AUSTRALIAN COMMISSION ON SAFETY AND QUALITY IN HEALTH CARE

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AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Surveillance Outcome Programs

Bloodstream infections

2023 report

AGAR

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Note regarding alternative descriptions

Due to the complexity of this document no alternative descriptions have been provided. If you need assistance with the structure of any graphs or charts, please email the Commission at AURA@safetyandquality.gov.au.

Contents

Overview

The Australian Group on Antimicrobial Resistance (AGAR), which is auspiced by the Australian Society for Antimicrobials (ASA), conducts targeted surveillance of selected pathogens in Australia via the:

- Australian Enterococcal Surveillance Outcome Program (AESOP)
- Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP)
- Gram-negative Surveillance Outcome Program (GnSOP).

AGAR collects data on antimicrobial resistance (AMR) in bacteria that cause life-threatening infections, and analyses and reports on these as part of the Antimicrobial Use and Resistance in Australia (AURA) surveillance program. These data complement two AMR surveillance programs developed and managed by the Australian Commission on Safety and Quality in Health Care (the Commission) that also contribute to AURA: the National Alert System for Critical Antimicrobial Resistances (CARAlert) and Australian Passive AMR Surveillance (APAS). Funding for the Commission's AURA Project and AGAR is provided by the Australian Government Department of Health and Aged Care, with contributions from states and territories as part of the collection and analysis of their data.

AGAR and APAS data are submitted to the World Health Organization (WHO) Global Antimicrobial Resistance and Use Surveillance System (GLASS).[1]

Implications for health care identified by analyses of 2023 AGAR data include:

- A longitudinal trend of increasing rates of resistance in Gram-negative organisms
- Prevalence of extended spectrum β-lactamases in hospital-onset *Escherichia coli* infections and variations between states and territories
- Uncommon, but concerning, carbapenemase-producing Gram-negative organisms
- Changing patterns of resistance in *Enterococcus* species
- Methicillin resistance in *S. aureus*
- Epidemiology of clinical manifestations of bacteraemia
- Variation across states and territories in patterns of resistance
- Variation between hospital and community settings in patterns of resistance – overwhelmingly, onset of episodes of bacteraemia occurred in the community
- Extended lengths of stay for patients with enterococcal and staphylococcal bacteraemias.

To ensure patients receive safe and high-quality health care, the Commission will continue to support states and territories, the private health sector and the primary and aged care sectors to use AGAR and other AURA data to refine and strengthen their approaches to infection prevention and control and antimicrobial stewardship. The Commission will also continue to support the implementation of National Safety and Quality Standards[2, 3] and Clinical Care Standards[4-6] and to work with developers of prescribing guidelines, to ensure AMR data informs guidelines and are promoted to prescribers.

Key findings and implications for health care: 2023 AGAR data

A. Key findings

Enterococcus species

- Between 1 January to 31 December 2023, a total of 1,599 episodes of bacteraemia were reported; the majority (92.9%) of enterococcal bacteraemia episodes were caused by *Enterococcus faecalis* (51.8%) or *E. faecium* (41.1%).
- Thirty-five episodes caused by *E. lactis* were identified. Prior to 2022, this species was mis-identified as *E. faecium*.
- Approximately two-thirds (67.3%) of *E. faecalis* bacteraemias were community-onset (CO), while only 26.5% of *E. faecium* bacteraemias were CO.
- The most frequent source of bacteraemia or principal clinical manifestation for *E. faecalis* was urinary tract infection (21.8%); for *E. faecium*, it was intra-abdominal infection other than biliary tract (17.7%) or febrile neutropenia (16.9%).
- The combined 30-day all-cause mortality for *E. faecalis* and *E. faecium* was 21.3%.
- There was a significant difference in 30-day all-cause mortality between *E. faecalis* (17.0%) and *E. faecium* (26.3%) ($P < 0.01$). However, there was no significant difference between vancomycin-resistant and vancomycin-susceptible *E. faecium* episodes (28.7% and 23.6%, respectively).
- The length of stay in hospital following enterococcal bacteraemia was more than 30 days for 23.8% of patients.
- Of bacteraemias caused by *E. faecium* in 2023, 50.8% were phenotypically vancomycin-resistant; up from 46.9% in 2022.
- In 2023, 53.2% of *E. faecium* harboured *vanA* and/or *vanB* genes (*vanA* 14.6%, *vanB* 38.3%, *vanA* plus *vanB* 0.3%). These proportions were similar to 2022, when 48.8% of *E. faecium* harboured *vanA* (13.7%) or *vanB* (35.1%) genes.
- Of vancomycin-resistant *E. faecium* bacteraemia, 26.9% were due to *vanA*-harbouring isolates. *vanA* was the dominant genotype in Queensland and Tasmania.
- There were 58 different *E. faecium* multi-locus sequence types (STs) identified, of which ST78, ST1424, ST17, ST780, ST796, ST1421, and ST555 were the most frequent.
- v*anA* genes were detected in eight STs, *vanB* genes were detected in 13 STs; and *vanA* plus *vanB* in two STs. The clonal diversity of *E. faecium* harbouring van genes varied across Australia.
- Two linezolid-resistant *E. faecium* from Victoria were confirmed. Both harboured the *optrA* gene and were vancomycin susceptible.
- In 2022, Australia ranked in the top four in rates of resistance to vancomycin in *E. faecium* when compared to the European Antimicrobial Resistance Surveillance Network (EARs-NET) countries.

Staphylococcus aureus

- A total of 3,422 *S. aureus* bacteraemia (SAB) episodes were reported from 1 January to 31 December 2023, 77.0% of which were CO. Of all episodes, 16.1% were due to methicillin-resistant isolates.
- The 30-day all-cause mortality was 16.2%. There was no significant difference in mortality due to place of onset (hospital, community), methicillin susceptibility (susceptible, resistant) or, for methicillin-resistant strains, by methicillin-resistant *Staphylococcus aureus* (MRSA) type (healthcare-associated MRSA [HA-MRSA] and community-associated MRSA [CA-MRSA]).
- The 30-day all-cause mortality for *S. aureus* was significantly lower among children (<18 years) (2/228, 0.9%) compared to adults (434/2,458, 17.7%) ($P < 0.01$). For adults aged 18-64 years,

the rate was 8.4% increasing to 16.0% for those in the 65-74 age group, and 31.7% in those aged greater than 74 years.
- Osteomyelitis/septic arthritis (20.6%) and skin and skin structure infections (19.2%) were the most common principal clinical manifestations.
- The hospital length of stay was more than 30 days in 26.9% of patients (30.3% in MRSA; 26.3% in MSSA).
- Resistances to non-β-lactam antimicrobials in MRSA has continued to decline overall, largely due to the substantial decline in the multi-resistant ST239-III clone.
- Daptomycin resistance was confirmed in two MRSA and three methicillin-susceptible *Staphylococcus aureus* (MSSA) isolates.
- CA-MRSA strains were the dominant cause of MRSA bacteraemia.
- Three HA-MRSA clones were identified; ST22-IV (EMRSA-15) which was the main HA-MRSA clone, ST239-III (Aus 2/3 EMRSA) and ST9276-III (a single locus variant of ST239-III). No HA-MRSA isolates harboured the Panton-Valentine leucocidin (PVL)-associated genes.
- The majority of ST22-IV (EMRSA-15) bacteraemias were community-onset.
- Eighty-four CA-MRSA clones were identified. The dominant CA-MRSA clone was ST93-IV (Queensland clone), accounting for 25.7% of CA-MRSA clones followed by the ST5-IV clone at 9.8%.
- Overall, 45.8% of CA-MRSA isolates harboured Panton-Valentine Leukocidin (PVL) genes.
- The Queensland clone of CA-MRSA (ST93-IV), which harbours PVL-associated genes, was seen in all states and territories; it is now the most common CA-MRSA clone in all regions except Tasmania.

Gram-negative species

- From 1 January 2023 to 31 December 2023, a total of 10,453 episodes of Gram-negative bacteraemia were reported, including *Enterobacterales* (90.9%), *Pseudomonas aeruginosa* (7.7%) and *Acinetobacter* species (1.4%). Three genera – *Escherichia* (60.1%), *Klebsiella* (20.3%) and *Enterobacter* (5.9%) – contributed to 86.3% of all *Enterobacterales* bacteraemias.
- The all-cause 30-day mortality rate for Gram-negative bacteraemia was 12.0% (11.5% for *Enterobacterales,* 17.3% for *P. aeruginosa*, and 8.5% for *Acinetobacter* species).
- Urinary tract infections were the most frequent source of bacteraemia or clinical manifestation (*Enterobacterales,* 43.3%; *P. aeruginosa,* 27.4%). For *Enterobacterales*, device-related urinary tract infections were more common in hospital-onset (HO) than CO episodes (23.1% versus 10.4%, $P < 0.01$).
- Of all *E. coli* isolates, 84.3% were from CO episodes, of which 12.2% were ceftriaxone-resistant.
- There was a significant difference in 30-day all-cause mortality between children and adults (4.5% versus 12.0%, respectively, $P < 0.01$) from *Enterobacterales* bacteraemia episodes. For adults aged 18-64 years, the rate was 7.6%, increasing to 11.7% for those in the 65-74 age group, and 16.3% in those aged greater than 74 years.
- In 2023, 15.2% of *E. coli isolates* (CO 14.1%; HO 21.6%) exhibited an extended-spectrum β-lactamase (ESBL) phenotype up from 14.2% in 2022 (CO 13.8%; HO 17.2%). Similarly, 8.5% of *K. pneumoniae* complex isolates (CO 7.1%; HO 12.4%) had and ESBL phenotype, an increase from 7.5%.
- Fluoroquinolone resistance in *E. coli* increased to 14.5% in 2023 (up from 13.7% in 2022), most notably in the Australian Capital Territory (ACT) (16.5%, up from 10.0% in 2022).
- Almost one-quarter (24.5%) of *E. coli* isolates were classified as multidrug-resistant (MDR), a proportion little changed from the 2022 survey (23.4%). The proportion of MDR *K. pneumoniae* complex isolates was 8.8% in 2023, it was 8.0% in 2022.
- Rates of carbapenemase-producing *Enterobacterales* (CPE) remained low among bacteraemic isolates (0.3%). In 2023, three-quarters (22/30, 73.3%) of CPE carried a $bla_{\text{OXA-48}}$-like and/or bla_{NDM} gene and one-quarter ($n = 8$, 26.7%) carried a $bla_{\text{IMP-4}}$ gene.
- Compared to European countries reporting to the EARs-Net, Australia ranks in the bottom quarter for rates of resistance to fluoroquinolones in *E. coli* and *K. pneumoniae* complex

isolates, and to third-generation cephalosporins in *K. pneumoniae* complex isolates. It ranks towards the middle in rates of resistance to third-generation cephalosporins in *E. coli.*

B. Implications of key findings for health care

When interpreting AGAR data, it is important to consider changes in surveillance coverage between 2013 and 2023. The number of hospitals that contribute to AGAR increased from 27 in 2013 to 43 in 2015, 56 in 2022, and 57 in 2023. Additionally, the relative distribution of sites has changed. Paediatric and/or facilities providing specialist obstetric services increased from three in 2013, to six in 2017, seven in 2019 and eight in 2020. Since 2015, 13 sites have been added including hospitals from north-west regional Western Australia (WA).

Overall, 23.6% of patients remained in hospital for more than 30 days after enterococcal bacteraemia, and 26.9% after staphylococcal bacteraemia. Bacteraemias caused by multidrug-resistant organisms result in increased death rates as well as increased lengths of hospital stay and morbidity. There are also many more costs to patients in terms of a poorer quality of life and increased chances of death and suffering besides the additional financial burdens on the health system. Hospital-onset *Enterococcus* and *S. aureus* bacteraemias were frequently device-related, which underscores the importance of appropriate infection prevention and control practices, aseptic technique and timely removal for the management of devices such as urinary catheters, peripheral cannulas, and central lines.

Gram-negative resistance

The percentage resistance in *E. coli* and *K. pneumoniae* complex isolates in 2023 was similar to 2022 for all antimicrobial agents tested.

Previous AGAR reports indicate a longitudinal trend from 2013 to 2020 of increasing *E. coli* resistance to key anti-Gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin. Resistance to both agents stabilised from 2018 to 2020, declined in 2021 and remained steady in 2022. These declines may be due to the effects of COVID-19 pandemic restrictions in place during 2020 and 2021. The steady rise in resistance to fluoroquinolones has been more striking in hospital-onset bacteraemia with a change from 13.7% to 19.8% between 2013 and 2018, to 21.3% in 2019 and 21.8% in 2020. In 2021, the percentage resistance rate fell to 16.7%, but increased slightly in 2022 to 17.8% and 17.7% in 2023.

Increasing resistance to third-generation cephalosporins and fluoroquinolones in *E. coli* strains is of concern, given that access to these agents on the Pharmaceutical Benefits Scheme (PBS) is quite restricted. It is likely that high community use of unrestricted agents, such as amoxicillin and cefalexin, which these strains are co-resistant to, contributes to this increase. A marked decrease in the numbers of tourists and returning travellers from countries with very high levels of resistance to third-generation cephalosporins and fluoroquinolones (mostly in Asia) from 2020 to 2022 is also a likely factor in the changes in percentage rates of resistance during that period.[7, 8]

Prevalence of extended-spectrum β-lactamases

The emergence of specific types of ESBLs (CTX-M enzymes) in *E. coli* from the community is part of a global epidemic.[9-11] It remains unclear what factors are driving the community expansion of CTX-M ESBLs in Australia, as third-generation cephalosporins are not widely used in this setting. It is thought to be driven by cross-resistance and co-resistance to agents used in community practice and returning travellers to Australia.[8, 12] There is also increasing recognition that ESBLs are becoming established in long-term care facilities in Australia.[13]

ESBLs in Gram-negative organisms have a considerable impact on resistance patterns and limit therapeutic options. In 2023, almost 1 in 7 (15.2%) *E. coli* isolates displayed this phenotype, and after a fall in rates in 2021 were at similar levels to 2018. This phenotype is significantly more common in hospital-onset infection compared to community-onset *E. coli* infection, with 21.6% of

isolates demonstrating this pattern in hospital-onset infection compared to 14.1% for community-onset isolates in 2023 ($P < 0.0001$). In hospital-onset *K. pneumoniae* complex isolates, this phenotype was also more common than for community-onset isolates (12.4% versus 7.1%, P <0.01).

The prevalence of ESBLs also varies by state and territory. For *E. coli*, the proportions are noticeably lower in Tasmania, and higher in the Northern Territory (NT). For *K. pneumoniae* complex isolates, proportions are noticeably higher in the NT.

Carbapenemase-producing Gram-negative organisms

Carbapenem resistance attributable to acquired carbapenemase genes is still uncommon in patients with bacteraemia in Australia. Carbapenemase types (IMP, NDM, OXA-48-like, KPC, and OXA-23 genes, either alone or co-produced) were detected in isolates from 18 of the contributing hospitals from six states and territories. No CPE were found in Tasmania or the NT. In 2023, almost three-quarters (22/30, 73.3%) of CPE carried a $bla_{\text{OXA-48}}$-like and/or bla_{NDM} gene(s), while only one-quarter ($n = 8$, 26.7%) carried $bla_{\text{IMP-4}}$. In contrast, in 2022, $bla_{\text{IMP-4}}$ accounted for 62.1% (18/29) of all carbapenemase-producing *Enterobacterales* (CPE).

Notwithstanding low rates of CPE from blood culture isolates reported to AGAR, CARAlert showed increasing rates of CPE in Australian hospitals in 2023 in non-blood isolates.[14] Carbapenemase-producing *Enterobacterales* were the most commonly reported critical antimicrobial resistance (CAR) in 2023, with a 45.4% increase in CPE reports in 2023 compared with 2022.

In addition to the *Australian Guidelines for the Prevention and Control of Infection in Healthcare*[15] (AICGs), specific guidance about reducing acquisition and subsequent invasive infection due to carbapenem-resistant organisms and CPE is available in *Recommendations for the control of carbapenemase-producing* Enterobacterales *(CPE): a guide for acute care health facilities*.[16]

Changing patterns in *Enterococcus* species

The total number of enterococcal bacteraemias identified by AGAR, excluding two hospitals that contributed in 2022 or 2023 only, increased from 1,478 in 2022 to 1,566 in 2023 (up 5.3%). This rise was mainly driven by *E. faecium* cases (588 in 2022; 648 in 2023, up 10.2%) rather than *E. faecalis* cases (786 in 2022; 799 in 2023, up 1.7%). The number of vancomycin-resistant *E. faecium* (VRE) isolates increased from 274 in 2022 to 328 in 2023.

Vancomycin resistance rates in *E. faecium* rose from 46.9% in 2022 to 50.8% and VRE as a proportion of all enterococcal isolates increased from 18.6% to 20.8%. The overall contribution of *vanA* and *vanB* genes to VRE varied by state or territory. *vanA*-harbouring types were dominant in Queensland and Tasmania, *vanA*- and *vanB*-harbouring types were similar in proportion in the NT, and *vanB*-harbouring types were dominant for the remainder of Australia.

Optimising all VRE prevention and control mechanisms will be required to respond effectively to resistance in *E. faecium* in Australia.

Changing patterns in *Staphylococcus* species

The proportion of *S. aureus* that are methicillin-resistant throughout Australia has remained relatively stable from 2013 to 2023, with some notable variations between states and territories.

The total number of *S. aureus* bacteraemia (SAB) isolates identified by AGAR in 2023, excluding isolates from one hospital that only contributed in 2023, was similar to 2022 (3,214 in 2022; 3,287 in 2023). There was a significant increase in the total number of SAB from New South Wales (NSW) (982 to 1,104, $P < 0.01$) due to an increase in the numbers of methicillin-susceptible *S. aureus* (807 to 908, $P < 0.01$). In Queensland, SAB cases decreased (536 to 472, $P = 0.0102$) driven by a drop in methicillin-susceptible *S. aureus* (473 to 408, $P = 0.0112$). The total number of

SAB increased slightly in Victoria, Tasmania and the NT; and decreased slightly in South Australia (SA), WA, and the ACT.

Overall, between 2022 and 2023, the proportion of MRSA increased from 15.0% to 16.1%. Over the same period, hospital-onset MRSA infections increased from 24.5% to 25.3%. Relative to 2022, there were no significant differences in the proportion of MRSA across all states and territories.

In 2023, community-associated MRSA clones accounted for 12.4% (417/3,363) of all *S. aureus*; in 2022 it was 12.2% (388/3,182). ST93-IV was the most prevalent community-associated-MRSA clone (107/417, 25.7%) and was dominant across all states and territories. Healthcare-associated-MRSA clones accounted for only 2.2% (74/3,422) of all *S. aureus* in 2023 and ST22-IV was the most common healthcare-associated MRSA clone (64/74, 86.5%); it was found in all states and territories.

MRSA is now dominated by community-associated strains, which are found in both community- and hospital onset settings. Strategies for control of MRSA in all settings, particularly in the community and in northern Australia where rates are higher, continue to be a priority.

Epidemiology of clinical manifestations

Urinary tract infection remains the most common manifestation associated with bacteraemia in *Enterobacterales*, *P. aeruginosa*, and *E. faecalis* episodes. In 2023, intra-abdominal infection other than biliary tract and febrile neutropenia were the most common clinical manifestations associated with *E. faecium* bacteraemia. For *Acinetobacter* species, device-related infection without metastatic focus or those with no identifiable focus were the most common.

Device-related bacteraemia accounted for 8.4% (1,117/13,302) of bacteraemia across all the AGAR surveillance programs in 2023, a slight increase from 8.2% in 2022. The majority of these infections were caused by Gram-negative bacteria (*n* = 357) and *S. aureus* (*n* = 557).

Gram-negative bacteraemias frequently originate from urinary tract infections associated with the use of indwelling catheters and urinary stents, as well as from biliary stents. In contrast, SAB is commonly associated with intra-vascular catheters and/or devices and prosthetic joints. Continued adherence to the requirements of the National Safety and Quality Health Service (NSQHS) Standards[2], the National Safety and Quality Primary and Community Care Standards (Primary and Community Care Standards)[3] and the AICGs for optimal medical device management[15] are important for all health service organisations to prevent and contain these infections. Additionally, the Commission's *Management of Peripheral Intravenous Catheters Clinical Care Standard*[5] provides important guidance for all health service organisations.

Whilst noting that it is not possible to distinguish aged care residents from other older people who are diagnosed with bacteraemia, the strengthened Aged Care Clinical Standard[17] will provide additional support for prevention of device-related infections.[5]

Variation across states and territories

Resistance rates vary considerably across states and territories. Methicillin resistance in *S. aureus* 16.1%) ranged from 8.0% in Tasmania to 43.7% in the NT.

E. coli resistance to third-generation cephalosporins (13.5%), ranged from 4.9% in Tasmania to 24.7% in the NT; ciprofloxacin resistance (14.5%) ranged from 8.3% in Tasmania to 18.7% in the NT; and aminoglycoside resistance (8.9%) ranged from 1.9% in Tasmania to 19.1% in the NT.

For *K. pneumoniae* complex, resistance to third-generation cephalosporins (7.8%) ranged from 2.4% in Tasmania to 13.6% in the NT; ciprofloxacin resistance (7.8%) ranged from 0.0% in Tasmania to 18.6% in the NT; and aminoglycoside resistance (4.0%) ranged from 0.0% in Tasmania to 8.9% in the ACT.

Vancomycin resistance in *E. faecium* (50.8%) ranged from 25.0% in WA to 88.2% in the NT. Teicoplanin resistance (12.7%) ranged from 0.0% in the ACT to 24.1% in Tasmania.

To minimise the use of broad-spectrum antimicrobials while ensuring the most appropriate treatment for severe infections, national treatment guidelines informed by local antibiograms should be adopted.

Variations between hospital and community settings

Bacteraemia and associated resistance varied between hospital and community settings. Organisms such as *E. cloacae* complex, *P. aeruginosa* and *Acinetobacter* species were evenly distributed between community- and hospital-onset infections, whilst others such as *E. coli* and *S. aureus* were more commonly community-onset. *E. faecium* was much more commonly hospital-onset (73.5%) than *E. faecalis* (32.7%). Vancomycin-resistant *E. faecium* bacteraemia accounted for 9.0% (72/801) of all community-onset enterococcal bacteraemia, compared to 32.7% (261/798) in hospital-onset disease.

These variations have implications for choice of empiric antimicrobial therapy and guidelines in community- versus hospital-onset infections, and accounting for infections in aged care home residents[13, 18, 19] Infections in aged care residents are included in the community-onset group in the AGAR data, but not distinguished as such in this report.

International comparisons

In 2023, Australia had relatively lower rates of resistance compared to available data from the European Union (EU) and European Economic Area (EEA) countries reporting to EARS-Net[20] or the WHO European Region countries (excluding EU/EEA countries) reporting to the Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network[21], and the SENTRY Antimicrobial Surveillance Program.[22] Australia ranks towards the middle for rates of resistance to methicillin in *S. aureus* compared to all European countries, but was ranked fifth highest in rates of resistance to vancomycin in *E. faecium*. From SENTRY data (2019-2021) the prevalence of both methicillin-resistant *S. aureus* and vancomycin-resistant *E. faecium* phenotypes were higher in the United States of America compared to European countries.

Australia also ranks towards the middle for resistance to third-generation cephalosporins in *E. coli*, but in the bottom quarter for fluoroquinolone resistance. In *K. pneumoniae* complex isolates, resistance to both fluoroquinolones and third-generation cephalosporins is low (<10.0%) compared to European countries (EU/EEA average 32.0% and 32.7%, respectively).

C. Response

In response to the themes and issues identified through analyses of AGAR data, the Commission will continue to:

- Report on the surveillance of AMR and use AURA data to refine and strengthen guidance for prevention and control of specific organisms and resistances, to inform strategies for antimicrobial stewardship (AMS) and appropriate antimicrobial use
- Support the implementation of the NSQHS Standards[2] relevant to the control of hospital-onset bacteraemia, particularly in relation to invasive medical devices
- Support the implementation of Primary and Community Healthcare Standards[3], particularly in relation to community-onset infections and community-associated MRSA
- Collaborate with the Aged Care Quality and Safety Commission, aged care providers and general practitioners to promote appropriate personal and clinical care, AMS and infection prevention and control for residents of aged care homes consistent with the requirements of the strengthened Aged Care Quality Standards
- Support the implementation of the Clinical Care Standard for Management of Peripheral Intravenous Catheters[5] to prevent bloodstream infections, and the Clinical Care Standards for AMS and Sepsis
- Promote effective infection prevention and control practices in health and aged care settings consistent with the AICGs[15], the *Recommendations for the control of carbapenemase-producing* Enterobacterales *(CPE). A guide for acute care health service organisations*[16] and the Aged Care Infection Prevention and Control Guide[23]
- Support collaboration and coordination between states and territories, and between hospital and community care settings to explore the drivers of variation and improve local prevention and control efforts
- Promote the use of the *Priority Antibacterial List for Antimicrobial Resistance Containment*[23] to support AMS programs to analyse antimicrobial usage in terms of preferred or optimal prescribing choices
- Work with developers of prescribing guidelines to ensure AMR data informs guidelines and promote these guidelines to prescribers
- Promote adaption of national prescribing practices to local resistance patterns and regular review of prescribing guidance by local AMS services
- Encourage states and territories and the private laboratory sector to consider geographic variation of AMR through the use of local antibiograms by AMS services
- Advocate for selected resistances to be made nationally notifiable under public health legislation
- Support submission of AGAR data and APAS data annually to the WHO GLASS.[1]

1. Background and objectives

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

AGAR's focus on bacteraemia allows examination of laboratory-confirmed, invasive infections and comparison of rates over time for hospitals, states and territories. AGAR compares Australian data with the European countries from the European Antimicrobial Resistance Surveillance Network (EARS-Net)[20] and the Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network,[21] enabling benchmarking and trend projections. AGAR has collected ongoing data on the prevalence of AMR in Australia over a long period using standardised methods.

This eighth amalgamated report on Surveillance Outcome Programs operated by AGAR presents analyses of AMR associated with episodes of bacteraemia (bloodstream infection) that were reported by 33 participating public and private laboratories servicing 57 hospitals across Australia in 2023.

The 57 hospitals that currently contribute to AGAR, including six private hospitals, are listed in Table 1. In 2023, one hospital from NSW was not able to contribute data to AESOP, or Quarter four of ASSOP. One hospital from Queensland was only able to participate for Quarter one of GnSOP.

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

AGAR contributes to the Antimicrobial Use and Resistance in Australia (AURA) surveillance program funded and coordinated by the Australian Government Department of Health and Aged Care, and to the World Health Organization (WHO) Global Antimicrobial Resistance and Use Surveillance System (GLASS).[1]

Table 1: Hospitals that contributed to AGAR, by state and territory, 2023

State or territory	Hospital
New South Wales	Children's Hospital Westmead
	Concord Repatriation General Hospital
	Gosford Hospital
	John Hunter and John Hunter Children's Hospitals
	Liverpool Hospital
	Nepean Hospital
	Prince of Wales Hospital
	Royal North Shore Hospital
	Royal Prince Alfred Hospital
	St Vincent's Hospital, Sydney*
	Sydney Children's Hospital
	Westmead Hospital
	Wollongong Hospital
Victoria	Alfred Hospital
	Austin Hospital (Austin Health)
	Monash Children's Hospital†

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

* Public/Private hospital
† Microbiology services provided by Monash Medical Centre (Monash Health)
§ Microbiology services provided by Sullivan Nicolaides Pathology
# Private hospital
** Microbiology services provided by Pathology Queensland Central Laboratory
‡ Microbiology services provided by SA Pathology, Royal Adelaide Hospital
§§ Microbiology services provided by PathWest Laboratory Medicine WA, Queen Elizabeth II Medical Centre
Microbiology services provided by PathWest Laboratory Medicine WA, Fiona Stanley Hospital
Note: In 2023, one hospital from NSW was not able to contribute data to AESOP, or Quarter four of ASSOP. One hospital from Queensland was only able to participate for Quarter one of GnSOP.

1.1. Australian Enterococcal Surveillance Outcome Program

Globally, enterococci are thought to account for approximately 10% of all bacteraemias, and in North America and Europe are the fourth and fifth leading causes of sepsis, respectively.[24, 25] In the 1970s, healthcare-associated enterococcal infections were primarily due to *Enterococcus faecalis*, however subsequently there has been a steady increase in prevalence of *E. faecium* nosocomial infections.[26-28] Worldwide, the increase in nosocomial *E. faecium* infections has primarily been due to the expansion of polyclonal hospital-adapted clonal complex (CC) 17 isolates. While innately resistant to many classes of antimicrobials, *E. faecium* CC17 has demonstrated a remarkable capacity to evolve new antimicrobial resistances. In 2009, the Infectious Diseases Society of America highlighted *E. faecium* as one of the key problem bacteria or ESKAPE (*E. faecium, S. aureus, Klebsiella pneumoniae, Acinetobacter baumannii, P. aeruginosa,* and *Enterobacter* species) pathogens requiring new therapies.[29]

AGAR began surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[30] In 2011, AGAR commenced the Australian Enterococcal Sepsis Outcome Program (AESOP). The term "Sepsis" was changed in 2021 to "Surveillance" to better reflect AGAR's surveillance of episodes of bacteraemia rather than sepsis.

In order to provide data to support improved antimicrobial prescribing and patient care, the objective of AESOP 2023 was to determine the proportion of *E. faecalis* and *E. faecium* bloodstream infection isolates demonstrating AMR with particular emphasis on:

- Assessing susceptibility to ampicillin
- Assessing susceptibility to glycopeptides, and the associated resistance genes
- Monitoring the molecular epidemiology of *E. faecium.*

1.2. Australian *Staphylococcus aureus* Surveillance Outcome Program

Globally *S. aureus* is one of the most frequent causes of hospital- and community-acquired bloodstream infections.[31] Although there are a wide variety of manifestations of serious invasive infection caused by *S. aureus*, in the great majority of cases the organism can be detected in blood cultures. Therefore, *S. aureus* bacteraemia (SAB) is considered a very useful marker for serious invasive infection.[32]

Despite standardised treatment protocols for SAB, including prolonged antimicrobial therapy and prompt source control[33], mortality can range from as low as 2.5% to as high as 40%.[34-36] Mortality rates are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[37, 38] A prospective study of SAB conducted by 27 laboratories in Australia and New Zealand found increased 30-day all-cause mortality was significantly associated with older age, European ethnicity, methicillin resistance, infections not originating from a medical device, sepsis syndrome, pneumonia/empyema and treatment with a glycopeptide or other non-β-lactam antibiotic.[39]

AGAR began surveillance of antimicrobial resistance in *S. aureus* in 1986.[40] In 2013, AGAR commenced the Australian *Staphylococcus aureus* Sepsis Outcome Program (ASSOP).[41] The term "Sepsis" was changed in 2021 to "Surveillance" to better reflect AGAR's surveillance of episodes of bacteraemia rather than sepsis.

The primary objective of ASSOP 2023 was to determine the proportion of SAB isolates demonstrating antimicrobial resistance with particular emphasis on:

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

1.3. Gram-negative Surveillance Outcome Program

In many healthcare settings, Gram-negative organisms, such as *E. coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and others, are commonly responsible for bacteremias.[22, 24] Many of these organisms have developed resistance to multiple antimicrobials, rendering conventional treatments ineffective. This phenomenon poses a significant global threat, as it can lead to difficult-to-treat infections and increased mortality rates.[42-44]

AGAR began surveillance of the key Gram-negative pathogens *E. coli* and *Klebsiella* species in 1992. Surveys were conducted every two years until 2008, when annual surveys commenced, alternating between community-onset and hospital-onset infections.

E. coli is the most common cause of community-onset urinary tract infections, whereas *Klebsiella* species are less common but are known to harbour important resistance mechanisms. In 2004, another genus of Gram-negative pathogens in which resistance can be of clinical importance – *Enterobacter* – was added. *Enterobacter* species are less common in the community, but of high

importance because of their intrinsic resistance to first-line antimicrobials used in this setting.[45] Taken together, the three groups of species surveyed are valuable sentinels for multidrug resistance (MDR) and emerging resistance in enteric Gram-negative bacilli. In 2013, AGAR initiated the yearly *Enterobacterales* Sepsis Outcome Program (EnSOP), which focused on the prospective collection of resistance and demographic data on all isolates from patients with documented bacteraemia. In 2015, *Pseudomonas aeruginosa* and *Acinetobacter* species were added, and the program evolved into the Gram-negative Sepsis Outcome Program (GnSOP), since renamed the Gram-negative Surveillance Outcome Program. The term “Sepsis” was changed in 2021 to “Surveillance” to better reflect AGAR’s surveillance of episodes of bacteraemia rather than sepsis.

Resistance to β-lactams due to β-lactamases is of particular interest, especially extended-spectrum β-lactamases (ESBLs) which inactivate third-generation cephalosporins. Other resistance of interest is to agents that are important for treatment of these serious infections, such as gentamicin, and to reserve agents such as ciprofloxacin and meropenem.

The objectives of the 2023 surveillance program were to:

- Monitor resistance in *Enterobacterales*, *P. aeruginosa* and *Acinetobacter* species isolated from blood cultures taken from patients presenting to the hospital or already in hospital
- Study the extent of co-resistance and multidrug resistance in the major species
- Detect emerging resistance to reserve agents such as carbapenems and colistin
- Examine the molecular basis of resistance to third-generation cephalosporins, quinolones and carbapenems.

2. Summary of methods

Fifty-seven hospitals, in each state and territory of Australia, were enrolled in the 2023 AGAR programs. The 33 laboratories that serviced the hospitals participating in AGAR collected all isolates from unique patient episodes of bacteraemia for ASSOP and AESOP, or either all or up to 200 isolates for GnSOP, from 1 January 2023 to 31 December 2023. Approval to conduct the prospective data collection, including de-identified demographic data, was given by the research ethics committees associated with each participating hospital.

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

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

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

2.1. Data fields

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

2.2. Species identification

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

For this report, the following organism complexes are defined:

- *Acinetobacter baumannii* complex (*A. calcoaceticus*, *A. baumannii*, *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*).

2.3. Susceptibility testing

Susceptibility testing of isolates is described in Appendix B. The analysis used breakpoints from the Clinical and Laboratory Standards Institute (CLSI) M100–Ed34[46] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v14.0.[47]

2.4. Whole genome sequencing

The following Gram-negative isolates were referred to a central laboratory (Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research):

- *E. coli*, *Klebsiella* spp. (excluding *K. aerogenes*), *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone minimum inhibitory concentration (MIC) > 1 mg/L, or cefoxitin MIC > 8 mg/L
- any other *Enterobacterales* with cefepime MIC > 1 mg/L
- *Salmonella* spp. with ciprofloxacin MIC > 0.25 mg/L
- all *Enterobacterales* with meropenem MIC > 0.125 mg/L (> 0.25 mg/L if tested using Vitek®)
- all *Acinetobacter* spp. or *P. aeruginosa* with meropenem MIC > 4 mg/L
- all isolates with amikacin MIC > 32 mg/L
- and all isolates with colistin MIC > 4 mg/L (except those with intrinsic resistance to colistin).

Whole genome sequencing (WGS) was performed on all referred Gram-negative 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 or the Australian Genome Research Facility (AGRF) or using Illumina platforms. Data were assembled and analysed using a modified version of the Nullarbor bioinformatic pipeline[48] and a custom pipeline to accurately detect AMR genes.

WGS using the Illumina NextSeq™ 500 platform was performed on all *E. faecium,* and methicillin-resistant *S. aureus* (MRSA) referred to the Antimicrobial Resistance and Infectious Diseases Research Laboratory (ARMID), Murdoch University, WA. The multi-locus sequence type (MLST) was determined using the PubMLST sequence definition database (*S. aureus* or *E. faecium*) and *van* genes (*E. faecium*) were identified using nucleotide sequences from the NCBI database and a BLAST interface.[49] SCC*mec* (MRSA) elements were identified using KmerFinder v3.2 and the SCC*mec* database curated from the Center for Genomic Epidemiology website. The Panton-Valentine leucocidin (PVL) (MRSA) associated genes, *lukF-PV* and *lukS-PV*, were identified using nucleotide sequences from the NCBI database and a BLAST interface.[49]

2.5. Statistical analysis

Confidence intervals of proportions, Fisher's exact test for categorical variables, and chi-square test for trend were calculated, if appropriate, using GraphPad Prism version 10.3.1 for Windows (GraphPad Software, La Jolla, California).

3. Results

3.1. Isolates recovered

During 2023, a total of 15,474 bloodstream isolates were reported from 57 participating hospitals. Overall, 1,036 (6.7%) of isolates were from children (<18 years of age). The proportion of *S. aureus* isolates from children was 9.4%, *Enterococcus* species 6.4%, *Enterobacterales* 5.9%, *P. aeruginosa* 3.7% and *Acinetobacter* species 16.7%.

A total of 10,453 Gram-negative bloodstream isolates (60 species/complex, 22 genera,) were reported. *Enterobacterales* accounted for 90.9%, followed by *P. aeruginosa* (7.7%) and *Acinetobacter* (1.4%). Three genera of *Enterobacterales* - *Escherichia* (54.8%), *Klebsiella* (18.3%) and *Enterobacter* (5.4%) - contributed 78.4% of all isolates. Overall, the top 10 species by rank were:

- *E. coli* (54.6%)
- *K. pneumoniae* complex (13.8%)
- *P. aeruginosa* (7.7%)
- *E. cloacae* complex (5.3%)
- *Proteus mirabilis* (3.4%)
- *K. oxytoca* (3.0%)
- *Serratia marcescens* (2.3%)
- *K. aerogenes* (1.6%)
- *Salmonella* species (non-typhoidal) (1.3%)
- *Citrobacter freundii* complex (1.1%).

These 10 species comprised 94.1% of all isolates (Table 2).

The proportion of isolates from children was 5.8% (*n* = 611; *Enterobacterales n* = 557, *P. aeruginosa n* = 30, *Acinetobacter* species *n* = 24). *Enterobacter cloacae* complex and *Salmonella* species episodes were more common among children than adults (8.8% versus 5.1% and 15.7% versus 1.4%, respectively) (data not shown).

Of 3,422 SAB episodes, 550 (16.1%; 95% confidence interval [CI]: 14.8-17.5) were methicillin-resistant, ranging from 8.0% (95% CI: 4.2-13.6) in Tasmania to 43.7% (95% CI: 32.6-57.3) in the NT (Table 2). There was no significant difference in the proportion of MRSA among children (14.9%, 95% CI: 11.0-19.7) and adults (16.2%, 95% CI: 14.8-17.7) (data not shown).

There were 1,599 episodes of enterococcal bloodstream infection. *E. faecalis* and *E. faecium* accounted for 92.9% of all enterococcal isolates (Table 2).

Table 2: Number of each species recovered, by state and territory, AGAR, 2023

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Enterococcus species	472	363	221	140	227	88	31	57	1,599
Enterococcus faecalis	243	168	125	73	122	57	14	26	828
Vancomycin-resistant, percent*	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Vancomycin-susceptible, percent*	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Enterococcus faecium	196	178	76	56	80	29	17	25	657
Vancomycin-resistant, percent*	55.9	60.1	32.9	62.5	25.0	31.0	88.2	52.0	50.8
Vancomycin-susceptible, percent*	44.1	39.9	67.1	37.5	75.0	69.0	11.8	48.0	49.2
Other enterococcal species	33	17	20	11	25	2	0	6	114
Enterococcus lactis†	11	3	6	2	9	0	0	4	35
Enterococcus gallinarum	7	9	6	1	4	0	0	1	28
Enterococcus casseliflavus	7	4	3	5	5	0	0	1	25
Enterococcus avium	2	1	3	0	3	1	0	0	10

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Enterococcus raffinosus	3	0	0	0	2	1	0	0	6
Enterococcus durans	2	0	1	2	0	0	0	0	5
Enterococcus hirae	0	0	1	0	1	0	0	0	2
Enterococcus mundtii	0	0	0	0	1	0	0	0	1
Enterococcus cecorum	1	0	0	0	0	0	0	0	1
Enterococcus gilvus	0	0	0	1	0	0	0	0	1
Staphylococcus aureus	1,104	614	607	229	489	163	119	97	3,422
Methicillin-resistant, percent	17.8	12.9	14.3	13.1	16.6	8.0	43.7	12.4	16.1
Methicillin-susceptible, percent	82.2	87.1	85.7	86.9	83.4	92.0	56.3	87.6	83.9
Gram-negative species#	3,270	2,073	1,688	731	1,584	429	323	355	10,453
Acinetobacter	31	22	37	10	21	8	14	1	144
Acinetobacter baumannii complex	14	10	26	4	13	6	13	1	87
Acinetobacter species§	4	4	4	4	3	1	1	0	21
Acinetobacter ursingii	3	3	2	1	2	1	0	0	12
Other *Acinetobacter* (*n* = 9)	10	5	5	1	3	0	0	0	24
Enterobacterales	3,011	1,923	1,468	641	1,453	391	287	329	9,503
Escherichia coli	1,804	1,110	848	385	917	264	194	183	5,705
Klebsiella pneumoniae complex	445	304	260	83	208	41	44	57	1,442
Enterobacter cloacae complex	176	129	96	36	75	14	9	22	557
Proteus mirabilis	131	63	49	33	53	14	7	4	354
Klebsiella oxytoca	94	74	30	35	44	16	1	21	315
Serratia marcescens	90	46	47	8	39	5	1	6	242
Klebsiella aerogenes	56	40	12	9	29	5	7	8	166
Salmonella species (non-typhoidal)	35	26	36	2	20	9	10	2	140
Citrobacter freundii complex	36	30	15	7	14	2	2	6	112
Morganella morganii	36	16	24	13	10	2	0	5	106
Salmonella species (typhoidal)	16	31	10	0	19	3	5	6	90
Citrobacter koseri	26	15	14	6	5	1	4	3	74
Raoultella ornithinolytica	11	3	2	3	6	2	0	4	31
Pantoea agglomerans	10	4	3	1	3	1	0	0	22
Proteus vulgaris	8	1	3	1	7	0	0	0	20
Providencia rettgeri	7	3	5	1	0	1	1	0	18
Hafnia alvei	5	3	2	0	3	2	0	1	16
Pantoea species§	2	6	3	1	0	0	1	0	13
Other *Enterobacterales* (*n* = 29)	23	19	9	17	1	9	1	1	80
Pseudomonas aeruginosa	228	128	183	80	110	30	22	25	806

* Vancomycin susceptibility was not available for five *E. faecalis* (NSW [2], Qld [2], Tas [1]) and one *E. faecium* (NSW)
† Prior to 2022 *E. lactis* was identified as *E. faecium*
§ Species not determined
\# *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*

Notes:
1. *Acinetobacter baumannii* complex includes *A. nosocomialis* (*n* = 5), *A. pittii* (*n* = 5), *A. seifertii* (*n* = 2)
2. *Citrobacter freundii* complex includes *C. braakii* (*n* = 16), *C. youngae* (*n* = 2). *C. werkmanii* (*n* = 1)
3. *Enterobacter cloacae* complex includes E. *hormaechei* (n = 54), *E. kobei* (*n* = 6), *E. ludwigii* (*n* = 4), *E. bugandensis* (*n* = 2)
4. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 121) and *K. quasipneumoniae* (*n* = 7).

3.2. Place of onset of bacteraemia

Almost all patients with bacteraemia were admitted to hospital (10,199, 97.6% Gram-negative species; 1,578, 98.7% *Enterococcus* species; 3,350, 97.9% *S. aureus*).

Information on place of onset of bacteraemia was available for all Gram-negative, *Enterococcus* species and *S. aureus* episodes (Table 3).

For Gram-negative species, 77.0% of all episodes were community-onset, with differences seen between *Enterobacterales* (78.7%), *Acinetobacter* species (63.9%) and *P. aeruginosa* (59.4%). The proportion of *Enterobacterales* that were community-onset was significantly lower among children (70.2%, 391/557) than adults (79.2%, 7,087/8,946) ($P < 0.0001$), most notable among *E. coli* (children 77.4%, adults 84.6%) and *K. pneumoniae* complex (children 46.8%, adults 74.8%) (data not shown).

Episodes involving *E. faecalis* and non-*E. faecium* enterococci were predominantly community-onset (*E. faecalis* [67.3%, 95% CI: 61.8-73.1]; other non-*E. faecium* species [61.4%, CI: 47.5-77.3]). However, *E. faecium* episodes were predominantly hospital-onset (73.5%; 95% CI: 67.0-80.3). The proportion of *E. faecalis* that were community-onset was significantly lower among paediatrics (29.0%, 20/69) than adults (70.8%, 537/759) ($P < 0.01$) (data not shown).

Most SABs were community-onset (77.0%; 95% CI: 74.1-80.0). The proportion of MRSA episodes that were community-onset was higher among children (81.3%, 39/48) than adults (74.1%, 372/502).

Table 3: Species recovered, by place of onset, AGAR, 2023

Organism	Community-onset % (*n*)	Hospital-onset % (*n*)	Total, 100%
Enterococcus species	50.1 (801)	49.9 (798)	1,599
Enterococcus faecalis	67.3 (557)	32.7 (271)	828
Vancomycin-resistant	–* (0)	–* (0)	0
Vancomycin-susceptible	67.6 (556)	32.4 (267)	823
Enterococcus faecium	26.5 (174)	73.5 (483)	657
Vancomycin-resistant	21.6 (72)	78.4 (261)	333
Vancomycin-susceptible	31.5 (102)	68.5 (222)	324
Other *Enterococcus* species (*n* = 10)	61.4 (70)	38.6 (44)	114
Staphylococcus aureus	77.0 (2,636)	22.9 (785)	3,422
Methicillin-resistant	74.7 (411)	25.3 (139)	550
Methicillin-susceptible	77.5 (2,225)	22.5 (647)	2,872
Gram-negative species	77.0 (8,049)	23.0 (2,404)	10,453
Acinetobacter	63.9 (92)	36.1 (52)	144
Acinetobacter baumannii complex	58.6 (51)	41.4 (36)	87
Acinetobacter species†	57.1 (12)	42.9 (9)	21
Acinetobacter ursingii	83.3 (10)	16.7 (2)	12
Other *Acinetobacter* species (*n* = 9)	79.2 (19)	20.8 (5)	24
Enterobacterales	78.7 (7,478)	21.3 (2,025)	9,503
Escherichia coli	84.3 (4,808)	15.7 (897)	5,705
Klebsiella pneumoniae complex	73.6 (1,061)	26.4 (381)	1,442
Enterobacter cloacae complex	54.0 (301)	46.0 (256)	557
Proteus mirabilis	81.9 (290)	18.1 (64)	354
Klebsiella oxytoca	70.5 (222)	29.5 (93)	315
Serratia marcescens	59.5 (144)	40.5 (98)	242
Klebsiella aerogenes	57.8 (96)	42.2 (70)	166
Salmonella species (non-typhoidal)	91.4 (128)	8.6 (12)	140
Citrobacter freundii complex	67.9 (76)	32.1 (36)	112
Morganella morganii	67.9 (72)	32.1 (34)	106
Salmonella species (typhoidal)	97.8 (88)	2.2 (2)	90
Citrobacter koseri	71.6 (53)	28.4 (21)	74
Raoultella ornithinolytica	61.3 (19)	38.7 (12)	31
Pantoea agglomerans	68.2 (15)	31.8 (7)	22
Proteus vulgaris	75.0 (15)	25.0 (5)	20
Providencia rettgeri	83.3 (15)	16.7 (3)	18
Hafnia alvei	50.0 (8)	50.0 (8)	16
Pantoea species†	69.2 (9)	30.8 (4)	13
Other Gram-negative species (*n* = 29)	72.5 (58)	27.5 (22)	80
Pseudomonas aeruginosa	59.4 (479)	40.6 (327)	806

* Insufficient numbers (<10) to calculate percentage
† Species not determined
Note: Vancomycin susceptibility was not available for five *E. faecalis* (community-onset [1], hospital-onset [4]) and one *E. faecium* (hospital-onset).

3.3. 30-day all-cause mortality and onset

All-cause or crude mortality removes the need for assessment of attributable mortality, which may be subjective. Mortality at 30-days is one of the commonest endpoints used for benchmarking.

Information on patient outcome was available for 7,153 (68.4%) episodes involving Gram-negative species; 1,335 (83.5%) involving *Enterococcus* and 2,686 (78.5%) involving *S. aureus*.

For patient episodes involving Gram-negative species, the 30-day all-cause mortality was 11.5% (742/6,433) for *Enterobacterales*, 17.3% (106/613) for *P. aeruginosa*, and 8.4% (9/107) for *Acinetobacter* species. A significant difference was seen between the 30-day all-cause mortality for community-onset (10.4%, 506/4,853) and hospital-onset (14.9%, 236/1,580) episodes for *Enterobacterales* ($P < 0.0001$), notably for *E. coli* (community-onset 9.1%, hospital-onset 13.7%) (Table 4). A significant difference in 30-day all-cause mortality was seen between children (4.5%, 17/379) and adults (12.0%, 725/6,054) for *Enterobacterales* ($P < 0.0001$). The 30-day all-cause mortality among infants aged 90 days or less was 9.7% (13/134).

The 30-day all-cause mortality rate for patients with *Enterococcus* species was significantly lower among children (4.5%, 4/88) compared to adults (21.6%, 269/1,247) ($P < 0.01$). Overall, there was a significant difference in the 30-day all-cause mortality between *E. faecium* (26.3%, 150/571) and *E. faecalis* (17.0%, 115/675) ($P < 0.01$). There was no significant difference between vancomycin-resistant (28.7%, 85/296) and vancomycin-susceptible (23.6%, 65/275) *E. faecium* episodes.

For patient episodes involving *S. aureus*, the 30-day all-cause mortality was significantly lower among children (0.9%, 2/228) compared to adults (17.7%, 434/2,458) ($P < 0.01$). There was no significant difference in 30-day all-cause mortality between methicillin-susceptible *S. aureus* (MSSA) and MRSA episodes (16.5% and 14.8%, respectively), or between healthcare-associated MRSA (HA MRSA) (17.5%) and community-associated MRSA (CA-MRSA) (13.6%) clones).

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), AGAR, 2023

Organism	Community-onset		Hospital-onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Enterococcus species	636	17.1 (109)	699	23.5 (164)	1,335	20.4 (273)
Enterococcus faecalis	441	16.6 (73)	234	17.9 (42)	675	17.0 (115)
Vancomycin-resistant	0	–* (0)	0	–* (0)	0	–* (0)
Vancomycin-susceptible	441	16.6 (73)	231	18.2 (42)	672	17.1 (115)
Enterococcus faecium	142	21.1 (30)	429	28.0 (120)	571	26.3 (150)
Vancomycin-resistant	60	21.7 (13)	236	30.5 (72)	296	28.7 (85)
Vancomycin-susceptible	82	20.7 (17)	193	24.9 (48)	275	23.6 (65)
Other enterococcal species (*n* = 10)	53	11.3 (6)	36	5.6 (2)	89	9.0 (8)
Staphylococcus aureus	2,048	15.9 (325)	638	17.4 (111)	2,686	16.2 (436)
Methicillin-resistant	323	15.5 (50)	115	13.0 (15)	438	14.8 (65)
CA-MRSA	251	14.3 (36)	81	11.1 (9)	332	13.6 (45)
HA-MRSA	42	19.0 (8)	21	14.3 (3)	63	17.5 (11)
Methicillin susceptible	1,725	15.9 (275)	523	18.4 (96)	2,248	16.5 (371)
Gram-negative species	5,270	10.8 (568)	1,883	15.3 (289)	7,153	12.0 (857)
Acinetobacter	69	10.1 (7)	38	5.3 (2)	107	8.4 (9)
Acinetobacter baumannii complex	35	14.3 (5)	25	4.0 (1)	60	10.0 (6)
Acinetobacter species†	11	9.1 (1)	8	12.5 (1)	19	10.5 (2)
Acinetobacter ursingii	9	0.0 (0)	2	0.0 (0)	11	0.0 (0)
Other *Acinetobacter* species (*n* = 9)	14	7.1 (1)	3	0.0 (0)	17	5.9 (1)

Organism	Community-onset		Hospital-onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Enterobacterales	4,853	10.4 (506)	1,580	14.9 (236)	6,433	11.5 (742)
Escherichia coli	3,064	9.1 (280)	695	13.7 (95)	3,759	10.0 (375)
Klebsiella pneumoniae complex	711	12.7 (90)	310	14.8 (46)	1,021	13.3 (136)
Enterobacter cloacae complex	197	14.2 (28)	197	16.2 (32)	394	15.2 (60)
Proteus mirabilis	217	15.7 (34)	42	23.8 (10)	259	17.0 (44)
Klebsiella oxytoca	172	14.0 (24)	74	13.5 (10)	246	13.8 (34)
Serratia marcescens	94	9.6 (9)	74	18.9 (14)	168	13.7 (23)
Klebsiella aerogenes	63	12.7 (8)	57	10.5 (6)	120	11.7 (14)
Citrobacter freundii complex	54	20.4 (11)	29	24.1 (7)	83	21.7 (18)
Salmonella species (non-typhoidal)	64	6.3 (4)	9	0.0 (0)	73	5.5 (4)
Morganella morganii	48	8.3 (4)	24	25.0 (6)	72	13.9 (10)
Citrobacter koseri	36	11.1 (4)	18	5.6 (1)	54	9.3 (5)
Salmonella species (typhoidal)	36	0.0 (0)	2	0.0 (0)	38	0.0 (0)
Raoultella ornithinolytica	14	14.3 (2)	11	27.3 (3)	25	20.0 (5)
Pantoea agglomerans	8	0.0 (0)	6	0.0 (0)	14	0.0 (0)
Proteus vulgaris	12	33.3 (4)	2	50.0 (1)	14	35.7 (5)
Hafnia alvei	6	0.0 (0)	6	0.0 (0)	12	0.0 (0)
Providencia rettgeri	9	22.2 (2)	2	50.0 (1)	11	27.3 (3)
Pantoea species†	6	0.0 (0)	4	0.0 (0)	10	0.0 (0)
Other *Enterobacterales* species (*n* = 26)	42	4.8 (2)	18	22.2 (4)	60	10.0 (6)
Pseudomonas aeruginosa	348	15.8 (55)	265	19.2 (51)	613	17.3 (106)

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

* Not applicable (no isolates)

† Species not determined

Notes:

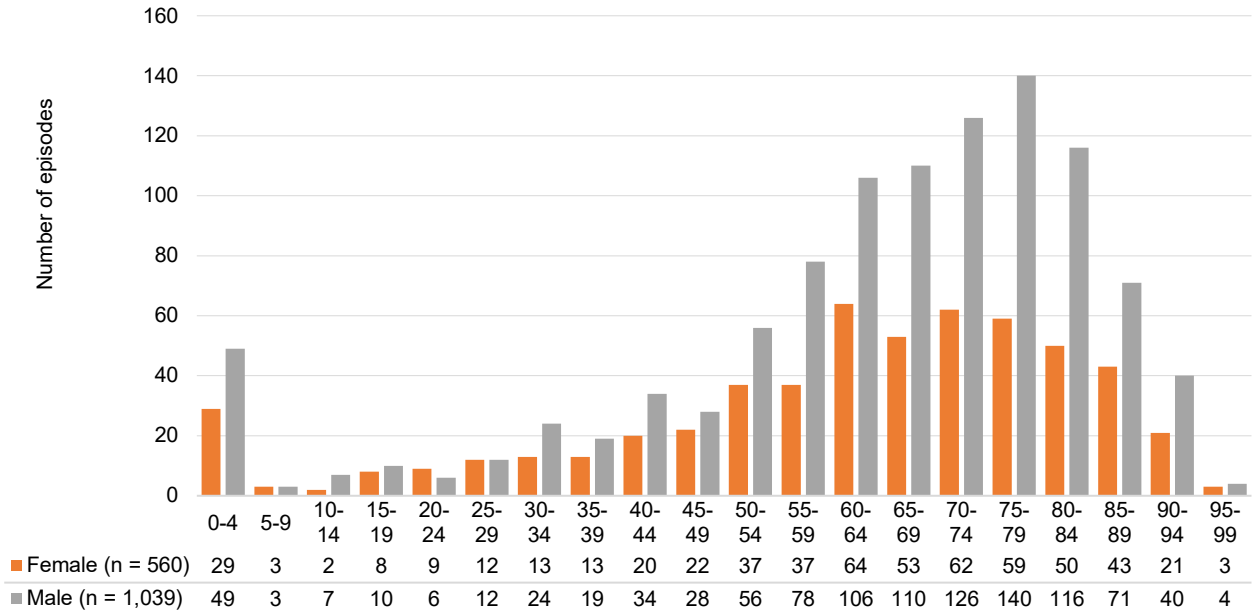
1. Forty-three methicillin-resistant *Staphylococcus aureus* were not available for whole genome sequencing.
2. Vancomycin susceptibility was not available for five *Enterococcus faecalis* (community-onset [1], hospital-onset [4]) and one *E. faecium* (hospital-onset).

3.4. Patient age and sex

Age and sex were available for all patients with Gram-negative, enterococcal or staphylococcal bacteraemia. For Gram-negative bloodstream infection, the proportion of males was 53.5% and females 46.5%. For *Enterococcus* species, 65.0% were male and 35.0% female; for SAB, 66.0% were male and 34.0% female.

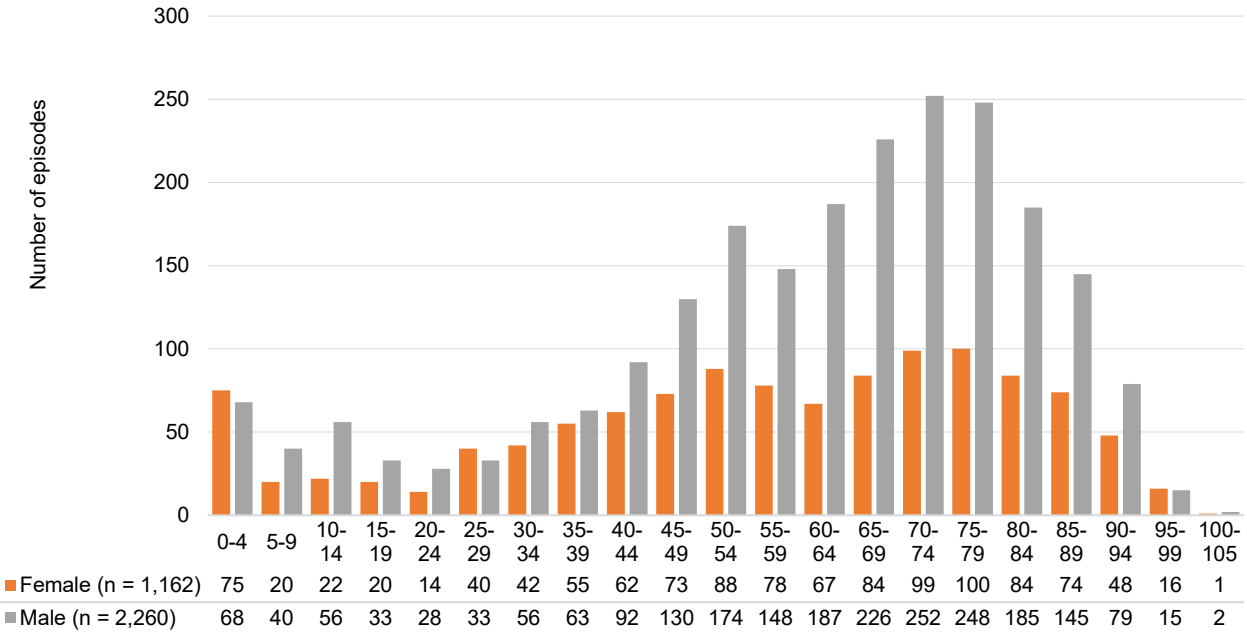
Increasing age was a surrogate risk factor for bacteraemia (Figures 1–3); only 13.7% of *Enterococcus* species episodes,19.4% of *S. aureus* episodes and 14.5% of Gram-negative species episodes, were in patients aged less than 40 years. The proportion of patients aged <18 years was 6.4% (*n* = 102), 9.4% (*n* = 323) and 5.8% (*n* = 611) among enterococcal episodes, *S. aureus* episodes, and Gram-negative episodes, respectively.

Figure 1: Number of episodes of bacteraemia due to *Enterococcus* species, by patient age group and sex, AGAR, 2023



Note: x-axis = age group in years.

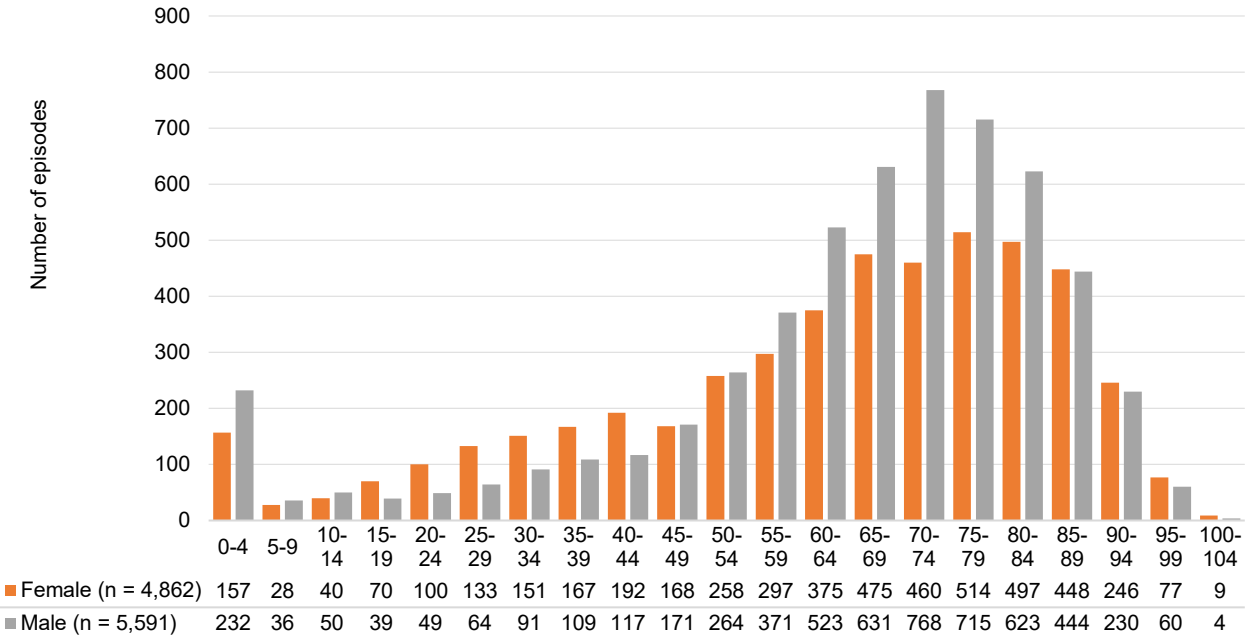
Figure 2: Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient age group and sex, AGAR, 2023



	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	80-84	85-89	90-94	95-99	100-105
Female (n = 1,162)	75	20	22	20	14	40	42	55	62	73	88	78	67	84	99	100	84	74	48	16	1
Male (n = 2,260)	68	40	56	33	28	33	56	63	92	130	174	148	187	226	252	248	185	145	79	15	2

Note: x-axis = age group in years.

Figure 3: Number of episodes of bacteraemia due to Gram-negative species, by patient age group and sex, AGAR, 2023



	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	80-84	85-89	90-94	95-99	100-104
Female (n = 4,862)	157	28	40	70	100	133	151	167	192	168	258	297	375	475	460	514	497	448	246	77	9
Male (n = 5,591)	232	36	50	39	49	64	91	109	117	171	264	371	523	631	768	715	623	444	230	60	4

Note: x-axis = age group in years.

3.5. Principal clinical manifestation

The principal clinical manifestations, which represent the most likely primary site or source for the origin of the bloodstream infection, are described below for patients with enterococcal, staphylococcal, or Gram-negative bacteraemia.

Enterococcus species

The principal clinical manifestation was known for 1,503 (94.0%) patient episodes of enterococcal bacteraemia. Overall, where the focus of infection was known, the most frequent principal clinical manifestations were urinary tract infection (14.7%) or biliary tract infection (14.0%) (Table 5). There was a significant gender difference in terms of principal clinical manifestation for endocarditis left-sided infections.

Of the hospital-onset episodes where data were available, the most frequent principal clinical manifestations were febrile neutropenia (15.0%), intra-abdominal infection other than biliary tract (14.9%), or device-related infection without metastatic focus (14.6%), Of the community-onset episodes where data were available, the most frequent principal clinical manifestations were urinary tract infection (21.5%) (data not shown).

Table 5: Principal clinical manifestation for enterococcal bacteraemia, by patient sex, AGAR, 2023

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance*
No identifiable focus	16.2 (86)	15.1 (147)	15.5 (233)	ns
Urinary tract infection	13.3 (71)	15.4 (150)	14.7 (221)	ns
Biliary tract infection (including cholangitis)	15.4 (82)	13.3 (129)	14.0 (211)	ns
Intra-abdominal infection other than biliary tract	14.3 (76)	11.3 (110)	12.4 (186)	ns
Device-related infection without metastatic focus	11.3 (60)	10.4 (101)	10.7 (161)	ns
Febrile neutropenia	7.9 (42)	9.3 (90)	8.8 (132)	ns
Other clinical syndrome	7.9 (42)	8.2 (80)	8.1 (122)	ns
Endocarditis left-sided	5.3 (28)	8.4 (82)	7.3 (110)	*P* = 0.0272
Skin and skin structure infection	3.6 (19)	3.0 (29)	3.2 (48)	ns
Device-related infection with metastatic focus	2.6 (14)	2.9 (28)	2.8 (42)	ns
Osteomyelitis/septic arthritis	1.5 (8)	1.9 (18)	1.7 (26)	ns
Endocarditis right-sided	0.8 (4)	0.7 (7)	0.7 (11)	ns
Total	532	971	1,503	

ns = not significant
* Fisher's exact test for difference in principal clinical manifestation and sex

The principal manifestation was known for 93.9% (1,395/1,485) of the *E. faecalis* or *E. faecium* episodes (Table 6). The most common clinical manifestation for *E. faecalis* was urinary tract infection (21.8%), whereas for *E. faecium* it was intra-abdominal infection other than biliary tract (17.7%) or febrile neutropenia (16.9%). Significant differences were seen between *E. faecalis* and *E. faecium* for a number of clinical manifestations.

Table 6: Principal clinical manifestation for *Enterococcus faecalis* and *E. faecium* bacteraemia, AGAR, 2023

Principal clinical manifestation	*E. faecalis* % (*n*)	*E. faecium* % (*n*)	Total % (*n*)	Significance*
Urinary tract infection	21.8 (168)	8.5 (53)	15.8 (221)	$P < 0.01$
No identifiable focus	17.5 (135)	13.2 (82)	15.6 (217)	$0.01 < P < 0.05$
Intra-abdominal infection other than biliary tract	8.5 (66)	17.7 (110)	12.6 (176)	$P < 0.01$
Biliary tract infection (including cholangitis)	9.1 (70)	15.4 (96)	11.9 (166)	$P < 0.01$
Device-related infection without metastatic focus	9.2 (71)	13.0 (81)	10.9 (152)	$0.01 < P < 0.05$
Febrile neutropenia	2.6 (20)	16.9 (105)	9.0 (125)	$P < 0.01$
Other clinical syndrome	8.0 (62)	7.4 (46)	7.7 (108)	$P < 0.01$
Endocarditis left-sided	13.2 (102)	1.0 (6)	7.7 (108)	ns
Skin and skin structure infection	4.1 (32)	2.4 (15)	3.4 (47)	ns
Device-related infection with metastatic focus	2.3 (18)	3.5 (22)	2.9 (40)	ns
Osteomyelitis/septic arthritis	2.3 (18)	1.0 (6)	1.7 (24)	ns
Endocarditis right-sided	1.3 (10)	0.2 (1)	0.8 (11)	$0.01 < P < 0.05$
Total	772	623	1,395	

ns = not significant
* Fisher's exact test for difference in principal clinical manifestation between *E. faecalis* and *E. faecium*

Staphylococcus aureus

The principal clinical manifestation was known for 3,058 (89.4%) episodes of SAB (Table 7). Overall, the most frequent principal clinical manifestation was osteomyelitis/septic arthritis (20.6%) followed by skin and skin structure infection (19.2%). Of the clinical manifestations in children a little over one-third (34.7%, 103/297) were due to osteomyelitis/septic arthritis (data not shown).

Of the hospital-onset SABs where data were available, the most common principal clinical manifestation was device-related infection without metastatic focus (32.7%, 239/730) (Table 7). Of the community-onset SABs, the most common principal clinical manifestation was osteomyelitis/septic arthritis (24.4%, 567/2,328).

Table 7: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by place of onset, AGAR, 2023

Principal clinical manifestation	Community-onset % (*n*)	Hospital-onset% (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	24.4 (567)	8.5 (62)	20.6 (629)
Skin and skin structure infection	20.4 (474)	15.5 (113)	19.2 (587)
Device-related infection without metastatic focus	10.5 (245)	32.7 (239)	15.8 (484)
No identifiable focus	14.7 (342)	12.3 (90)	14.1 (432)
Other clinical syndrome	10.4 (242)	10.7 (78)	10.5 (320)
Endocarditis left-sided	5.7 (133)	3.2 (23)	5.1 (156)
Pneumonia/empyema	3.6 (84)	3.8 (28)	3.7 (112)
Deep abscess(es) excluding those in the CNS	3.0 (69)	1.2 (9)	2.6 (78)
Endocarditis right-sided	2.8 (65)	1.2 (9)	2.4 (74)
Device-related infection with metastatic focus	1.4 (32)	5.6 (41)	2.4 (73)
CNS infection (meningitis, abscess(es))	2.4 (55)	1.0 (7)	2.0 (62)
Febrile neutropenia	0.9 (20)	4.2 (31)	1.7 (51)
Total	2,328	730	3,058

CNS = central nervous system

The most common principal clinical manifestation for MSSA was osteomyelitis/septic arthritis (21.0%, 544/2,586), whereas for MRSA it was skin and skin structure infection (23.7%, 112/472) (Table 8).

Table 8: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, AGAR, 2023

Principal clinical manifestation	Methicillin-resistant % (*n*)	Methicillin-susceptible % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	18.0 (85)	21.0 (544)	20.6 (629)
Skin and skin structure infection	23.7 (112)	18.4 (475)	19.2 (587)
Device-related infection without metastatic focus	11.4 (54)	16.6 (430)	15.8 (484)
No identifiable focus	13.3 (63)	14.3 (369)	14.1 (432)
Other clinical syndrome	12.7 (60)	10.1 (260)	10.5 (320)
Endocarditis left-sided	4.4 (21)	5.2 (135)	5.1 (156)
Pneumonia/empyema	6.4 (30)	3.2 (82)	3.7 (112)
Deep abscess(es) excluding those in the CNS	3.6 (17)	2.4 (61)	2.6 (78)
Endocarditis right-sided	2.3 (11)	2.4 (63)	2.4 (74)
Device-related infection with metastatic focus	1.7 (8)	2.5 (65)	2.4 (73)
CNS infection (meningitis, abscess(es))	1.1 (5)	2.2 (57)	2.0 (62)
Febrile neutropenia	1.3 (6)	1.7 (45)	1.7 (51)
Total	472	2,586	3,058

CNS = central nervous system

Gram-negative species

The principal clinical manifestation was documented for 8,771 (83.9%) patient episodes of Gram-negative bacteraemia. The most frequent clinical manifestations for episodes caused by *Enterobacterales* were urinary tract infection (43.3%) and biliary tract infection (16.2%); for *P. aeruginosa*, urinary tract infections (27.4%) and febrile neutropenia (17.4%) were the most common. For *Acinetobacter*, device-related infection without metastatic focus (23.4%) was the most common while 21.8% had no identifiable focus (Table 9).

Urinary tract infection was the most frequent principal manifestation for community-onset episodes caused by *Enterobacterales* (51.7%). For *P. aeruginosa*, febrile neutropenia (19.3%) and urinary tract infection (17.5%) were the most common. For hospital-onset episodes, urinary tract infection (*Enterobacterales* 35.6%, *P. aeruginosa* 31.9%), biliary tract infections (including cholangitis) (*Enterobacterales* 18.8%), and febrile neutropenia (*P. aeruginosa* 16.5%) were the most common.

For episodes involving *Enterobacterales* where urinary tract infection was reported as the principal clinical manifestation, a small proportion (409/3,444, 11.9%) were regarded as a device-related infection. This was higher for hospital-onset than community-onset episodes (hospital-onset: 94/407, 23.1%, community-onset: 315/3,037, 10.4%; $P < 0.0001$).

Table 9: Principal clinical manifestation for Gram-negative bacteraemia, by patient sex, AGAR, 2023

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Gram-negative species*	4,051	4,720	8,771
Acinetobacter	80	44	124
Device-related infection without metastatic focus	21.3 (17)	27.3 (12)	23.4 (29)
No identifiable focus	26.3 (21)	13.6 (6)	21.8 (27)
Other clinical syndrome	15.0 (12)	22.7 (10)	17.7 (22)
Skin and skin structure infection	16.3 (13)	11.4 (5)	14.5 (18)
Urinary tract infection	6.3 (5)	4.5 (2)	5.6 (7)
Febrile neutropenia	2.5 (2)	11.4 (5)	5.6 (7)
Biliary tract infection (including cholangitis)	5.0 (4)	2.3 (1)	4.0 (5)
Osteomyelitis/septic arthritis	2.5 (2)	2.3 (1)	2.4 (3)
Device-related infection with metastatic focus	2.5 (2)	2.3 (1)	2.4 (3)
Intra-abdominal infection other than biliary tract	2.5 (2)	2.3 (1)	2.4 (3)
Enterobacterales	6,210	1,758	7,968
Urinary tract infection	49.0 (3,040)	23.2 (407)	43.3 (3,447)
Biliary tract infection (including cholangitis)	17.9 (1,109)	10.5 (185)	16.2 (1,294)
Intra-abdominal infection other than biliary tract	9.3 (576)	13.2 (232)	10.1 (808)
Other clinical syndrome	7.3 (454)	11.4 (200)	8.2 (654)
No identifiable focus	7.6 (472)	9.6 (169)	8.0 (641)
Febrile neutropenia	4.5 (282)	19.9 (349)	7.9 (631)
Device-related infection without metastatic focus	1.8 (111)	6.8 (119)	2.9 (230)
Skin and skin structure infection	1.7 (104)	3.7 (65)	2.1 (169)
Osteomyelitis/septic arthritis	0.9 (53)	0.9 (16)	0.9 (69)
Device-related infection with metastatic focus	0.1 (9)	0.9 (16)	0.3 (25)
Pseudomonas aeruginosa	398	281	679
Urinary tract infection	29.6 (118)	24.2 (68)	27.4 (186)
Febrile neutropenia	14.8 (59)	21.0 (59)	17.4 (118)
Other clinical syndrome	13.1 (52)	14.2 (40)	13.5 (92)
No identifiable focus	12.6 (50)	5.7 (16)	9.7 (66)
Device-related infection without metastatic focus	6.3 (25)	13.2 (37)	9.1 (62)
Intra-abdominal infection other than biliary tract	7.8 (31)	8.2 (23)	8.0 (54)
Skin and skin structure infection	8.3 (33)	5.7 (16)	7.2 (49)
Biliary tract infection (including cholangitis)	6.5 (26)	4.6 (13)	5.7 (39)
Device-related infection with metastatic focus	0.3 (1)	2.5 (7)	1.2 (8)
Osteomyelitis/septic arthritis	0.8 (3)	0.7 (2)	0.7 (5)

* *Acinetobacter*, *Enterobacterales* and *Pseudomonas aeruginosa*

3.6. Length of hospital stay following bacteraemic episode

Information on length of stay following bacteraemia was available for 1,479 (92.5%) episodes involving *Enterococcus* species, 3,180 (92.9%) episodes involving *S. aureus* and 9,035 (86.4%) episodes involving Gram-negative species.

Overall, 23.8% of patients remained in hospital for more than 30 days after enterococcal bacteraemia (Table 10) and 26.9% after staphylococcal bacteraemia (Table 11). Just over one-half (3,685/6,832, 53.9%) of patients with a community-onset Gram-negative bacteraemia had a length of hospital stay less than seven days. A little over one-third of patients with hospital-onset bacteraemia caused by *Acinetobacter* (18/47, 38.3%) remained in hospital for more than 30 days (Table 12).

Table 10: Length of stay following *Enterococcus* species bacteraemia, by vancomycin resistance and place of onset, AGAR, 2023

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
All species	25.2 (372)	26.5 (392)	24.5 (363)	23.8 (352)	1,479
E. faecalis	27.8 (215)	27.4 (212)	20.6 (159)	24.2 (187)	773
Vancomycin-resistant	–* (0)	–* (0)	–* (0)	–* (0)	0
Vancomycin-susceptible	27.9 (214)	27.5 (211)	20.3 (156)	24.3 (187)	768
E. faecium	20.8 (126)	25.4 (154)	29.5 (179)	24.4 (148)	607
Vancomycin-resistant	22.7 (68)	21.0 (63)	31.7 (95)	24.7 (74)	300
Vancomycin-susceptible	19.0 (58)	29.7 (91)	27.5 (84)	23.9 (73)	306
Other *Enterococcus* species (*n* = 10)	31.3 (31)	26.3 (26)	25.3 (25)	17.2 (17)	99
Community-onset					
E. faecalis	33.3 (176)	29.4 (155)	17.2 (91)	20.1 (106)	528
Vancomycin-resistant	–* (0)	–* (0)	–* (0)	–* (0)	0
Vancomycin-susceptible	33.4 (176)	29.2 (154)	17.3 (91)	20.1 (106)	527
E. faecium	25.9 (43)	34.9 (58)	23.5 (39)	15.7 (26)	166
Vancomycin-resistant	31.8 (21)	28.8 (19)	25.8 (17)	13.6 (9)	66
Vancomycin-susceptible	22.0 (22)	39.0 (39)	22.0 (22)	17.0 (17)	100
Hospital-onset					
E. faecalis	15.9 (39)	23.3 (57)	27.8 (68)	33.1 (81)	245
Vancomycin-resistant	–* (0)	–* (0)	–* (0)	–* (0)	0
Vancomycin-susceptible	15.8 (38)	23.7 (57)	27.0 (65)	33.6 (81)	241
E. faecium	18.8 (83)	21.8 (96)	31.7 (140)	27.7 (122)	441
Vancomycin-resistant	20.1 (47)	18.8 (44)	33.3 (78)	27.8 (65)	234
Vancomycin-susceptible	17.5 (36)	25.2 (52)	30.1 (62)	27.2 (56)	206

* Insufficient numbers (<10) to calculate percentage

Note: Vancomycin susceptibility not available for five *E. faecalis* (community-onset [1]; hospital-onset [4]) and one *E. faecium* (hospital-onset).

Table 11: Length of stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, AGAR, 2023

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Staphylococcus aureus	19.4 (616)	25.0 (794)	28.7 (913)	26.9 (857)	3,180
Methicillin-resistant	20.4 (100)	20.4 (100)	28.8 (141)	30.3 (148)	489
Community-onset	23.0 (84)	20.5 (75)	27.9 (102)	28.7 (105)	366
Hospital-onset	13.0 (16)	20.3 (25)	31.7 (39)	35.0 (43)	123
Methicillin-susceptible	19.2 (516)	25.8 (694)	28.7 (772)	26.3 (709)	2,691
Community-onset	19.6 (411)	27.0 (566)	26.6 (558)	26.8 (562)	2,097
Hospital-onset	17.7 (105)	21.5 (128)	36.0 (214)	24.7 (147)	594

Table 12: Length of stay following Gram-negative bacteraemia, by species and place of onset, AGAR, 2023

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Gram-negative species	45.7 (4,129)	29.0 (2,617)	14.7 (1,328)	10.6 (961)	9,035
Community-onset	53.9 (3,685)	29.0 (1,978)	11.3 (775)	5.8 (394)	6,832
Hospital-onset	20.2 (444)	29.0 (639)	25.1 (553)	25.7 (567)	2,203
Acinetobacter	34.4 (42)	24.6 (30)	18.0 (22)	23.0 (28)	122
Community-onset	49.3 (37)	25.3 (19)	12.0 (9)	13.3 (10)	75
Hospital-onset	10.6 (5)	23.4 (11)	27.7 (13)	38.3 (18)	47
Enterobacterales	47.0 (3,862)	28.8 (2,367)	14.2 (1,166)	9.9 (816)	8,211
Community-onset	54.9 (3,486)	28.7 (1,825)	10.9 (690)	5.5 (352)	6,353
Hospital-onset	20.2 (376)	29.2 (542)	25.6 (476)	25.0 (464)	1,858
Escherichia coli	51.8 (2,543)	28.1 (1,379)	12.0 (591)	8.0 (393)	4,906
Community-onset	57.7 (2,356)	27.7 (1,132)	9.6 (392)	4.9 (202)	4,082
Hospital-onset	22.7 (187)	30.0 (247)	24.2 (199)	23.2 (191)	824
Klebsiella pneumoniae complex	39.3 (484)	32.9 (406)	16.4 (202)	11.4 (141)	1,233
Community-onset	48.2 (424)	32.7 (288)	13.2 (116)	5.9 (52)	880
Hospital-onset	17.0 (60)	33.4 (118)	24.4 (86)	25.2 (89)	353
Enterobacter cloacae complex	28.7 (141)	28.9 (142)	26.3 (129)	16.1 (79)	491
Community-onset	42.8 (110)	30.4 (78)	18.3 (47)	8.6 (22)	257
Hospital-onset	13.2 (31)	27.4 (64)	35.0 (82)	24.4 (57)	234
Other *Enterobacterales* (*n* = 44)	43.9 (694)	27.8 (440)	15.4 (244)	12.8 (203)	1,581
Pseudomonas aeruginosa	32.1 (225)	31.3 (220)	19.9 (140)	16.7 (117)	702
Community-onset	40.1 (162)	33.2 (134)	18.8 (76)	7.9 (32)	404
Hospital-onset	21.1 (63)	28.9 (86)	21.5 (64)	28.5 (85)	298

3.7. Susceptibility testing results

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

Percentages of non-susceptibility in national priority indicator species

Overall percentages of resistance or non-susceptibility in the indicator species of national priority[50] using both CLSI breakpoints and EUCAST breakpoints, are shown in Table 13. Resistances (as defined by EUCAST), by state and territory to glycopeptides in *E. faecium*, and high-level gentamicin in *E. faecalis* are shown in Figure 4; to key antimicrobial categories (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) for *E. coli* (Figure 5) and *K. pneumoniae* complex (Figure 6); key antipseudomonal agents (Figure 7); and methicillin resistance in *S. aureus* (Figure 8). Detailed resistance by state and territory can be found in Appendix C.

Table 13: Activity of antimicrobial agents tested against isolates recovered from patients with bacteraemia, AGAR, 2023

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Acinetobacter baumannii complex					
Piperacillin–tazobactam	75	10.7 (8)	6.7 (5)	–*	–*
Ceftriaxone	77	63.6 (49)	7.8 (6)	–*	–*
Ceftazidime	77	19.5 (15)	2.6 (2)	–*	–*
Cefepime	48	8.3 (4)	4.2 (2)	–*	–*
Gentamicin	83	1.2 (1)	0.0 (0)	–†	1.2 (1)
Tobramycin	80	0.0 (0)	0.0 (0)	–†	0.0 (0)
Amikacin	74	0.0 (0)	0.0 (0)	–†	1.4 (1)
Ciprofloxacin	81	1.2 (1)	0.0 (0)	98.8 (80)	1.2 (1)
Meropenem	82	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Enterobacter cloacae complex					
Piperacillin–tazobactam	553	4.9 (27)	16.5 (91)	–†	23.3 (129)
Ceftriaxone	555	0.5 (3)	25.0 (139)	0.5 (3)	25.0 (139)
Ceftazidime	555	0.7 (4)	21.3 (118)	1.8 (10)	22.0 (122)
Cefepime	555	3.2 (18)§	2.7 (15)	8.5 (47)	3.8 (21)
Gentamicin	555	0.2 (1)	3.2 (18)	–†	4.1 (23)
Tobramycin	543	1.3 (7)	2.6 (14)	–†	4.1 (22)
Amikacin	555	0.0 (0)	0.0 (0)	–†	0.5 (3)
Ciprofloxacin	554	1.4 (8)	3.2 (18)	1.4 (8)	3.2 (18)
Meropenem	554	0.2 (1)	1.4 (8)	0.4 (2)	1.1 (6)
Enterococcus faecalis					
Ampicillin	818	–*	0.0 (0)	0.0 (0)	0.0 (0)
Benzylpenicillin	638	–*	0.6 (4)	–†	–†
Daptomycin	761	33.5 (255)	0.0 (0)	–†	–†
Linezolid	820	0.4 (3)	0.2 (2)	–*	0.2 (2)
Teicoplanin	821	0.0 (0)	0.0 (0)	–*	0.0 (0)
Vancomycin	821	0.0 (0)	0.0 (0)	–*	0.0 (0)
Enterococcus faecium					
Ampicillin	652	–*	94.2 (614)	0.0 (0)	94.2 (614)

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Benzylpenicillin	498	–*	93.2 (464)	–†	–†
Daptomycin	82	100.0 (82)§	0.0 (0)	–†	–†
Linezolid	653	0.3 (2)	0.0 (0)	–*	0.0 (0)
Teicoplanin	647	1.5 (10)	8.3 (54)	–*	12.7 (82)
Vancomycin	656	0.6 (4)	50.2 (329)	–*	50.8 (333)
Escherichia coli					
Ampicillin	5,648	1.8 (100)	50.6 (2,856)	–†	52.3 (2,956)
Amoxicillin–clavulanic acid (2:1 ratio)#	4,295	9.4 (405)	8.2 (351)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	1,315	–*	–*	–†	37.7 (496)
Piperacillin–tazobactam	5,629	2.3 (128)	2.9 (163)	–†	6.0 (336)
Cefazolin	4,921	–#	22.7 (1,118)	77.3 (3,803)	22.7 (1,118)
Cefuroxime	548	1.5 (8)	16.1 (88)	82.5 (452)	17.5 (96)
Ceftriaxone	5,649	0.1 (6)	12.9 (729)	0.1 (6)	12.9 (729)
Ceftazidime	5,647	1.4 (77)	5.2 (291)	7.7 (437)	6.5 (368)
Cefepime	5,646	1.8 (102)§	2.8 (156)	6.4 (361)	3.4 (191)
Gentamicin	5,645	0.1 (8)	7.5 (424)	–†	8.1 (455)
Tobramycin	5,616	5.5 (311)	2.6 (148)	–†	8.6 (481)
Amikacin	5,646	0.1 (7)	0.2 (9)	–†	1.3 (73)
Ciprofloxacin	5,634	5.0 (282)	14.5 (816)	5.0 (282)	14.5 (816)
Meropenem	5,649	0.0 (2)	0.2 (13)	0.1 (4)	0.2 (9)
Klebsiella aerogenes					
Piperacillin–tazobactam	165	7.9 (13)	27.9 (46)	–†	41.2 (68)
Ceftriaxone	165	1.2 (2)	39.4 (65)	1.2 (2)	39.4 (65)
Ceftazidime	165	3.0 (5)	34.5 (57)	3.6 (6)	37.6 (62)
Cefepime	165	1.2 (2)§	3.0 (5)	3.0 (5)	3.6 (6)
Gentamicin	165	0.6 (1)	1.8 (3)	–†	2.4 (4)
Tobramycin	163	1.2 (2)	1.8 (3)	–†	3.1 (5)
Amikacin	165	0.0 (0)	0.0 (0)	–†	0.6 (1)
Ciprofloxacin	164	2.4 (4)	3.0 (5)	2.4 (4)	3.0 (5)
Meropenem	165	0.6 (1)	3.0 (5)	1.8 (3)	1.2 (2)
Klebsiella oxytoca					
Amoxicillin–clavulanic acid (2:1 ratio)#	234	2.6 (6)	8.1 (19)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	75	–*	–*	–†	10.7 (8)
Piperacillin–tazobactam	311	0.6 (2)	10.9 (34)	–†	12.5 (39)
Ceftriaxone	312	0.6 (2)	7.4 (23)	0.6 (2)	7.4 (23)
Ceftazidime	312	0.3 (1)	1.6 (5)	0.6 (2)	1.9 (6)
Cefepime	312	1.0 (3)§	0.3 (1)	2.2 (7)	0.3 (1)
Gentamicin	312	0.0 (0)	1.6 (5)	–†	1.9 (6)
Tobramycin	308	0.3 (1)	1.0 (3)	–†	1.9 (6)
Amikacin	312	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	311	0.3 (1)	0.6 (2)	0.3 (1)	0.6 (2)
Meropenem	312	0.0 (0)	1.0 (3)	0.0 (0)	1.0 (3)
Klebsiella pneumoniae complex					
Amoxicillin–clavulanic acid (2:1	1,030	3.4 (35)	3.9 (40)	–*	–*

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
ratio)[#]					
Amoxicillin–clavulanic acid (fixed ratio IV)	377	–*	–*	–†	13.3 (50)
Piperacillin–tazobactam	1,425	2.3 (33)	3.8 (54)	–†	9.4 (134)
Cefazolin	1,246	–[#]	11.3 (141)	88.7 (1,105)	11.3 (141)
Cefuroxime	139	3.6 (5)	7.2 (10)	89.2 (124)	10.8 (15)
Ceftriaxone	1,428	0.1 (2)	6.9 (98)	0.1 (2)	6.9 (98)
Ceftazidime	1,428	1.3 (18)	4.7 (67)	2.0 (28)	6.0 (85)
Cefepime	1,428	0.7 (10)[§]	1.9 (27)	3.4 (49)	2.2 (32)
Gentamicin	1,427	0.2 (3)	3.0 (43)	–†	3.3 (47)
Tobramycin	1,414	1.7 (24)	1.8 (26)	–†	3.7 (53)
Amikacin	1,428	0.1 (1)	0.2 (3)	–†	0.5 (7)
Ciprofloxacin	1,421	3.9 (55)	7.8 (111)	3.9 (55)	7.8 (111)
Meropenem	1,427	0.1 (2)	0.5 (7)	0.1 (1)	0.4 (6)
Proteus mirabilis					
Ampicillin	353	0.8 (3)	17.8 (63)	–†	18.7 (66)
Amoxicillin–clavulanic acid (2:1 ratio)[#]	262	8.4 (22)	4.6 (12)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	89	–*	–*	–†	2.2 (2)
Piperacillin–tazobactam	353	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ceftriaxone	353	0.8 (3)	2.0 (7)	0.8 (3)	2.0 (7)
Ceftazidime	351	0.6 (2)	1.1 (4)	1.4 (5)	1.7 (6)
Cefepime	353	0.8 (3)[§]	1.1 (4)	0.8 (3)	1.1 (4)
Gentamicin	352	2.0 (7)	2.0 (7)	–†	7.7 (27)
Tobramycin	352	1.7 (6)	1.7 (6)	–†	6.3 (22)
Amikacin	353	0.3 (1)	0.0 (0)	–†	1.4 (5)
Ciprofloxacin	351	0.6 (2)	3.4 (12)	0.6 (2)	3.4 (12)
Meropenem	352	0.0 (0)	0.3 (1)	0.3 (1)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin–tazobactam	788	7.7 (61)	6.0 (47)	86.3 (680)	13.7 (108)
Ceftazidime	790	3.3 (26)	5.6 (44)	91.1 (720)	8.9 (70)
Cefepime	787	2.4 (19)	3.4 (27)	94.2 (741)	5.8 (46)
Tobramycin	786	0.1 (1)	0.3 (2)	–†	0.9 (7)
Amikacin	785	0.8 (6)	0.3 (2)	–†	1.0 (8)
Ciprofloxacin	789	3.3 (26)	4.3 (34)	92.4 (729)	7.6 (60)
Meropenem	789	3.9 (31)	2.8 (22)	4.7 (37)	2.0 (16)
Salmonella species (non-typhoidal)					
Ampicillin	138	0.0 (0)	4.3 (6)	–†	4.3 (6)
Amoxicillin–clavulanic acid (2:1 ratio)[#]	94	0.0 (0)	0.0 (0)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	44	–*	–*	–†	0.0 (0)
Piperacillin–tazobactam	138	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ceftriaxone	138	0.0 (0)	1.4 (2)	0.0 (0)	1.4 (2)
Ceftazidime	138	0.0 (0)	2.2 (3)	0.0 (0)	2.2 (3)
Cefepime	138	0.0 (0)[§]	1.4 (2)	0.0 (0)	1.4 (2)
Ciprofloxacin[‡]	134	6.0 (8)	11.2 (15)	–†	17.2 (23)

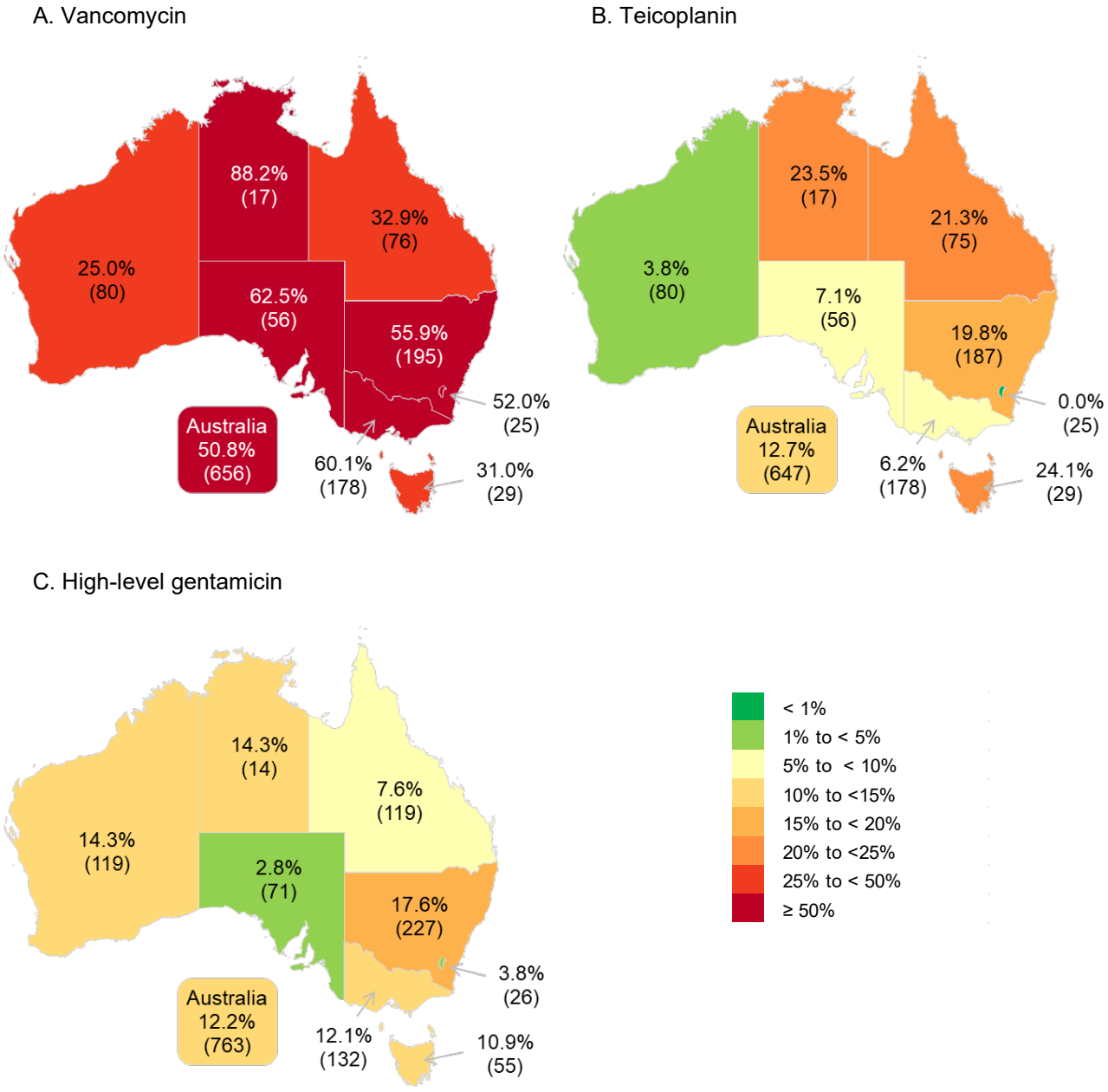
Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Meropenem	138	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	188	1.1 (2)	0.5 (1)	–†	1.6 (3)
Ceftriaxone	239	0.4 (1)	3.3 (8)	0.4 (1)	3.3 (8)
Ceftazidime	239	0.0 (0)	0.4 (1)	0.4 (1)	0.4 (1)
Cefepime	239	0.0 (0)§	0.0 (0)	0.4 (1)	0.0 (0)
Gentamicin	239	0.0 (0)	0.4 (1)	–†	2.1 (5)
Tobramycin	230	14.3 (33)	0.9 (2)	–†	36.1 (83)
Amikacin	239	0.4 (1)	0.0 (0)	–†	0.8 (2)
Ciprofloxacin	237	1.3 (3)	1.7 (4)	1.3 (3)	1.7 (4)
Meropenem	239	0.0 (0)	0.4 (1)	0.0 (0)	0.4 (1)
Staphylococcus aureus					
Benzylpenicillin§§	3,368	–†	80.6 (2,713)	–†	80.6 (2,713)
Cefoxitin (methicillin)##	3,422	–†	16.1 (550)	–†	16.1 (550)
Ciprofloxacin	3,401	0.5 (18)	7.2 (244)	92.3 (3,139)	7.7 (262)
Clindamycin (constitutive)	3,400	0.0 (0)	3.5 (120)	0.0 (0)	3.7 (127)
Clindamycin (constitutive + inducible resistance)	3,400	0.0 (0)	13.8 (468)	0.0 (0)	14.7 (500)
Daptomycin	3,412	–†	<0.1 (5)***	–†	0.1 (5)
Erythromycin	3,367	27.9 (938)	16.7 (561)	–†	18.0 (605)
Fusidic acid	3,366	–*	–*	–†	2.8 (93)
Gentamicin	3,383	1.6 (55)	2.0 (68)	–†	5.9 (201)
Linezolid	3,412	–†	0.0 (0)	–†	0.0 (0)
Mupirocin (high-level)‡†	2,372	–†	1.9 (46)	–†	1.9 (46)
Rifampicin	3,396	0.1 (3)	0.3 (11)	–§§§	1.3 (17)
Teicoplanin	3,411	0.0 (0)	0.0 (0)	–*	0.1 (4)
Tetracycline/doxycycline)###	3,397	0.0 (0)	4.2 (142)	–†	4.9 (165)
Trimethoprim–sulfamethoxazole****	3,379	0.1 (4)	0.8 (28)	0.1 (3)	0.9 (29)
Vancomycin	3,409	0.0 (0)	0.0 (0)	–†	0.0 (0)

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

* No guidelines for indicated species
† No category defined
§ Susceptible dose dependent category for CLSI
# For susceptibility testing purposes, EUCAST fixes the concentration of clavulanic acid at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines
** The cefazolin concentration range available on the Vitek® card used restricts the ability to accurately identify CLSI susceptible and intermediate categories
‡ The ciprofloxacin concentration range available on the Vitek® card used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. Results of MIC gradient strips, where available, were provided
§§ Benzylpenicillin resistance including β-lactamase producers
Resistance as determined by cefoxitin screen (Vitek®) or cefoxitin MIC (Phoenix™)
*** Non-susceptible, resistance not defined
‡† Mupirocin high-level resistance screen
§§§ The rifampicin concentration range on the Phoenix™ card and Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility for EUCAST (*n* = 1,242)
The doxycycline concentration range available on the Phoenix™ card used restricts the ability to accurately identify CLSI intermediate and resistant categories for *S. aureus*
**** Trimethoprim–sulfamethoxazole resistance, as determined by Vitek® or Phoenix™, confirmed by disc diffusion

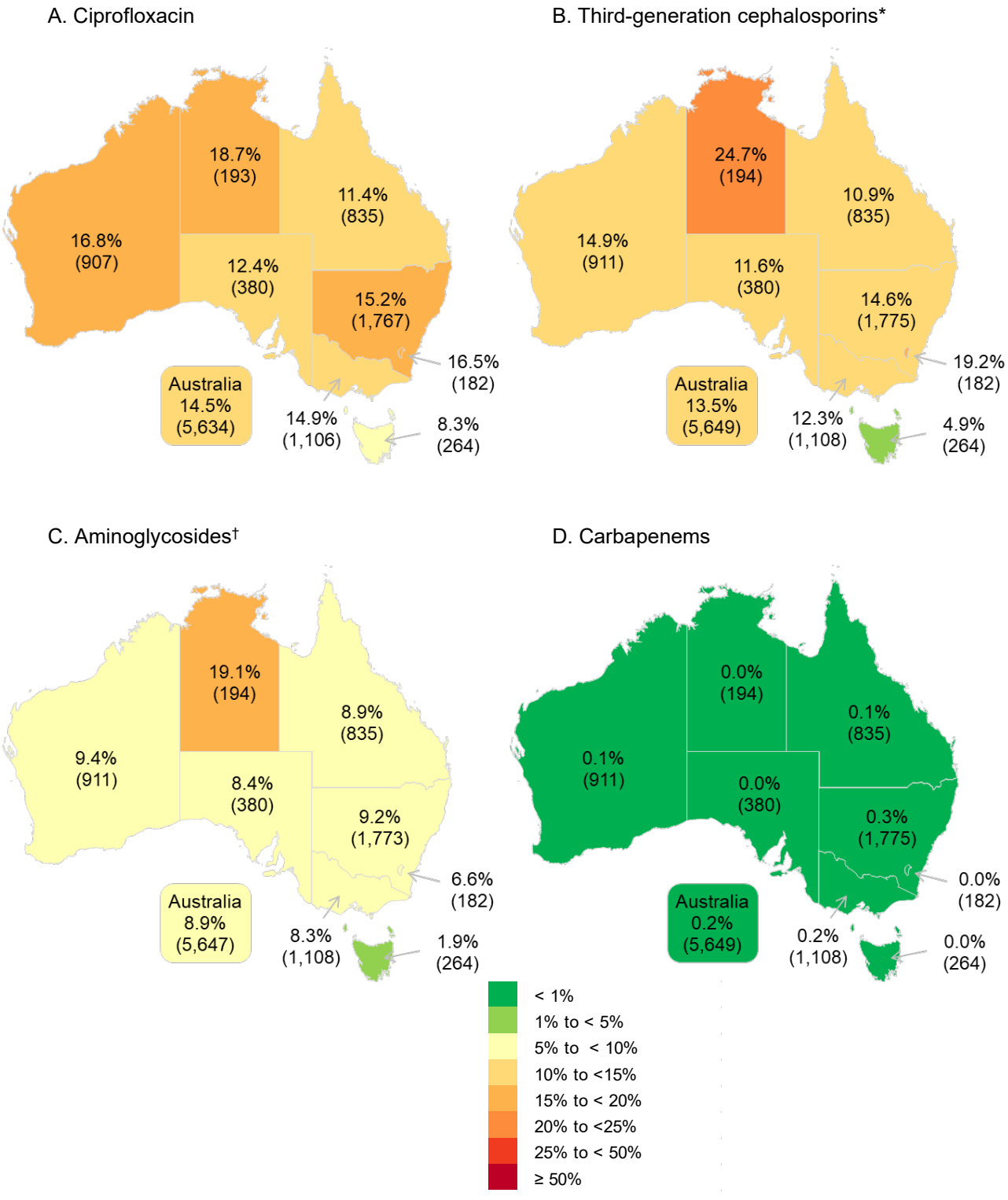
Note: *E. faecium* are usually susceptible dose dependent to daptomycin (CLSI).

Figure 4: Percentage of *Enterococcus faecium* from patients with bacteraemia with resistance, as defined by EUCAST, to vancomycin (A) and teicoplanin (B), and *Enterococcus faecalis* with resistance to high-level gentamicin (C), Australia, AGAR, 2023



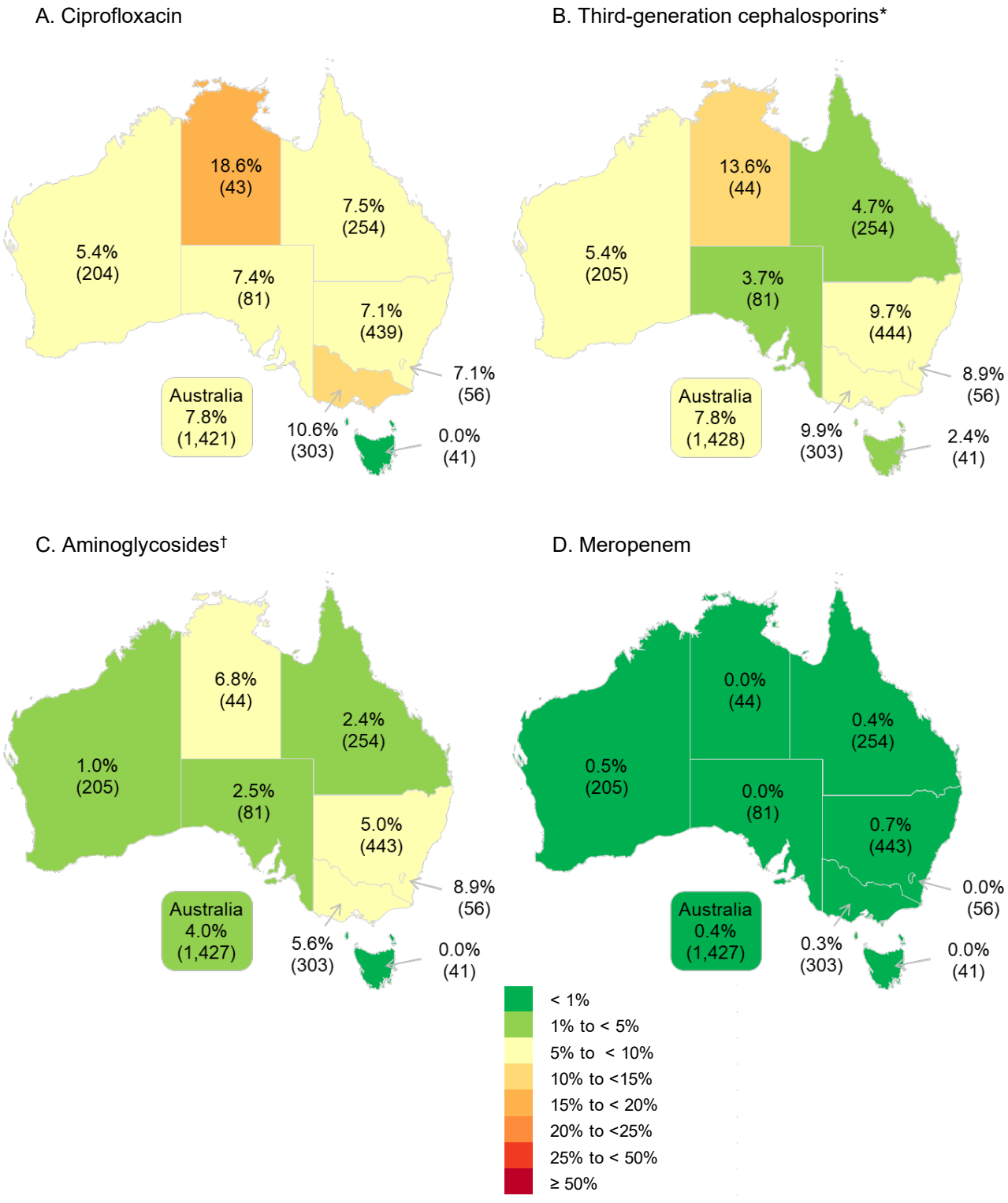
EUCAST = European Committee on Antimicrobial Susceptibility Testing

Figure 5: Percentage of *Escherichia coli* from patients with bacteraemia with resistance, as defined by EUCAST, to ciprofloxacin (A), third-generation cephalosporins (B), aminoglycosides (C) and meropenem (D), Australia, AGAR, 2023



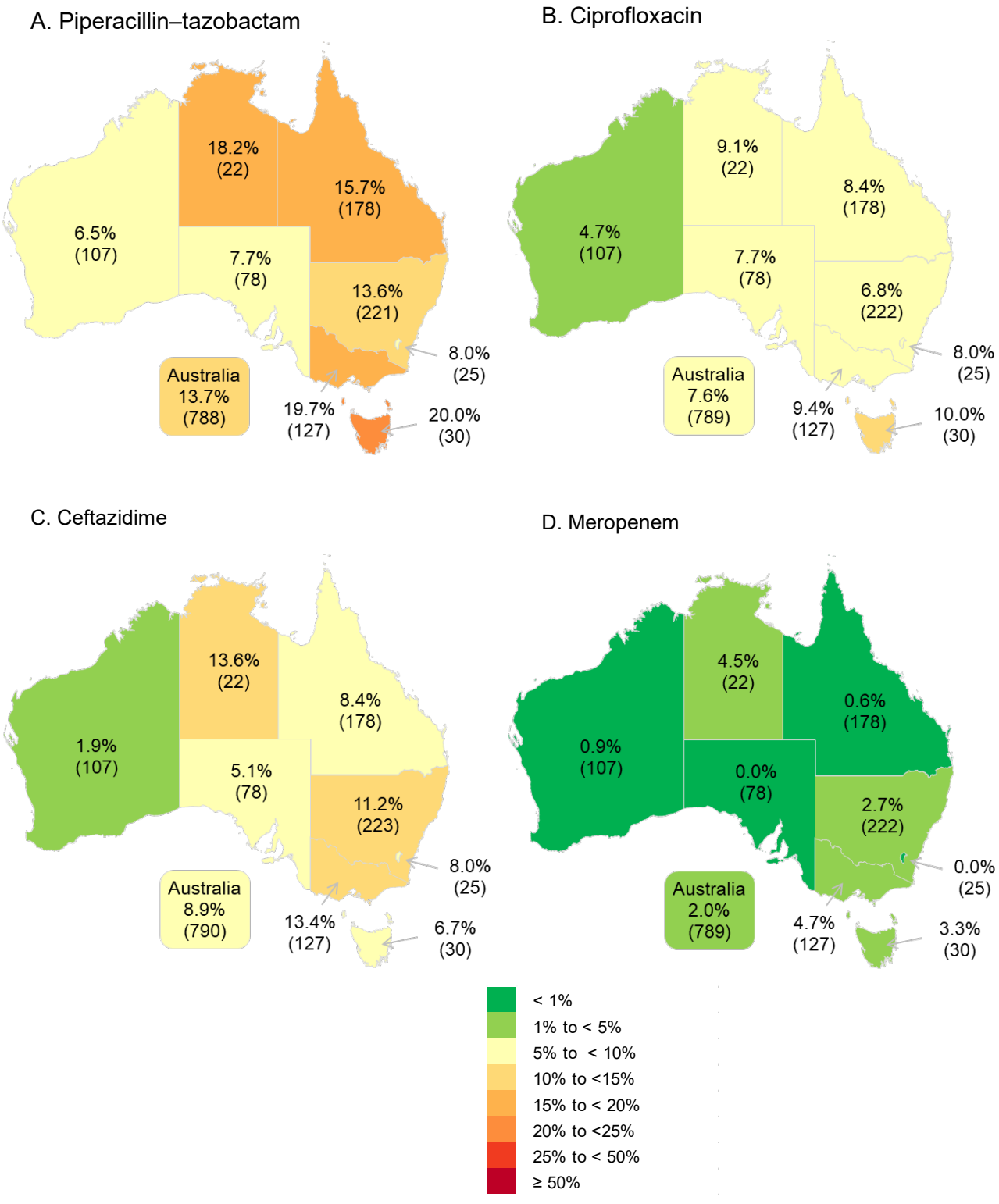
EUCAST = European Committee on Antimicrobial Susceptibility Testing
* Third-generation cephalosporins refers to ceftriaxone and/or ceftazidime
† Aminoglycosides refers to gentamicin or tobramycin

Figure 6: Percentage of *Klebsiella pneumoniae* complex from patients with bacteraemia with resistance, as defined by EUCAST, to ciprofloxacin (A), third-generation cephalosporins (B), aminoglycosides (C) and meropenem (D), Australia, AGAR, 2023



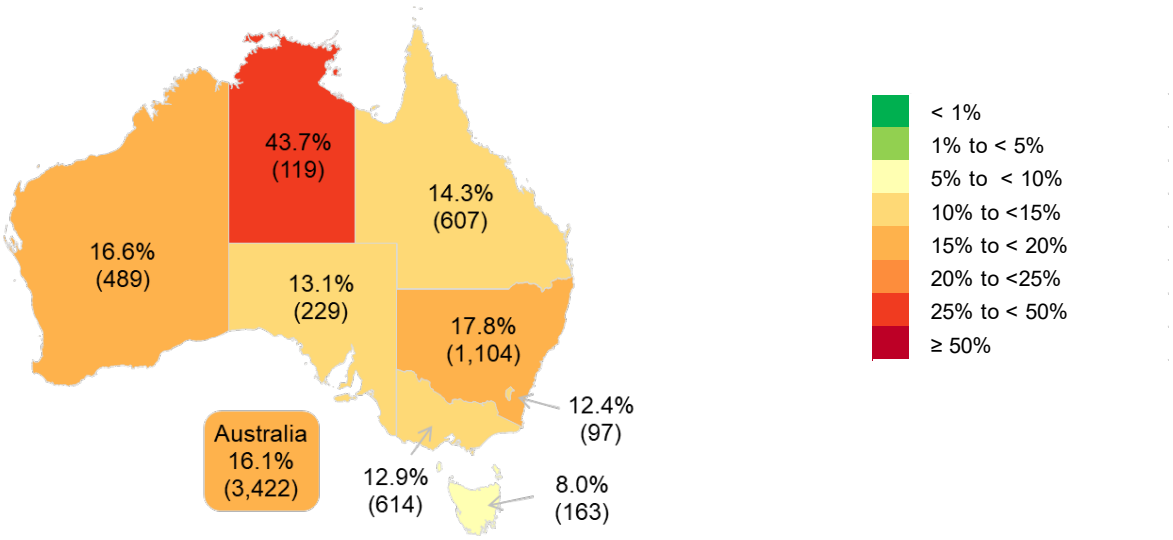
EUCAST = European Committee on Antimicrobial Susceptibility Testing
* Third-generation cephalosporins refers to ceftriaxone and/or ceftazidime
† Aminoglycosides refers to gentamicin or tobramycin

Figure 7: Percentage of *Pseudomonas aeruginosa* from patients with bacteraemia with resistance, as defined by EUCAST, to piperacillin–tazobactam (A), ciprofloxacin (B), ceftazidime (C) and meropenem (D), Australia, AGAR, 2023



EUCAST = European Committee on Antimicrobial Susceptibility Testing

Figure 8: Percentage of *Staphylococcus aureus* from patients with bacteraemia with resistance, as defined by EUCAST, to methicillin, Australia, AGAR, 2023



EUCAST = European Committee on Antimicrobial Susceptibility Testing

Antimicrobial resistance by place of onset

Antimicrobial resistances (CLSI and EUCAST) in indicator species by place of onset, if known, are shown in Table 14.

Table 14: Activity of antimicrobial agents tested against species recovered from patients with bacteraemia, by place of onset, AGAR, 2023

	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
Species and antimicrobial	No.	I	R	S, IE	R	No.	I	R	S, IE	R
Acinetobacter baumannii complex										
Piperacillin–tazobactam	42	9.5	7.1	–*	–*	33	12.1	6.1	–*	–*
Ceftriaxone	44	65.9	4.5	–*	–*	33	60.6	12.1	–*	–*
Ceftazidime	44	9.1	2.3	–*	–*	33	33.3	3.0	–*	–*
Cefepime	30	0.0	3.3	–*	–*	18	22.2	5.6	–*	–*
Gentamicin	48	0.0	0.0	–†	0.0	35	2.9	0.0	–†	2.9
Tobramycin	47	0.0	0.0	–†	0.0	33	0.0	0.0	–†	0.0
Amikacin	43	0.0	0.0	–†	0.0	31	0.0	0.0	–†	3.2
Ciprofloxacin	48	2.1	0.0	97.9	2.1	33	0.0	0.0	100.0	0.0
Meropenem	48	0.0	0.0	0.0	0.0	34	0.0	0.0	0.0	0.0
Enterobacter cloacae complex										
Piperacillin–tazobactam	297	4.0	9.8	–†	15.8	256	5.9	24.2	–†	32.0
Ceftriaxone	299	0.7	18.7	0.7	18.7	256	0.4	32.4	0.4	32.4
Ceftazidime	299	0.3	14.0	2.7	14.4	256	1.2	29.7	0.8	30.9
Cefepime	299	2.7§	2.3	5.0	3.7	256	3.9§	3.1	12.5	3.9
Gentamicin	299	0.3	3.0	–†	3.3	256	0.0	3.5	–†	5.1
Tobramycin	292	1.4	2.4	–†	3.8	251	1.2	2.8	–†	4.4
Amikacin	299	0.0	0.0	–†	0.7	256	0.0	0.0	–†	0.4
Ciprofloxacin	298	1.7	3.7	1.7	3.7	256	1.2	2.7	1.2	2.7
Meropenem	298	0.3	1.7	0.7	1.0	256	0.0	1.2	0.0	1.2
Enterococcus faecalis										
Ampicillin	555	–†	0.0	0.0	0.0	263	–†	0.0	0.0	0.0
Benzylpenicillin	440	–†	0.5	–*	–*	198	–†	1.0	–*	–*
Daptomycin	515	33.0	0.0	–*	–*	246	34.6	0.0	–*	–*
Linezolid	555	0.2	0.2	–†	0.2	265	0.8	0.4	–†	0.4
Teicoplanin	555	0.0	0.0	–†	0.0	266	0.0	0.0	–†	0.0
Vancomycin	555	0.0	0.0	–†	0.0	266	0.0	0.0	–†	0.0
Enterococcus faecium										
Ampicillin	171	–†	84.8	0.0	84.8	481	–†	97.5	0.0	97.5
Benzylpenicillin	124	–†	80.6	–*	–*	374	–†	97.3	–*	–*
Daptomycin	24	100.0§	0.0	–*	–*	58	100.0§	0.0	–*	–*
Linezolid	173	0.0	0.0	–†	0.0	480	0.4	0.0	–†	0.0
Teicoplanin	171	1.2	9.4	–†	11.7	476	1.7	8.0	–†	13.0
Vancomycin	174	0.0	41.4	–†	41.4	482	0.8	53.3	–†	54.1
Escherichia coli										
Ampicillin	4,758	1.9	48.9	–†	50.8	890	0.9	59.7	–†	60.6
Amoxicillin–clavulanic acid (2:1 ratio)#	3,642	9.7	7.2	–*	–*	653	8.1	13.8	–*	–*

Species and antimicrobial	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
	No.	I	R	S, IE	R	No.	I	R	S, IE	R
Amoxicillin–clavulanic acid (fixed ratio IV)	1,089	–*	–*	–†	35.4	226	–*	–*	–†	48.7
Piperacillin–tazobactam	4,743	2.1	1.9	–†	4.8	886	3.0	8.4	–†	12.0
Cefazolin	4,167	–#	21.2	78.8	21.2	754	–#	31.0	69.0	31.0
Cefuroxime	437	1.4	13.3	85.4	14.6	111	1.8	27.0	71.2	28.8
Ceftriaxone	4,759	0.1	12.0	0.1	12.0	890	0.1	17.8	0.1	17.8
Ceftazidime	4,757	1.3	4.4	7.4	5.7	890	1.7	9.1	9.8	10.8
Cefepime	4,757	1.6§	2.3	6.2	2.8	889	2.7§	5.4	7.5	6.3
Gentamicin	4,757	0.1	7.4	–†	7.9	888	0.2	8.1	–†	9.1
Tobramycin	4,735	5.5	2.4	–†	8.3	881	5.6	4.0	–†	10.1
Amikacin	4,757	0.1	0.1	–†	1.1	889	0.1	0.4	–†	2.1
Ciprofloxacin	4,746	5.0	13.9	5.0	13.9	888	5.3	17.7	5.3	17.7
Meropenem	4,759	0.0	0.1	0.0	0.1	890	0.1	0.8	0.3	0.4
Klebsiella aerogenes										
Piperacillin–tazobactam	96	5.2	25.0	–†	35.4	69	11.6	31.9	–†	49.3
Ceftriaxone	96	1.0	33.3	1.0	33.3	69	1.4	47.8	1.4	47.8
Ceftazidime	96	4.2	28.1	3.1	32.3	69	1.4	43.5	4.3	44.9
Cefepime	96	0.0§	2.1	2.1	2.1	69	2.9§	4.3	4.3	5.8
Gentamicin	96	0.0	1.0	–†	1.0	69	1.4	2.9	–†	4.3
Tobramycin	96	1.0	1.0	–†	2.1	67	1.5	3.0	–†	4.5
Amikacin	96	0.0	0.0	–†	0.0	69	0.0	0.0	–†	1.4
Ciprofloxacin	95	2.1	3.2	2.1	3.2	69	2.9	2.9	2.9	2.9
Meropenem	96	0.0	1.0	1.0	0.0	69	1.4	5.8	2.9	2.9
Klebsiella oxytoca										
Amoxicillin–clavulanic acid (2:1 ratio)#	168	1.2	6.5	–*	–*	66	6.1	12.1	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	50	–*	–*	–†	8.0	25	–*	–*	–†	16.0
Piperacillin–tazobactam	218	0.5	7.8	–†	8.7	93	1.1	18.3	–†	21.5
Ceftriaxone	219	0.5	5.5	0.5	5.5	93	1.1	11.8	1.1	11.8
Ceftazidime	219	0.5	1.4	0.5	1.8	93	0.0	2.2	1.1	2.2
Cefepime	219	0.9§	0.0	2.3	0.0	93	1.1§	1.1	2.2	1.1
Gentamicin	219	0.0	1.4	–†	1.8	93	0.0	2.2	–†	2.2
Tobramycin	216	0.5	0.5	–†	1.9	92	0.0	2.2	–†	2.2
Amikacin	219	0.0	0.0	–†	0.0	93	0.0	0.0	–†	0.0
Ciprofloxacin	218	0.5	0.5	0.5	0.5	93	0.0	1.1	0.0	1.1
Meropenem	219	0.0	0.5	0.0	0.5	93	0.0	2.2	0.0	2.2
Klebsiella pneumoniae complex										
Amoxicillin–clavulanic acid (2:1 ratio)#	767	2.7	2.1	–*	–*	263	5.3	9.1	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	270	–*	–*	–†	11.1	107	–*	–*	–†	18.7
Piperacillin–tazobactam	1,046	2.2	2.2	–†	7.0	379	2.6	8.2	–†	16.1
Cefazolin	927	–*	9.4	90.6	9.4	319	–*	16.9	83.1	16.9
Cefuroxime	92	3.3	5.4	91.3	8.7	47	4.3	10.6	85.1	14.9
Ceftriaxone	1,049	0.2	6.3	0.2	6.3	379	0.0	8.4	0.0	8.4
Ceftazidime	1,049	1.2	4.0	1.2	5.2	379	1.3	6.6	4.0	7.9
Cefepime	1,049	0.5§	1.4	3.4	1.7	379	1.3§	3.2	3.4	3.7

Species and antimicrobial	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
	No.	I	R	S, IE	R	No.	I	R	S, IE	R
Gentamicin	1,048	0.2	2.8	–†	3.0	379	0.3	3.7	–†	4.2
Tobramycin	1,042	1.4	1.3	–†	3.1	372	2.4	3.2	–†	5.6
Amikacin	1,049	0.0	0.1	–†	0.2	379	0.3	0.5	–†	1.3
Ciprofloxacin	1,043	3.5	6.9	3.5	6.9	378	5.0	10.3	5.0	10.3
Meropenem	1,049	0.1	0.4	0.0	0.4	378	0.3	0.8	0.3	0.5
Proteus mirabilis										
Ampicillin	289	0.7	16.3	–†	17.0	64	1.6	25.0	–†	26.6
Amoxicillin–clavulanic acid (2:1 ratio)#	215	7.9	4.2	–*	–*	47	10.6	6.4	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	73	–*	–*	–†	2.7	16	–*	–*	–†	0.0
Piperacillin–tazobactam	289	0.0	0.0	–†	0.0	64	0.0	0.0	–†	0.0
Ceftriaxone	289	1.0	1.7	1.0	1.7	64	0.0	3.1	0.0	3.1
Ceftazidime	288	0.3	0.7	1.7	1.0	63	1.6	3.2	0.0	4.8
Cefepime	289	1.0§	0.7	1.0	0.7	64	0.0§	3.1	0.0	3.1
Gentamicin	288	1.4	1.4	–†	6.9	64	4.7	4.7	–†	10.9
Tobramycin	288	1.0	1.4	–†	5.6	64	4.7	3.1	–†	9.4
Amikacin	289	0.3	0.0	–†	1.0	64	0.0	0.0	–†	3.1
Ciprofloxacin	288	0.7	2.4	0.7	2.4	63	0.0	7.9	0.0	7.9
Meropenem	289	0.0	0.3	0.3	0.0	63	0.0	0.0	0.0	0.0
Pseudomonas aeruginosa										
Piperacillin–tazobactam	466	7.3	4.1	88.6	11.4	322	8.4	8.7	82.9	17.1
Ceftazidime	466	2.1	4.1	93.8	6.2	324	4.9	7.7	87.3	12.7
Cefepime	466	2.4	2.6	95.1	4.9	321	2.5	4.7	92.8	7.2
Tobramycin	464	0.2	0.0	–†	0.6	322	0.0	0.6	–†	1.2
Amikacin	464	0.6	0.2	–†	0.9	321	0.9	0.3	–†	1.2
Ciprofloxacin	465	3.4	4.1	92.5	7.5	324	3.1	4.6	92.3	7.7
Meropenem	466	2.6	1.7	3.2	1.1	323	5.9	4.3	6.8	3.4
Salmonella species (non-typhoidal)										
Ampicillin	126	0.0	4.8	–†	4.8	12	0.0	0.0	–†	0.0
Amoxicillin–clavulanic acid (2:1 ratio)#	85	0.0	0.0	–*	–*	9	n/a	n/a	–*	–*
Amoxicillin–clavulanic acid (fixed ratio IV)	41	–*	–*	–†	0.0	3	–*	–*	–†	n/a
Piperacillin–tazobactam	126	0.0	0.0	–†	0.0	12	0.0	0.0	–†	0.0
Ceftriaxone	126	0.0	1.6	0.0	1.6	12	0.0	0.0	0.0	0.0
Ceftazidime	126	0.0	2.4	0.0	2.4	12	0.0	0.0	0.0	0.0
Cefepime	126	0.0§	1.6	0.0	1.6	12	0.0§	0.0	0.0	0.0
Ciprofloxacin‡	123	6.5	12.2	–†	18.7	11	0.0	0.0	–†	0.0
Meropenem	126	0.0	0.0	0.0	0.0	12	0.0	0.0	0.0	0.0
Serratia marcescens										
Piperacillin–tazobactam	114	0.0	0.0	–†	0.0	74	2.7	1.4	–†	4.1
Ceftriaxone	142	0.7	1.4	0.7	1.4	97	0.0	6.2	0.0	6.2
Ceftazidime	142	0.0	0.0	0.0	0.0	97	0.0	1.0	1.0	1.0
Cefepime	142	0.0§	0.0	0.0	0.0	97	0.0§	0.0	1.0	0.0
Gentamicin	142	0.0	0.0	–†	1.4	97	0.0	1.0	–†	3.1
Tobramycin	140	15.0	0.7	–†	35.7	90	13.3	1.1	–†	36.7

Species and antimicrobial	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
	No.	I	R	S, IE	R	No.	I	R	S, IE	R
Amikacin	142	0.7	0.0	–†	1.4	97	0.0	0.0	–†	0.0
Ciprofloxacin	140	1.4	1.4	1.4	1.4	97	1.0	2.1	1.0	2.1
Meropenem	142	0.0	0.0	0.0	0.0	97	0.0	1.0	0.0	1.0
Staphylococcus aureus										
Benzylpenicillin§§	2,597	–†	79.7	–†	79.7	771	–†	83.3	–†	83.3
Cefoxitin (methicillin)##	2,636	–†	15.6	–†	15.6	786	–†	17.7	–†	17.7
Ciprofloxacin	2,623	0.6	6.6	92.8	7.2	778	0.4	9.1	90.5	9.5
Clindamycin (constitutive)	2,621	0.0	3.8	0.0	4.0	779	0.0	2.6	0.0	2.7
Clindamycin (constitutive + inducible resistance)	2,621	0.0	14.0	0.0	14.9	779	0.0	12.8	0.0	14.0
Daptomycin	2,630	0.1***	–†	–†	0.1	782	0.3***	–†	–†	0.3
Erythromycin	2,595	27.3	16.6	–†	17.8	772	29.8	16.7	–†	18.5
Fusidic acid	2,595	–*	–*	–†	2.6	771	–*	–*	–†	3.1
Gentamicin	2,612	1.1	2.0	–†	5.9	771	2.2	1.9	–†	6.0
Linezolid	2,630	–†	0.0	–†	0.0	782	–†	0.0	–†	0.0
Mupirocin (high-level) ‡†	1,835	–†	1.9	–†	1.9	537	–†	2.2	–†	2.2
Rifampicin	2,620	0.0	0.3	–†	1.2§§§	776	0.1	0.5	–†	1.6
Teicoplanin	2,630	0.0	0.0	–†	0.1	781	0.0	0.0	–†	0.3
Tetracycline/doxycycline###	2,618	0.1	4.0	–†	4.7	779	0.0	4.9	–†	5.4
Trimethoprim–sulfamethoxazole****	2,608	0.2	0.8	0.1	0.8	771	0.0	0.9	0.0	0.9
Vancomycin	2,627	0.0	0.0	–†	0.0	782	0.0	0.0	–†	0.0

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate; IV = intravenous; n/a = not applicable, insufficient numbers (<10) to calculate percentage; No. = number of isolates; R = resistant; S, IE = susceptible, increased exposure

* No guidelines for indicated species
† No category defined
§ Includes susceptible dose dependent category for CLSI
# For susceptibility testing purposes, EUCAST fixes the concentration of clavulanic acid at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines
** The cefazolin concentration range available on the Vitek® card used restricts the ability to accurately identify CLSI susceptible and intermediate categories
‡ The ciprofloxacin concentration range available on the Vitek® card used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. Results of MIC gradient strips, where available, were provided
§§ Benzylpenicillin resistance including β-lactamase producers
Resistance as determined by cefoxitin screen (Vitek®) or cefoxitin MIC (Phoenix™)
*** Non-susceptible, resistance not defined
‡† Mupirocin high-level resistance screen
§§§ The rifampicin concentration range on the Phoenix™ card and Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility for EUCAST (community-onset, *n* = 936; hospital-onset, *n* = 306)
The doxycycline concentration range available on the Phoenix™ card used restricts the ability to accurately identify CLSI intermediate and resistant categories for *S. aureus*
**** Trimethoprim–sulfamethoxazole resistance, as determined by Vitek® or Phoenix™, confirmed by disc diffusion

3.8. Multi-drug resistance

The most problematic pathogens are those with multiple acquired resistances. The definitions proposed by Magiorakos et al.[51] were applied in this survey, where multi-drug resistance was defined as resistance to at least one agent in three or more antimicrobial categories. For each species, antimicrobials were excluded from the count if natural resistance mechanisms are present.

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

Multiple acquired resistances for key species are shown in Tables 15 to 20. The agents included for each species are listed in the notes after each table. For other common species, refer to Appendix D.

Enterococci have expected resistant phenotypes to several antimicrobial categories and any additional acquired resistance severely limits the number of treatment options. The limited range of antimicrobials available on the test panels limits the ability to determine multiple acquired resistance in *E. faecalis* and *E. faecium*. Vancomycin-resistant *E. faecium* are included in the WHO high-priority category list,[52] and are listed as a serious threat to public health by the CDC.[42] They have also been identified as a major AMR threat in Australian healthcare facilities.[53]

Table 15: Multiple acquired resistance in *Enterobacter cloacae* complex, by state and territory, AGAR, 2023

State or territory	Total	Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)				
		0	1	2	%	3	4	5	6	%
NSW	175	106	17	34	89.7	6	5	6	1	10.3
Vic	126	91	5	19	91.3	5	2	3	1	8.7
Qld	95	62	17	15	98.9	1	0	0	0	1.1
SA	36	21	5	9	97.2	1	0	0	0	2.8
WA	74	55	4	13	97.3	2	0	0	0	2.7
Tas	14	6	5	3	–*	0	0	0	0	–*
NT	9	5	1	1	–*	1	1	0	0	–*
ACT	22	19	0	2	–*	1	0	0	0	–*
Total	**551**	**365**	**54**	**96**	**93.5**	**17**	**8**	**9**	**2**	**6.5**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Insufficient numbers (<30) to calculate percentage
Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Enterobacter cloacae* complex includes *E. hormaechei* (*n* = 54), *E. kobei* (*n* = 6), *E. ludwigii* (*n* = 4), *E. bugandensis* (*n* = 2), and *E. asburiae* (*n* = 2).

Table 16: Multiple acquired resistance in *Escherichia coli*, by state and territory, AGAR, 2023

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)							
		0	1	2	%	3	4	5	6	7	8	9	%
NSW	1,714	729	290	249	74.0	121	124	135	45	15	3	3	26.0
Vic	1,074	449	226	136	75.5	85	83	45	34	9	6	1	24.5
Qld	830	359	145	149	78.7	55	56	43	14	6	3	0	21.3
SA	379	173	78	61	82.3	21	10	22	10	4	0	0	17.7
WA	901	390	153	134	75.1	65	52	61	33	7	6	0	24.9
Tas	157	84	36	18	87.9	12	4	2	1	0	0	0	12.1
NT	192	53	21	40	59.4	23	21	20	12	1	1	0	40.6
ACT	182	86	30	12	70.3	25	14	11	4	0	0	0	29.7
Total	**5,429**	**2323**	**979**	**799**	**75.5**	**407**	**364**	**339**	**153**	**42**	**19**	**4**	**24.5**

MDR = multi-drug resistant; resistant to at least one agent in three or more antimicrobial groups
Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), non-extended-spectrum cephalosporins (cefazolin or cefuroxime), and aminopenicillins (ampicillin).

Table 17: Multiple acquired resistance in *Klebsiella pneumoniae* complex isolates, by state and territory, AGAR, 2023

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)						
		0	1	2	%	3	4	5	6	7	8	%
NSW	417	318	32	30	91.1	11	10	5	8	0	3	8.9
Vic	295	219	25	13	87.1	14	8	4	9	3	0	12.9
Qld	254	196	25	17	93.7	2	11	1	1	0	1	6.3
SA	81	62	9	4	92.6	3	0	3	0	0	0	7.4
WA	203	167	11	15	95.1	3	4	1	1	0	1	4.9
Tas	25	23	1	0	–*	1	0	0	0	0	0	–*
NT	42	27	6	2	83.3	2	3	0	2	0	0	16.7
ACT	56	46	1	3	89.3	1	2	2	0	1	0	10.7
Total	**1,373**	**1058**	**110**	**84**	**91.2**	**37**	**38**	**16**	**21**	**4**	**5**	**8.8**

MDR = multi-drug resistant; resistant to at least one agent in three or more antimicrobial groups
* Insufficient numbers (<30) to calculate percentage
Notes:
1. Antimicrobial categories (agents) are aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and non-extended-spectrum cephalosporins (cefazolin or cefuroxime).
2. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 114) and *K. quasipneumoniae* (*n* = 6).

Table 18: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, AGAR, 2023

State or territory		Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)			
	Total	0	1	2	%	3	4	5	%
NSW	216	171	22	14	95.8	9	0	0	4.2
Vic	127	98	10	10	92.9	6	3	0	7.1
Qld	177	135	28	11	98.3	3	0	0	1.7
SA	78	68	6	2	97.4	2	0	0	2.6
WA	107	96	7	2	98.1	2	0	0	1.9
Tas	30	22	6	1	96.7	0	0	1	3.3
NT	22	17	2	1	–*	2	0	0	–*
ACT	25	22	0	2	–*	1	0	0	–*
Total	**782**	**629**	**81**	**43**	**96.3**	**25**	**3**	**1**	**3.7**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Insufficient numbers (<30) to calculate percentage
Note: Antimicrobial categories (agents) were aminoglycosides (tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftazidime), fluoroquinolones (ciprofloxacin).

Table 19: Multiple acquired resistance in *Staphylococcus aureus* (methicillin-resistant), by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)									
	Total	0	1	2	%	3	4	5	6	7	8	9	10	11	%
NSW	179	72	26	27	69.8	28	10	7	8	0	1	0	0	0	30.2
Vic	74	30	17	8	74.3	11	5	3	0	0	0	0	0	0	25.7
Qld	87	52	12	13	88.5	4	2	2	2	0	0	0	0	0	11.5
SA	27	11	8	3	–*	3	2	0	0	0	0	0	0	0	–*
WA	81	42	17	15	91.4	3	2	2	0	0	0	0	0	0	8.6
Tas	12	3	2	6	–*	1	0	0	0	0	0	0	0	0	–*
NT	52	39	3	8	96.2	2	0	0	0	0	0	0	0	0	3.8
ACT	12	3	3	4	–*	0	2	0	0	0	0	0	0	0	–*
Total	**524**	**252**	**88**	**84**	**80.9**	**52**	**23**	**14**	**10**	**0**	**1**	**0**	**0**	**0**	**19.1**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Insufficient numbers (<30) to calculate percentage
Note: Antimicrobials were aminoglycosides (gentamicin), ansamycins (rifampicin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), fucidanes (fusidic acid), glycopeptides (vancomycin or teicoplanin), lincosamides (clindamycin), lipopeptides (daptomycin), macrolides (erythromycin), oxazolidinones (linezolid), and tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™).

Table 20: Multiple acquired resistance in *Staphylococcus aureus* (methicillin-susceptible), by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)									
	Total	0	1	2	%	3	4	5	6	7	8	9	10	11	%
NSW	866	670	78	86	96.3	29	2	1	0	0	0	0	0	0	3.7
Vic	520	414	48	42	96.9	16	0	0	0	0	0	0	0	0	3.1
Qld	506	355	57	62	93.7	29	3	0	0	0	0	0	0	0	6.3
SA	197	155	23	15	98.0	2	2	0	0	0	0	0	0	0	2.0
WA	406	322	30	33	94.8	19	2	0	0	0	0	0	0	0	5.2
Tas	150	121	7	17	96.7	5	0	0	0	0	0	0	0	0	3.3
NT	67	43	9	3	82.1	11	0	1	0	0	0	0	0	0	17.9
ACT	83	63	10	8	97.6	2	0	0	0	0	0	0	0	0	2.4
Total	**2,795**	**2143**	**262**	**266**	**95.6**	**113**	**9**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**4.4**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
Note: Antimicrobials were aminoglycosides (gentamicin), ansamycins (rifampicin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), fucidanes (fusidic acid), glycopeptides (vancomycin or teicoplanin), lincosamides (clindamycin), lipopeptides (daptomycin), macrolides (erythromycin), oxazolidinones (linezolid), and tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™).

Nationally, 54.4% of all *E. coli* isolates were resistant to at least one of five key antimicrobial categories (aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 21). For *K. pneumoniae* complex, 11.5% were resistant to at least one antimicrobial group (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 22). For *P. aeruginosa,* 19.6% were resistant to at least one antimicrobial group (piperacillin–tazobactam, fluoroquinolones, ceftazidime, aminoglycosides and carbapenems) (Table 23). For *S. aureus*, the most common resistance combination was resistance to methicillin and fluoroquinolones (Table 24).

Table 21: Resistance combinations among *Escherichia coli* tested against aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems, AGAR, 2023

Resistance pattern	Number	% of total*
Fully susceptible	2,566	45.6
Single resistance	1,924	34.2
Aminopenicillins	1,810	32.1
Fluoroquinolones	96	1.7
Aminoglycosides	18	0.3
Resistance to two antimicrobial categories	510	9.1
Aminopenicillins + third-generation cephalosporins	230	4.1
Aminopenicillins + fluoroquinolones	188	3.3
Aminopenicillins + aminoglycosides	88	1.6
Fluoroquinolones + aminoglycosides	4	<0.1
Resistance to three antimicrobial categories	443	7.9
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	238	4.2
Aminopenicillins + third-generation cephalosporins + aminoglycosides	102	1.8
Aminopenicillins + fluoroquinolones + aminoglycosides	101	1.8
Aminopenicillins + third-generation cephalosporins + carbapenems	2	<0.1
Resistance to four antimicrobial categories	184	3.3
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	181	3.2
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + carbapenems	2	<0.1
Aminopenicillins + third-generation cephalosporins + aminoglycosides + carbapenems	1	<0.1
Resistance to five antimicrobial categories	4	<0.1
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	4	<0.1

Note: Only data from isolates tested against all five antimicrobial categories were included (n = 5,631).

Table 22: Resistance combinations among *Klebsiella pneumoniae* complex tested against fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems, AGAR, 2023

Resistance pattern	Number	% of total
Fully susceptible	1,256	88.5
Single resistance	82	5.8
Fluoroquinolones	44	3.1
Third-generation cephalosporins	33	2.3
Aminoglycosides	5	0.4
Resistance to two antimicrobial categories	45	3.2
Third-generation cephalosporins + fluoroquinolones	28	2.0
Third-generation cephalosporins + aminoglycosides	13	0.9
Fluoroquinolones + aminoglycosides	3	0.2
Third-generation cephalosporins + carbapenems	1	<0.1
Resistance to three antimicrobial categories	31	2.2
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	31	2.2
Resistance to four antimicrobial categories	5	0.4
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	5	0.4

Notes:
1. Only data from isolates tested against all four antimicrobial categories were included (*n* = 1,419).
2. *K. pneumoniae* complex includes *K. variicola* (*n* = 121) *and K. quasipneumoniae* (*n* = 7).

Table 23: Resistance combinations among *Pseudomonas aeruginosa* tested against piperacillin–tazobactam, ceftazidime, ciprofloxacin, aminoglycosides and meropenem, AGAR, 2023

Resistance pattern	Number	% of total
Fully susceptible	629	80.4
Single resistance	81	10.4
Piperacillin–tazobactam	39	5.0
Ciprofloxacin	34	4.3
Ceftazidime	4	0.5
Aminoglycosides	2	0.3
Meropenem	2	0.3
Resistance to two antimicrobial categories	43	5.5
Piperacillin–tazobactam + ceftazidime	36	4.6
Piperacillin–tazobactam + ciprofloxacin	2	0.3
Piperacillin–tazobactam + meropenem	2	0.3
Ciprofloxacin + aminoglycosides	1	0.1
Ceftazidime + meropenem	1	0.1
Piperacillin–tazobactam + aminoglycosides	1	0.1
Resistance to three antimicrobial categories	25	3.2
Piperacillin–tazobactam + ceftazidime + ciprofloxacin	17	2.2
Piperacillin–tazobactam + ceftazidime + meropenem	5	0.6
Ceftazidime + aminoglycosides + meropenem	1	0.1
Piperacillin–tazobactam + ciprofloxacin + meropenem	1	0.1
Piperacillin–tazobactam + ciprofloxacin + aminoglycosides	1	0.1
Resistance to four antimicrobial categories	3	0.4
Piperacillin–tazobactam + ceftazidime + ciprofloxacin + meropenem	3	0.4
Resistance to five antimicrobial categories	1	0.1
Piperacillin–tazobactam + ceftazidime + ciprofloxacin + aminoglycosides + meropenem	1	0.1

Note: Only data from isolates tested against all five antimicrobial categories were included (*n* = 782).

Table 24: Resistance combinations among *Staphylococcus aureus* tested against methicillin, ciprofloxacin and rifampicin, AGAR, 2023

Resistance pattern	N	% of total
Fully susceptible	2,709	81.6
Single resistance	437	13.2
Methicillin	351	10.6
Ciprofloxacin	75	2.3
Rifampicin	11	0.3
Resistance to two antimicrobial categories	171	5.2
Methicillin + ciprofloxacin	168	5.1
Methicillin + rifampicin	3	<0.1
Resistance to three antimicrobial categories	2	<0.1
Methicillin + ciprofloxacin + rifampicin	2	<0.1

Note: Only data from isolates tested against all five antimicrobial categories were included (*n* = 3,319).

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

Multi-drug resistances by onset setting (community or hospital) and 30-day all-cause mortality for the most common species are shown in Table 25.

E. coli had a significantly higher 30-day all-cause mortality for hospital-onset than community-onset bacteraemia (hospital-onset 94/664, 14.2%; community-onset 264/2,894, 9.1%, $P < 0.01$). In *P. aeruginosa*, there was a significant association between multidrug-resistance and 30-day all-cause mortality for hospital-onset bacteraemia (MDR: 6/13, 46.2%; non-MDR: 45/247, 18.2%, $P = 0.0242$).

Table 25: Multi-drug resistance, by onset setting and 30-day all-cause mortality, AGAR, 2023

Species	Category	Total		Community-onset		Hospital-onset	
		Number	Deaths, % (n)	Number	Deaths,% (n)	Number	Deaths, % (n)
Enterobacter cloacae complex	Total	389	15.2 (59)	192	14.1 (27)	197	16.2 (32)
	Non-MDR (≤2)	364	14.3 (52)	184	13.0 (24)	180	15.6 (28)
	MDR (>2)	25	28.0 (7)	8	37.5 (3)	17	23.5 (4)
Escherichia coli	Total	3,558	10.1 (358)	2,894	**9.1 (264)**	664	**14.2 (94)**
	Non-MDR (≤2)	2,657	9.9 (263)	2,215	9.1 (201)	442	14.0 (62)
	MDR (>2)	901	10.5 (95)	679	9.3 (63)	222	14.4 (32)
Klebsiella pneumoniae complex	Total	966	13.4 (129)	671	12.7 (85)	295	14.9 (44)
	Non-MDR (≤2)	864	13.3 (115)	610	12.6 (77)	254	15.0 (38)
	MDR (>2)	102	13.7 (14)	61	13.1 (8)	41	14.6 (6)
Pseudomonas aeruginosa	Total	594	17.3 (103)	334	15.6 (52)	260	19.6 (51)
	Non-MDR (≤2)	570	17.0 (97)	323	16.1 (52)	247	**18.2 (45)**
	MDR (>2)	24	25.0 (6)	11	0.0 (0)	13	**46.2 (6)**
Staphylococcus aureus	Total	2,597	16.6 (431)	1,987	16.2 (321)	610	19.3 (110)
	Non-MDR (≤2)	2,088	16.9 (353)	1,604	16.3 (262)	484	18.8 (91)
	MDR (>2)	509	15.3 (78)	383	15.4 (59)	126	21.0 (19)

MDR = multidrug-resistant; resistant to at least one agent in three or more antimicrobial groups. The agents included for each species are listed in the notes after each table (Tables 15 to 20)

Blue text indicates a significant association between place of onset and death (Fisher's exact test, $P < 0.01$).
Bold text indicates a significant association between MDR and death (Fisher's exact test, $0.01 < P < 0.05$).

Notes:
1. Antimicrobial categories (agents) for each species are listed under Tables 15 to 20. For *Staphylococcus aureus,* anti-staphylococcal β-lactams (cefoxitin) is also included.
2. *Enterobacter cloacae* complex includes *E. hormaechei* (*n* = 45), *E. kobei* (*n* = 5), *E. ludwigii* (*n* = 3), *E. bugandensis* (*n* = 2), and *E. asburiae* (*n* = 2).
3. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 91) and *K. quasipneumoniae* (*n* = 3).

3.9. PCR and whole genome sequencing

This section describes the molecular epidemiology of *E. faecium* and MRSA, and the resistance mechanisms of Gram-negative organisms identified by WGS in the 2023 dataset. The benefits of this method include increased accuracy in detecting the genetic mechanisms for AMR and clarifying the underlining epidemiology. Molecular methods also detect *van* genes in vancomycin variable enterococci which are vancomycin-susceptible enterococci harbouring *van* genes.

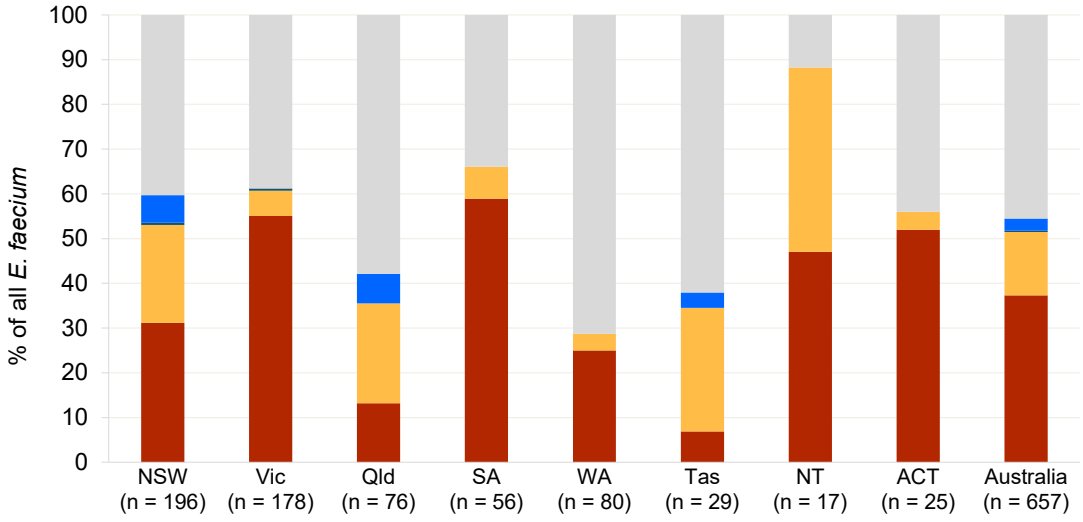
Molecular epidemiology of *Enterococcus faecium*

van genes

Results of PCR testing for *vanA* and *vanB* genes were available for 639 (97.3%) of the 657 *E. faecium* isolates. *van* genes were detected in 340/639 (53.2%) of *E. faecium*; *vanA* in 93 (14.6%), *vanB* in 245 (38.3%), or *vanA* plus *vanB* in 2 (0.3%) (Figure 9).

For vancomycin-resistant *E. faecium* (MIC > 4 mg/L), *vanA* was detected in 87/324 (26.9%), *vanB* in 235 (72.5%), and both *vanA* and *vanB* in 2 (0.6%). In 16 of 315 (5.1%) vancomycin-susceptible *E. faecium*, *van* genes were detected: 10 with *vanB* and six with *vanA*. All 16 isolates had vancomycin MIC ≤ 4 mg/L.

Figure 9: Vancomycin genotype of *Enterococcus faecium* isolates, by state and territory, and nationally, AGAR, 2023



	NSW (n = 196)	Vic (n = 178)	Qld (n = 76)	SA (n = 56)	WA (n = 80)	Tas (n = 29)	NT (n = 17)	ACT (n = 25)	Australia (n = 657)
Not detected (n = 299)	40.3	38.8	57.9	33.9	71.3	62.1	11.8	44.0	45.5
Not determined (n = 18)	6.1	0.0	6.6	0.0	0.0	3.4	0.0	0.0	2.7
vanA and vanB (n = 2)	0.5	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.3
vanA (n = 93)	21.9	5.6	22.4	7.1	3.8	27.6	41.2	4.0	14.2
vanB (n = 245)	31.1	55.1	13.2	58.9	25.0	6.9	47.1	52.0	37.3

Note: vancomycin genotype as detected by WGS, or PCR performed by the participating laboratory

Multi-locus sequence type

Of the 657 *E. faecium* isolates reported, 610 (92.8%) were available for typing by WGS (Table 26). Based on the MLST, 58 sequence types were identified. Overall, 85.7% of *E. faecium* could be characterised into seven major sequence types (10 or more isolates): ST78 (*n* = 141); ST1424 (*n* = 113); ST17, (*n* = 96); ST780 (*n* = 70); ST796 (*n* = 47); ST1421 (*n* = 37); and ST555 (*n* = 19). There were 37 sequence types with a single isolate.

ST78 was the predominant sequence type in Victoria, SA and the ACT; ST1424 in Tasmania; ST17 in WA; and ST1421 in the NT. ST78 and ST1424 were the dominant sequence types in NSW; and ST1424 and ST17 in Queensland.

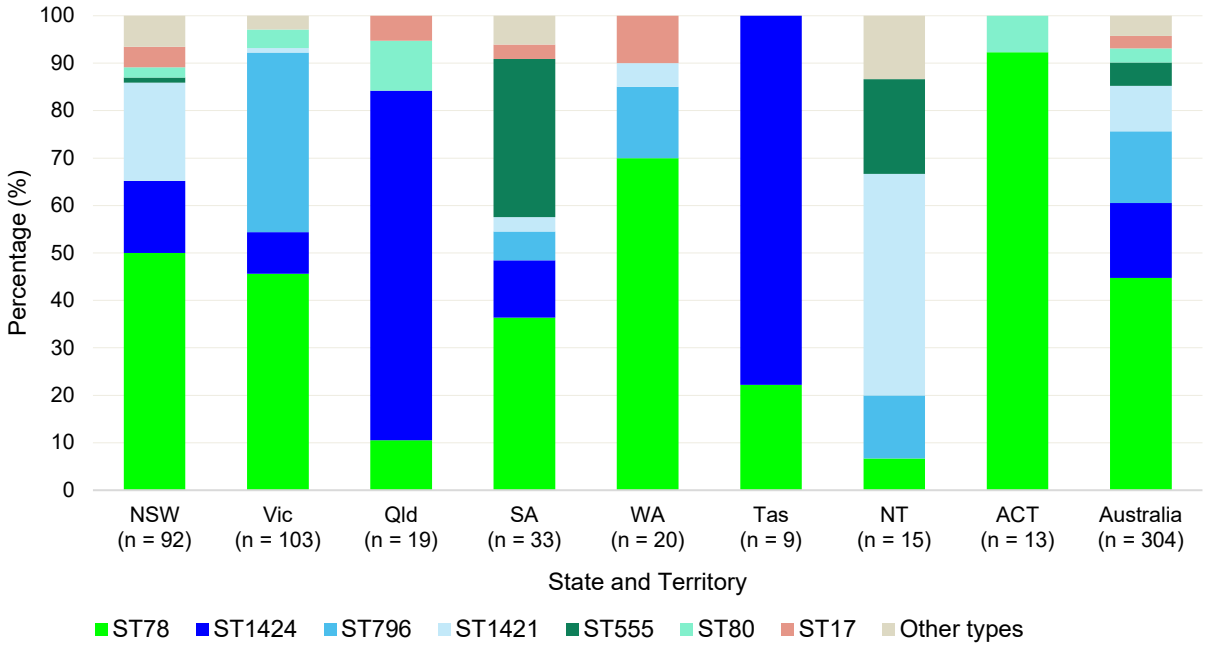
The distribution of vancomycin-resistant *E. faecium* sequence types throughout Australian states and territories are shown in Figure 10.

Table 26: *Enterococcus faecium* MLST, by state and territory, AGAR, 2023

	Percentage, % (*n*)								
MLST	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST78	28.5 (49)	27.5 (47)	4.7 (3)	22.2 (12)	19.0 (15)	7.1 (2)	5.9 (1)	48.0 (12)	23.1 (141)
ST1424	26.7 (46)	12.9 (22)	32.8 (21)	9.3 (5)	0.0 (0)	53.6 (15)	0.0 (0)	16.0 (4)	18.5 (113)
ST17	7.6 (13)	9.4 (16)	31.3 (20)	9.3 (5)	43.0 (34)	25.0 (7)	0.0 (0)	4.0 (1)	15.7 (96)
ST80	6.4 (11)	12.9 (22)	20.3 (13)	3.7 (2)	20.3 (16)	3.6 (1)	0.0 (0)	20.0 (5)	11.5 (70)
ST796	0.0 (0)	23.4 (40)	0.0 (0)	3.7 (2)	3.8 (3)	0.0 (0)	11.8 (2)	0.0 (0)	7.7 (47)
ST1421	12.8 (22)	0.6 (1)	3.1 (2)	3.7 (2)	2.5 (2)	0.0 (0)	41.2 (7)	4.0 (1)	6.1 (37)
ST555	0.6 (1)	0.6 (1)	0.0 (0)	24.1 (13)	1.3 (1)	0.0 (0)	17.6 (3)	0.0 (0)	3.1 (19)
ST117	17.4 (30)	12.9 (22)	7.8 (5)	24.1 (13)	10.1 (8)	10.7 (3)	23.5 (4)	8.0 (2)	14.3 (87)
Other types (*n* = 51)	28.5 (49)	27.5 (47)	4.7 (3)	22.2 (12)	19.0 (15)	7.1 (2)	5.9 (1)	48.0 (12)	23.1 (141)
Total	**172**	**171**	**64**	**54**	**79**	**28**	**17**	**25**	**610**

MLST = multi-locus sequence type

Figure 10: Distribution of vancomycin-resistant *Enterococcus faecium* sequence types, by state and territory, AGAR, 2023



MLST and *van* genes

The *vanA* gene alone was detected in eight sequence types; ST1424 (*n* = 45), ST1421 (*n* = 31), ST817 (*n* = 3), ST17 (*n* = 2) and one each of ST80, ST375, ST761 and ST2220.

The *vanB* gene alone was detected in 13 sequence types: ST78 (*n* = 141), ST796 (*n* = 46), ST555 (*n* = 17), ST17 (*n* = 8), ST80 (n = 7), ST1424 (*n* = 4), ST2439 (*n* = 4), and one each of ST192, ST203, ST1421, ST2682, ST2693 and ST2690 (Table 27).

Both *vanA* and *vanB* genes were detected in two sequence types, ST80 and ST796.

Table 27: *Enterococcus faecium* MLST harbouring *van* genes, AGAR, 2023

	Percentage* (*n*)				
MLST	*vanA*	*vanB*	*vanA* + *vanB*	*van* genes not detected	Total, *n*
ST78	0.0 (0)	100.0 (141)	0.0 (0)	0.0 (0)	141
ST1424	39.8 (45)	3.5 (4)	0.0 (0)	56.6 (64)	113
ST17	2.1 (2)	8.3 (8)	0.0 (0)	89.6 (86)	96
ST80	1.4 (1)	10.0 (7)	1.4 (1)	87.1 (61)	70
ST796	0.0 (0)	97.9 (46)	2.1 (1)	0.0 (0)	47
ST1421	83.8 (31)	2.7 (1)	0.0 (0)	13.5 (5)	37
ST555	0.0 (0)	89.5 (17)	0.0 (0)	10.5 (2)	19
Other types (*n* =51)	6.9 (6)	10.3 (9)	0.0 (0)	82.8 (72)	87
Total	13.9 (85)	38.2 (233)	0.3 (2)	47.5 (290)	610

MLST = multi-locus sequence type
* Percentage of total with *van* genes

Linezolid resistance

Two linezolid-resistant *E. faecalis* from Victoria were confirmed. Both isolates harboured the *optrA* gene, had linezolid MIC = 6 mg/L and were vancomycin susceptible. One isolate was identified as ST16, the other ST86.

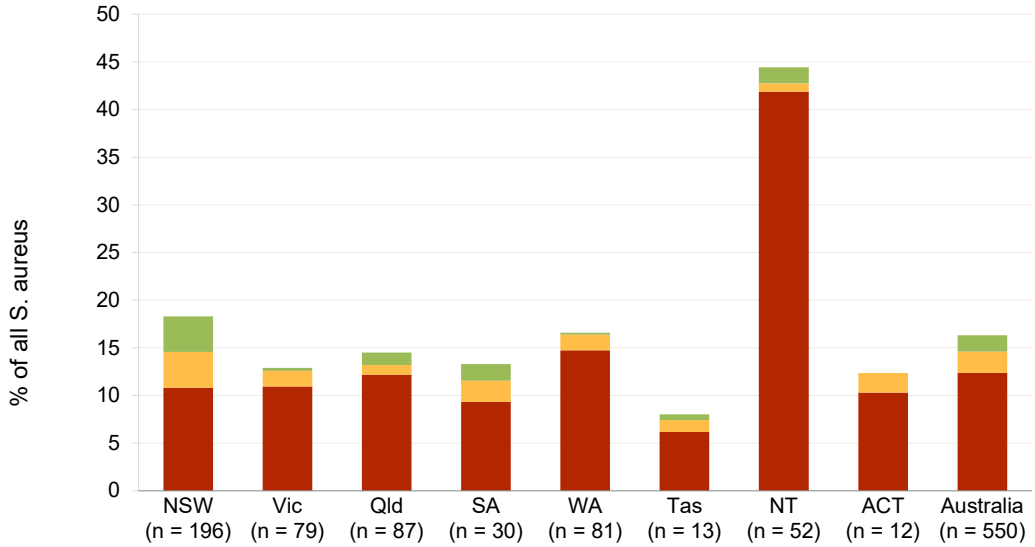
Daptomycin resistance

No daptomycin-resistant Enterococcus species were confirmed in the 2023 survey.

Molecular epidemiology of methicillin-resistant *Staphylococcus aureus*

Of the 550 MRSA reported, 491 (89.3%) were available for typing by WGS. There were marked differences among the states and territories in the percentage and types of MRSA clones. Prevalence of MRSA ranged from 8.0% (13/163) in Tasmania to 43.7% (52/119) in the NT (Figure 11).

Figure 11: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, AGAR, 2023



	NSW (n = 196)	Vic (n = 79)	Qld (n = 87)	SA (n = 30)	WA (n = 81)	Tas (n = 13)	NT (n = 52)	ACT (n = 12)	Australia (n = 550)
Not available (n = 59)	3.7	0.3	1.3	1.7	0.2	0.6	1.7	0.0	1.7
Healthcare associated (n = 74)	3.8	1.6	1.0	2.2	1.6	1.2	0.9	2.1	2.2
Community associated (n = 417)	10.8	10.9	12.2	9.3	14.8	6.2	41.9	10.3	12.4

MRSA = methicillin-resistant *Staphylococcus aureus*
Notes:
1. *S. aureus* were categorised as MRSA based on cefoxitin screen (Vitek®) or cefoxitin MIC (Phoenix™).
2. Fifty-nine MRSA were not available for whole genome sequencing to determine association.

Healthcare-associated MRSA

Based on the MLST and SCC*mec* type, three HA-MRSA clones were identified: ST22-IV (EMRSA-15), ST239-III (Aus 2/3 EMRSA), and ST9276-III (a single locus variant of ST239 (Table 28). PVL associated genes were not identified in HA-MRSA.

The most frequently isolated HA-MRSA clone, PVL-negative ST22-IV, was identified in all states and territories. ST239-III was only identified in NSW and Queensland (Table 29).

Community-associated MRSA

Based on the MLST and SCC*mec* type, 84 CA-MRSA clones were identified. There were 52 sequence types with a single isolate. PVL was detected in 28 CA-MRSA clones. Overall, 45.8% (191/417) of CA-MRSA were PVL positive (Table 30). The most frequently isolated CA-MRSA clone, ST93-IV (Qld CA-MRSA), was isolated in all states and territories.

Nine PVL positive ST22-IV isolates were identified: two each in Victoria, Tasmania and the ACT, and one each in NSW, Queensland, and the NT (data not shown). PVL positive ST22-IV are frequently isolated in the South Asian subcontinent; they are not related to EMRSA-15, and are not considered to be a HA-MRSA clone.[54]

Of the hospital-onset MRSA, 80.3% (98/122) were caused by CA-MRSA.

Table 28: MRSA clones, association, place of onset and PVL carriage, AGAR, 2023

Clone	Clonal complex	Total, *n*	Community-onset, % (*n*)*	Hospital-onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)	CC22	64	62.5 (40)	37.5 (24)	0.0 (0)
ST239-III (Aus2/3 EMRSA)	CC239	9	–† (9)	–† (0)	–† (0)
ST9276-III§	CC239	1	–† (1)	–† (0)	–† (0)
Total HA-MRSA		74	67.6 (50)	32.4 (24)	0.0 (0)
Community-associated					
ST93-IV (Qld CA-MRSA)	CC93	107	83.2 (89)	16.8 (18)	96.3 (103)
ST5-IV	CC5	41	85.4 (35)	14.6 (6)	43.9 (18)
ST1-IV (WA1 MRSA)	CC1	35	82.9 (29)	17.1 (6)	5.7 (2)
ST45-V	CC45	34	67.6 (23)	32.4 (11)	0.0 (0)
ST30-IV (SWP MRSA)	CC30	20	70.0 (14)	30.0 (6)	90.0 (18)
ST8-IV	CC8	17	70.6 (12)	29.4 (5)	82.4 (14)
ST6-IV	CC6	15	86.7 (13)	13.3 (2)	6.7 (1)
ST97-IV	CC97	13	76.9 (10)	23.1 (3)	0.0 (0)
ST953-IV	CC97	11	72.7 (8)	27.3 (3)	0.0 (0)
Other (*n* = 75)		124	69.4 (86)	30.6 (38)	28.2 (35)
Total CA-MRSA		417	76.5 (319)	23.5 (98)	45.8 (191)
MRSA		491	75.2 (369)	24.8 (122)	38.9 (191)

CC = clonal complex; MRSA = methicillin-resistant *Staphylococcus aureus*; PVL = Panton-Valentine leucocidin
* Percentage of the clone
† Insufficient numbers (<10) to calculate percentage
§ Single locus variant of ST239-III

Table 29: Healthcare-associated MRSA clones, by state and territory, AGAR, 2023

	Percentage (*n*)								
Clone	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15)	80.0 (32)	100.0 (10)	–* (4)	–* (5)	–* (8)	–* (2)	–* (1)	–* (2)	86.5 (64)
ST239-III (Aus2/3 EMRSA)	17.5 (7)	0.0 (0)	–* (2)	–* (0)	–* (0)	–* (0)	–* (0)	–* (0)	12.2 (9)
ST9276-III	2.5 (1)	0.0 (0)	–* (0)	–* (0)	–* (0)	–* (0)	–* (0)	–* (0)	1.4 (1)
Total	40	10	6	5	8	2	1	2	74

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

Table 30: Major community-associated MRSA clones (>10 isolates) by state and territory and PVL carriage, AGAR, 2023

	Percentage (*n*)								
Clone	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST93-IV (Qld CA-MRSA)	16.5 (19)	13.4 (9)	34.2 (25)	33.3 (7)	27.8 (20)	10.0 (1)	51.0 (25)	10.0 (1)	25.7 (107)
Number PVL positive	17	9	24	7	19	1	25	1	103
Number PVL negative	2	0	1	0	1	0	0	0	4
ST5-IV	6.1 (7)	6.0 (4)	11.0 (8)	14.3 (3)	12.5 (9)	0.0 (0)	18.4 (9)	10.0 (1)	9.8 (41)
Number PVL positive	1	1	1	0	6	0	9	0	18
Number PVL negative	6	3	7	3	3	0	0	1	23
ST45-V	7.0 (8)	4.5 (3)	12.3 (9)	4.8 (1)	11.1 (8)	20.0 (2)	8.2 (4)	0.0 (0)	8.4 (35)
Number PVL positive	0	0	1	0	1	0	0	0	2
Number PVL negative	8	3	8	1	7	2	4	0	33
ST1-IV	13.0 (15)	11.9 (8)	5.5 (4)	4.8 (1)	4.2 (3)	20.0 (2)	0.0 (0)	10.0 (1)	8.2 (34)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	15	8	4	1	3	2	0	1	34
ST30-IV	8.7 (10)	6.0 (4)	5.5 (4)	0.0 (0)	1.4 (1)	10.0 (1)	0.0 (0)	0.0 (0)	4.8 (20)
Number PVL positive	10	4	2	0	1	1	0	0	18
Number PVL negative	0	0	2	0	0	0	0	0	2
ST97-IV	7.8 (9)	7.5 (5)	2.7 (2)	4.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	4.1 (17)
Number PVL positive	8	3	2	1	0	0	0	0	14
Number PVL negative	1	2	0	0	0	0	0	0	3
ST953-IV	8.7 (10)	1.5 (1)	4.1 (3)	0.0 (0)	1.4 (1)	0.0 (0)	0.0 (0)	0.0 (0)	3.6 (15)
Number PVL positive	1	0	0	0	0	0	0	0	1
Number PVL negative	9	1	3	0	1	0	0	0	14
ST8-IV	4.3 (5)	7.5 (5)	2.7 (2)	0.0 (0)	0.0 (0)	0.0 (0)	2.0 (1)	0.0 (0)	3.1 (13)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	5	5	2	0	0	0	1	0	13
ST953-IV	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	15.3 (11)	0.0 (0)	0.0 (0)	0.0 (0)	2.6 (11)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	0	0	0	0	11	0	0	0	11
Other clones (*n* = 75)	27.8 (32)	41.8 (28)	21.9 (16)	38.1 (8)	26.4 (19)	40.0 (4)	20.4 (10)	70.0 (7)	29.7 (124)
Number PVL positive	7	10	4	1	3	2	5	3	35
Number PVL negative	25	18	12	7	16	2	5	4	89
Total	**115**	**67**	**73**	**21**	**72**	**10**	**49**	**10**	**417**
PVL positive	44	27	34	9	30	4	39	4	191
PVL negative	71	40	39	12	42	6	10	6	226

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

* Insufficient numbers (<10) to calculate percentage

Daptomycin resistance

Five isolates were confirmed as daptomycin-resistant. Two MRSA from NSW, both with daptomycin MIC = 4 mg/L, were ST22-IV carrying the V351E MprF mutation or ST45-V carrying the T345I MprF mutation. Three MSSA, one from Tasmania with a daptomycin MIC = 2 mg/L was ST9295 and carried the L341I MprF mutation, one from NSW (MIC = 4 mg/L) was ST97 and carried the L776S MprF mutation, and one from WA (MIC = 2 mg/L) was ST5. No mutations in known loci were detected in the WA isolate.[55, 56]

Gram-negative species

All referred Gram-negative isolates were sequenced and analysed for antimicrobial resistance mechanisms.

Third-generation cephalosporin resistance

Extended-spectrum β-lactamases

ESBLs are important because 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 often have co-resistance to other non-β-lactam agents. This can result in delays in the use of effective empirical therapy. The lack of available oral options for treatment can result in unnecessary hospitalisation and, in the setting of sepsis, increased mortality risk.

Initially, ESBLs were more common in *Klebsiella* species than in *E. coli*. The emergence of specific types of ESBLs (CTX-M enzymes) in *E. coli* from the community is part of a global epidemic.[9-11] It is unclear what is driving the community expansion of CTX-M ESBLs in Australia, as third-generation cephalosporins are not widely used in this setting; it is thought to be driven by cross-resistance and co-resistance to agents used in community practice. There is also increasing recognition that ESBLs are becoming established in long-term care facilities in Australia.[13] Returning travellers and visitors from high prevalence areas such as Asia, are also likely a factor.[7, 8]

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. Isolates with either ceftriaxone or ceftazidime MICs above 1 mg/L were referred and underwent sequencing.

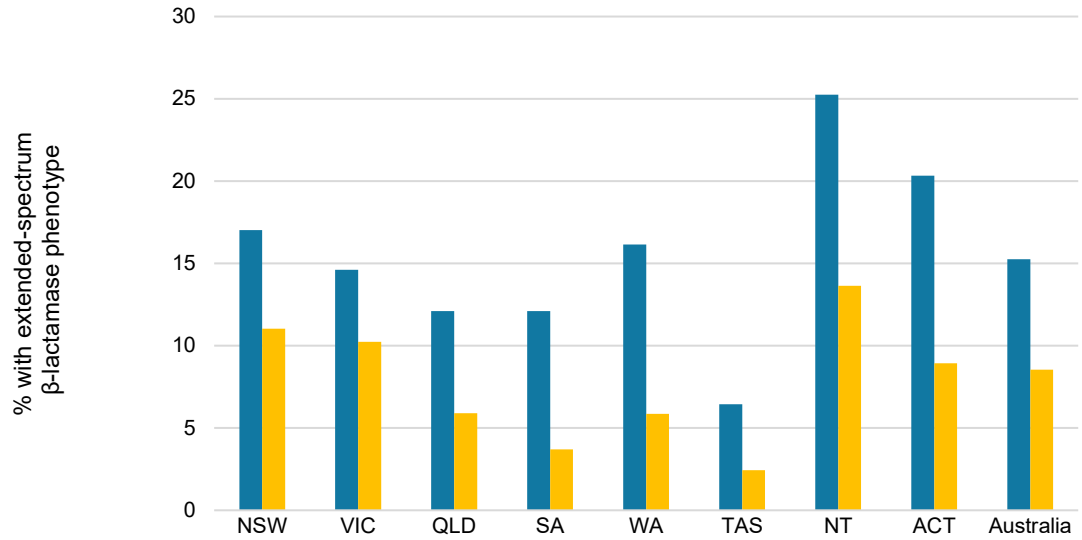
Neither ceftriaxone nor ceftazidime testing will identify ESBL production in *Enterobacter* species because of their intrinsic chromosomal AmpC β-lactamase. In *Enterobacter*, cefepime MICs of greater than 0.25 mg/L suggest that an isolate of this genus may harbour an ESBL.[57] However, due to the cefepime concentration range available on the susceptibility cards, isolates with a cefepime MIC of greater than 1 mg/L were referred and underwent sequencing.

Sequences of all referred isolates were screened for the presence of β-lactamase genes using methods outlined in Appendix B.

E. coli and *K. pneumoniae* complex isolates resistant to ceftriaxone and/or ceftazidime (MIC > 1 mg/L), and their variation across states and territories, are shown in Figure 12. An ESBL phenotype was more common among *E. coli* (861/5647, 15.2%) than *K. pneumoniae* complex (122/1428, 8.5%)

The percentage of *E. coli* with an ESBL phenotype was highest in the NT (25.3%, 49/194) and lowest in Tasmania (6.4%, 17/264). The percentage of *K. pneumoniae* complex with an ESBL phenotype ranged from 13.6% (6/44) in the NT, to 2.4% (1/41) in Tasmania.

Figure 12: Percentage of *Escherichia coli* and *Klebsiella pneumoniae* complex isolates with an extended-spectrum β-lactamase phenotype, by state and territory, and nationally, AGAR, 2023



	NSW	VIC	QLD	SA	WA	TAS	NT	ACT	Australia
E. coli, %	17.0	14.6	12.1	12.1	16.2	6.4	25.3	20.3	15.2
K. pneumoniae complex, %	11.0	10.2	5.9	3.7	5.9	2.4	13.6	8.9	8.5
E. coli (n = 5,647)	302	162	101	46	147	17	49	37	861
K. pneumoniae complex (n = 1,428)	49	31	15	3	12	1	6	5	122

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

An ESBL phenotype was significantly more prevalent among hospital-onset than community-onset episodes of *E. coli* (192/890 [21.6%] vs 669/4,757 [14.1%], $P < 0.0001$) and *K. pneumoniae* complex bacteraemia (47/379 [12.4%] vs 75/1,049 [7.1%], $P < 0.01$).

For 60 *E. cloacae* complex isolates with cefepime MIC >1 mg/L, 14 (23.3%; 2.5% overall) contained a non-intrinsic β-lactamase gene(s): ESBL only (*n* = 9), ESBL + carbapenemase (*n* = 3), or carbapenemase only (*n* = 2) (Table 31).

Almost one-quarter (5/22, 22.7%) of *K. oxytoca* isolates with a ceftriaxone-resistant phenotype carried an ESBL and/or a carbapenemase gene. The remainder are presumably hyperproducers of OXY, the natural chromosomal β-lactamase in this species, with characteristic resistance to piperacillin–tazobactam and borderline resistance to cefepime, but susceptibility to ceftazidime (data not shown).[58, 59]

Table 31: β-lactamase genes detected in *Enterobacterales* with extended-spectrum β-lactamase phenotype, AGAR, 2023

β-lactamase mechanism	*Escherichia coli*	*Klebsiella pneumoniae* complex	*Enterobacter cloacae* complex	*Proteus mirabilis*	*Klebsiella oxytoca*	*Salmonella* spp.†
Total	5,647	1,428	555	351	312	226
ESBL phenotype*, % (n)	15.2 (861)	8.5 (122)	12.2 (68)	4.0 (14)	8.3 (26)	1.8 (4)
β-lactamase genes confirmed/number tested (%)	753/791 (95.2)	97/110 (88.2)	14/60 (23.3)	6/11 (54.5)	5/22 (22.7)	1/2 (50.0)
ESBL	579	74	9	4	3	1
ESBL, AmpC	29	2	0	0	0	0
ESBL, AmpC, Carb	1	1	0	0	0	0
ESBL, Carb	5	2	3	0	1	0
AmpC	133	16	0	2	0	0
AmpC, Carb	3	1	0	0	0	0
Carb	3	1	2	0	1	0
Not detected	38	13	46	5	17	1
Not determined§	43	7	5	3	2	2

AmpC = plasmid-borne *ampC*; Carb = carbapenemase; ESBL = extended-spectrum β-lactamase
* ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L; for *E. cloacae* complex, cefepime MIC > 1 mg/L
† Non-typhoidal (*n* = 138), typhoidal (*n* = 88)
§ Isolate not available for confirmation

The β-lactamase genes confirmed in *Enterobacterales* with an ESBL phenotype are shown in Table 32. *bla*CTX-M genes continue to be the dominant β-lactamase genes in *E. coli*. Of 753 with confirmed β-lactamase gene(s), 609 (80.9%) had at least one *bla*CTX-M genes, either *bla*CTX-M group 1 (*n* = 296), *bla*CTX-M group 9 (*n* = 310), or *bla*CTX-M group 1 + *bla*CTX-M group 9 (*n* = 3). CTX-M group 1 types were dominant in SA, WA, and the ACT. CTX-M group 9 types were more prevalent in NSW, Queensland, and the NT.

Among *K. pneumoniae* complex isolates with confirmed β-lactamase genes, 78 of 97 (80.4%) contained a *bla*CTX-M gene: *bla*CTX-M group 1 (*n* = 65), or *bla*CTX-M group 9 (*n* = 13) (Table 32).

Table 32: β-lactamase genes among *Enterobacterales* with extended-spectrum β-lactamase phenotype, by state and territory, AGAR, 2023

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,774	1,108	835	380	910	264	194	182	5,647
ESBL phenotype*, % (*n*)	17.0 (302)	14.6 (162)	12.1 (101)	12.1 (46)	16.2 (147)	6.4 (17)	25.3 (49)	20.3 (37)	15.2 (861)
Confirmed β-lactamase genes/number tested	256/ 271	130/ 136	88/ 97	40/ 42	141/ 142	15/ 17	49/ 49	34/ 37	753/ 791
ESBL types	204	99	68	34	118	13	48	30	614
CTX-M-types	202	98	68	33	117	13	48	30	609
group 1	86	48	20	26	65	7	21	23	296
group 9	113	50	48	7	52	6	27	7	310
group 1 + group 9	3	0	0	0	0	0	0	0	3
SHV (ESBL types)	2	1	0	1	1	0	0	0	5
Plasmid-borne AmpC	64	38	24	8	23	2	2	5	166
CMY-2-like	15	11	9	2	9	0	0	4	50
DHA-1	49	27	15	6	14	2	2	1	116
Carbapenemases	6	3	1	0	2	0	0	0	12
OXA-48-like	2	2	0	0	1	0	0	0	5
NDM-5	2	1	0	0	1	0	0	0	4
NDM-7	1	0	0	0	0	0	0	0	1
IMP-4	0	0	1	0	0	0	0	0	1
NDM-5 + OXA-48-like	1	0	0	0	0	0	0	0	1
Klebsiella pneumoniae complex	444	303	254	81	205	41	44	56	1,428
ESBL phenotype*, % (*n*)	11.0 (49)	10.2 (31)	5.9 (15)	3.7 (3)	5.9 (12)	2.4 (1)	13.6 (6)	8.9 (5)	8.5 (122)
Confirmed β-lactamase genes/number tested	39/44	22/26	11/14	3/3	11/12	1/1	5/5	5/5	97/110
ESBL types	30	18	10	1	10	0	5	5	79
CTX-M-types	29	18	10	1	10	0	5	5	78
group 1	23	15	9	0	10	0	4	4	65
group 9	6	3	1	1	0	0	1	1	13
SHV (ESBL types)	2	1	0	0	0	0	0	1	4
Plasmid-borne AmpC	9	5	1	3	1	1	0	0	20
DHA-1	8	5	1	3	1	1	0	0	19
CMY-2-like	1	0	0	0	0	0	0	0	1
Carbapenemases	2	1	1	0	1	0	0	0	5
NDM-1	0	0	1	0	1	0	0	0	2
OXA-48-like	0	1	0	0	0	0	0	0	1
NDM-5 + OXA-48-like	1	0	0	0	0	0	0	0	1
KPC-2 + NDM-5 + OXA-48-like	1	0	0	0	0	0	0	0	1

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Enterobacter cloacae complex	176	129	96	36	75	14	9	22	557
ESBL phenotype*, % (*n*)	15.3 (27)	12.4 (16)	7.3 (7)	22.2 (8)	5.3 (4)	14.3 (2)	11.1 (1)	13.6 (3)	12.2 (68)
Confirmed β-lactamase genes/number tested (%)	6/22	5/14	0/7	0/8	1/4	0/1	1/1	1/3	14/60
ESBL types	5	4	0	0	1	0	1	1	12
CTX-M-types	1	3	0	0	1	0	1	1	7
group 1	1	2	0	0	1	0	0	1	5
group 9	0	1	0	0	0	0	1	0	2
SHV (ESBL types)	2	2	0	0	0	0	1	0	5
VEB	2	0	0	0	0	0	0	0	2
Carbapenemases	3	2	0	0	0	0	0	0	5
IMP-4	3	0	0	0	0	0	0	0	3
NDM-1	0	2	0	0	0	0	0	0	2

ESBL = extended-spectrum β-lactamase; n/a = Insufficient numbers (<10) to calculate percentage
* ESBL phenotype = ceftriaxone and/or ceftazidime MIC > 1 mg/L; for *E. cloacae* complex, cefepime MIC > 1 mg/L
Note: Isolates may possess more than one type of β-lactamase gene.

bla$_{\text{CTX-M}}$ genes were detected in 77.0% (609/791) of *E. coli* with an ESBL phenotype (Table 33). In the *bla*$_{\text{CTX-M-1}}$ group, *bla*$_{\text{CTX-M-15}}$ accounted for 90.6% (271/299). In the *bla*$_{\text{CTX-M-9}}$ group, *bla*$_{\text{CTX-M-27}}$ and *bla*$_{\text{CTX-M-14}}$ were the major genotypes, accounting for 87.4% (271/310) and 11.0% (34/310), respectively.

Table 33: *Escherichia coli*, CTX-M variants, ESBL phenotype, sequence type, AGAR, 2023

		Phenotype		Sequence type						
CTX-M variant	Number	ESBL	Non-ESBL	131	69	1193	73	38	-*	Other types (*n* = 107)
Not detected	275	182	93	12	49	11	18	10	19	156
CTX-M-1 group	296	296	0	109	19	26	29	11	11	91
bla$_{\text{CTX-M-15}}$	267	267	0	109	12	25	28	11	11	71
bla$_{\text{CTX-M-55}}$	19	19	0	0	4	1	0	0	0	14
bla$_{\text{CTX-M-3}}$	5	5	0	0	0	0	0	0	0	5
bla$_{\text{CTX-M-231}}$	3	3	0	0	3	0	0	0	0	0
bla$_{\text{CTX-M-1}}$	1	1	0	0	0	0	1	0	0	0
bla$_{\text{CTX-M-15}}$-like[†]	1	1	0	0	0	0	0	0	0	1
CTX-M-9 group	311	310	1	211	12	19	5	20	10	34
bla$_{\text{CTX-M-27}}$	270	270	0	197	10	19	4	12	8	20
bla$_{\text{CTX-M-14}}$	33	33	0	10	2	0	1	6	1	13
bla$_{\text{CTX-M-24}}$	4	4	0	0	0	0	0	2	1	1
bla$_{\text{CTX-M-27}}$-like[§]	1	1	0	1	0	0	0	0	0	0
bla$_{\text{CTX-M-174}}$	1	1	0	1	0	0	0	0	0	0
bla$_{\text{CTX-M-14}}$-like[#]	1	1	0	1	0	0	0	0	0	0
bla$_{\text{CTX-M-255}}$	1	0	1	1	0	0	0	0	0	0
CTX-M group 1 + group 9	3	3	0	3	0	0	0	0	0	0
bla$_{\text{CTX-M-15, CTX-M-27}}$	2	2	0	2	0	0	0	0	0	0
bla$_{\text{CTX-M-15, CTX-M-24}}$	1	1	0	1	0	0	0	0	0	0
	885	791	94	335	80	56	52	41	40	281

ESBL = extended-spectrum β-lactamase
* Not available
[†] *bla*$_{\text{CTX-M-15}}$-like: 3 SNPs (239 Gly to Ser, 241 Gly to Cys, 242 Gly to Ala)
§ *bla*$_{\text{CTX-M-27}}$-like: 1 SNP (86 Gln to Leu)
# *bla*$_{\text{CTX-M-14}}$-like: 1 SNP (23 Ser to Asn)

bla$_{\text{SHV}}$- or *bla*$_{\text{TEM}}$-type ESBL genes were not detected in isolates with a *bla*$_{\text{CTX-M}}$ gene. Among 182 isolates with an ESBL phenotype but no *bla*$_{\text{CTX-M}}$ gene, 133 harboured either plasmid *ampC* gene only (*bla*$_{\text{DHA}}$ *n* = 94, *bla*$_{\text{CMY}}$ *n* = 39), both a plasmid *ampC* gene and a carbapenemase gene (*n* = 3), a *bla*$_{\text{SHV}}$ gene only (*n* = 4), both a *bla*$_{\text{SHV}}$ and a plasmid *ampC* gene (*n* = 1), or a carbapenemase gene only (*n* = 3). β-lactam resistance mechanisms were not detected in the remaining 38 isolates.

Among the 791 *E. coli* with an ESBL phenotype, 86 sequence types (ST) were detected, although 67 had less than five isolates. ST131 was dominant (*n* = 328, 41.5%), followed by ST69 (*n* = 76, 9.6%), ST1193 (*n* = 52, 6.6%) and ST73 (*n* = 41, 5.2%) (Table 33).

Just over half (52.3%, 321/614) of the ESBL-producing *E. coli* with confirmed ESBL gene(s) belong to sequence type 131 (ST131) (Table 34). The fluoroquinolone-resistant subclade, H30R, was the most prevalent subclade of ST131 (45.2%, 145/321). Within ST131, all isolates identified as H30Rx (subclade C2) (*n* = 79) carried *bla*$_{\text{CTX-M-15}}$, as reported globally.[60-62] A little over two-thirds (72.7%, 197/271) of isolates with *bla*$_{\text{CTX-M-27}}$-like genes were ST131; 120 belonged to H41 subclade A; 50 to H30R subclade C1-M27.

ST1193 has recently been identified as an emerging MDR type.[63, 64] In the 2023, all ST1193 isolates were ciprofloxacin resistant, and nearly all of these isolates harboured either an ESBL gene (*bla*$_{\text{CTX-M}}$, *n* = 44), a plasmid *ampC* gene (*n* = 4), or both (*n* = 2).

Table 34: ESBL-producing *Escherichia coli* subset, *fimH* allele, H30Rx, AGAR, 2023

		ST131						
			H30					
ESBL type	Number	All	H41*	H99	H30Rx	H30R	Others†	Non-ST131
CTX-M-15	267	109	26	0	79	2	2	158
CTX-M-27	270	196	119*	13	0	50	14	74
CTX-M-14	33	10	0	0	0	9	1	23
CTX-M-55	19	0	0	0	0	0	0	19
CTX-M-3	5	0	0	0	0	0	0	5
CTX-M-24	4	0	0	0	0	0	0	4
CTX-M-231	3	0	0	0	0	0	0	3
CTX-M-15, CTX-M-27	2	2	0	0	0	2	0	0
CTX-M-15, CTX-M-24	1	1	0	0	0	1	0	0
CTX-M-27-like§	1	1	1	0	0	0	0	0
CTX-M-1	1	0	0	0	0	0	0	1
CTX-M-14-like#	1	1	0	0	0	1	0	0
CTX-M-174	1	1	0	0	0	1	0	0
CTX-M-15-like**	1	0	0	0	0	0	0	1
SHV-12	4	0	0	0	0	0	0	4
SHV-2	1	0	0	0	0	0	0	1
	614	321	146	13	79	66	17	293

ESBL = extended-spectrum β-lactamase
* Includes H41-like (*n* = 4)
† H54 (*n* = 3), H141 (*n* = 1), H1196 (*n* = 1), unknown (*n* = 12)
§ CTX-M-27-like: 1 SNP (86 Gln to Leu)
# CTX-M-14-like: 1 SNP (23 Ser to Asn)
** CTX-M-15-like: 3 SNPs (239 Gly to Ser, 241 Gly to Cys, 242 Gly to Ala)

Plasmid-borne AmpC β-lactamases

Plasmid-borne *ampC* β-lactamase genes have emerged internationally as a potential Gram-negative resistance problem. They arise by mobilisation of intrinsic chromosomal genes found in common (notably Enterobacter spp.) and uncommon species of *Enterobacterales* onto transmissible plasmids, and transmission into more common pathogens. There are currently six separate classes of plasmid-encoded AmpC β-lactamases. Like ESBLs, these enzymes confer resistance to the important third-generation cephalosporins, such as ceftriaxone and ceftazidime. Routine phenotypic detection methods have not yet been developed. Nevertheless, it is possible to exploit a special feature of these enzymes: their ability to inactivate the cephamycins, represented by cefoxitin.

Plasmid-borne *ampC* (*bla*$_{CMY-2}$-like, *bla*$_{DHA}$, *bla*$_{FOX}$, *bla*$_{MOX}$, *bla*$_{ACT/MIR}$, *bla*$_{ACC}$) genes were screened for in WGS data using the methods outlined in Appendix B.

The proportions of *E. coli* and *K. pneumoniae* complex isolates with a cefoxitin MIC > 8 mg/L (non-wild type) remain low (6.3% and 5.9% respectively) (Table 35). One-half (162/319, 50.8%) of *E. coli* and 26.8% (19/71) of *K. pneumoniae* complex isolates with cefoxitin MIC > 8 mg/L that were available for confirmation contained at least one plasmid-borne *ampC* genes (Table 35). In most cases the plasmid-borne *ampC* gene type was *bla*$_{DHA}$, found in 70.4% (114/162) of *E. coli* and 94.7% (18/19) of *K. pneumoniae* complex isolates.

Table 35: Numbers of isolates with a plasmid-borne *ampC* gene, by state and territory, AGAR, 2023

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Escherichia coli	1,759	1,108	835	380	910	264	194	182	5,632
Cefoxitin MIC > 8 mg/L (%)	143 (8.1)	83 (7.5)	48 (5.7)	15 (3.9)	43 (4.7)	11 (4.2)	5 (2.6)	8 (4.4)	356 (6.3)
Confirmed/number tested	63/126	37/69	24/43	8/14	22/43	2/11	2/5	4/8	162/319
bla$_{DHA-1}$	48	27	15	6	13	2	2	1	114
bla$_{CMY-2}$	11	7	6	2	8	0	0	3	37
bla$_{CMY-42}$	4	1	3	0	1	0	0	0	9
bla$_{CMY-4}$	0	1	0	0	0	0	0	0	1
bla$_{CMY-145}$	0	1	0	0	0	0	0	0	1
Klebsiella pneumoniae complex	441	303	254	81	205	41	44	56	1,425
Cefoxitin MIC > 8 mg/L (%)	29 (6.6)	18 (5.9)	12 (4.7)	6 (7.4)	12 (5.9)	2 (4.9)	1 (2.3)	4 (7.1)	84 (5.9)
Confirmed/number tested	9/29	5/9	1/10	2/5	1/11	1/2	0/1	0/4	19/71
bla$_{DHA-1}$	8	5	1	2	1	1	0	0	18
bla$_{CMY-2}$	1	0	0	0	0	0	0	0	1

MIC = minimum inhibitory concentration

Of cefoxitin non-wild type (MIC > 8 mg/L) isolates without a plasmid-borne *ampC* gene, at least one carbapenemase genes were detected in seven of 157 (4.5%) *E. coli* (*bla*$_{NDM-5}$ [2], *bla*$_{OXA-244}$ [2], *bla*$_{NDM-7}$ [1], *bla*$_{OXA-484}$ [1], *bla*$_{IMP-4}$ [1]), and three of 52 (5.8%) *K. pneumoniae* complex (*bla*$_{KPC-2}$, *bla*$_{NDM-1}$, *bla*$_{NDM-5}$+*bla*$_{OXA-181}$).

Four *E. coli* with a wild type cefoxitin MIC (≤ 8 mg/L) contained a plasmid *ampC* gene (*bla*$_{CMY-4}$ [2], *bla*$_{DHA-1}$ [2]), and one *K. pneumoniae* complex isolate with a cefoxitin MIC ≤ 8 mg/L contained *bla*$_{DHA-1}$ (data not shown).

Carbapenem resistance

Only 0.4% (*n* = 40) of *Enterobacterales* had a meropenem MIC > 2 mg/L; an additional 39 had meropenem MIC between 1 and 2 mg/L. Meropenem resistance (MIC > 8 mg/L) was 2.0% (16/789) for *P. aeruginosa*, and 0.8% (1/126) for *Acinetobacter* species (Table 36).

Among meropenem-resistant (MIC >8 mg/L) isolates, carbapenemase genes were found in 81.8% (18/22) of *Enterobacterales*, 6.3% (1/16) *P. aeruginosa*, and the only *Acinetobacter* (Table 36). Carbapenemase genes were found in four *Enterobacterales* with meropenem MIC = 0.5 mg/L (*bla*$_{OXA-48}$-like (*n* = 3), *bla*$_{NDM-5}$ (*n* = 1)), and one with meropenem MIC = 0.25 mg/L (*bla*$_{OXA-48}$-like). A further two *Enterobacterales* with a *bla*$_{OXA-48}$-like gene had meropenem MICs of ≤0.125 and ≤0.25 mg/L.

Table 36: Number of isolates with carbapenemase genes, organism group, meropenem MIC, AGAR, 2023

	Acinetobacter (*n* = 126)			*Enterobacterales* (*n* = 9,397)				*Pseudomonas* (*n* = 789)		
	Meropenem MIC (mg/L)			Meropenem MIC (mg/L)				Meropenem MIC (mg/L)		
	≤2	4-8	>8	≤0.5	1-2	4-8	>8	≤2	4-8	>8
Number	125	0	1	9,318	39	11	29	736	37	16
Confirmed/number tested	1/3	–*	1/1	7/1,315	2/35	1/8	18/22	0/2	0/5	1/16
Carbapenemase type†										
Class B	0	0	0	1	0	0	15	0	0	1
bla$_{IMP-4}$§	0	0	0	0	0	0	6	0	0	1
bla$_{NDM-1}$	0	0	0	0	0	0	4	0	0	0
bla$_{NDM-5}$	0	0	0	1	0	0	3	0	0	0
bla$_{NDM-7}$	0	0	0	0	0	0	2	0	0	0
Class D	1	0	0	6	2	0	1	0	0	0
bla$_{OXA-244}$	0	0	0	3	1	0	0	0	0	0
bla$_{OXA-48}$	0	0	0	2	0	0	0	0	0	0
bla$_{OXA-181}$	0	0	0	0	0	0	1	0	0	0
bla$_{OXA-232}$	0	0	0	0	1	0	0	0	0	0
bla$_{OXA-484}$	0	0	0	1	0	0	0	0	0	0
bla$_{OXA-23}$	1	0	0	0	0	0	0	0	0	0
Class B + class D	0	0	1	0	0	1	1	0	0	0
bla$_{NDM-5}$ + *bla*$_{OXA-181}$	0	0	0	0	0	0	1	0	0	0
bla$_{NDM-5}$ + *bla*$_{OXA-484}$	0	0	0	0	0	1	0	0	0	0
bla$_{IMP-4}$ + *bla*$_{OXA-23}$ + *bla*$_{OXA-58}$	0	0	1	0	0	0	0	0	0	0
Class A + class B + class D	0	0	0	0	0	0	1	0	0	0
bla$_{KPC-2}$ + *bla*$_{NDM-5}$ + *bla*$_{OXA-181}$	0	0	0	0	0	0	1	0	0	0

MIC = minimum inhibitory concentration
* not applicable
† Carbapenemase molecular class: class A, *bla*$_{KPC}$; class B (metallo-β-lactamases),*bla*$_{IMP}$, *bla*$_{NDM}$); class D (oxacillinases), including those mainly found in *Acinetobacter* (*bla*$_{OXA-23}$, *bla*$_{OXA-58}$) - *bla*$_{OXA-48}$-like (*bla*$_{OXA-48}$, *bla*$_{OXA-244}$) or *bla*$_{OXA-181}$-like (*bla*$_{OXA-181}$, *bla*$_{OXA-232}$, *bla*$_{OXA-484}$)
§ Meropenem MIC was not known for two *Enterobacterales*
Note: For carbapenemase screening, a meropenem screening cut-off of >0.125 mg/L is recommended. The lowest meropenem MIC on the Vitek® cards used in the survey was ≤ 0.25 mg/L

Thirty-three (0.3%) isolates from 33 patients were found to harbour a carbapenemase gene (Table 37). The overall prevalence of carbapenemase genes among *Enterobacterales* was 0.3% (30/9,338), although for *E. cloacae* complex isolates it was 0.9% (5/547). In 2023, almost three-quarters (22/30, 73.3%) of CPE carried a *bla*$_{OXA-48}$-like and/or a *bla*$_{NDM}$ gene(s), with only one-quarter (*n* = 8, 26.7%) carrying a *bla*$_{IMP-4}$ gene. In 2022, 62.1% (18/29) carried *bla*$_{IMP-4}$.

Two of 142 *Acinetobacter* isolates (1.4%) harboured at least one carbapenemase genes, one *A. baumannii* complex (*bla*$_{OXA-23}$) and one *A. radioresistens* (*bla*$_{IMP-4}$, *bla*$_{OXA-23}$, *bla*$_{OXA-58}$). Only one of 801 (0.1%) *P. aeruginosa* isolates carried a carbapenemase gene (*bla*$_{IMP-4}$).

Isolates carrying carbapenemase genes were detected in 18 hospitals from six states and territories. CPE infections are particularly notable in NSW (17/2,939, 0.6%) and Victoria (6/1,866, 0.3%), compared to other states and territories (Table 38). One-half (9/18, 50.0%) of the hospitals had only one carbapenemase-producing isolate.

Table 37: Carbapenemase-producing organisms, carbapenemase genes, AGAR, 2023

Species	Total	Carbapenemase type, number							
		IMP-4	NDM types	OXA-48-like types	OXA-23	NDM + OXA-48-like types	IMP-4 + OXA-23 + OXA-58	KPC-2 + NDM-5, OXA-181	% (*n*)
Acinetobacter	142	0	0	0	1	0	1	0	1.4 (2)
Acinetobacter baumannii complex	86	0	0	0	1	0	0	0	1.2 (1)
Acinetobacter radioresistens	9	0	0	0	0	0	1	0	11.1 (1)
Enterobacterales	9,338	8	10	9	0	2	0	1	0.3 (30)
Escherichia coli	5,493	2	5	7	0	1	0	0	0.3 (15)
Klebsiella pneumoniae complex*	1,382	0	2	1	0	1	0	1	0.4 (5)
Enterobacter cloacae complex†	536	3	2	0	0	0	0	0	0.9 (5)
Klebsiella oxytoca	298	1	1	0	0	0	0	0	0.7 (2)
Citrobacter freundii complex	102	1	0	0	0	0	0	0	1.0 (1)
Klebsiella aerogenes	153	0	0	1	0	0	0	0	0.7 (1)
Serratia marcescens	233	1	0	0	0	0	0	0	0.4 (1)
Pseudomonas aeruginosa	801	1	0	0	0	0	0	0	0.1 (1)
All species	10,281	9	10	9	1	2	1	1	0.3 (33)

* *K. pneumoniae* (*n* = 4: bla_{NDM-1} [1], $bla_{OXA-232}$ [1], bla_{NDM-5} + $bla_{OXA-181}$ [1], bla_{KPC-2} + bla_{NDM-5} + $bla_{OXA-181}$ [1]); *K. variicola* (*n* = 1: bla_{NDM-1})
† *E. hormaechei* (bla_{NDM-1} [2]), bla_{IMP-4} [1]); *E. cloacae* complex 'Hoffmann cluster III' (bla_{IMP-4} [2])

Table 38: Carbapenemase genes, organism group, state and territory, AGAR, 2023

Organism group and carbapenemase	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Total species, *n*	3,194	2,016	1,671	722	1,574	427	322	355	10,281
Acinetobacter	30	22	37	9	21	8	14	1	142
Carbapenemase, % (*n*)	0.0 (0)	4.5 (1)	0.0 (0)	11.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	1.4 (2)
bla_{OXA-23}	0	0	1	0	0	0	1	0	2
bla_{IMP-4} + bla_{OXA-23} + bla_{OXA-58}									
Enterobacterales	2,939	1,866	1,451	634	1,444	389	286	329	9,338
Carbapenemase, % (*n*)	0.6 (17)	0.3 (6)	0.1 (2)	0.1 (0)	0.2 (3)	0.0 (0)	0.0 (0)	0.6 (2)	0.3 (30)
bla_{IMP-4}	6	0	1	0	0	0	0	1	8
bla_{NDM-1}	0	2	1	0	1	0	0	0	4
$bla_{OXA-244}$	2	1	0	0	1	0	0	0	4
bla_{NDM-5}	2	1	0	0	1	0	0	0	4
bla_{OXA-48}	2	0	0	0	0	0	0	0	2
bla_{KPC-2} + bla_{NDM-5} + $bla_{OXA-181}$	1	0	0	0	0	0	0	0	1
bla_{NDM-5} + $bla_{OXA-181}$	1	0	0	0	0	0	0	0	1
bla_{NDM-5} + $bla_{OXA-484}$	1	0	0	0	0	0	0	0	1
bla_{NDM-7}	2	0	0	0	0	0	0	0	2
$bla_{OXA-181}$	0	0	0	0	0	0	0	1	1
$bla_{OXA-232}$	0	1	0	0	0	0	0	0	1
$bla_{OXA-484}$	0	1	0	0	0	0	0	0	1
Pseudomonas aeruginosa	225	128	183	79	109	30	22	25	801
Carbapenemase, % (*n*)	0.4 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.1 (1)
bla_{IMP-4}	1	0	0	0	0	0	0	0	1
Overall prevalence, % (n)	0.6 (18)	0.3 (7)	0.1 (2)	0.1 (1)	0.2 (3)	0.0 (0)	0.0 (0)	0.6 (2)	0.3 (33)

Fluoroquinolone resistance

Multiple resistance mechanisms against quinolones have been described. Resistance is most commonly due to mutations in DNA gyrase (*gyrA*, *gyrB*) and topoisomerase IV (*parC*, *parE*) genes. Transmissible plasmid-mediated quinolone resistance (PMQR) has emerged in *Enterobacterales*. PMQR determinants include *qnr* genes (*qnrA, qnrB, qnrC, qnrD, qnrE, qnrS, qnrVC); aac(6')-Ib-cr*, coding for a variant aminoglycoside acetyltransferase enzyme, and genes coding for efflux pumps (*qepA*, *oqxAB*).[65, 66] *oqxAB* genes are intrinsic in *Klebsiella* and *Enterobacter*.

Escherichia coli

Nationally, 19.5% (1,098/5,634) of *E. coli* had a ciprofloxacin MIC >0.25 mg/L, ranging from 10.6% (28/264) in Tasmania to 29.0% in the NT (56/193). A subset of 910 *E. coli* (16.2% of total) was referred and underwent WGS. This included 811 with an ESBL phenotype and 587 with ciprofloxacin MIC >0.25 mg/L (Table 39).

Table 39: *Escherichia coli*, ciprofloxacin susceptibility, ESBL phenotype, AGAR, 2023

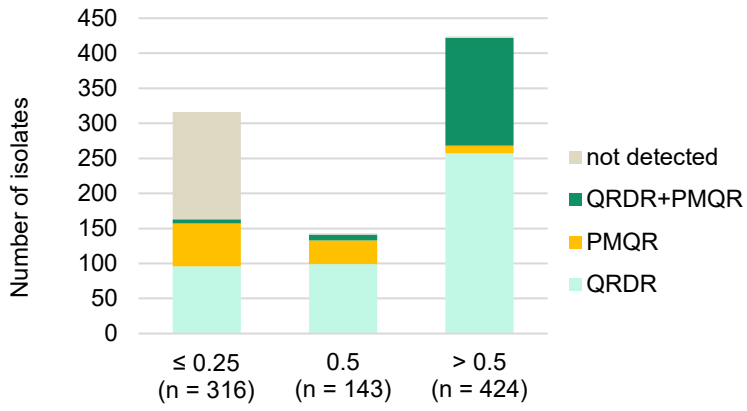
		Ciprofloxacin MIC (mg/L)				
Subset	Phenotype	≤0.25	0.5	>0.5	Total	% of total
Total	ESBL	31.3 (268)	17.0 (146)	51.7 (443)	857	15.2
	non-ESBL	89.3 (4,266)	2.8 (136)	7.8 (373)	4,775	84.8
	Total	80.5 (4,534)	5.0 (282)	14.5 (816)	5,632	
WGS	ESBL	248	143	420	811	
	non-ESBL	75	3	21	99	
	Total	323	146	441	910	

ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; WGS = whole genome sequencing
Note: ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L.

Almost all (563/567, 99.3%) of the *E. coli* subset that had ciprofloxacin MIC > 0.25 mg/L harboured fluoroquinolone resistance determinants (Figure 13). The vast majority (90.8%, 515/567) of this group had a QRDR mutation in codon 83 of *gyrA*. A substantial majority (79.5%, 337/424) of isolates resistant to ciprofloxacin (MIC >0.5 mg/L) also had a second mutation in *gyrA* (codon 87), and 83.5% (354/424) had at least one mutation in *parC* (refer to Appendix E1).

PMQR genes (*qnr* variants) without QRDR mutations were more common in ciprofloxacin susceptible isolates. Of 179 *E. coli* with confirmed *qnr*, most had a *qnrB* (*n* = 116, 64.8%) gene, while some had a *qnrS* gene (*n* = 60, 33.5%) or *qnrB* + *qnrS* genes (*n* = 3) (data not shown). *qepA4* was found in one *E. coli* isolate from NSW.

Figure 13: *Escherichia coli* (*n* = 883), fluoroquinolone resistance mechanisms, ciprofloxacin MIC, AGAR, 2023



MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*), QRDR = quinolone resistance-determining region (*gyrA*, *gyrB*, *parC*, *parE*).

A substantial majority (67.5%, 286/424) of ciprofloxacin resistant *E. coli* belong to either ST131 (*n* = 225, 53.1%) or ST1193 (*n* = 61, 14.4%), which have reported distinguishing *parE* mutations (I529L and L416F, respectively).[67] Almost one-quarter (103/424, 24.3%) have *aac(6')-Ib-cr*, almost all (95.1%, 98/103) of which have $bla_{CTX\text{-}M\text{-}15}$ (*n* = 97) or $bla_{CTX\text{-}M\text{-}14}$ (*n* = 1) (data not shown).

Klebsiella pneumoniae complex

Nationally, 11.7% (166/1,421) of *K. pneumoniae* complex isolates had a ciprofloxacin MIC >0.25 mg/L, ranging from 0.0% in Tasmania (0/41) to 20.9% in the NT (9/43). A subset of 162 *K. pneumoniae* complex (11.4% of total) was referred and underwent WGS. This included 115 with an ESBL phenotype and 103 with ciprofloxacin MIC >0.25 mg/L (Table 40).

Table 40: *Klebsiella pneumoniae* complex, ciprofloxacin susceptibility, ESBL phenotype, AGAR, 2023

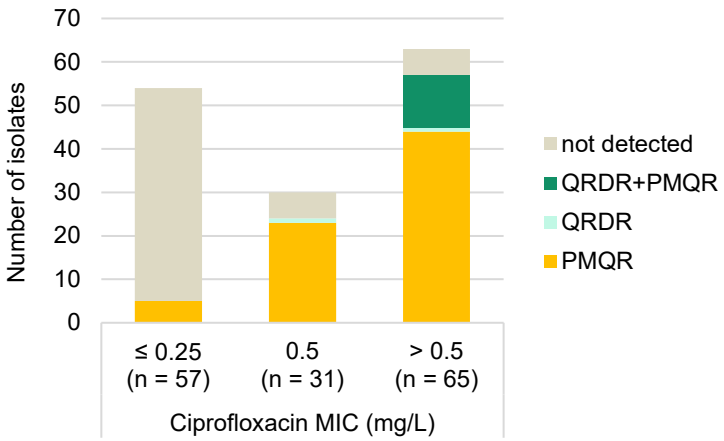
Subset	Phenotype	Ciprofloxacin MIC (mg/L)			Total	% of total
		≤0.25	0.5	>0.5		
Total	ESBL	23.8 (29)	21.3 (26)	54.9 (67)	122	8.6
	non-ESBL	94.4 (1,226)	2.2 (29)	3.4 (44)	1,299	91.4
	Total	88.3 (1,255)	3.9 (55)	7.8 (111)	1,421	
WGS	ESBL	26	25	64	115	
	non-ESBL	33	6	8	47	
	Total	59	31	72	162	

ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; WGS = whole genome sequencing
Note: ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L.

Of the subset of *K. pneumoniae* complex isolates with a ciprofloxacin MIC >0.25 mg/L, 87.5% (84/96) harboured fluoroquinolone resistance determinants (Figure 14) PMQR genes either alone (83.3%, 70/84) or in combination with QRDR mutations in codon 83 of *gyrA* (14.3%, 12/84) were prevalent; only 1/84 had *parC* (*n* = 1) mutations alone (refer to Appendix Table E2).

In *K. pneumoniae* complex isolates, when PMQR genes (*qnr* variants) were found alone (62/78, 79.5%) they were usually in isolates with ciprofloxacin MIC >0.25 mg/L (57/62, 91.9%). In 78 *K. pneumoniae* complex isolates with confirmed *qnr*, most had *qnrS* (*n* = 40, 51.3%), while some had *qnrB* (*n* = 32) or both *qnrS* and *qnrB* (*n* = 6).

Figure 14: *Klebsiella pneumoniae* complex (*n* = 153), fluoroquinolone resistance mechanisms, ciprofloxacin MIC, AGAR, 2023



MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*), QRDR = quinolone resistance-determining region (*gyrA*, *gyrB*, *parC*, *parE*).

Pseudomonas aeruginosa

Of 23 *P. aeruginosa* isolates referred for sequencing two harboured QRDR mutations, one in codon 83 (T83I) of *gyrA*, and one in codon 87 (D87N). The ciprofloxacin MIC for both isolates was ≥ 2 mg/L. No PMQR genes were detected.

Salmonella species

Ciprofloxacin resistance (MIC > 0.06 mg/L) among non-typhoidal species was 17.2% (23/134 confirmed). For the typhoidal species, 97.8% (88/90) were resistant, comprising 66/68 (97.1%) *S*. Typhi and all *S*. Paratyphi A (*n* = 21) and *S*. Paratyphi B (*n* = 1) (Table 41).

Table 41: *Salmonella* species, ciprofloxacin minimum inhibitory concentrations, AGAR, 2023

	Ciprofloxacin minimum inhibitory concentration (mg/L)							
Organism	**≤0.06**	**0.125**	**0.25**	**0.5**	**1**	**2**	**≥4**	**Total**
Salmonella species (non-typhoidal)	111	3	3	7	8	0	2	134
Salmonella species (typhoidal)	2	1	6	22	39	2	18	90
S. Typhi	2	1	5	21	21	2	16	68
S. Paratyphi A	0	0	0	1	18	0	2	21
S. Paratyphi B	0	0	1	0	0	0	0	1
Total	**113**	**4**	**9**	**29**	**47**	**2**	**20**	**224**

Notes:
1. MICs were determined using MIC strips on Salmonella where Vitek® MIC ≤0.25 mg/L.
2. For some laboratories using EUCAST interpretative criteria, a perfloxacin disc was used to screen for ciprofloxacin resistance. If susceptible to a 5 mg/L disc, the isolate was recorded as MIC≤ 0.06 mg/L (susceptible).

All typhoidal isolates that were resistant to ciprofloxacin harboured a mutation in the QRDR of *gyrA*, either in codon 83 (*n* = 62), codon 87 (n = 1) or both codons 83 and 57 (*n* = 14), known mutations conferring quinolone resistance (refer to Appendix E1).[68]

One *Salmonella* (non-typhoidal) isolate from Queensland with QRDR mutations also harboured an ESBL gene ($bla_{\text{CTX-M-55}}$).

Plasmid-mediated colistin determinants

Two isolates with bla_{NDM} carbapenemase genes also harboured *mcr-9.1 (E. cloacae* complex $bla_{\text{NDM-1}}$, *K. oxytoca* $bla_{\text{NDM-7}}$).

Seven additional isolates (*E. cloacae* complex, *n* = 5; *E. coli*, *n* = 1), and *K. oxytoca*, *n* = 1) that did not carry a carbapenemase gene had either *mcr-9* (*n* = 5) or *mcr-10* (*n* = 2). *mcr-9* has recently been found among several species of *Enterobacterales*. It is not associated with a resistant phenotype[69], but is typically carried on HI2 plasmids.[70, 71]

Ribosomal methyltransferases

Simultaneous resistance to gentamicin, tobramycin and/or amikacin is often due to ribosomal methyltransferases (RMT), which are frequently coproduced with ESBL and carbapenemases.[72, 73]

In the 2023 survey, seven *Enterobacterales* were resistant to amikacin (MIC > 32 mg/L), gentamicin (MIC > 8 mg/L) and tobramycin (MIC > 8 mg/L). RMT genes were detected in four of five isolates that were available for WGS; *rmtB1* in three (*E. coli n* = 2, *K. pneumoniae* (*n* = 1), and both *rmtB1* and *rmtF1* in one *K. pneumoniae*. All four isolates carried β-lactamase gene(s).

Hypervirulent *Klebsiella pneumoniae* complex

Hypervirulent *K. pneumoniae* (hvKp) has emerged as a concerning global pathogen.[74-76] In GnSOP 2023, 12 *K. pneumoniae* isolates (and one *K. oxytoca*) would be classified as hypervirulent (virulence score ≥3) by Kleborate.[77] Nine isolates have a K1 or K2 capsule serotype, the most

common types in hvKp. Five isolates are ST23-K1, already identified globally as a high-risk clone of hvKp carrying carbapenamase genes.[78, 79] Four of these have a virulence score of 5 and carry *ybt*, *clb* and *iuc*, but no ESBL or carbapenemase genes. One ST23-K1 isolate with a virulence score of 3 (*iuc* only) has $bla_{\text{CTX-M-15}}$. The other hvKp isolates belong to ST25 (*n* = 2), ST29, ST86, ST91, ST260 or ST420, all previously associated with hypervirulence.[80-84] Two carry a plasmid *ampC* gene ($bla_{\text{CMY-2}}$ or $bla_{\text{DHA-1}}$) and one carries $bla_{\text{CTX-M-14}}$.

3.10. Trend analysis (2014–2023)

Trend data were available for *Enterococcus* species, *S. aureus* and *Enterobacterales,* for the ten-year period 2014 to 2023. *Acinetobacter* species and *P. aeruginosa* were introduced to the program in 2015.

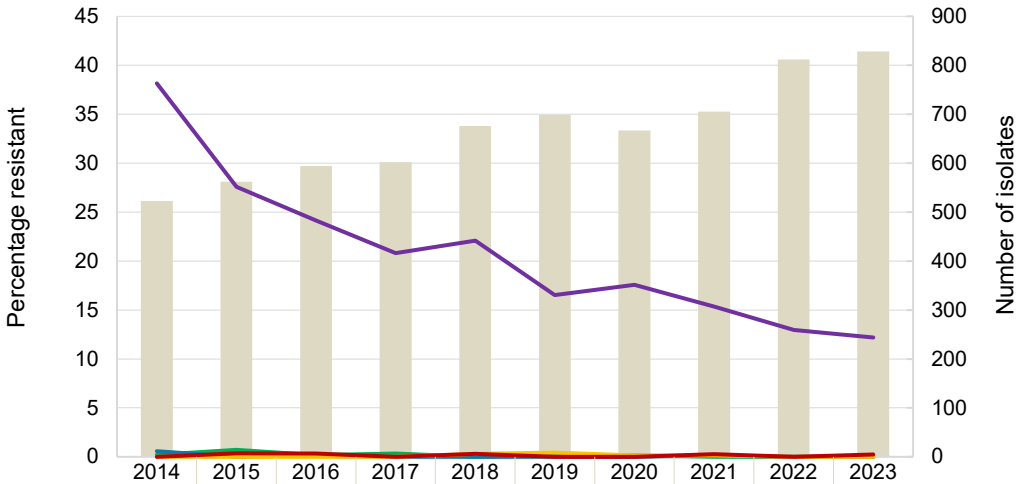
Enterococcus species

The 2023 program focused on the proportions of *E. faecium* and *E. faecalis* bloodstream isolates demonstrating resistance to ampicillin, glycopeptides and other anti-enterococcal agents. Important trends for the period 2014 to 2023 are described below.

Enterococcus faecalis

National
Resistance (EUCAST) to key antimicrobial agents for *E. faecalis* over the ten-year period from 2014 to 2023 is shown in Figure 15. Resistance to ampicillin, vancomycin, teicoplanin and linezolid remains rare. There was a significant decreasing trend in high-level gentamicin resistance (X^2 for linear trend = 163.0, $P < 0.01$).

Figure 15: *Enterococcus faecalis*, antimicrobial resistance (EUCAST), AGAR, 2014–2023



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Number of isolates	523	562	594	602	676	699	667	705	812	828
Gentamicin (high-level)	38.2	27.6	24.1	20.8	22.1	16.5	17.6	15.3	13.0	12.2
Vancomycin	0.2	0.7	0.2	0.3	0.0	0.1	0.2	0.0	0.0	0.0
Ampicillin	0.6	0.0	0.2	0.0	0.0	0.0	0.0	0.1	0.0	0.0
Teicoplanin	0.0	0.0	0.0	0.0	0.3	0.4	0.2	0.1	0.0	0.0
Linezolid	0.0	0.4	0.3	0.0	0.3	0.0	0.0	0.3	0.0	0.2

EUCAST = European Committee on Antimicrobial Susceptibility Testing
Notes:
1. Percentage resistance determined using EUCAST 2024 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2014; *n* = 43 in 2015; *n* = 44 in 2016; *n* = 48 in 2017 and 2018; *n* = 51 in 2019, 2020 and 2021; *n* = 55 in 2022 and 2023.

State and territory

There were no significant changes in antimicrobial resistance in *E. faecalis* in 2023, compared to 2022.

From 2019 to 2023, there was a significant decreasing trend in high-level gentamicin resistance in Australia (X^2 for linear trend = 10.07, $P < 0.01$), notably in Victoria (X^2 for linear trend = 10.34, $P < 0.01$), and the ACT (X^2 for linear trend = 6.370, $P < 0.01$) (Table 42).

Table 42: *Enterococcus faecalis*, percentage resistant to gentamicin (high-level) (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
South Australia	35.3 (51)	28.1 (57)	29.4 (51)	35.5 (31)	23.6 (55)	9.4 (64)	13.8 (58)	17.4 (69)	10.8 (74)	2.8 (71)	↔
Australian Capital Territory	54.5 (33)	34.3 (35)	22.5 (40)	35.7 (28)	38.5 (26)	**44.4 (36)**	**19.4 (31)**	**27.8 (36)**	**15.2 (33)**	**3.8 (26)**	▼
Queensland	34.3 (102)	25.5 (94)	28.6 (98)	21.2 (99)	16.3 (129)	13.0 (123)	9.3 (97)	9.0 (100)	11.2 (89)	7.6 (119)	↔
Tasmania	30.8 (13)	25.0 (12)	14.8 (27)	19.4 (31)	16.1 (31)	12.2 (41)	7.4 (27)	9.1 (33)	12.0 (50)	10.9 (55)	↔
Victoria	38.7 (119)	27.4 (106)	21.7 (129)	19.7 (117)	23.1 (117)	**22.2 (126)**	**24.8 (133)**	**16.0 (131)**	**11.2 (125)**	**12.1 (132)**	▼
Western Australia	28.6 (63)	23.3 (90)	16.1 (87)	22.5 (89)	21.1 (90)	12.8 (78)	15.9 (88)	9.4 (106)	12.0 (117)	14.3 (119)	↔
Northern Territory	–† (6)	40.0 (10)	–† (7)	10.0 (10)	18.2 (11)	–† (7)	–† (5)	–† (8)	42.9 (14)	14.3 (14)	↔
New South Wales	42.4 (132)	29.3 (140)	28.2 (149)	16.7 (186)	24.2 (207)	15.3 (215)	19.0 (221)	19.8 (162)	13.8 (239)	17.6 (227)	↔
Australia	38.2 (519)	27.6 (544)	24.1 (588)	20.8 (591)	22.1 (666)	**16.5 (690)**	**17.6 (660)**	**15.3 (645)**	**13.0 (741)**	**12.2 (763)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing
* Chi-square test for trend for past five years (2019–2023), **bold** text significant decrease ▼ ($P < 0.01$), ↔ no significant difference
† Not applicable, insufficient numbers (<10) to calculate percentage
Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

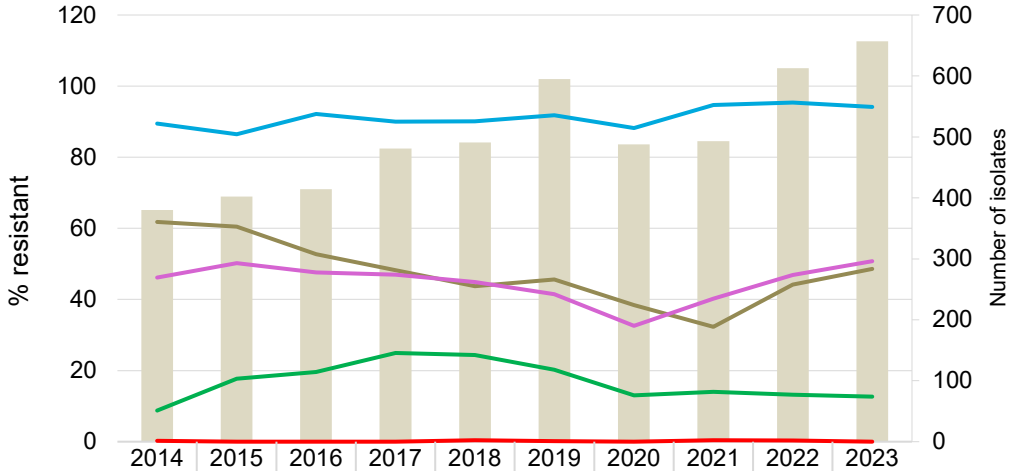
Enterococcus faecium

National

The total number of *E. faecium* isolated from patients with bacteraemia increased in 2023 compared to 2022 (*n* = 613 in 2022; *n* = 657 in 2023, up 7.2%) (Figure 16).

Nationally, the proportion of *E. faecium* resistant to vancomycin increased from 46.9% (285/608) in 2022 to 50.8% (333/656) in 2023 (Figure 16). Teicoplanin resistance in vancomycin-resistant *E. faecium* isolates decreased (28.4% in 2022, 25.3% in 2023), and high-level gentamicin resistance in vancomycin-susceptible *E. faecium* isolates increased (263.8% in 2022, 32.3% in 2023) (Figure 17).

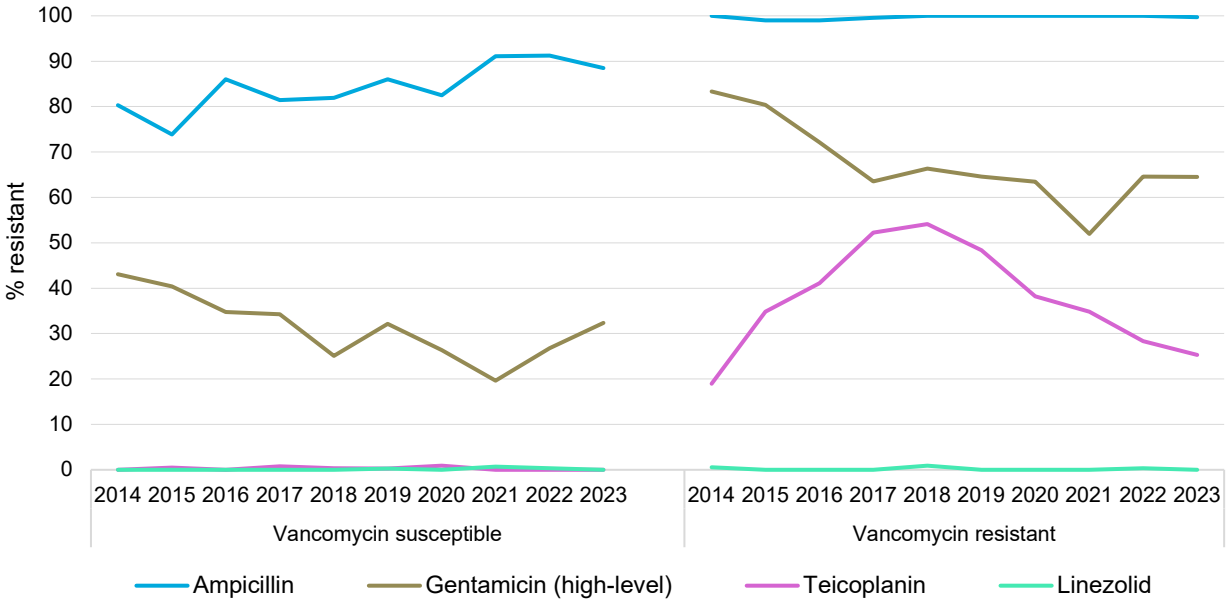
Figure 16: *Enterococcus faecium*, antimicrobial resistance (EUCAST), AGAR, 2014–2023



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Total, n	380	402	414	481	491	595	488	493	613	657
Ampicillin	89.4	86.5	92.2	90.0	90.1	91.9	88.2	94.7	95.4	94.2
Gentamicin (high-level)	61.8	60.5	52.7	48.2	43.7	45.6	38.4	32.3	44.2	48.6
Vancomycin	46.2	50.2	47.6	47.0	44.9	41.5	32.6	40.2	46.9	50.8
Teicoplanin	8.8	17.7	19.6	24.9	24.4	20.2	13.0	14.0	13.2	12.7
Linezolid	0.3	0.0	0.0	0.0	0.4	0.2	0.0	0.4	0.3	0.0

EUCAST = European Committee on Antimicrobial Susceptibility Testing
Notes:
1. Percentage resistance determined using EUCAST 2024 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2014; *n* = 43 in 2015; *n* = 44 in 2016; *n* = 48 in 2017 and 2018; *n* = 51 in 2019, 2020 and 2021; *n* = 55 in 2022 and 2023.

Figure 17: *Enterococcus faecium,* antimicrobial resistance (EUCAST), by vancomycin susceptibility, AGAR, 2014–2023



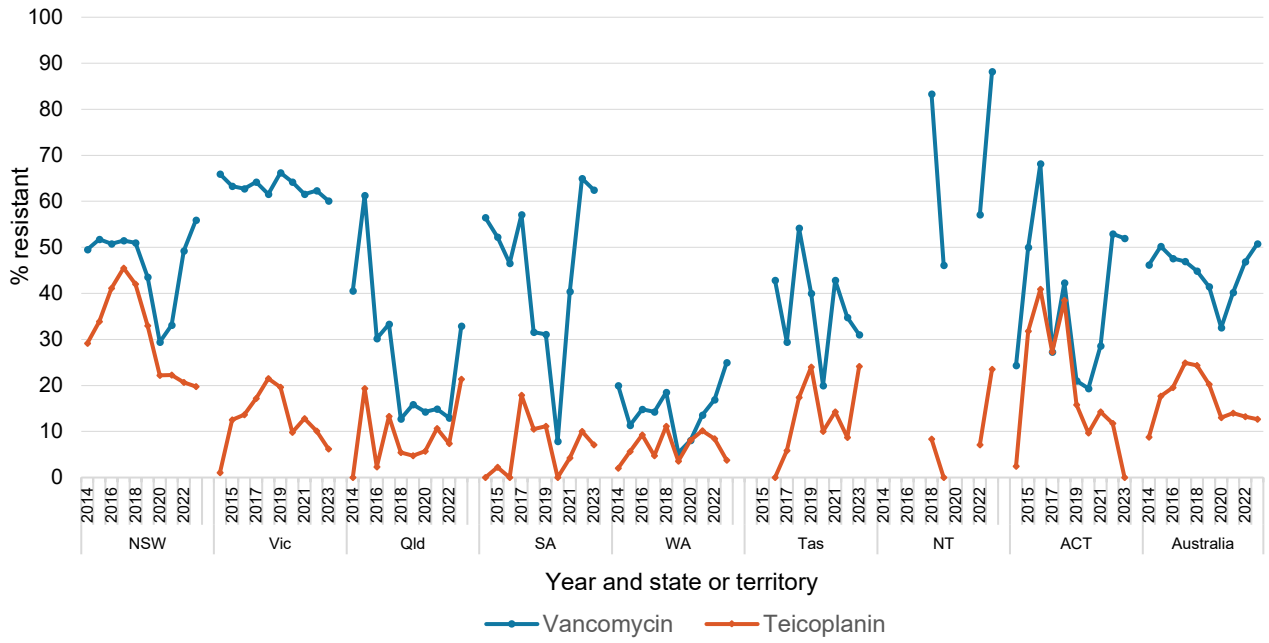
EUCAST = European Committee on Antimicrobial Susceptibility Testing
Notes:
1. Percentage resistance determined using EUCAST 2024 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2014; *n* = 43 in 2015; *n* = 44 in 2016; *n* = 48 in 2017 and 2018; *n* = 51 in 2019, 2020 and 2021; *n* = 55 in 2022 and 2023.

State and territory

The proportion of glycopeptide-resistant *E. faecium* by state and territory is shown in Figure 18. In Queensland, there was an increase in the proportion of vancomycin resistance (7/54, 13.0% in 2022; 25/76, 32.9% in 2023, $P = 0.0126$), and teicoplanin-resistance *E. faecium* isolates (7/54, 13.0% in 2022; 25/76, 32.9% in 2023, $P = 0.0468$).

The overall increase in high-level gentamicin resistance in *E. faecium* isolates (44.2% in 2022, 48.6% in 2023) (Figure 16) was most notable in Victoria (37/134, 27.6% in 2022; 65/143, 45.5% in 2023, $P < 0.01$), and Queensland (14/52, 26.9% in 2022; 23/73, 31.5% in 2023, $P < 0.01$) (data not shown).

Figure 18: *Enterococcus faecium*, glycopeptide resistance (EUCAST), by state and territory, and nationally, AGAR, 2014–2023



EUCAST = European Committee on Antimicrobial Susceptibility Testing

Notes:

1. Percentage resistance determined using EUCAST 2024 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2014; *n* = 43 in 2015; *n* = 44 in 2016; *n* = 48 in 2017 and 2018; *n* = 51 in 2019, 2020 and 2021; *n* = 55 in 2022 and 2023.
3. Insufficient numbers (<10) to calculate percentage for Tasmania (2014–2015) and the NT (2014–2017, 2020, 2021).

Over the past five years (2019–2023), a significant increasing trend in vancomycin resistance in *E. faecium* was observed in Australia (X^2 for linear trend = 25.25, $P < 0.0001$). The increases were observed in most regions except for Victoria, Tasmania and the NT (Table 43). Over the same period, teicoplanin resistance in *E. faecium* decreased significantly nationally (X^2 for linear trend = 11.32, $P < 0.01$); notably in NSW (X^2 for linear trend = 9.14, $P < 0.01$), and Victoria (X^2 for linear trend = 12.42, $P < 0.01$), but teicoplanin resistance increased in Queensland (X^2 for linear trend = 8.77, $P < 0.01$) (Table 44).

Table 43: *Enterococcus faecium*, percentage resistant to vancomycin (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Western Australia	20.0 (50)	11.3 (53)	14.8 (54)	14.3 (63)	18.5 (54)	**5.4 (56)**	**8.1 (62)**	**13.6 (59)**	**16.9 (71)**	**25.0 (80)**	▲
Tasmania	–† (7)	–† (8)	42.9 (14)	27.8 (18)	54.2 (24)	40.0 (25)	20.0 (10)	42.9 (14)	34.8 (23)	31.0 (29)	↔
Queensland	40.5 (37)	61.3 (31)	30.2 (43)	32.6 (46)	12.7 (55)	**15.9 (63)**	**14.3 (35)**	**14.9 (47)**	**13.0 (54)**	**32.9 (76)**	▲
Australian Capital Territory	24.4 (41)	50.0 (22)	68.2 (22)	27.3 (22)	42.3 (26)	**21.1 (19)**	**19.4 (31)**	**28.6 (14)**	**52.9 (17)**	**52.0 (25)**	▲
New South Wales	49.5 (103)	51.7 (116)	50.8 (124)	51.5 (167)	51.0 (151)	**43.5 (209)**	**29.4 (180)**	**33.1 (139)**	**49.3 (211)**	**55.9 (195)**	▲
Victoria	66.0 (94)	63.3 (120)	62.2 (111)	63.7 (135)	61.5 (130)	66.3 (163)	64.2 (123)	61.6 (164)	62.4 (178)	60.1 (178)	↔
South Australia	56.5 (46)	52.3 (44)	46.5 (43)	57.1 (28)	31.6 (38)	**31.1 (45)**	**7.9 (38)**	**40.4 (47)**	**65.0 (40)**	**62.5 (56)**	▲
Northern Territory	–† (1)	–† (8)	–† (4)	–† (5)	83.3 (12)	46.2 (13)	–† (6)	–† (8)	57.1 (14)	88.2 (17)	NA
Australia	46.2 (379)	50.2 (402)	47.5 (415)	46.7 (484)	44.9 (490)	**41.5 (593)**	**32.6 (485)**	**40.2 (492)**	**46.9 (608)**	**50.8 (656)**	▲

EUCAST = European Committee on Antimicrobial Susceptibility Testing; NA = Not applicable
* Chi-square test for trend for past five years (2019–2023), bold text significant increase ▲ ($P < 0.01$), ▲ ($< 0.01 < P < 0.05$), ↔ no significant difference
† Not applicable, insufficient numbers (<10) to calculate percentage
Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

Table 44: *Enterococcus faecium*, percentage resistant to teicoplanin (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Australian Capital Territory	2.4 (41)	31.8 (22)	40.9 (22)	27.3 (22)	38.5 (26)	15.8 (19)	9.7 (31)	14.3 (14)	11.8 (17)	0.0 (25)	↔
Western Australia	2.0 (50)	5.7 (53)	9.3 (54)	4.8 (63)	11.1 (54)	3.6 (56)	8.1 (62)	10.2 (59)	8.5 (71)	3.8 (80)	↔
Victoria	1.1 (94)	12.5 (120)	13.6 (110)	17.2 (134)	21.5 (130)	**19.6 (163)**	**9.8 (122)**	**12.8 (164)**	**10.1 (178)**	**6.2 (178)**	▼
South Australia	0.0 (45)	2.3 (44)	0.0 (43)	17.9 (28)	10.5 (38)	11.1 (45)	0.0 (39)	4.3 (47)	10.0 (40)	7.1 (56)	↔
New South Wales	29.1 (103)	33.9 (115)	41.1 (124)	45.5 (167)	42.0 (150)	**33.0 (209)**	**22.2 (180)**	**22.3 (139)**	**20.7 (208)**	**19.8 (187)**	▼
Queensland	0.0 (36)	19.4 (31)	2.3 (43)	13.3 (45)	5.5 (55)	**4.8 (63)**	**5.7 (35)**	**10.6 (47)**	**7.4 (54)**	**21.3 (75)**	▲
Northern Territory	–† (1)	–† (8)	–† (4)	–† (5)	8.3 (12)	0.0 (13)	–† (6)	–† (8)	7.1 (14)	23.5 (17)	NA
Tasmania	–† (7)	–† (8)	0.0 (14)	5.9 (17)	17.4 (23)	24.0 (25)	10.0 (10)	14.3 (14)	8.7 (23)	24.1 (29)	↔
Australia	8.8 (377)	17.7 (401)	19.6 (414)	24.9 (481)	24.4 (488)	**20.2 (593)**	**13.0 (485)**	**14.0 (492)**	**13.2 (605)**	**12.7 (647)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing; NA = Not applicable
* Chi-square test for trend for past five years (2019–2023), **bold** text indicates significant increase ▲ ($P < 0.01$), significant decrease ▼ ($P < 0.01$), ↔ no significant difference
† Not applicable, insufficient numbers (<10) to calculate percentage
Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

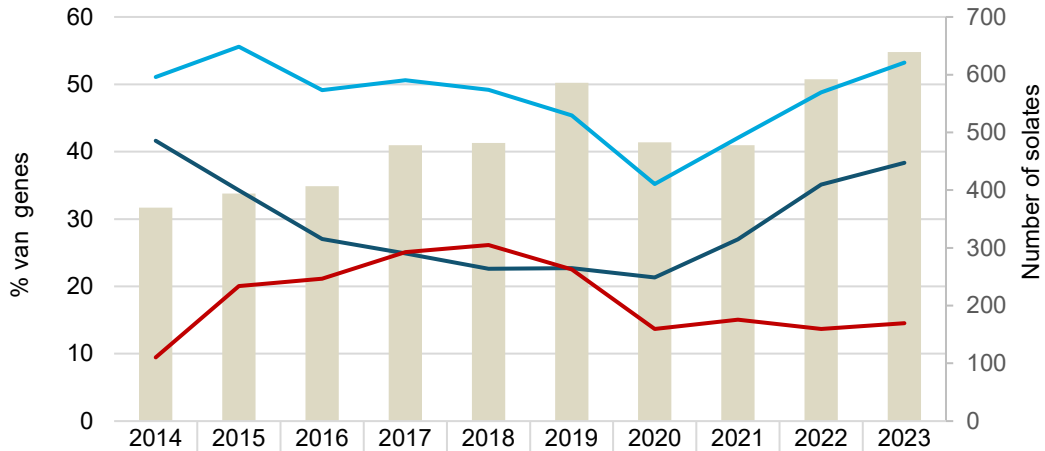
Glycopeptide-resistance and *van* genes in *Enterococcus faecium*

National

In 2023, glycopeptide resistance in *E. faecium* was predominantly due to *vanB* genes. Overall, the proportion of *vanB E. faecium* increased from 21.3% in 2020 to 38.3% in 2023 (P < 0.01), and the proportion of *vanA E. faecium* remained stable (Figure 19).

Over the past five-years (2019-2023), there was a significantly increasing trend in the proportion of *E. faecium* with *vanB* genes (X^2 for linear trend = 54.69, $P < 0.0001$), and a significantly decreasing trend in the proportion of *vanA* genes (X^2 for linear trend = 12.81, $P < 0.01$).

Figure 19: Ten-year trend in percent *Enterococcus faecium* with *van* genes, AGAR, 2014–2023



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
E. faecium, n	370	394	407	478	482	586	483	478	592	639
Any van gene, %	51.1	55.6	49.1	50.6	49.2	45.4	35.2	42.1	48.8	53.2
vanB, %	41.6	34.3	27.0	24.9	22.6	22.7	21.3	27.0	35.1	38.3
vanA,%	9.5	20.1	21.1	25.1	26.1	22.5	13.7	15.1	13.7	14.6

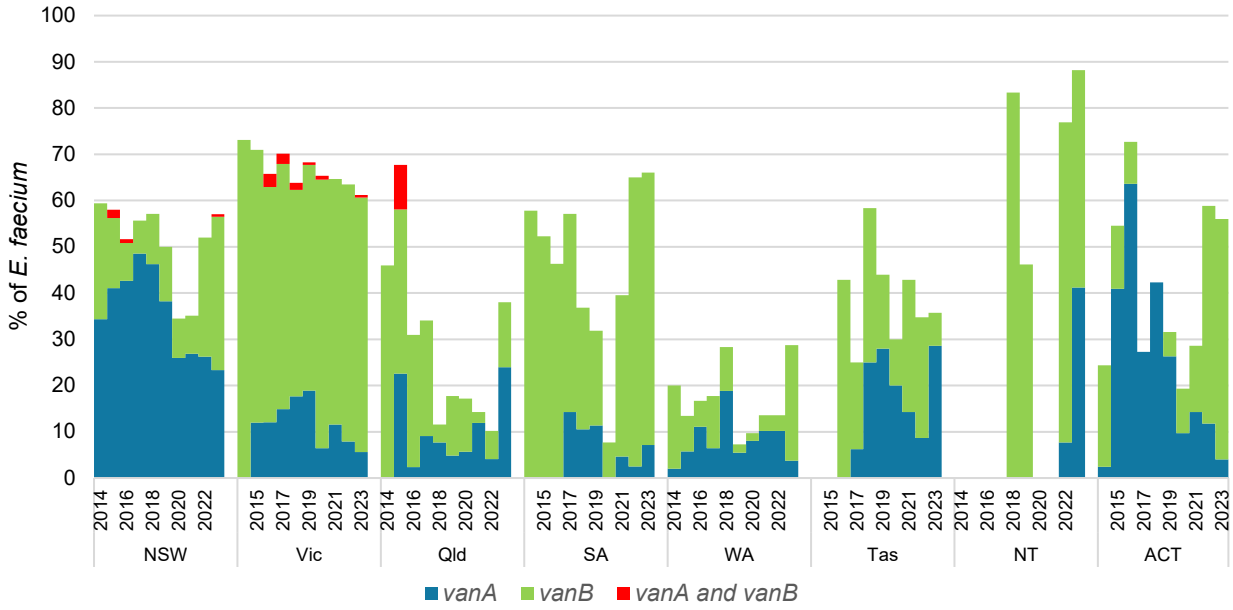
State and territory

There is considerable variation in the proportion of *E. faecium* with *van* genes by state and territory, and the *van* type (Figure 20).

In 2023, there was a notable increase in *vanB E. faecium* in WA (6/63, 8.7% in 2022; 20/60, 25.0% in 2022, $P < 0.01$). There was a significant increase in *vanA E. faecium* in Queensland (1/47, 2.1% in 2022; 17/54, 23.9% in 2023, $P = 0.0159$).

Over the past five-years (2019-2023), there was a significantly increasing trend in the proportion of *E. faecium* with *vanB* genes nationally (X^2 for linear trend = 56.69, $P < 0.0001$), most notably in NSW (X^2 for linear trend = 45.66, $P < 0.0001$), SA (X^2 for linear trend = 32.45, $P < 0.0001$), WA (X^2 for linear trend = 25.55, $P < 0.0001$), and the ACT (X^2 for linear trend = 20.48, $P < 0.0001$). Over the same period, there was a significantly decreasing trend in the proportion of *vanA* genes in NSW (X^2 for linear trend = 8.09, $P < 0.01$) and Victoria (X^2 for linear trend = 12.72, $P < 0.01$). There was a significantly increasing trend in the proportion of *vanA* genes in Queensland (X^2 for linear trend = 9.446, $P < 0.01$ and the NT (X^2 for linear trend = 9.89, $P < 0.01$).

Figure 20: Proportion of *van* genes in *Enterococcus faecium* by state and territory, AGAR, 2014–2023



Note: Insufficient number of *E. faecium* isolates (<10) to calculate percentage for Tasmania 2014-2015) and the Northern Territory (2014-2017, 2020, 2021).

Staphylococcus aureus

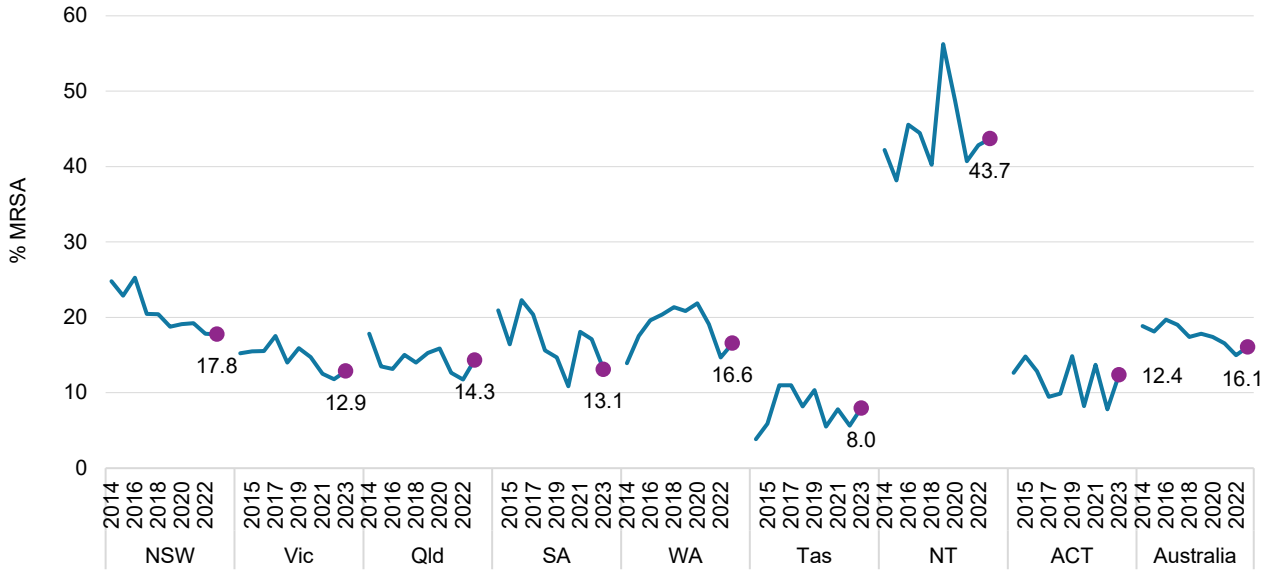
A primary objective of the ASSOP 2023 survey was to determine the proportion of SAB isolates demonstrating resistance to methicillin and other important anti-staphylococcal agents. The following sections describe the major trends observed for the ten-year period 2014 to 2023.

Methicillin-resistant *Staphylococcus aureus*

Since 2016, the proportion of *S. aureus* that was methicillin-resistant began to decline nationally in Australia, although there were notable variations at state and territory level (Figure 21). Relative to 2022, there were no significant differences in the proportion of MRSA in the states and territories.

From 2019 to 2023, there was a significantly decreasing trend in MRSA in Australia (X^2 for linear trend = 9.95, $P < 0.01$), notably in WA (X^2 for linear trend = 7.88, $P < 0.01$) (Table 45).

Figure 21: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, AGAR, 2014–2023



MRSA = methicillin-resistant *Staphylococcus aureus*
Notes:

1. Percentage resistance determined using EUCAST 2023 breakpoints for all years. Filled circles indicate values for 2023.
2. Number of contributors per year: *n* = 27 in 2014; *n* = 43 in 2015; *n* = 44 in 2016; *n* = 48 in 2017 and 2018; *n* = 51 in 2019, 2020 and 2021; *n* = 55 in 2022, *n* = 56 in 2023.

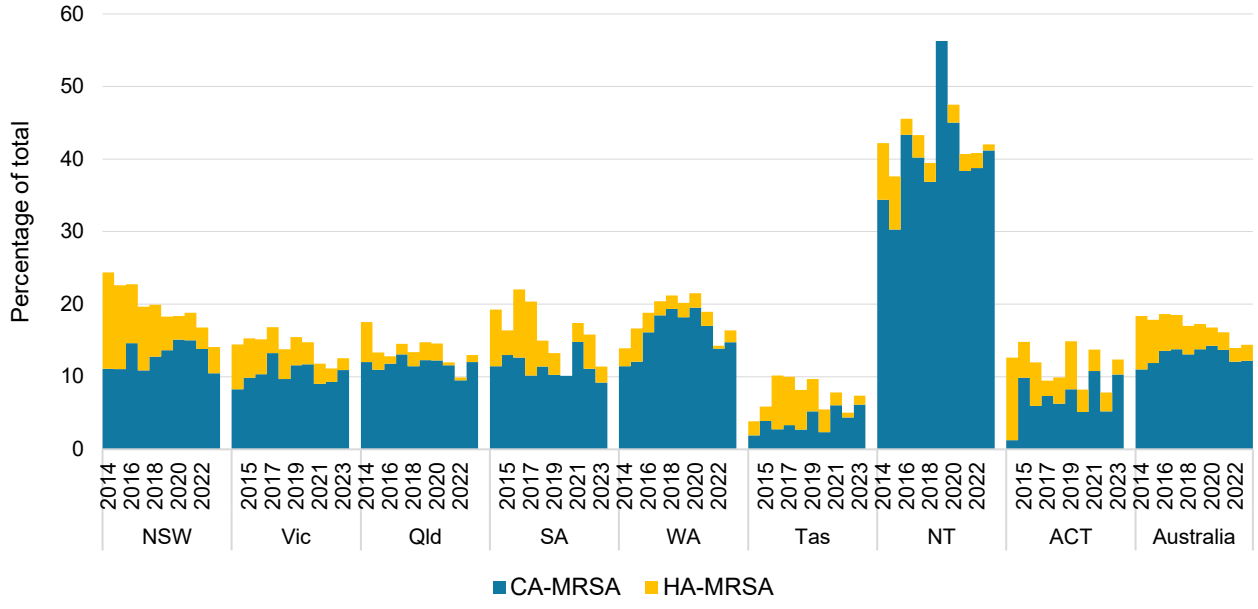
Table 45: *Staphylococcus aureus*, percentage resistant to methicillin (EUCAST) and number tested, state and territory, AGAR, 2014–2023

	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Tasmania	3.8 (52)	5.9 (51)	11.0 (109)	11.0 (91)	8.2 (110)	10.4 (135)	5.5 (127)	7.8 (115)	5.7 (159)	8.0 (163)	↔
Australian Capital Territory	12.7 (79)	14.8 (81)	12.9 (101)	9.5 (95)	9.9 (111)	14.9 (121)	8.2 (97)	13.7 (102)	7.8 (115)	12.4 (97)	↔
Victoria	15.3 (426)	15.5 (407)	15.6 (418)	17.5 (365)	14.0 (414)	15.9 (546)	14.8 (461)	12.5 (615)	11.8 (593)	12.9 (614)	↔
South Australia	20.9 (196)	16.4 (262)	22.3 (278)	20.4 (167)	15.6 (256)	14.7 (238)	10.9 (239)	18.1 (232)	17.1 (234)	13.1 (229)	↔
Queensland	17.8 (550)	13.5 (503)	13.2 (494)	15.0 (553)	14.0 (571)	15.3 (647)	15.9 (473)	12.6 (514)	11.8 (536)	14.3 (607)	↔
Western Australia	13.9 (323)	17.5 (394)	19.6 (413)	20.4 (466)	21.4 (487)	**20.8 (499)**	**21.9 (448)**	**19.1 (513)**	**14.7 (497)**	**16.6 (489)**	▼
New South Wales	24.8 (516)	22.9 (590)	25.3 (637)	20.5 (679)	20.4 (647)	18.7 (907)	19.1 (807)	19.2 (770)	17.8 (982)	17.8 (1,104)	↔
Northern Territory	42.2 (64)	38.2 (110)	45.6 (90)	44.4 (99)	40.3 (77)	56.3 (64)	48.8 (82)	40.7 (86)	42.9 (98)	43.7 (119)	↔
Australia	18.9 (2,206)	18.1 (2,398)	19.7 (2,540)	19.0 (2,515)	17.4 (2,673)	**17.8 (3,157)**	**17.4 (2,734)**	**16.6 (2,947)**	**15.0 (3,214)**	**16.1 (3,422)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing
* Chi-square test for trend for past five years (2019–2023), **bold** text significant decrease ▼ ($P < 0.01$), ↔ no significant difference
Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years.

Since 2014, there were significant decreases in the proportion of HA-MRSA clones nationally (X^2 for linear trend = 178.9, $P < 0.01$); this decrease was seen in all states and territories.

Figure 22: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory and association, AGAR, 2014–2023

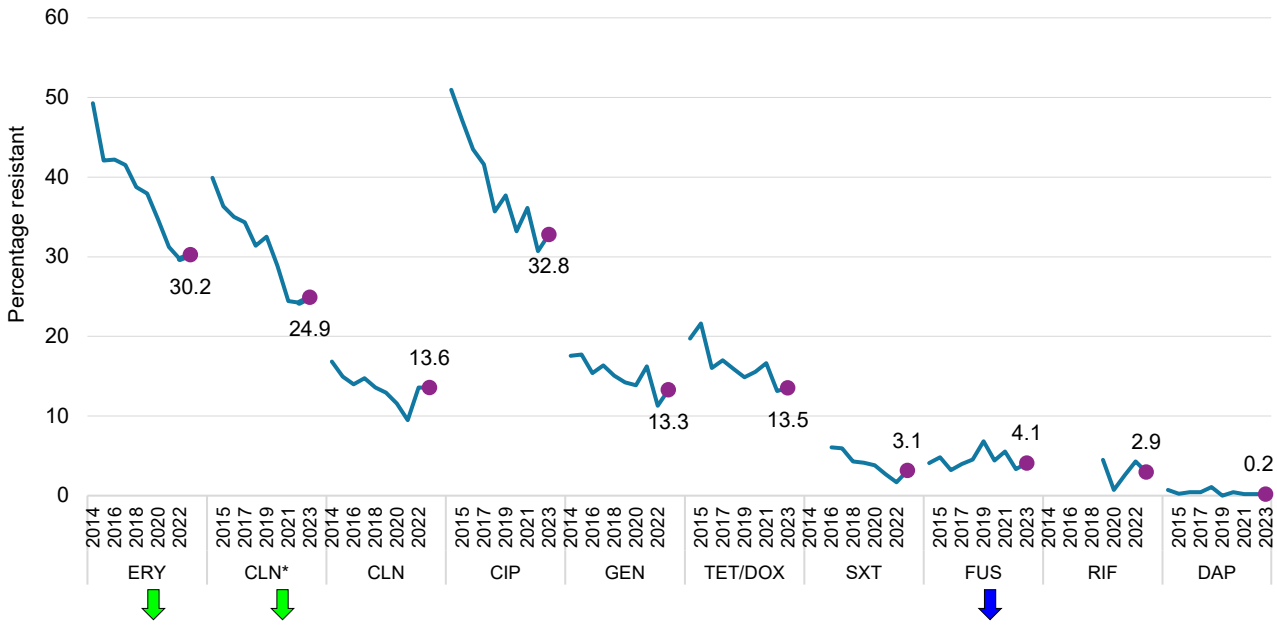


MRSA = methicillin-resistant *Staphylococcus aureus*; CA-MRSA = community-associated MRSA; HA-MRSA = healthcare-associated MRSA

Relative to 2022, the percentage resistance to antimicrobial agents tested against MRSA in 2023 remained stable (Figure 23).

Rates of resistance in MRSA from 2019 to 2023 decreased for erythromycin (χ^2 for linear trend = 9.99, P = < 0.01), clindamycin (inducible + constitutive resistance, [χ^2 for linear trend = 10.63, P < 0.01], and fusidic acid (χ^2 for linear trend = 5.01, P = 0.0252) (Figure 23).

Figure 23: Methicillin-resistant *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2014–2023



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

Notes:

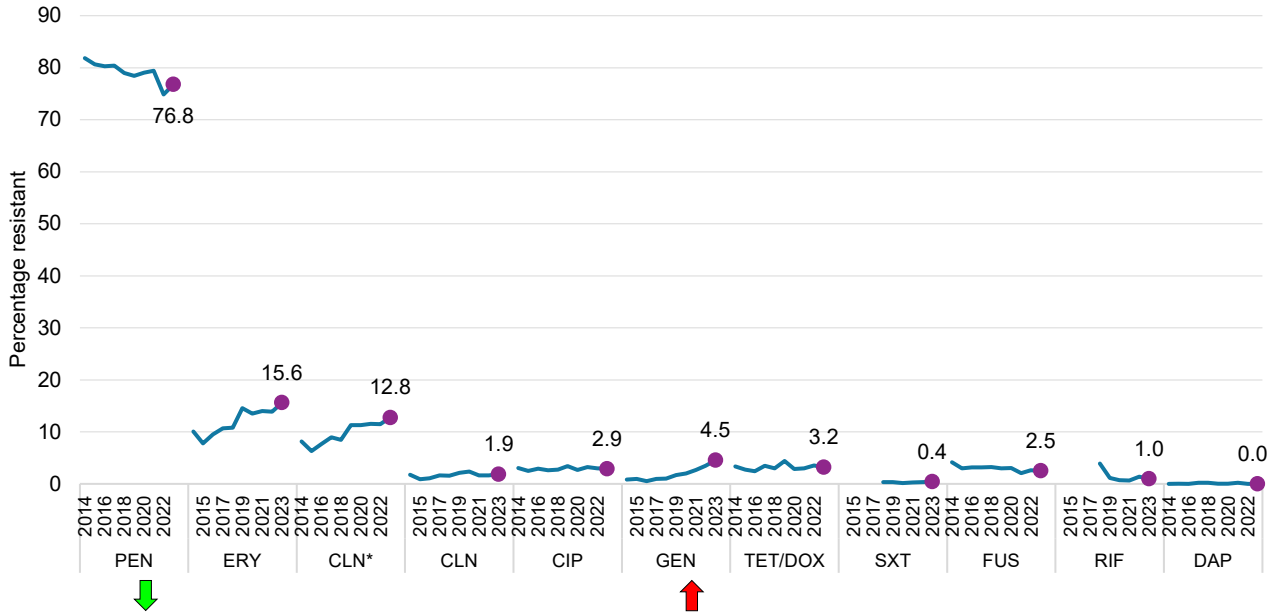
1. Percentage resistance determined using EUCAST 2024 breakpoints for all years Filled circles indicate values for 2023.
2. Down arrows indicate antimicrobial agents for which resistance rates have decreased significantly over the past five years (2019 to 2023), with P < 0.01, shown in green and 0.01 < P < 0.05 in blue.
3. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek® or Phoenix™) was not confirmed by an alternative method in 2014 to 2015.
4. Rifampicin concentration on the Phoenix™ and one Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility (EUCAST) from 2014 to 2018.

Methicillin-susceptible *Staphylococcus aureus*

The percentage resistance for MSSA in 2023 was similar to 2021 for the antimicrobial agents tested, except for gentamicin (3.5% in 2022, 4.5% in 2023, $P = 0.0402$) (Figure 24).

Rates of resistance in MSSA over the past five years increased for gentamicin (χ^2 for linear trend = 47.48, $P < 0.0001$), and decreased for benzylpenicillin (χ^2 for linear trend = 8.34, $P < 0.01$) (Figure 24).

Figure 24: Methicillin-susceptible *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2014–2023



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

Notes:

1. Percentage resistance determined using EUCAST 2024 breakpoints for all years.
2. Down arrows indicate antimicrobial agents for which resistance rates have decreased significantly over the past five years (2019 to 2023), with $P < 0.01$, shown in green.
3. Up arrows indicate antimicrobial agents for which resistance rates have increased significantly over the past five years (2019 to 2023), with $P < 0.01$, shown in red.
4. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek® or Phoenix™) was not confirmed by an alternative method in 2014–2017.
5. Rifampicin concentration on the Phoenix™ and one Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility (EUCAST) from 2014 to 2018.

Gram-negative species

The following sections describe the major trends observed for key Gram-negative species for the period 2014 to 2023.

EUCAST interpretive criteria have been used throughout, with the notable exception of amoxicillin–clavulanic acid. Eighty-two percent of the pathology services used Vitek® cards which have the CLSI formulation (2:1 ratio) for interpretation for susceptibility for this agent.

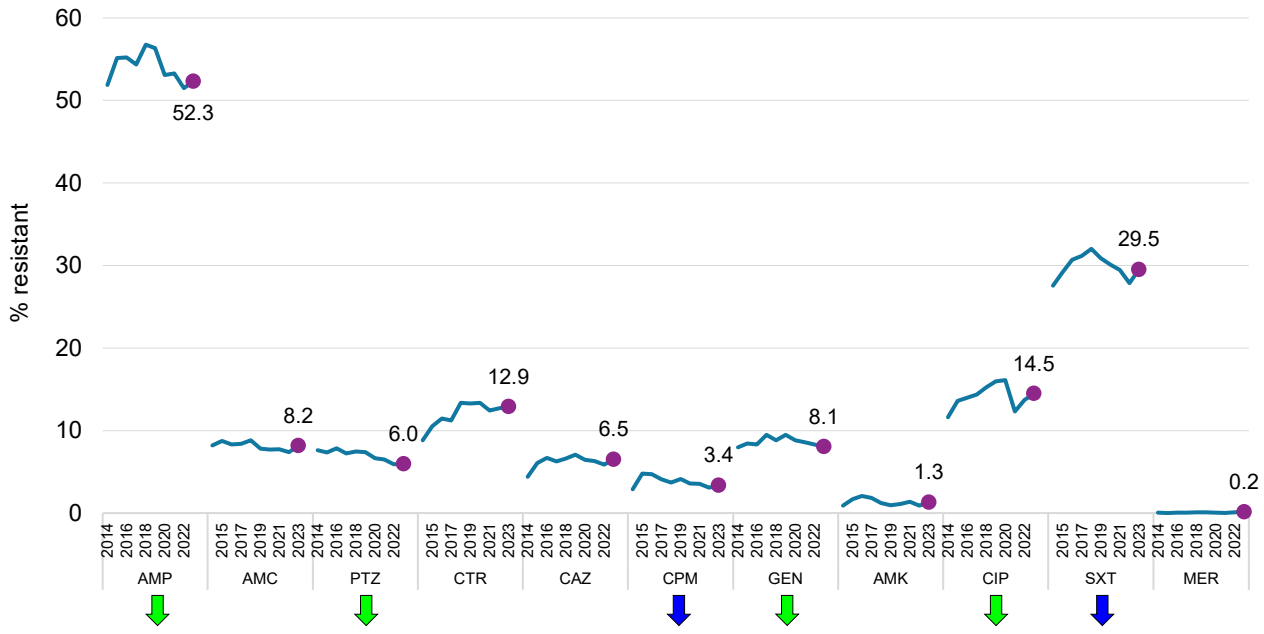
Escherichia coli

National

The percentage resistance for *E. coli* in 2023 was similar to that seen in 2022. There was a slight increase (1.7 percentage point) in resistance to trimethoprim–sulfamethoxazole (Figure 25).

Rates of resistance to several key antimicrobial agents have decreased over the past five years (2019–2023), most notably to ampicillin (X^2 for linear trend = 18.40, $P < 0.001$), piperacillin–tazobactam (X^2 for linear trend = 10.65, $P < 0.01$), ciprofloxacin (X^2 for linear trend = 10.76, $P < 0.01$), and gentamicin (X^2 for linear trend = 7.228, $P < 0.01$) (Figure 25).

Figure 25: *Escherichia coli* resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2014–2023



AMC = amoxicillin–clavulanic acid (2:1 ratio); AMK = amikacin; AMP = ampicillin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; SXT = trimethoprim–sulfamethoxazole

Notes:

1. Percentage resistance determined using EUCAST 2024 breakpoints for all years. Filled circles indicate values for 2023.
2. Down arrows indicate antimicrobial agents for which resistance rates have decreased significantly over the past five years (2019 to 2023), with $P < 0.01$, shown in green and $0.01 < P < 0.05$ in blue.

By state and territory

In 2023, there were no significant changes in ciprofloxacin, third-generation cephalosporin or aminoglycoside resistance for any state or territory compared to 2022.

Over the past five years (2019-2023), in Victoria there was significantly decreasing trends in resistance to ciprofloxacin (X^2 for linear trend = 12.94, $P < 0.01$), third generation cephalosporins (X^2 for linear trend = 17.63, $P < 0.0001$), and aminoglycosides (X^2 for linear trend = 22.53, $P < 0.0001$) in *E. coli* isolates (Tables 46-48). There were increasing resistance trends to third-generation cephalosporins in the NT (X^2 for linear trend = 7.892, $P < 0.01$) and Queensland (X^2 for linear trend = 4.115, $P = 0.0425$) (Figure 47), and decreasing resistance trends to aminoglycosides in Tasmania (X^2 for linear trend = 6.781, $P < 0.01$) (Figure 48).

Table 46: *Escherichia coli*, percentage resistant to ciprofloxacin (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Tas	7.6 (79)	7.6 (79)	10.7 (168)	5.7 (174)	7.6 (184)	12.9 (201)	8.0 (201)	10.6 (218)	6.9 (231)	8.3 (264)	↔
Qld	7.1 (742)	8.7 (691)	9.0 (811)	12.9 (858)	10.3 (868)	10.4 (817)	11.6 (628)	8.5 (693)	10.0 (711)	11.4 (835)	↔
SA	10.9 (386)	9.0 (454)	13.3 (429)	8.3 (288)	11.6 (405)	13.9 (440)	9.8 (479)	8.5 (470)	14.6 (439)	12.4 (380)	↔
Vic	16.2 (722)	14.4 (727)	15.7 (709)	15.6 (794)	18.1 (770)	**18.3 (919)**	**20.0 (899)**	**13.2 (1,085)**	**13.1 (1,053)**	**14.9 (1,106)**	▼
NSW	11.8 (781)	17.7 (1,107)	17.3 (993)	16.3 (1,170)	15.8 (1,224)	16.9 (1,379)	17.5 (1,492)	12.1 (1,281)	16.4 (1,770)	15.2 (1,767)	↔
ACT	12.5 (168)	10.7 (149)	13.6 (154)	12.0 (158)	17.8 (157)	20.5 (185)	15.2 (198)	13.6 (206)	10.0 (190)	16.5 (182)	↔
WA	12.7 (510)	16.2 (650)	15.7 (677)	16.2 (770)	20.5 (801)	17.3 (736)	17.5 (776)	16.2 (740)	14.0 (695)	16.8 (907)	↔
NT	8.2 (97)	9.5 (137)	9.8 (153)	15.6 (141)	12.5 (160)	20.0 (205)	20.8 (197)	17.0 (224)	15.3 (170)	18.7 (193)	↔
Australia	11.6 (3,485)	13.6 (3,994)	14.0 (4,094)	14.4 (4,353)	15.2 (4,569)	**16.0 (4,882)**	**16.1 (4,870)**	**12.3 (4,917)**	**13.7 (5,259)**	**14.5 (5,634)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing
* Chi-square test for trend for past five years (2019–2023), **bold** text significant decrease ▼ ($P < 0.01$), ↔ no significant difference
Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

Table 47: *Escherichia coli*, percentage resistant to ceftriaxone and/or ceftazidime (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Tas	10.1 (79)	0.0 (79)	6.5 (168)	5.2 (174)	7.6 (184)	7.0 (201)	6.0 (201)	6.0 (218)	5.2 (231)	4.9 (264)	↔
Qld	7.1 (742)	6.1 (691)	8.1 (811)	9.4 (858)	11.5 (868)	**8.4 (817)**	**8.9 (628)**	**10.5 (693)**	**11.0 (711)**	**10.9 (835)**	▲
SA	6.2 (386)	7.5 (454)	12.3 (431)	4.8 (289)	9.1 (405)	12.5 (440)	9.2 (479)	11.9 (471)	12.5 (439)	11.6 (380)	↔
Vic	13.0 (722)	12.5 (727)	13.7 (709)	14.2 (794)	17.1 (770)	**16.9 (922)**	**17.0 (899)**	**13.5 (1,086)**	**11.5 (1,054)**	**12.3 (1,108)**	▼
NSW	10.0 (781)	15.4 (1,107)	15.1 (993)	14.4 (1,170)	13.5 (1,224)	15.4 (1,379)	15.7 (1,493)	14.1 (1,280)	14.6 (1,771)	14.6 (1,775)	↔
WA	6.3 (510)	9.7 (650)	11.7 (677)	11.5 (771)	15.6 (801)	12.2 (736)	12.5 (776)	14.4 (741)	12.1 (695)	14.9 (911)	↔
ACT	8.9 (168)	10.7 (149)	9.7 (154)	12.0 (158)	12.7 (157)	16.7 (186)	13.1 (198)	13.1 (206)	16.8 (190)	19.2 (182)	↔
NT	9.3 (97)	8.8 (137)	9.2 (153)	9.2 (141)	17.5 (160)	**16.1 (205)**	**19.8 (197)**	**13.4 (224)**	**28.8 (170)**	**24.7 (194)**	▲
Australia	9.0 (3,485)	10.7 (3,994)	11.8 (4,096)	11.6 (4,355)	13.6 (4,569)	13.5 (4,886)	13.6 (4,871)	12.9 (4,919)	13.1 (5,261)	13.5 (5,649)	↔

EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Chi-square test for trend for past five years (2019–2023), **bold** text significant increase ▲ ($P < 0.01$), ▲ ($< 0.01 < P < 0.05$), significant decrease ▼ ($P < 0.01$), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

Table 48: *Escherichia coli*, percentage resistant to gentamicin and/or tobramycin (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Tas	8.9 (79)	2.5 (79)	6.0 (168)	3.4 (174)	3.8 (184)	**7.0 (201)**	**4.5 (201)**	**3.2 (218)**	**3.9 (231)**	**1.9 (264)**	▼
ACT	10.7 (168)	5.4 (149)	7.1 (154)	13.3 (158)	8.9 (157)	11.3 (186)	10.1 (198)	9.2 (206)	7.4 (190)	6.6 (182)	↔
Vic	10.9 (722)	10.2 (727)	9.3 (709)	12.8 (794)	10.5 (770)	**12.9 (922)**	**11.8 (899)**	**7.7 (1,086)**	**6.7 (1,054)**	**8.3 (1,108)**	▼
SA	6.5 (386)	9.0 (454)	10.7 (431)	6.6 (289)	9.6 (405)	9.3 (440)	8.1 (479)	8.1 (471)	12.3 (439)	8.4 (380)	↔
Qld	8.1 (742)	7.7 (691)	8.1 (811)	9.7 (858)	7.7 (868)	8.4 (817)	8.3 (628)	7.5 (693)	7.5 (711)	8.9 (835)	↔
NSW	9.5 (781)	11.4 (1,107)	9.0 (993)	10.4 (1,170)	10.8 (1,225)	10.4 (1,379)	9.7 (1,493)	10.1 (1,281)	9.5 (1,769)	9.2 (1,773)	↔
WA	7.8 (511)	11.8 (650)	14.8 (677)	12.2 (771)	13.0 (801)	9.6 (736)	9.7 (776)	11.6 (741)	8.8 (695)	9.4 (911)	↔
NT	15.5 (97)	11.7 (137)	12.4 (153)	12.8 (141)	16.9 (160)	18.5 (205)	20.8 (197)	17.4 (224)	22.9 (170)	19.1 (194)	↔
Australia	9.1 (3,486)	9.9 (3,994)	9.9 (4,096)	10.7 (4,355)	10.3 (4,570)	**10.6 (4,886)**	**10.0 (4,871)**	**9.2 (4,920)**	**8.9 (5,259)**	**8.9 (5,647)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Chi-square test for trend for past five years (2019–2023), **bold** text significant decrease ▼ ($P<0.01$), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years

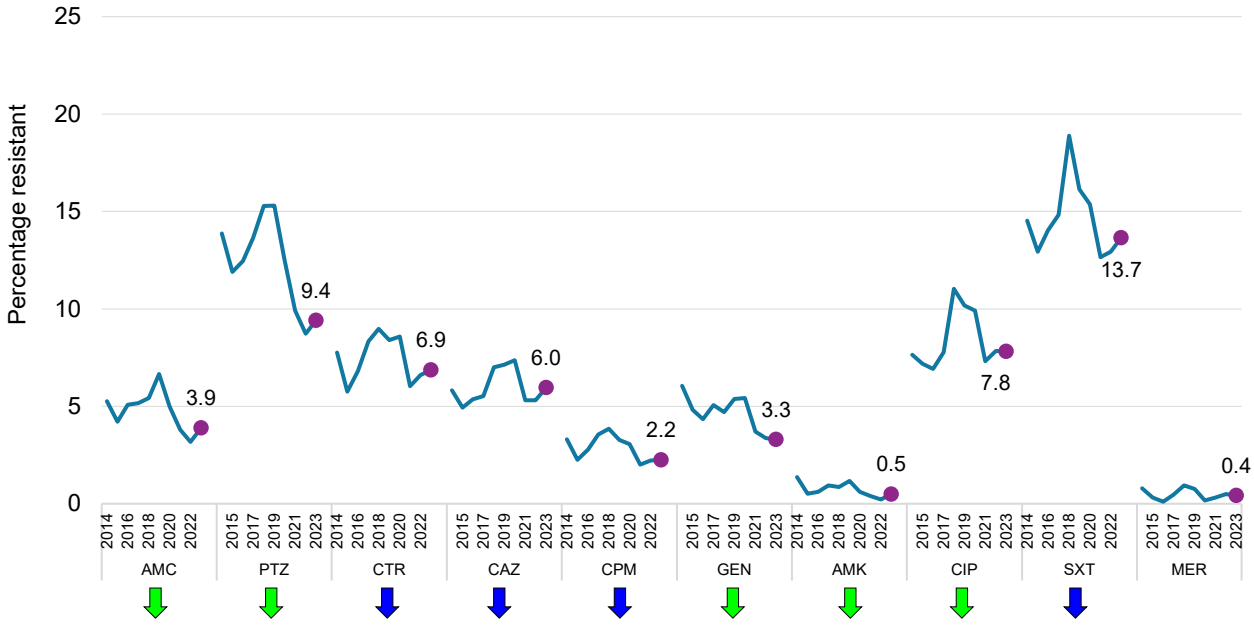
Klebsiella pneumoniae complex

National

The percentage resistance for *K. pneumoniae* complex isolates in 2023 was similar to that seen in 2022. There was a slight increase (0.7 percentage point) in resistance to amoxicillin–clavulanic acid, piperacillin–tazobactam, and trimethoprim–sulfamethoxazole (Figure 26).

Over the past five years (2019–2023), there was a significant decreasing trend in resistance to all antimicrobial agents tested except meropenem. The most notable downward trends were observed for resistance to amoxicillin–clavulanic acid (X^2 for linear trend = 14.15, $P < 0.01$), piperacillin–tazobactam (X^2 for linear trend = 30.59, $P < 0.0001$), gentamicin (X^2 for linear trend = 12.17, $P < 0.01$), amikacin (X^2 for linear trend = 6.747, $P < 0.01$), and ciprofloxacin (X^2 for linear trend = 7.185, $P < 0.01$) (Figure 26).

Figure 26: *Klebsiella pneumoniae* complex resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2014–2023



AMC = amoxicillin–clavulanic acid (2:1 ratio); AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; SXT = trimethoprim–sulfamethoxazole

Notes:

1. Percentage resistance determined using EUCAST 2024 breakpoints for all years. Filled circles indicate values for 2023.
2. Down arrows indicate antimicrobial agents for which resistance rates have decreased significantly over the past five years (2019 to 2023), with $P < 0.01$ shown in green and $0.01 < P < 0.05$ shown in blue.

By state and territory

In 2023, there were no significant changes in ciprofloxacin (Table 49), third-generation cephalosporin (Table 50), or aminoglycoside resistance relative to 2022 (Table 51) in *K. pneumoniae* complex in any state or territory.

Over the past five years (2019-2023), in Victoria there was significantly decreasing trends in resistance to fluoroquinolones (X^2 for linear trend = 11.17, $P < 0.01$), third generation cephalosporins (X^2 for linear trend = 11.32, $P < 0.01$), and aminoglycosides (X^2 for linear trend = 19.59, $P < 0.0001$) in *K. pneumoniae* complex isolates (Tables 49-51). There were decreasing resistance trends in SA for resistance to fluoroquinolones (X^2 for linear trend = 6.121, $P = 0.0134$) (Figure 34), and to aminoglycosides in NSW (X^2 for linear trend = 9.164, $P < 0.01$) and Tasmania (X^2 for linear trend = 4.050, $P = 0.0442$) (Figure 36).

Table 49: *Klebsiella pneumoniae* complex, percentage resistant to ciprofloxacin (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Tas	11.1 (9)	5.6 (18)	5.6 (36)	0.0 (30)	11.8 (34)	7.8 (51)	6.7 (30)	4.5 (44)	8.0 (50)	0.0 (41)	↔
WA	4.7 (149)	5.9 (187)	2.8 (181)	6.3 (159)	7.5 (186)	5.0 (160)	2.6 (189)	3.9 (204)	8.5 (212)	5.4 (204)	↔
NSW	9.3 (205)	7.2 (236)	8.4 (226)	5.5 (293)	9.3 (301)	10.4 (347)	10.2 (371)	8.6 (337)	8.4 (443)	7.1 (439)	↔
ACT	7.7 (26)	5.7 (35)	5.3 (38)	7.7 (39)	8.3 (36)	8.3 (36)	13.2 (38)	4.3 (46)	11.9 (42)	7.1 (56)	↔
SA	5.4 (74)	4.7 (85)	7.4 (81)	2.8 (71)	8.8 (91)	**15.7 (89)**	**9.9 (81)**	**9.6 (114)**	**2.4 (83)**	**7.4 (81)**	▼
Qld	5.3 (208)	6.3 (189)	4.2 (189)	6.1 (246)	5.6 (270)	5.2 (249)	6.5 (185)	8.8 (205)	5.7 (227)	7.5 (254)	↔
Vic	10.3 (174)	11.9 (177)	13.3 (180)	17.6 (199)	24.3 (214)	**17.0 (212)**	**17.7 (209)**	**7.3 (260)**	**7.4 (282)**	**10.6 (303)**	▼
NT	16.1 (31)	4.3 (47)	2.6 (38)	6.7 (30)	13.5 (37)	15.6 (45)	16.2 (37)	6.1 (33)	17.3 (52)	18.6 (43)	↔
Australia	7.6 (876)	7.2 (974)	6.9 (969)	7.8 (1,067)	11.0 (1,169)	**10.2 (1,189)**	**9.9 (1,140)**	**7.3 (1,243)**	**7.8 (1,391)**	**7.8 (1,421)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Chi-square test for trend for past five years (2019–2023), **bold** text significant decrease ▼ ($P<0.01$), ▼ ($< 0.01 < P < 0.05$), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

Table 50: *Klebsiella pneumoniae* complex, percentage resistant to ceftriaxone and/or ceftazidime (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Tas	11.1 (9)	5.6 (18)	5.6 (36)	3.3 (30)	11.8 (34)	7.8 (51)	6.7 (30)	4.5 (44)	8.0 (50)	2.4 (41)	↔
SA	4.1 (74)	3.5 (85)	7.4 (81)	5.6 (72)	9.9 (91)	9.0 (89)	7.4 (81)	6.1 (114)	4.8 (83)	3.7 (81)	↔
Qld	4.3 (208)	3.7 (189)	3.7 (189)	3.3 (246)	5.9 (270)	4.4 (249)	3.8 (185)	2.4 (205)	3.5 (227)	4.7 (254)	↔
WA	4.0 (149)	3.7 (187)	5.5 (181)	5.7 (159)	4.3 (186)	4.4 (160)	3.7 (189)	3.9 (204)	5.2 (212)	5.4 (205)	↔
ACT	11.5 (26)	2.9 (35)	2.6 (38)	10.3 (39)	5.6 (36)	11.1 (36)	7.9 (38)	4.3 (46)	9.5 (42)	8.9 (56)	↔
NSW	12.1 (206)	7.6 (236)	9.7 (226)	7.5 (293)	8.9 (302)	9.8 (348)	9.2 (371)	12.2 (337)	8.1 (444)	9.7 (444)	↔
Vic	10.9 (174)	10.7 (177)	13.9 (180)	19.6 (199)	19.2 (214)	**16.0 (212)**	**16.7 (210)**	**5.0 (260)**	**6.4 (282)**	**9.9 (303)**	▼
NT	6.5 (31)	6.4 (47)	2.6 (38)	6.7 (30)	13.5 (37)	15.6 (45)	27.0 (37)	15.2 (33)	21.2 (52)	13.6 (44)	↔
Australia	7.8 (877)	6.1 (974)	7.6 (969)	8.3 (1,068)	9.6 (1,170)	**9.2 (1,190)**	**9.1 (1,141)**	**6.7 (1,243)**	**6.9 (1,392)**	**7.8 (1,428)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Chi-square test for trend for past five years (2019–2023), **bold** text significant decrease ▼ (P<0.01), ▼ (< 0.01 < P < 0.05), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

Table 51: *Klebsiella pneumoniae* complex, percentage resistant to gentamicin and/or tobramycin (EUCAST) and number tested, state and territory, AGAR, 2014–2023

State and territory	Percentage resistant, (*n*) by year										Trend 2019–2023*
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	
Tas	11.1 (9)	11.1 (18)	2.8 (36)	3.3 (30)	8.8 (34)	**5.9 (51)**	**6.7 (30)**	**0.0 (44)**	**2.0 (50)**	**0.0 (41)**	▼
WA	2.7 (149)	3.2 (187)	5.0 (181)	3.8 (159)	3.8 (186)	3.1 (160)	2.1 (189)	2.5 (204)	3.3 (212)	1.0 (205)	↔
Qld	4.3 (208)	4.2 (189)	3.7 (189)	3.3 (246)	3.0 (270)	2.4 (249)	2.7 (185)	3.4 (205)	2.2 (227)	2.4 (254)	↔
SA	1.4 (74)	5.9 (85)	3.7 (81)	4.2 (72)	7.7 (91)	7.9 (89)	3.7 (81)	6.1 (114)	2.4 (83)	2.5 (81)	↔
NSW	11.2 (206)	8.1 (236)	6.2 (226)	5.5 (293)	5.0 (302)	**9.5 (348)**	**8.9 (371)**	**5.9 (337)**	**5.6 (444)**	**5.0 (443)**	▼
Vic	9.8 (174)	7.9 (177)	10.0 (180)	15.6 (199)	18.7 (214)	**14.2 (212)**	**11.0 (210)**	**4.6 (260)**	**3.5 (282)**	**5.6 (303)**	▼
NT	16.1 (31)	10.6 (47)	2.6 (38)	6.7 (30)	16.2 (37)	13.3 (45)	24.3 (37)	9.1 (33)	13.5 (52)	6.8 (44)	↔
ACT	7.7 (26)	2.9 (35)	2.6 (38)	7.7 (39)	8.3 (36)	11.1 (36)	5.3 (38)	4.3 (46)	11.9 (42)	8.9 (56)	↔
Australia	7.1 (877)	6.2 (974)	5.6 (969)	6.6 (1,068)	7.6 (1,170)	**7.9 (1,190)**	**7.1 (1,141)**	**4.5 (1,243)**	**4.5 (1,392)**	**4.0 (1,427)**	▼

EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Chi-square test for trend for past five years (2019–2023), **bold** text significant decrease ▼ (P<0.01), ▼ (< 0.01 < P < 0.05), ↔ no significant difference

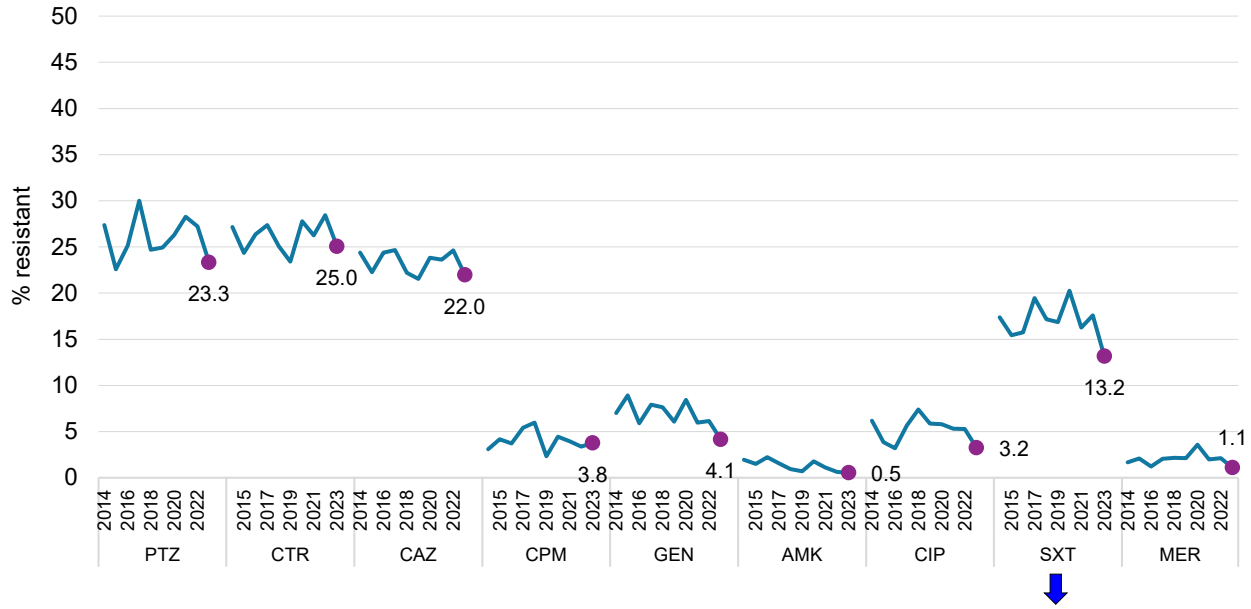
Note: Percentage resistance determined using EUCAST 2024 breakpoints for all years.

Enterobacter cloacae complex

National

For *E. cloacae* complex, the percentage resistance to all key antimicrobials in 2023 was similar to 2022. Over the past five years (2019–2023) there was a significant decreasing trend in resistance to trimethoprim–sulfamethoxazole (X^2 for linear trend = 4.121, P = 0.0424) (Figure 27).

Figure 27: *Enterobacter cloacae* complex resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2014–2023



AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; SXT = trimethoprim–sulfamethoxazole

Notes:

1. Percentage resistance determined using EUCAST 2024 breakpoints for all years. Filled circles indicate values for 2023.
2. Blue down arrows indicate antimicrobial agents with significant decrease ($0.01 < P < 0.05$) over the past five years (2019 to 2023).

Extended-spectrum β-lactamases

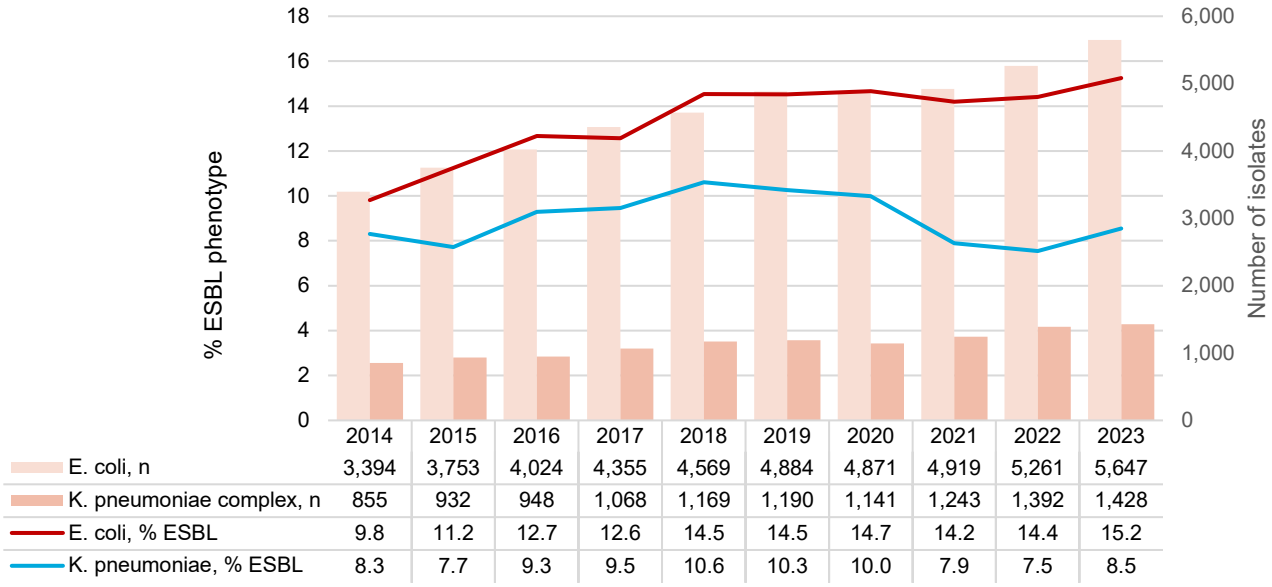
The frequency of *E. coli* with an ESBL phenotype increased from 9.8% in 2014 to 14.5% in 2018, remained at steady at around 14% from 2019 to 2022, and increased to 15.2% in 2023. For the *K. pneumoniae* complex, the frequency of an ESBL phenotype was lower than that observed for *E. coli* and increased from 8.3% in 2014 to around 10% in 2018 to 2020, decreasing to 7.9% in 2021 and 7.5% in 2022, and increasing to 8.5% in 2023 (Figure 28).

ESBL-type β-lactamase genes (alone or with other *bla* genes) continue to be the dominant β-lactam resistance mechanism among *E. coli* and *K. pneumoniae* complex isolates with an ESBL phenotype, with considerable regional variation noted.

Overall, in the 2023 survey there was little change in the proportion of *E. coli* (2022: 581/5226, 11.1%). 2023: 614/5577, 11.0%) (Figure 29), or *K. pneumoniae complex* isolates (2022: 80/1389, 5.8%); 2023: 79/1415, 5.6%) with confirmed ESBL genes relative to 2022 (Figure 30).

Over the past five years (2019–2023) in Victoria, there was a significantly decreasing trend in the proportion of both *E. coli* (X_2 for linear trend = 20.13, $P < 0.0001$) and *K. pneumoniae complex* isolates with at least one confirmed ESBL-genes (X_2 for linear trend = 9.592, $P < 0.01$) (Figures 29 and 30). There were significantly increasing trends in the proportion of *E. coli* with at least one confirmed ESBL-genes seen in the NT (X_2 for linear trend = 9.857, $P < 0.01$) and Queensland (X_2 for linear trend = 5.540, P = 0.0186).

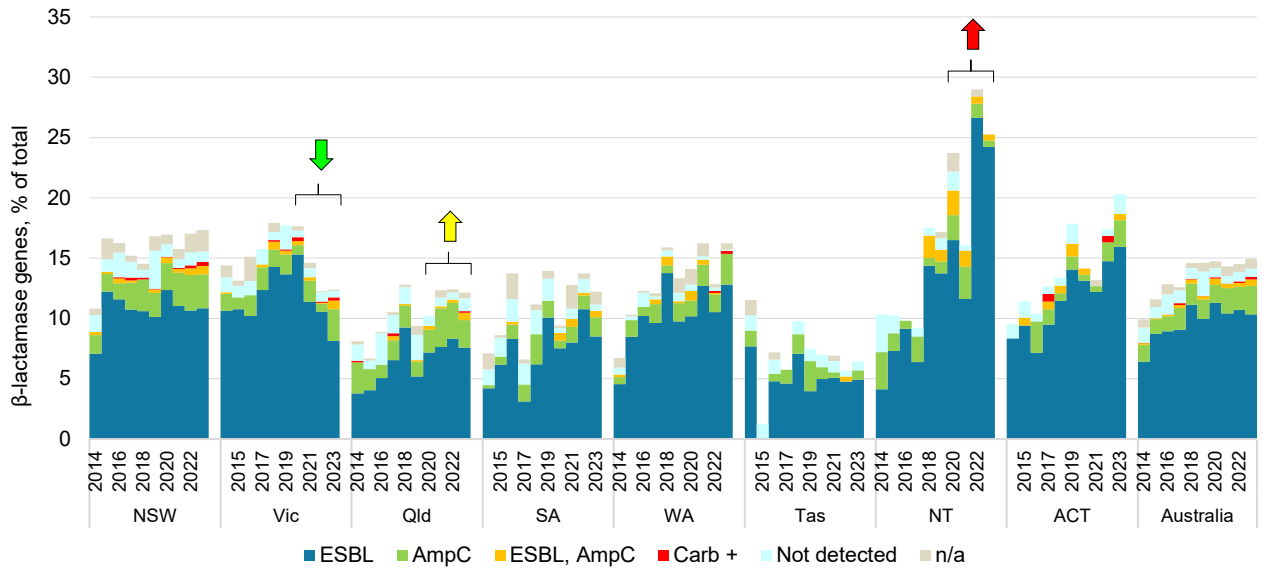
Figure 28: *Escherichia coli* and *Klebsiella pneumoniae* complex isolates with extended-spectrum β-lactamase phenotype, AGAR, 2014–2023



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
E. coli, n	3,394	3,753	4,024	4,355	4,569	4,884	4,871	4,919	5,261	5,647
K. pneumoniae complex, n	855	932	948	1,068	1,169	1,190	1,141	1,243	1,392	1,428
E. coli, % ESBL	9.8	11.2	12.7	12.6	14.5	14.5	14.7	14.2	14.4	15.2
K. pneumoniae, % ESBL	8.3	7.7	9.3	9.5	10.6	10.3	10.0	7.9	7.5	8.5

ESBL = extended-spectrum β-lactamase

Figure 29: β-lactamase genes in *Escherichia coli*, by state and territory, and nationally, AGAR, 2014–2023

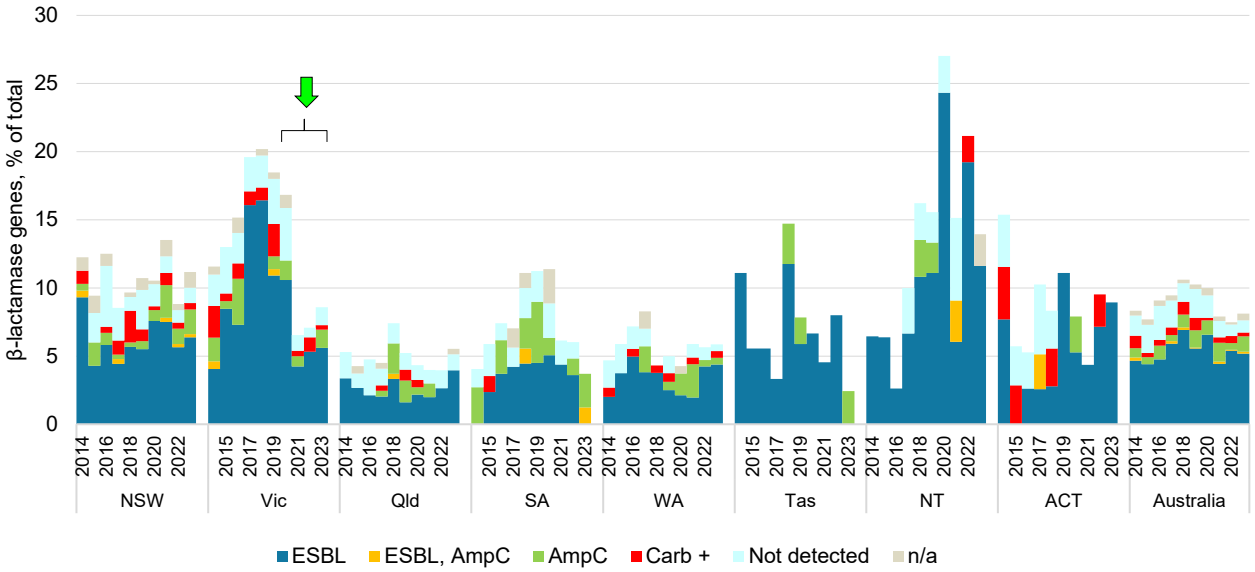


AmpC = plasmid-borne AmpC; Carb + = carbapenemase with or without other β-lactamase genes; ESBL = extended-spectrum β-lactamase; n/a = isolate not available for confirmation by whole genome sequencing

Notes:

1. β-lactamase genes (ESBL-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Down arrows indicate states and territories for which the percentage of ESBL genes have significantly decreased over the past five years (2019–2023), with $P < 0.01$ shown in green.
3. Up arrows indicate states and territories for which the percentage of β-lactamase genes have significantly increased over the past five years (2019–2023), with $P < 0.01$ shown in red, and $0.01 < P < 0.05$ shown in yellow.

Figure 30: β-lactamase genes in *Klebsiella pneumoniae* complex isolates by state and territory, and nationally, AGAR, 2014–2023



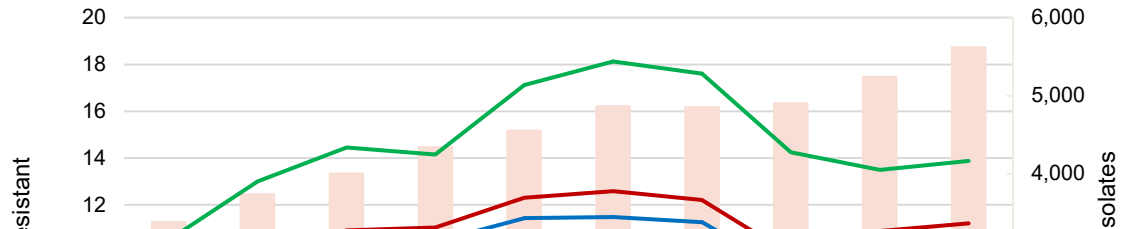
AmpC = plasmid-borne AmpC; Carb + = carbapenemase with or without other β-lactamase genes; ESBL = extended-spectrum β-lactamase; n/a = isolate not available for confirmation by whole genome sequencing
Notes:
1. β-lactamase genes (ESBL-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Green arrow indicates states and territories where there was a significant decrease ($P < 0.01$) in proportion of ESBL genes over the past five years (2019–2023).

Multi-drug resistance

In *E. coli*, the frequency of MDR (to five key antimicrobial groups; aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) increased from 7.9% in 2014 to 11.0% in 2017, remained steady at 12% from 2018 to 2020. There was a decrease in 2021 (9.9%) before increasing to 10.9% in 2022 and to 11.2% in 2023. MDR *E. coli* are more common in hospital-onset episodes, but the increase in overall frequency since 2021 was observed among isolates from community-onset episodes (Figure 31).

For the *K. pneumoniae* complex, the frequency of MDR (to fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) was more variable (Figure 32). For isolates from hospital-onset episodes, the highest frequency was observed from 2018 and 2019 (10.6%–11.2%). It fell sharply in 2020 to 5.4% but has remained stable at less than 4% since 2021. There was little change in frequency among isolates from community-onset episodes; the lowest rate was observed in 2021 (2.0%, down from 4.6% in 2018), and has remained steady at 2% since.

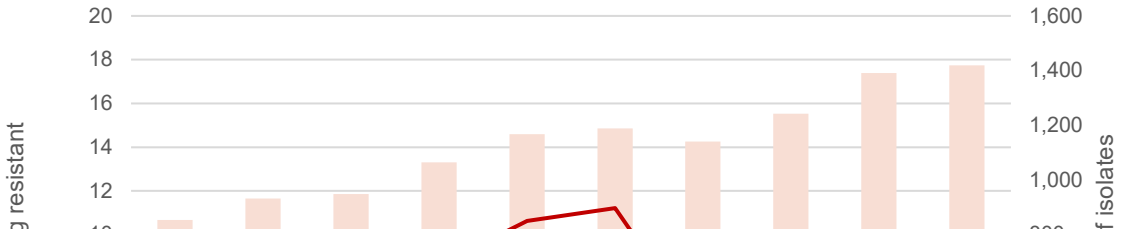
Figure 31: Trends in multi-drug resistance among *Escherichia coli*, by onset, AGAR, 2014 to 2023



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Isolates, n	3,392	3,751	4,016	4,352	4,566	4,878	4,865	4,914	5,254	5,631
Community onset	7.4	9.3	10.2	10.4	11.4	11.5	11.3	9.1	10.3	10.7
Hospital onset	10.5	13.0	14.5	14.1	17.1	18.1	17.6	14.2	13.5	13.9
Overall	7.9	9.9	10.9	11.0	12.3	12.6	12.2	9.9	10.9	11.2

Notes:
1. Multi-drug resistance was defined as resistance to at least one agent in three or more antimicrobial groups
2. Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), fluoroquinolones (ciprofloxacin), and aminopenicillins (ampicillin).

Figure 32: Trends in multi-drug resistance among *Klebsiella pneumoniae* complex isolates by onset, AGAR, 2014 to 2023



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Isolates, n	854	932	948	1,065	1,168	1,189	1,140	1,243	1,391	1,419
Community onset	3.4	2.7	3.2	3.0	4.6	3.5	4.0	2.0	2.2	2.1
Hospital onset	7.5	5.1	4.6	8.6	10.6	11.2	5.4	4.2	4.0	3.7
Overall	4.7	3.4	3.6	4.6	6.3	5.6	4.4	2.7	2.7	2.5

Notes:
1. Multi-drug resistance was defined as resistance to at least one agent in three or more antimicrobial groups.
2. Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), fluoroquinolones (ciprofloxacin).

4. International comparisons

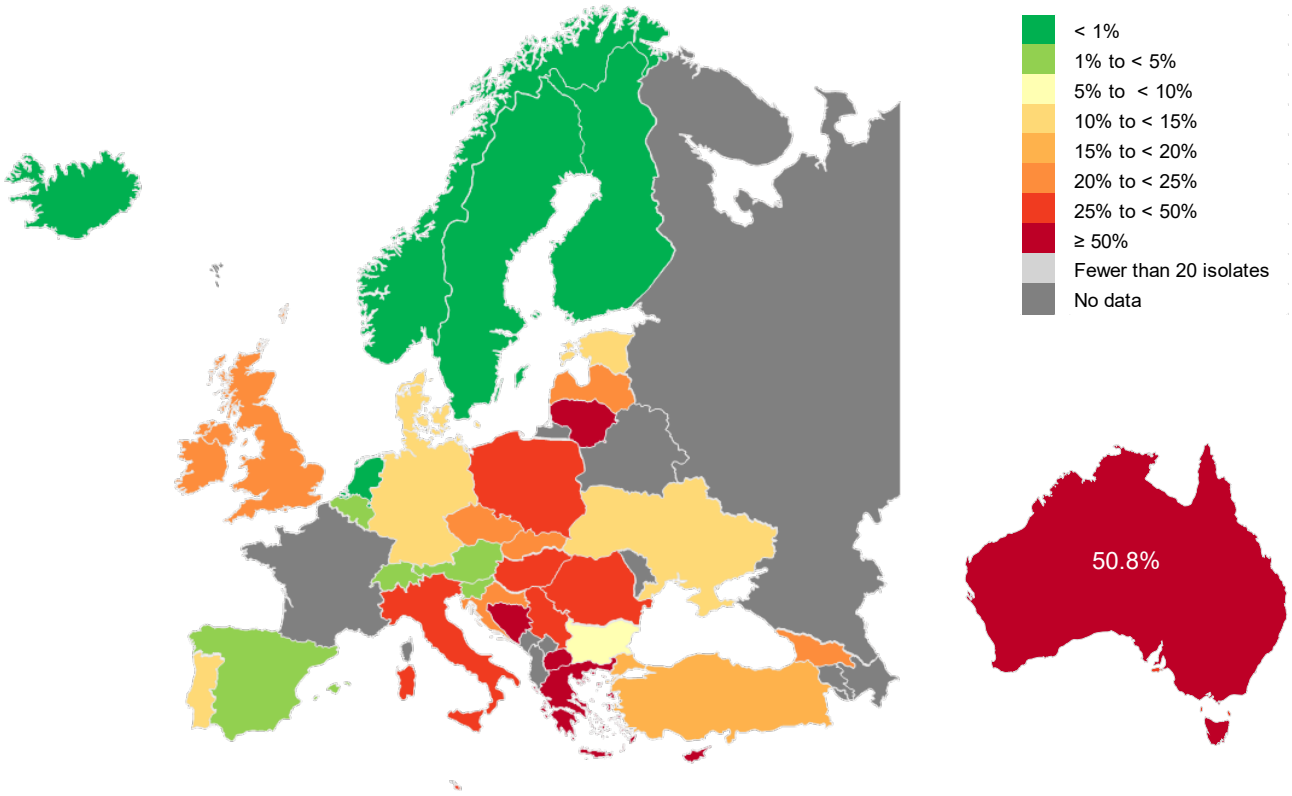
The main international AMR surveillance mechanisms in the WHO European Region are the European Antimicrobial Resistance Surveillance Network (EARS-Net)[20] and the Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network.[21] EARS-Net collects data from countries within the European Union and European Economic Area (EU/EEA), while CAESAR collects data from countries within the WHO European Region that are not included in EARS-Net. Through close collaboration and by using compatible methodologies, the two surveillance networks complement one another, contributing to a pan-European overview of the AMR situation.[21] Both of these programs examine resistance in bacterial pathogens found in bloodstream infections, allowing comparison with AGAR data.

Enterococcus faecium

Australia ranks fifth highest in rates of resistance to vancomycin in *E. faecium* compared to the WHO European region countries (Figure 33). The rate of vancomycin resistance in *E. faecium* in Australia increased from 46.9% in 2022 to 50.8% in 2023.

In 2023, five of the 40 (13%) European countries reported resistance percentages of below 1% (Finland, Iceland, the Netherlands, Norway, and Sweden). Resistance percentages equal to or above 25% were found in 11 (28%) countries, five of which reported percentages equal to or above 50% (Bosnia and Herzegovina, Cyprus, Greece, Lithuania, and Macedonia).

Figure 33: Comparison of *Enterococcus faecium* rates of resistance to vancomycin in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2023



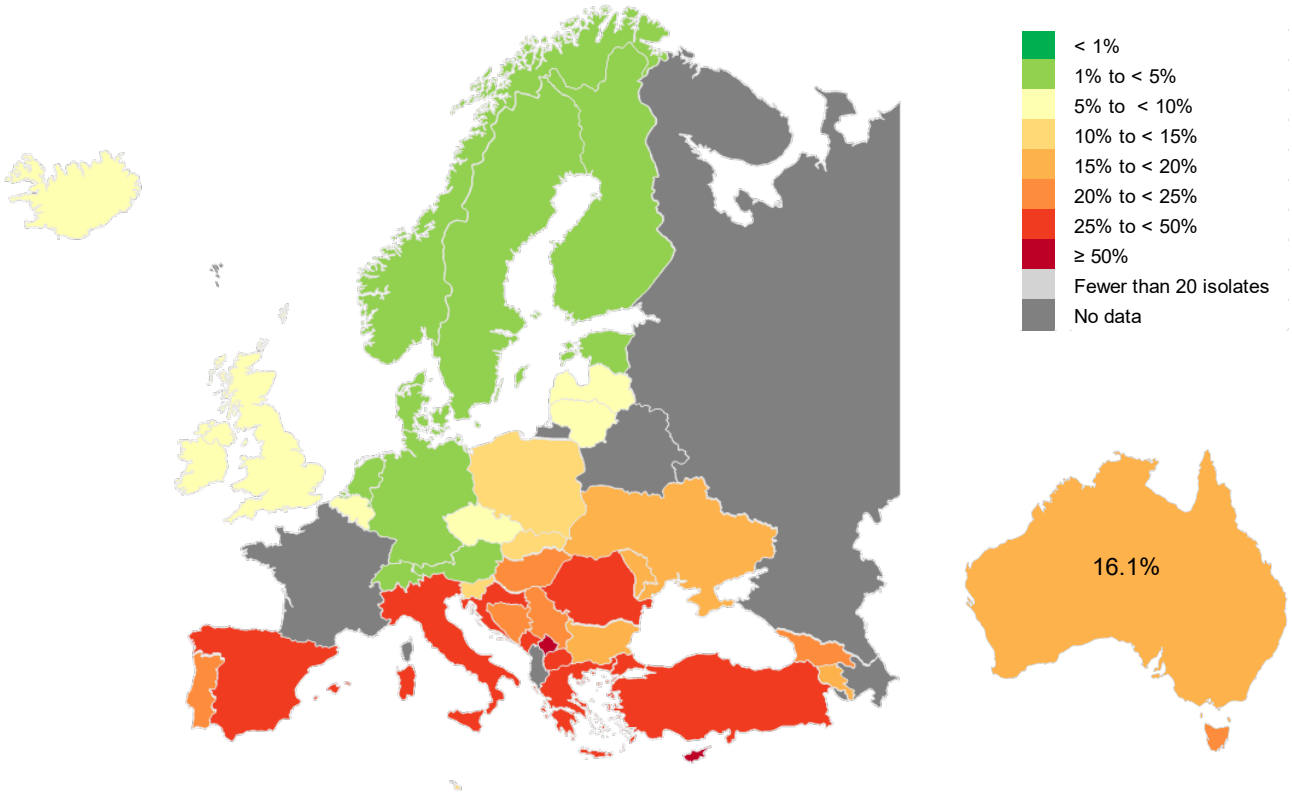
Source: Antimicrobial resistance in Europe[85]

Staphylococcus aureus

Australia ranks towards the middle in rates of resistance to methicillin in *S. aureus* compared to the WHO European region countries (Figure 34). The rate of methicillin resistance in *S. aureus* in Australia increased from 15.0% in 2022 to 16.1% in 2023.

In 2023, nine of the 44 (20%) European countries reporting data on *S. aureus* had MRSA percentages below 5%. MRSA percentages equal to or above 25% were found in 10 (23%) countries (Croatia, Cyprus, Greece, Italy, Kosova, Macedonia, Montenegro, Romania, Spain, and Türkiye), with the resistance rate over 50% in Cyprus and Kosova.

Figure 34: Comparison of *Staphylococcus aureus* rates of resistance to methicillin in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2023



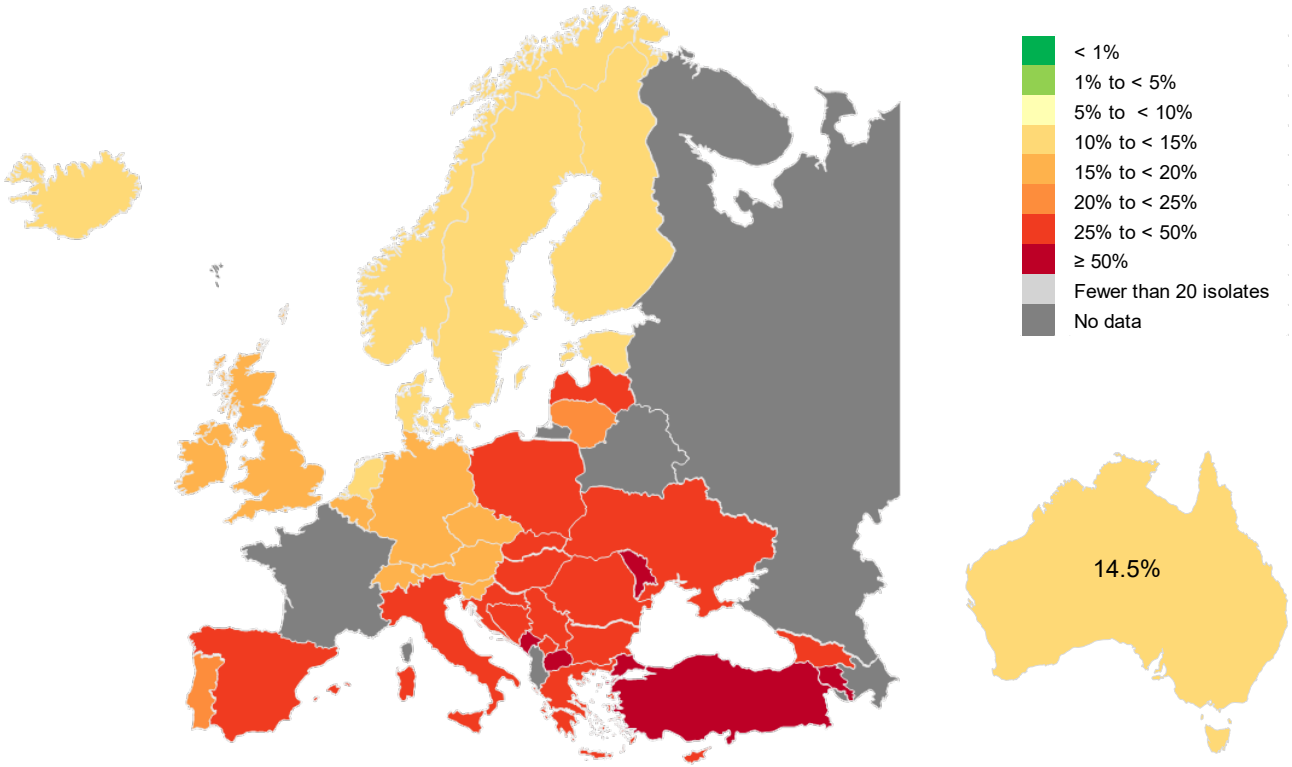
Source: Antimicrobial resistance in Europe[85]

Escherichia coli

Australia ranked in the bottom quarter in rates of resistance to ciprofloxacin in *E. coli* compared to the WHO European region countries (Figure 35). The rate of ciprofloxacin resistance in *E. coli* in Australia increased from 13.7% in 2022 to 14.5% in 2023.

Ciprofloxacin resistance was generally lowest in the northern and western parts of the European countries and highest in southern and eastern parts. In 2023, none of the 44 European countries reported a resistance percentage below 10% for this species. Just over one-half (23/44, 52%) of the countries reported a percentage of 25% or above. Percentages of 50% or more were observed in six countries (Armenia, Kyrgyzstan, North Macedonia, Moldova, Montenegro, and Türkiye).

Figure 35: Comparison of *Escherichia coli* rates of resistance to ciprofloxacin in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2023

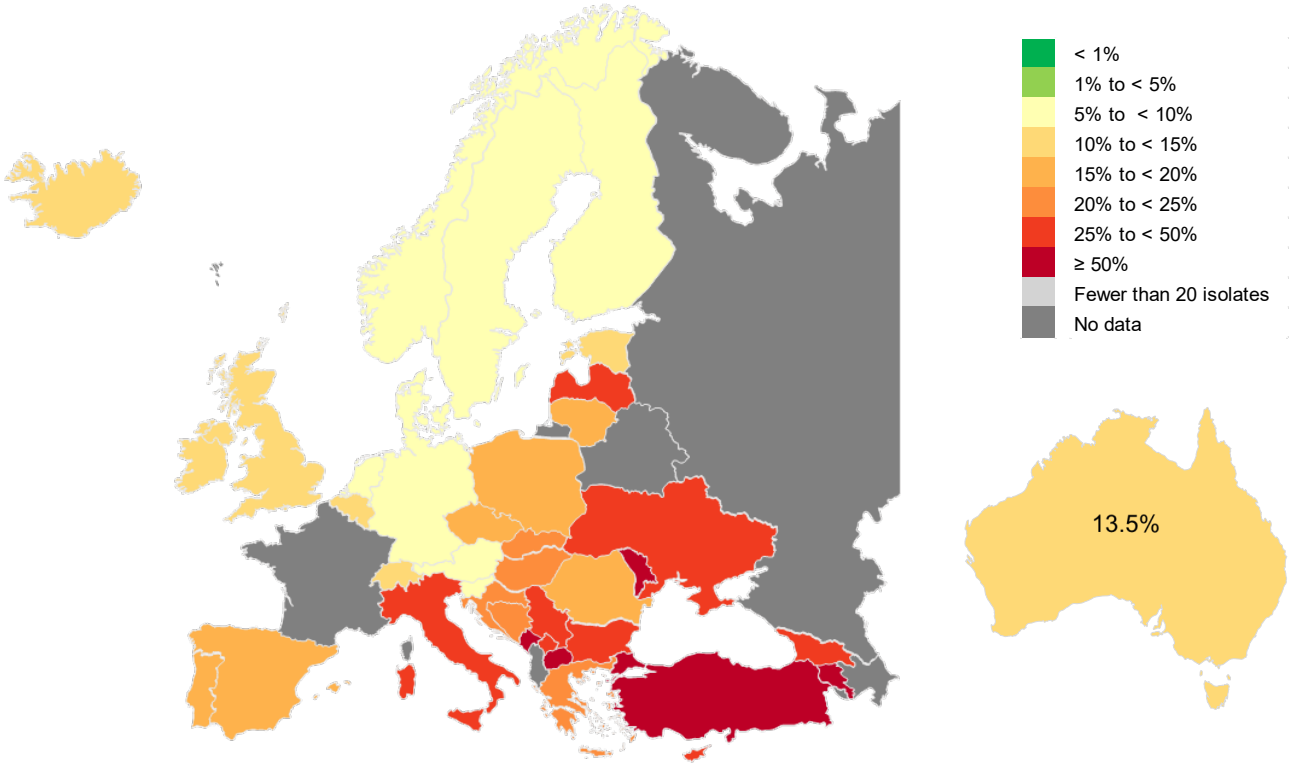


Source: Antimicrobial resistance in Europe[85]

Australia ranks towards the middle in resistance rates to third-generation resistance in *E. coli* compared to the WHO European region countries (Figure 36). The rate of third-generation cephalosporin resistance in *E. coli* in Australia has remained steady (13.1% in 2022, 13.5% in 2023).

For third-generation cephalosporin resistance in *E. coli,* eight (18%) of the 44 European countries reported percentages below 10% in 2023, Almost one-third (14/44, 32%) reported rates of 25% or more, including six (14%) countries of with resistance rates above 50% (Armenia, Kyrgyzstan, Moldova, Montenegro, North Macedonia, and Türkiye).

Figure 36: Comparison of *Escherichia coli* rates of resistance to third-generation cephalosporins in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2023



Source: Antimicrobial resistance in Europe[85]

Klebsiella pneumoniae complex

Australia ranked in the bottom three with Denmark and Finland, in rates of resistance to ciprofloxacin in the *K. pneumoniae* complex isolates compared to the WHO European region countries (Figure 37). The rate of ciprofloxacin resistance in the *K. pneumoniae* complex in Australia was 7.8% in 2022 and 2023.

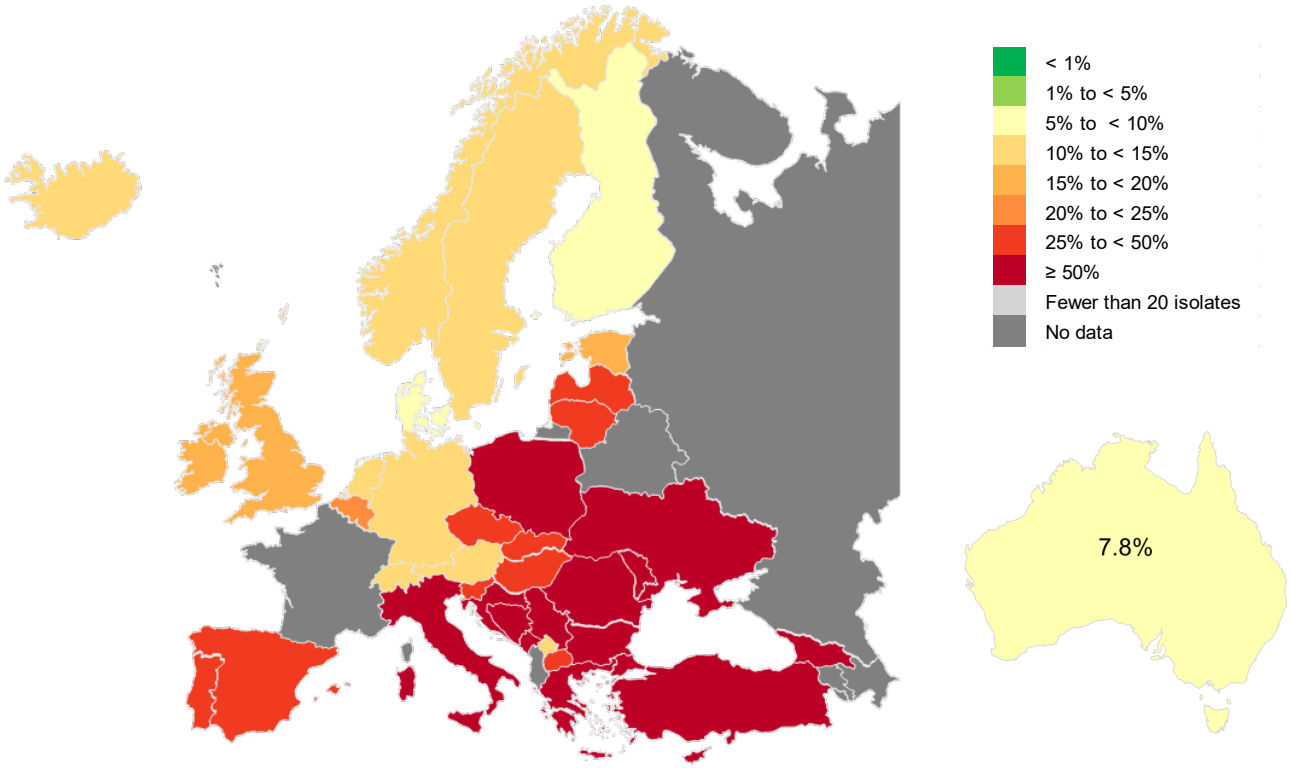
In 2023 resistance to fluoroquinolones in *K. pneumoniae* was generally lowest in the northern and western parts of the European countries and highest in southern and eastern parts (Figure 37). A resistance percentage below 10% was only observed in two (5%) of 44 European countries reporting data on this microorganism. Nineteen (43%) of these countries, particularly in the southern and eastern parts of the Region, reported a resistance percentage of 50% or above, with Ukraine, Serbia, and Moldova reporting rates of 80% or more.

Rates of resistance to third-generation cephalosporins in *K. pneumoniae* complex are low (< 10%) in Australia compared with most of the WHO European region countries (Figure 38). The rate of third-generation cephalosporin resistance in *K. pneumoniae* in Australia has increased slightly (6.9% in 2022; 7.8% in 2023).

Third-generation cephalosporin resistance in this species complex has become quite widespread in European countries. Resistance percentages below 10% were observed in seven (16%) of 44 countries in 2023, while 19 (43%), particularly in the southern and eastern parts of the Region, reported resistance percentages of 50% or above.

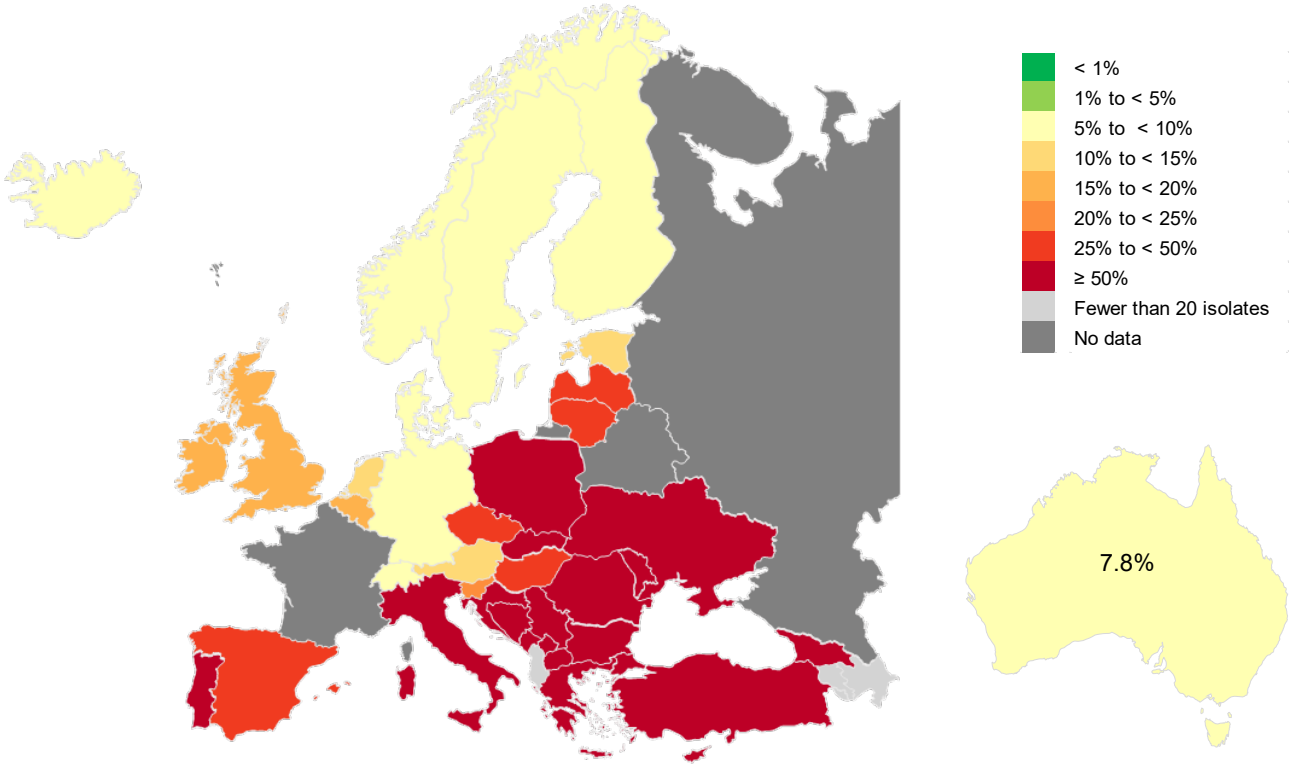
Carbapenem resistance rates in the *K. pneumoniae* complex were generally low in northern and western parts of the WHO European region countries. In 2023, nine (20%) of 44 countries reported resistance percentages below 1% (Figure 39). Fourteen (32%) countries reported percentages equal to or above 25%, eight of which reported resistance percentages equal to or above 50% (Bulgaria, Georgia, Greece, Italy, Moldova, Romania, Serbia, and Ukraine). The rate of carbapenem resistance in *K. pneumoniae* in Australia was very low (0.5% in 2022; 0.4% in 2023).

Figure 37: Comparison of *Klebsiella pneumoniae* complex rates of resistance to ciprofloxacin in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2023



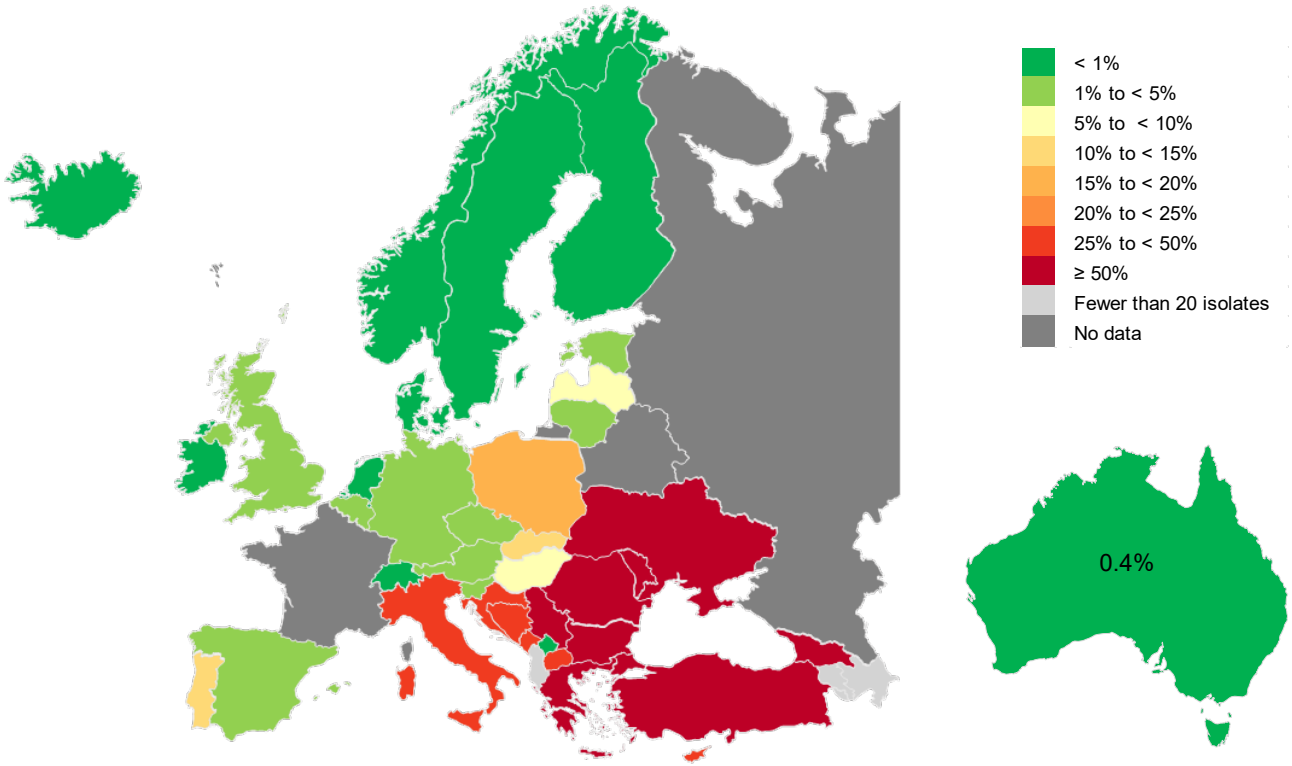
Source: Antimicrobial resistance in Europe[85]

Figure 38: Comparison of *Klebsiella pneumoniae* complex rates of resistance to third-generation cephalosporins in Australia (AGAR) WHO European Region countries, blood culture isolates, 2023



Source: Antimicrobial resistance in Europe[85]

Figure 39: Comparison of *Klebsiella pneumoniae* complex rates of resistance to carbapenems in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2023



Source: Antimicrobial resistance in Europe[85]

5. Limitations of the study

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

- The data are not denominator controlled, and there is currently no consensus on an appropriate denominator for such surveys; hospital size, patient throughput, patient complexity and local antimicrobial use patterns all influence the types of resistance that are likely to be observed
- Although data have been collected from 57 hospitals across Australia, it is not clear how representative the sample is of Australia as a whole, because the proportion of the population that is served by the laboratories that participate in AGAR is not accurately known. Further, it is likely that the proportion of the population served differs in each state and territory
- In 2023, one hospital participating in the GnSOP was unable to contribute at the level they enrolled in for the whole year which limits the available clinical and outcome data (device-related infection, principal clinical manifestation, 30-day all-cause mortality)
- The formulation of amoxicillin–clavulanic acid used in some of the Vitek® cards used in this survey, restricts the ability for interpretation using EUCAST guidelines. Less than 17% of all laboratories used cards that contained the EUCAST formulation in this survey
- Concentration ranges of some antimicrobial agents in both the Vitek® and Phoenix™ cards limit the ability to accurately identify ‘susceptible’ for some combinations of antimicrobial agents and species
- Data are classified into hospital-onset and community-onset infections; some community-onset infections may be healthcare-associated (e.g. discharged patients with indwelling devices)
- Association of resistance genes with relevant genetic mobile elements (for example, plasmid/s) is not included in this report.

6. Discussion and summary

Many of the organisms reported by the AGAR surveillance programs are included in the WHO bacterial priority pathogens list for 2024.[52]

AGAR data show that in 2023, onset of bacteraemia in Australia overwhelmingly occurred in the community, including for episodes of *S. aureus* (77.0%), *E. faecalis* (67.3%), and *Enterobacterales* (78.7%). However, the onset of only 26.6% of *E. faecium* episodes occurred in the community.

In 2023, intra-abdominal infections, other than biliary tract or febrile neutropenia, were the most common clinical manifestations associated with *E. faecium*. For *E. faecalis* episodes, urinary tract infections were the most frequent. Episodes with no detected focus and setting also contributed to high proportions of presentations for enterococcal bacteraemia overall, as well as for both *E. faecalis* and *E. faecium*.

For *S. aureus*, the most frequent principal clinical manifestations were osteomyelitis/septic arthritis and skin and skin structure infections. Strategies to reduce bloodstream infection should consider these clinical manifestations (sources of bloodstream infection). In hospital-onset and other healthcare-associated infections, intravascular devices remain a common source for bloodstream infection. In 2023, 11.9% of all *E. coli* bloodstream infections were associated with indwelling urinary devices such as urinary catheters; this proportion was 23.1% for hospital-onset episodes.

Previous AGAR reports showed a longitudinal trend of increasing *E. coli* resistance to key anti-Gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin.[40, 86] Resistance to both agents stabilised from 2018 to 2020 (ceftriaxone 13.3%–13.4%, ciprofloxacin 15.2%–16.1%); but declined to12.5% and 12.3% respectively in 2021. In 2023, resistance levels increased to12.9% and 14.5%, respectively. Resistance to fluoroquinolones rose steadily in hospital-onset bacteraemia, from 13.7% to 19.8% between 2013 and 2018, to 21.3% in 2019, and to 21.8% in 2020. Resistance decreased to 16.7% in 2021, rose slightly to 17.8% in 2022, and was 17.7% in 2023. In *K. pneumoniae* complex, rates of resistance to ciprofloxacin were lower than for *E. coli*. Resistance in this species complex peaked in 2018–2019 at 11.0%–10.2%, falling to 7.3% in 2021, and was 7.8% in 2022 and 2023.

Two decades ago, ciprofloxacin resistance rates were consistently between 1% and 4%.[40, 86] Despite the concerning recent increase, the percentage of fluoroquinolone-resistant *E. coli* in Australia remains low compared to most European countries.[20, 21] Because fluoroquinolone resistance is often linked to cephalosporin resistance caused by ESBLs of the CTX-M type, fluoroquinolone use alone may not be solely responsible for the increase. It is possible that the high use of oral cephalosporins in the community is driving this resistance.[87]

The proportion of *E. coli* with an ESBL phenotype increased slightly in 2023 compared to 2022 (2022 14.4%; 2023 15.2%). Similarly, the proportion of *K. pneumoniae* complex, with an ESBL phenotype also increased slightly (7.5% in 2022, 8.5% in 2023). A substantial majority (77.7%) of ESBL-producing *E. coli* bloodstream infections were community-onset. This indicates that a substantial reservoir of resistance exists in the community, particularly among the elderly population and in long-term residential care settings.[19, 88] In *E. coli* rates of resistance to ceftriaxone in hospital-onset bacteraemia rose from 13.0% in 2016 to 20.2% in 2019. Rates then declined to 18.8% in 2020, 17.8% in 2021, and to 15.2% in 2022 and were 17.8% in 2023. Community-onset ceftriaxone resistance has remained steady over the years (11.1% in 2016, 11.9% in 2019, 12.4% in 2020, 11.5% in 2021, 12.1% in 2022 and 12.0% in 2023).

To date, CPE remain relatively uncommon in patients with bacteraemia (0.3% in *E. coli* and 0.4% in *K. pneumoniae* complex isolates). While the overall low rates of CPE bloodstream infection are encouraging, some organisms are more likely to harbour them; Namely, 0.9% of *E. cloacae* complex infections harboured a carbapenemase in 2023. Almost three-quarters (22/30, 73.3%) of all CPE carried a $bla_{\text{OXA-48}}$-like gene and/or a bla_{NDM} gene(s), with only one-quarter (n = 8, 26.7%) carrying a $bla_{\text{IMP-4}}$ gene. In 2022, 62.1% (18/29) carried $bla_{\text{IMP-4}}$. Just over three-quarters (23/30, 76.7%) of all CPE were from NSW (n = 17, 56.7%) or Victoria (n = 6, 20.0%).

Eighteen of the participating hospitals, from six states and territories, had at least one isolate with a carbapenemase gene. This reinforces the importance of infection prevention and control programs and adherence to carbapenemase management guidelines to limit transmission of CPE.[16]

No mobile colistin resistance genes other than *mcr-9* or *mcr-10* were detected in any isolates referred for WGS (*n* = 1,344). Although *mcr-9* has recently been found among several species of *Enterobacterales*, it is not associated with a colistin resistant phenotype.[69] However, it is typically found on IncHI2 plasmids that may carry a carbapenemase gene.[70, 71]

E. faecium bacteraemia has significant clinical consequences and resource implications, particularly as it causes increased length of hospital stay. Bacteraemia episodes lead to prolonged hospital stays; the average length of stay in all Australian public hospitals in 2022–23 was 5.1 days without a hospital-acquired complication (HAC), and 21.7 days with a HAC.[89] In 2023, where data were available for episodes of bacteraemia caused by GnSOP isolates, a little over one-half (54.3%) had a length of stay of seven days or more. For episodes of enterococcal bacteraemia, almost one-quarter (23.8%) had a length of stay >30 days; for staphylococcal bacteraemia, this figure was 26.9%.

Thirty-day all-cause mortality due to *E. faecium* in 2023 was 26.3% (community-onset 21.1%; hospital-onset 28.0%). There was no significant difference in 30-day all-cause mortality between vancomycin-susceptible and resistant episodes (23.6% and 28.7%, respectively). The 30-day all-cause mortality associated with *E. coli* hospital-onset infections (13.7%) exceeded community-onset infections (9.1%).

In the 2023 survey, 53.2% of *E. faecium* harboured *vanA* and/or *vanB* genes; up from 48.8% in 2021. Vancomycin, which until recently was the mainstay of therapy for *E. faecium*, can no longer be recommended empirically due to rising resistance rates. Agents with less certain efficacy but much lower resistance rates, such as linezolid, are the alternative.

For almost two decades, unlike in most other countries where vancomycin resistance is problematic, vancomycin resistance in Australia has been dominated by the *vanB* genotype. However, in the 2018 survey, 52.8% of vancomycin-resistant *E. faecium* bloodstream infections were due to *vanA*; increasing from 6.1% in 2013. Since 2019, *vanA* genotype has declined from 48.4% to 28.3% in 2022. In the 2023 survey 14.6% of vancomycin-resistant *E. faecium* harboured the *vanA* gene.

The percentage of *E. faecium* bloodstream isolates that are resistant to vancomycin in Australia is higher than that seen in almost all European countries. In 2022, Australia ranked fourth highest in rates of resistance to vancomycin in *E. faecium* when compared with EU/EEA countries[90] The rate of vancomycin resistance in *E. faecium* in Australia increased to 50.8% in 2023.

Although infection prevention and control strategies are essential for control of this organism, many antimicrobials have been implicated in the development of vancomycin non-susceptible *E. faecium.* Vancomycin is used commonly to empirically treat MRSA. Other broad-spectrum antibiotics which select for enterococci due to intrinsic resistance, especially the third-generation cephalosporins, are widely used in Australia.

The overall rates of MRSA increased from 15.0% in 2022[91] to 16.1% in the 2023 study. This compares with the 2023 EU/EEA population-weighted mean MRSA percentage of 15.8%.[90]

The rate of community-onset SABs that are methicillin-resistant has remained steady. However, CA-MRSA clones (particularly ST93-IV, ST5-IV, ST1-IV, and ST45-V) are becoming an increasing source of hospital-onset bacteraemia. Meanwhile, HA-MRSA cases are decreasing significantly, but the ST22-IV clone of HA-MRSA is now more frequently found in community-onset bacteraemia. The molecular characterisation of MRSA contained within this report identifies opportunities for prevention and control of MRSA bloodstream infections in the Australian setting.

The rapidly changing landscape of MRSA in Australia, as captured by 15 years of AGAR surveillance, was further explored in *Methicillin-resistant* Staphylococcus aureus *in Australia. MRSA bacteraemia – 2013 to 2018*.[54]

In this survey, multi-drug resistance did not appear to influence the rates of 30-day all-cause mortality for *E. coli*, K. *pneumoniae* complex, *E. cloacae* complex, *P. aeruginosa* or *S. aureus* bacteraemia.

It should be noted that outbreaks of organisms can occur in hospitals and other institutional care settings, and substantial transmission occurs before invasive bloodstream infections develop. AGAR data may therefore underestimate local or regional spread of MDR organisms and may not assist with early detection of sentinel resistances, such as certain CPEs. AGAR surveillance data need to be considered alongside other sources of information to provide broader insights into antimicrobial resistance in Australia. The AURA surveillance program enables these assessments through the Australian Passive AMR Surveillance (APAS), National Alert System for Critical Antimicrobial Resistances (CARAlert), and data provided from Sullivan Nicolaides Pathology for private hospitals, aged care homes and general practices, all of which complement AGAR data.

The impact of the COVID-19 pandemic on AMR may be due to a number of contributing factors. COVID-19-related travel restrictions throughout much of 2020 and 2021[92], combined with increased awareness and implementation of antimicrobial stewardship as part of the National Safety and Quality Health Service Standards[2] across Australia, may have contributed to reduced resistance, particularly for ESBLs.

Pharmaceutical Benefits Scheme and Repatriation Pharmaceutical Benefits Scheme data indicate that the COVID-19 pandemic had a profound impact on antimicrobial use in 2020, with a 40% drop in antimicrobials dispensed between March and April in 2020, and usage remaining at this lower level for the rest of the year.[50, 87]

It is also possible that a reduction in elective surgery and, related to this, in post-surgical bloodstream infections, may have occurred during 2020 and 2021.

The 2023 survey suggests that there was a slight increase in resistance rates to pre-COVID levels. Future AGAR surveys will help determine whether the observed increase in resistance rates is sustained.

AGAR surveillance remains core to informing Australia's response to the growing problem of AMR, and it contributes to understanding AMR in Australian human health settings, and internationally through annual contribution of data on five pathogens from blood (*S. aureus*, *K. pneumoniae*, *E. coli*, *Acinetobacter* species and *Salmonella* species) to the WHO GLASS initiative.

Abbreviations

Abbreviation	Term
ACT	Australian Capital Territory
AESOP	Australian Enterococcal Surveillance Outcome Program
AGAR	Australian Group on Antimicrobial Resistance
AMR	antimicrobial resistance
AMS	antimicrobial stewardship
APAS	Australian Passive AMR Surveillance
ASA	Australian Society for Antimicrobials
ASSOP	Australian *Staphylococcus aureus* Surveillance Outcome Program
AURA	Antimicrobial Use and Resistance in Australia
CAESAR	Central Asian and European Surveillance of Antimicrobial Resistance
CA-MRSA	community-associated methicillin-resistant *Staphylococcus aureus*
CARAlert	National Alert System for Critical Antimicrobial Resistances
CI	confidence interval
CLSI	Clinical and Laboratory Standards Institute
CO	community-onset
CPE	carbapenemase-producing *Enterobacterales*
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECOFF	epidemiological cut-off value
ESBL	extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
GLASS	Global Antimicrobial Resistance and Use Surveillance System
GnSOP	Gram-negative Surveillance Outcome Program
HA-MRSA	healthcare-associated methicillin-resistant *Staphylococcus aureus*
HO	hospital-onset
IV	intravenous
MDR	multidrug-resistant
MIC	minimum inhibitory concentration
MLST	multi-locus sequence type
MRSA	methicillin-resistant *Staphylococcus aureus*
MSSA	methicillin-susceptible *Staphylococcus aureus*
NSQHS	National Safety and Quality Health Service
NSW	New South Wales
NT	Northern Territory
PCR	polymerase chain reaction
PMQR	plasmid mediated quinolone resistance
Qld	Queensland
QRDR	quinolone-resistant determining region
RMT	ribosomal methyltransferase

Abbreviation	Term
SA	South Australia
SAB	*Staphylococcus aureus* bacteraemia
Tas	Tasmania
Vic	Victoria
VRE	vancomycin-resistant enterococci
WA	Western Australia
WGS	whole genome sequencing
WHO	World Health Organization

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Appendix A. Study design

Fifty-seven hospitals participated in the 2023 survey, 49 adult and eight children's hospitals. All states and territories were represented. The hospital peer group/type[93] represented were:

Principal referral hospitals (*n* = 27)
Public acute group A hospitals (*n* = 6)
Children's hospitals (*n* = 7)
Combined Women's and children's hospitals (*n* = 1)
Private acute group A hospitals (*n* = 2)
Private acute group B hospitals (*n* = 1)
Regional and district hospitals from north-west regional WA (*n* = 13)

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

The 33 laboratories that serviced the hospitals participating in AGAR collected all enterococcal and staphylococcal isolates from different patient episodes of bloodstream infection, and either all isolates or up to 200 isolates for the Gram-negative Surveillance Outcome Program. In patients with more than one isolate, a new episode was defined as a new positive blood culture if collected more than two weeks after the initial positive culture.

An episode was defined as CO if the first positive blood culture was collected 48 hours or less after admission, and as HO if collected greater than 48 hours after admission.

All laboratories that participated in AGAR obtained basic laboratory information for each patient episode plus various demographic information, depending on the level at which they are enrolled in the program, Bronze or Silver (Tables A1–A3). Bronze level laboratories provided date of collection, date of birth, sex, postcode and admission date. Silver level laboratories also provided discharge date, device-related infection, principal clinical manifestation, outcome at seven and 30 days from date of collection, and date of death if appropriate.

In 2023, one hospital from Queensland was able to recommence their participation. One NSW hospital was not able to contribute data to AESOP or Quarter four of ASSOP. For GnSOP, one hospital from Queensland was only able to participate for Quarter one, and one hospital from NSW contributed Quarter One GnSOP data at Silver level, but at Bronze level for the remaining quarters

Table A1: Level of participation of laboratories that contributed data on Gram-negative* bacteraemia, by state and territory, 2023

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	14	2	12†
Victoria	8	0	8
Queensland	8§	1	7§
South Australia	3	0	3
Western Australia	19#	2	17#
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	57	6	51

* *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
† One hospital participated at Silver level for Quarter one and at Bronze level for the remaining quarters
§ One hospital participated for Quarter One only
# Includes 13 regional and district hospitals from north-west WA

Table A2: Level of participation of laboratories that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2023

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	14†	1	13
Victoria	8	0	8
Queensland	8	0	8
South Australia	3	0	3
Western Australia	19*	2	17*
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	57	4	53

* Includes 13 regional and district hospitals from north-west Western Australia
† One hospital participated for three quarters only

Table A3: Level of participation of laboratories that contributed data on enterococcal bacteraemia, by state and territory, 2023

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	13	2	11
Victoria	8	0	8
Queensland	8	0	8
South Australia	3	0	3
Western Australia	19*	2	17*
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	56	5	51

* Includes 13 regional and district hospitals from north-west Western Australia

Appendix B. Methods

Species identification

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

Susceptibility testing

Testing was performed using two commercial semi-automated methods: Vitek® 2 (bioMérieux) (*n* = 30) and Phoenix (BD) (*n* = 3), which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution. Commercially available Vitek® 2 (AST-N246, AST-N410, AST-N435, AST-P612, AST-P643, or AST-P656) or Phoenix™ (NMIC-422, or PMIC-84) cards were used by all participants throughout the survey period.

The CLSI M100[46] and the EUCAST v14.0[47] breakpoints from January 2024 were used in the analysis.

S. aureus were classified as MRSA if cefoxitin screen positive (Vitek®) or cefoxitin MIC > 4 mg/L (Phoenix™) and *mecA* or SCC*mec* was detected. Cefoxitin screen negative isolates that were oxacillin-resistant underwent *mecA*/*nuc* PCR or WGS. If *mecA* or SCC*mec* was detected, the isolate was reported as MRSA. All *S. aureus* with penicillin MIC ≤ 0.12 mg/L and no β-lactamase results provided were tested for penicillinase by disc diffusion. A sharp zone edge around a penicillin disc (1 unit, EUCAST or 10 unit, CLSI) was recorded as a penicillinase producer.[46, 47]

Additional tests were performed on *S. aureus* to confirm unusual resistances or to provide additional information for antimicrobials where issues have been reported with Vitek®/Phoenix™ panels.[94-96]

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

Additional tests performed on *E. faecalis* and *E. faecium* include:

- E-test MIC if:
  - Linezolid MIC > 4 mg/L, or if MIC not provided
  - Daptomycin MIC > 4 mg/L
  - Vancomycin and teicoplanin if MIC not provided or discrepant with *van* gene
  - Ampicillin MIC > 8 mg/L (*E. faecalis*) or ampicillin MIC ≤ 4 mg/L (*E. faecium*), or if MIC not provided.
- *van* gene PCR on *E. faecalis* if:
  - Vancomycin MIC > 4 mg/L or teicoplanin MIC > 2 mg/L, and *van* gene not provided.

Clinical and outcome data

Device-related infection
Device-related bloodstream infection is defined as a bloodstream infection 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 bloodstream infections associated with biliary stents.

Principal clinical manifestation

For AGAR surveys, the principal clinical manifestation for each patient episode was classified for each program as indicated in Table B1.

Table B1: Principal clinical manifestations for patient episodes of bacteraemia, AGAR, 2023

Principal Clinical Manifestation	ASSOP	AESOP	GnSOP
Biliary tract infection (including cholangitis)	No	Yes	Yes
CNS infection (meningitis, abscess(es))	Yes	No	No
Deep abscess(es) excluding those in the CNS	Yes	No	No
Device-related infection with metastatic focus	Yes	Yes	Yes
Device-related infection without metastatic focus	Yes	Yes	Yes
Endocarditis (left-sided)	Yes	Yes	No
Endocarditis (right-sided)	Yes	Yes	No
Febrile neutropenia	Yes	Yes	Yes
Intra-abdominal infection other than biliary tract	No	Yes	Yes
No identifiable focus	Yes	Yes	Yes
Osteomyelitis/septic arthritis	Yes	Yes	Yes
Other clinical syndrome	Yes	Yes	Yes
Pneumonia/empyema	Yes	No	No
Skin and skin structure infection	Yes	Yes	Yes
Urinary tract infection	No	Yes	Yes

AESOP = Australian Enterococcal Surveillance Outcome Program; ASSOP = Australian *Staphylococcus aureus* Surveillance Outcome Program; CNS = central nervous system; GnSOP = Gram-negative Surveillance Outcome Program; No = not included; Yes = included

Length of hospital stay following bacteraemia

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

All-cause mortality

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

Antimicrobials tested

The antimicrobials tested is shown in Table B2.

Table B2: Antimicrobials available on susceptibility testing cards and interpretive guidelines for CLSI and EUCAST

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v14.0†		
	S	SDD	I	R	S, SD	S, IE	R
Benzylpenicillin							
Enterococcus spp.	≤8		–§	≥16	–#	–#	–#
Staphylococcus aureus	≤0.12		–§	≥0.25	≤0.125	–§	>0.125
Amikacin							
Acinetobacter spp.	≤16		32	≥64	≤8	–§	>8
Enterobacterales	≤16		32	≥64	≤8	–§	>8
Pseudomonas spp.	≤16		32	≥64	≤16	–§	>16
Amoxicillin–clavulanic acid (2:1 ratio)**							
Enterobacterales	≤8/4		16/8	≥32/16	–#	–#	–#
Ampicillin							
Enterobacterales	≤8		16	≥32	≤8	–§	>8
Enterococcus spp.	≤8		–§	≥16	≤4	8	>8
Aztreonam (Phoenix™ card)							
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤0.001	0.002–16	>16
Cefazolin							
Enterobacterales	≤2‡		4‡	≥8	≤0.001	0.002–4	>4
Cefepime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤2	4–8	–§	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤0.001	0.002–8	>8
Cefalexin	–#		–#	–#	≤16	–§	>16
Cefuroxime (Phoenix™ card)							
Enterobacterales (parental)	≤8		16	≥32	≤0.001	0.002–8	>8
Enterobacterales (oral)	≤4		8–16	≥32	≤8	–§	>8
Cefoxitin							
Enterobacterales	≤8		16	≥32	–#	–#	–#
Ceftazidime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤0.001	0.002–8	>8
Ceftolozane–tazobactam							
Enterobacterales	≤2/4		4/4	≥8/4	≤2	–§	>2
Pseudomonas spp.	≤4/4		8/4	≥16/4	≤4	–§	>4
Ceftriaxone							
Acinetobacter spp.	≤8		16–32	≥64	–#	–#	–#
Enterobacterales	≤1		2	≥4	≤1	2	>2
Chloramphenicol (Phoenix™ card)							
Staphylococcus aureus	≤8		16	≥32	–#	–#	–#

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v14.0†		
	S	SDD	I	R	S, SD	S, IE	R
Ciprofloxacin							
Acinetobacter spp.	≤1		2	≥4	≤0.001	0.002–1	>1
Enterobacterales§§	≤0.25		0.5	≥1	≤0.25	0.5	>0.5
Salmonella spp.‡	≤0.06		0.12–0.5	≥1	≤0.06	–§	>0.06
Staphylococcus aureus	≤1		2	≥4	≤0.001	**0.002–2**	**>2**
Pseudomonas spp.	≤0.5		1	≥2	≤0.001	0.002–0.5	>0.5
Clindamycin							
Staphylococcus aureus	≤0.5		1–2	≥4	≤0.25	–§	>0.25
Colistin (Phoenix™ card)							
Acinetobacter spp.	–#		≤2	≥4	≤2	–§	>2
Enterobacterales	–#		≤2	≥4	≤2	–§	>2
Pseudomonas spp.	–#		≤2	≥4	≤4	–§	>4
Daptomycin							
Enterococcus faecium		≤4	–	≥8	–#	–#	–#
Enterococcus spp. other than *E. faecium*	≤2		4	≥8	–#	–#	–#
Staphylococcus aureus	≤1		–#	–#	≤1	–§	>1
Doxycycline (Phoenix™ card)							
Enterococcus spp.	≤4		8##	≥16##	–#	–#	–#
Staphylococcus aureus	≤4		8##	≥16##	≤1	–§	>1
Ertapenem (Phoenix™ card)	≤0.5		1	≥2	≤0.5	–§	>0.5
Erythromycin							
Enterococcus spp.	≤0.5		1–4	≥8	–#	–#	–#
Staphylococcus aureus	≤0.5		1–4	≥8	≤1	–§	>1
Fosfomycin (Phoenix™ card)							
Enterobacterales	≤64		128	≥256	≤32	–§	>32
Fusidic acid							
Staphylococcus aureus	–#		–#	–#	≤1	–§	>1
Gentamicin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	>4
Enterobacterales	≤4		8	≥16	≤2	–§	>2
Pseudomonas spp.	≤4		8	≥16	–#	–#	–#
Staphylococcus aureus	≤4		8	≥16	≤2	–§	>2
Imipenem (Phoenix™ card)							
Acinetobacter spp.	≤2		4	≥8	≤2	4	>4
Enterobacterales	≤1		2	≥4	≤2	4	>4
Enterococcus spp.	–#		–#	–#	≤0.001	0.002–4	>4
Pseudomonas spp.	≤2		4	≥8	≤0.001	0.002–4	>4
Linezolid							
Enterococcus spp.	≤2		4	≥8	≤4	–§	>4
Staphylococcus aureus	≤4		–§	≥8	≤4	–§	>4
Meropenem							
Acinetobacter spp.	≤2		4	≥8	≤2	4–8	>8
Enterobacterales	≤1		2	≥4	≤2	4–8	>8
Pseudomonas spp.	≤2		4	≥8	≤2	4–8	>8
Nitrofurantoin							

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v14.0†		
	S	SDD	I	R	S, SD	S, IE	R
Enterobacterales	≤32		64	≥128	≤64[***]	–[§]	>64[***]
Enterococcus spp.	≤32		64	≥128	≤64[‡†]	–[§]	>64[‡†]
Staphylococcus aureus	≤32		64	≥128	–[#]	–[#]	–[#]
Norfloxacin							
Enterobacterales	≤4		8	≥16	≤0.5	–[§]	>0.5
Pseudomonas spp.	≤4		8	≥16	–[#]	–[#]	–[#]
Oxacillin							
Staphylococcus aureus	≤2		–[§]	≥4	–[#]	–[#]	–[#]
Piperacillin–tazobactam							
Acinetobacter spp.	≤16/4		32/4–64/4	≥128/4	–[#]	–[#]	–[#]
Enterobacterales	≤16/4		32/4–64/4	≥128/4	≤8	–[§]	>8
Pseudomonas spp.	≤16/4		32/4–64/4	≥128/4	≤0.001	0.002–16	>16
Quinupristin/Dalfopristin							
Enterococcus faecium	≤1		2	≥4	≤1	–[§]	>1
Rifampicin							
Enterococcus spp.	≤1		2	≥4	–[#]	–[#]	–[#]
Staphylococcus aureus	≤1		2	≥4	≤0.06[§§§]	–[§]	>0.06[§§§]
Teicoplanin							
Enterococcus spp.	≤8		16	≥32	≤2	–[§]	>2
Staphylococcus aureus	≤8		16	≥32	≤2	–[§]	>2
Tetracycline							
Acinetobacter spp.	≤4		8	≥16	–[#]	–[#]	–[#]
Enterobacterales	≤4		8	≥16	–[#]	–[#]	–[#]
Enterococcus spp.	≤4		8	≥16	–[#]	–[#]	–[#]
Staphylococcus aureus	≤4		8	≥16	≤1	–[§]	>1
Ticarcillin–clavulanate							
Acinetobacter spp.	≤16/2		32/2–64/2	≥128/2	–[#]	–[#]	–[#]
Enterobacterales	≤16/2		32/2–64/2	≥128/2	≤8	16	>16
Pseudomonas spp.	≤16/2		32/2–64/2	≥128/2	≤0.001	0.002–16	>16
Tigecycline (Phoenix™ card)	–[#]		–[#]	–[#]	≤0.5	–[§]	>0.5
Tobramycin							
Acinetobacter spp.	≤4		8	≥16	≤4	–[§]	>4
Enterobacterales	≤4		8	≥16	≤2	–[§]	>2
Pseudomonas spp.	≤4		8	≥16	≤2	–[§]	>2
Trimethoprim							
Enterobacterales	≤8		–[§]	≥16	≤4	–[§]	>4
Staphylococcus aureus	≤8		–[§]	≥16	–[#]	–[#]	–[#]
Trimethoprim–sulfamethoxazole							
Acinetobacter spp.	≤2/38		–[§]	≥4/76	≤2/38	4/76	>4/76
Enterobacterales	≤2/38		–[§]	≥4/76	≤2/38	4/76	>4/76
Staphylococcus aureus	≤2/38		–[§]	≥4/76	≤2	4	>4
Vancomycin							
Enterococcus spp.	≤4		8–16	≥32	≤4	–[§]	>4
Staphylococcus aureus	≤2		4–8	≥16	≤2	–[§]	>2

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

Note: Information in **blue** boldface type is new or modified since 2023.

* The breakpoints selected to identify resistance are described in the *Performance Standards for Antimicrobial Susceptibility Testing.* 34th *Ed. CLSI supplement* M100, 2024
† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 14.0, 2024 (www.eucast.org)
§ No category defined
# No guidelines for indicated species
** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanic acid at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines. The EUCAST breakpoint is based in intravenous administration
‡ The cefazolin concentration range available on the current Vitek® card restricts the ability to identify the CLSI susceptible and intermediate categories.
§§ The ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. MIC strips were used to determine susceptibility on all *Salmonella* or on those where Vitek® MIC ≤ 0.25 mg/L
The concentration range available on the current Phoenix™ card restricts the ability to identify intermediate and resistant categories
*** Breakpoints apply to *E. coli* from uncomplicated urinary tract infections only
‡† Breakpoints apply to *E. faecalis* from uncomplicated urinary tract infections only
§§§ The rifampicin concentration on the cards restricts category interpretation to non-resistant or resistant

Molecular confirmation of resistance

E. coli, *Klebsiella* spp., and *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone MIC >1 mg/L, or cefoxitin MIC >8 mg/L; any other *Enterobacterales* with cefepime MIC >1 mg/L; all *Enterobacterales* with meropenem MIC >0.125 mg/L (>0.25 mg/L if tested using Vitek®); all *Acinetobacter* isolates and *P. aeruginosa* with meropenem MIC ≥ 8 mg/L; all isolates with amikacin MIC >32 mg/L, and all isolates with colistin MIC > 4 mg/L were referred to a central laboratory (Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research) for WGS.

WGS was performed by 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 or the Australian Genome Research Facility (AGRF) using Illumina platforms. Data were assembled and analysed using a modification of the Nullarbor bioinformatic pipeline[48], incorporating searching contigs against the NCBI AMRFinder database (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA313047) using ABRicate[97] and AMRFinder[98], followed by a custom AMR-specific pipeline which includes a read-based search using ARIBA[99] against the CARD[100] and NCBI databases. Ambiguities and potential multiple gene copies/variants were checked manually by mapping reads to reference genes from https://www.ncbi.nlm.nih.gov/pathogens/isolates#/refgene/ using Geneious. Reported chromosomal mutations were derived from ARIBA result tables (quinolone mutations) or its mapping-based reassemblies (all other mutations). Additional mutations in *gyr* and *par* genes identified by PointFinder[101] potentially contributing to resistance were also examined manually. *fimH* type was predicted by FimTyper.[102] Detection of *H30-Rx* specific SNPs were carried out by *in silico* PCR.[103] Kleborate[77] was used to screen *K. pneumoniae* complex species for virulence loci and K (capsule) serotype.

For ASSOP and AESOP WGS was performed by the Antimicrobial Resistance Infectious Diseases (AMRID) Research Laboratory at Murdoch University using the Illumina NextSeq™ 500 platform. The Nullarbor bioinformatic pipeline[48] was used to identify the multi-locus sequence type and Panton-Valentine leucocidin (MRSA). *van* genes (*E. faecium*), were identified using nucleotide sequences from the NCBI database and a BLAST interface. For MRSA SCC*mec* was determined using KmerFinder v3.2 and the SCCmec database curated from the Center for Genomic Epidemiology database (www.genomicepidemiology.org).

Quality control

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

Data validation

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

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

Appendix C. Susceptibility to antimicrobial agents

Overall percentages of resistance or non-susceptibility for the indicator species of national priority[23] are shown in Table C1. For some antimicrobials, the concentration range tested did not distinguish between intermediate susceptibility (I, CLSI) and resistant (R), and the term non-susceptible (NS) was used to describe these isolates.

Table C1: Activity of antimicrobial agents tested against isolates recovered from patients with bloodstream infection, by state and territory, AGAR, 2023

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Amikacin										
Acinetobacter baumannii complex	n	9	5	13	2	9	1	1	1	41
	%R	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Enterobacter cloacae complex	n	142	93	83	24	63	16	8	19	448
	%R	0.0, 2.1	0.0, 0.0	1.2, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 5.3	0.2, 1.1
Escherichia coli	n	1,281	1,086	686	471	741	218	224	206	4,913
	%R	0.0, 1.3	0.0, 0.8	0.1, 0.9	0.2, 1.1	0.3, 2.4	0.0, 0.0	0.0, 3.6	0.5, 2.4	0.1, 1.4
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%R	0.0, 0.0	0.0, 3.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
Klebsiella oxytoca	n	76	67	28	27	35	12	4	14	263
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%R	0.0, 0.0	0.0, 1.2	0.0, 0.0	0.9, 0.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.2, 2.2	0.2, 0.4
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312
	%R	1.2, 3.5	0.0, 1.2	0.0, 0.0	0.0, 3.3	0.0, 0.0	0.0, 0.0	n/a	n/a	0.3, 1.6
Pseudomonas aeruginosa	n	210	124	141	83	98	20	21	38	735
	%R	0.0, 0.5	0.0, 0.8	0.0, 0.0	0.0, 0.0	0.0, 1.0	5.0, 5.0	0.0, 0.0	0.0, 0.0	0.1, 0.5
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	42	35	15	34	4	1	10	200
	%R	0.0, 0.0	0.0, 4.8	0.0, 2.9	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 1.5
Amoxicillin–clavulanic acid (2:1 ratio)†										
Escherichia coli	n	952	1,086	686	185	740	218	224	206	4,297
	%I	11.0, –§	14.1, –§	8.6, –§	16.2, –§	15.4, –§	10.1, –§	18.3, –§	9.2, –§	12.6, –§
	%R	8.9, –§	7.3, –§	8.0, –§	4.9, –§	9.3, –§	4.6, –§	7.6, –§	4.4, –§	7.7, –§
Klebsiella oxytoca	n	58	67	28	13	35	12	4	14	231
	%I	3.4, –	1.5, –	3.6, –	7.7, –	0.0,	16.7,	n/a	7.1, –	3.5, –§

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		[§]	[§]	[§]	[§]	–[§]	–[§]		[§]	
	%R	3.4, –[§]	11.9, –[§]	3.6, –[§]	7.7, –[§]	11.4, –[§]	8.3, –[§]	n/a	0.0, –[§]	7.4, –[§]
Klebsiella pneumoniae complex	n	243	260	201	46	204	44	33	46	1,077
	%I	5.8, –[§]	4.2, –[§]	4.5, –[§]	8.7, –[§]	1.0, –[§]	11.4, –[§]	12.1, –[§]	2.2, –[§]	4.6, –[§]
	%R	7.0, –[§]	3.5, –[§]	2.0, –[§]	2.2, –[§]	4.4, –[§]	0.0, –[§]	3.0, –[§]	0.0, –[§]	3.8, –[§]
Proteus mirabilis	n	69	84	44	14	44	12	4	8	279
	%I	7.2, –[§]	13.1, –[§]	6.8, –[§]	0.0, –[§]	9.1, –[§]	16.7, –[§]	n/a	n/a	9.0, –[§]
	%R	1.4, –[§]	1.2, –[§]	0.0, –[§]	7.1, –[§]	2.3, –[§]	8.3, –[§]	n/a	n/a	1.8, –[§]
Salmonella species (non-typhoidal)	n	18	22	15	3	7	2	8	4	79
	%I	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	0.0, –[§]
	%R	0.0, –[§]	0.0, –[§]	6.7, –[§]	n/a	n/a	n/a	n/a	n/a	1.3, –[§]
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%I	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Ampicillin										
Enterococcus faecalis	n	237	168	122	73	122	56	14	26	818
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Enterococcus faecium	n	192	178	75	56	80	29	17	25	652
	%R	92.7, 92.7	93.8, 93.8	100.0, 100.0	91.1, 89.5	93.8, 93.8	96.6, 96.6	100.0, 100.0	92.0, 92.0	94.2, 94.0
Escherichia coli	n	1,280	1,086	686	471	741	218	224	206	4,912
	%I	1.3, –[#]	1.6, –[#]	1.9, –[#]	0.8, –[#]	2.6, –[#]	4.1, –[#]	1.8, –[#]	2.4, –[#]	1.8, –[#]
	%R	51.4, 52.7	52.6, 54.1	48.8, 50.7	49.3, 50.1	55.3, 57.9	36.2, 40.4	65.2, 67.0	46.6, 49.0	51.4, 53.2
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312
	%I	0.0, –[#]	1.2, –[#]	0.0, –[#]	0.0, –[#]	2.3, –[#]	0.0, –[#]	n/a	n/a	0.6, –[#]
	%R	16.3, 16.3	17.9, 19.0	4.5, 4.5	13.3, 13.3	18.2, 20.5	16.7, 16.7	n/a	n/a	14.7, 15.4
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%I	0.0, –[#]	0.0, –[#]	0.0, –[#]	n/a	n/a	n/a	n/a	n/a	0.0, –[#]
	%R	0.0, 0.0	4.5, 4.5	6.7, 6.7	n/a	n/a	n/a	n/a	n/a	3.8, 3.8
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%I	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Benzylpenicillin										
Enterococcus faecalis	n	187	101	120	71	119	0	14	26	638
	%R	0.5, –[#]	0.0, –[#]	1.7, –[#]	0.0, –[#]	0.8, –[#]	n/a	0.0, –[#]	0.0, –[#]	0.6, –[#]
Enterococcus faecium	n	167	82	75	53	79	0	17	25	498
	%R	91.0, –[#]	93.9, –[#]	97.3, –[#]	88.7, –[#]	94.9, –[#]	n/a	100.0, –[#]	92.0, –[#]	93.2, –[#]

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Staphylococcus aureus	n	1,077	614	586	225	489	162	119	96	3,368
	%R**	85.1, 85.1	76.9, 76.9	79.5, 79.5	81.3, 81.3	76.5, 76.5	73.5, 73.5	94.1, 94.1	74.0, 74.0	80.6, 80.6
Cefazolin										
Escherichia coli	n	952	1,085	686	185	741	218	224	206	4,297
	%R	23.8, 23.8	23.3, 23.3	20.6, 20.6	23.2, 23.2	27.1, 27.1	11.9, 11.9	28.6, 28.6	18.9, 18.9	23.1, 23.1
Klebsiella oxytoca	n	58	67	28	13	35	12	4	14	231
	%R	51.7, 51.7	55.2, 55.2	39.3, 39.3	61.5, 61.5	60.0, 60.0	66.7, 66.7	n/a	28.6, 28.6	52.4, 52.4
Klebsiella pneumoniae complex	n	240	260	201	46	204	44	33	46	1,074
	%R	15.4, 15.4	8.5, 8.5	6.5, 6.5	13.0, 13.0	8.8, 8.8	6.8, 6.8	15.2, 15.2	6.5, 6.5	10.0, 10.0
Proteus mirabilis	n	66	84	44	14	44	12	4	8	276
	%R	16.7, 16.7	22.6, 22.6	20.5, 20.5	14.3, 14.3	18.2, 18.2	25.0, 25.0	n/a	n/a	19.2, 19.2
Cefepime										
Acinetobacter baumannii	n	10	7	13	2	9	2	1	0	44
	%I	0.0, –§	n/a	0.0, –§	n/a	n/a	n/a	n/a	n/a	2.3, –§
	%R	10.0, –§	n/a	7.7, –§	n/a	n/a	n/a	n/a	n/a	6.8, –§
Enterobacter cloacae complex	n	142	93	83	24	63	16	8	19	448
	%SDD/I	5.6, 10.6	2.2, 8.6	3.6, 7.2	12.5, 16.7	0.0, 4.8	0.0, 6.3	n/a	5.3, 21.1	3.8, 9.4
	%R	5.6, 7.7	1.1, 2.2	1.2, 3.6	4.2, 4.2	0.0, 0.0	0.0, 0.0	n/a	5.3, 5.3	2.7, 4.0
Escherichia coli	n	1,281	1,086	686	471	741	218	224	206	4,913
	%SDD/I	2.4, 5.4	1.4, 6.5	1.3, 5.2	1.9, 3.4	2.4, 7.8	1.4, 2.3	2.7, 6.3	2.9, 6.3	2.0, 5.7
	%R	3.7, 4.9	2.2, 3.0	1.0, 1.5	5.1, 6.2	2.3, 3.1	0.9, 1.4	1.3, 2.7	1.9, 3.9	2.6, 3.6
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%SDD/I	0.0, 2.4	0.0, 6.3	8.3, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.8, 2.5
	%R	2.4, 2.4	3.1, 3.1	0.0, 8.3	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.7, 2.5
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%SDD/I	0.0, 0.0	0.0, 1.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.8
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%SDD/I	2.4, 5.0	0.4, 3.1	0.0, 2.0	0.9, 1.8	0.0, 1.5	0.0, 4.5	3.0, 6.1	4.3, 2.2	1.0, 3.1
	%R	3.0, 3.9	1.5, 1.5	0.5, 0.5	2.6, 3.5	1.0, 1.0	0.0, 0.0	0.0, 0.0	0.0, 2.2	1.6, 2.0
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312
	%SDD/I	3.5, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.3, 2.3	0.0, 0.0	n/a	n/a	1.3, 1.0
	%R	1.2, 2.3	1.2, 1.2	2.3, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	1.0, 1.3
Pseudomonas	n	210	124	141	83	98	20	21	38	735

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
aeruginosa	%I	3.3, 95.2	3.2, 92.7	2.1, 93.6	2.4, 91.6	8.2, 90.8	0.0, 100.0	0.0, 95.2	0.0, 97.4	3.3, 93.7
	%R	1.4, 4.8	4.0, 7.3	4.3, 6.4	6.0, 8.4	1.0, 9.2	0.0, 0.0	4.8, 4.8	2.6, 2.6	3.0, 6.3
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%SDD/I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%SDD/I	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	42	35	15	34	4	1	10	200
	%SDD/I	0.0, 1.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 0.5
	%R	1.7, 1.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.5, 0.5
Cefoxitin										
Escherichia coli	n	1,281	1,085	686	471	740	218	224	206	4,911
	%R/ECOFF	3.9, 6.5	2.8, 4.5	4.1, 6.7	2.3, 4.2	3.2, 5.7	2.3, 4.6	4.0, 6.3	0.5, 3.9	3.2, 5.5
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%R/ECOFF	1.3, 2.6	1.5, 1.5	3.6, 3.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.1, 1.5
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%R/ECOFF	5.3, 6.8	3.8, 6.2	4.5, 6.5	0.9, 1.8	6.4, 6.9	6.8, 13.6	3.0, 3.0	0.0, 2.2	4.4, 6.1
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312
	%R/ECOFF	1.2, 1.2	0.0, 1.2	0.0, 4.5	0.0, 0.0	0.0, 4.5	0.0, 8.3	n/a	n/a	0.3, 2.2
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%R/ECOFF	0.0, 0.0	0.0, 0.0	6.7, 6.7	n/a	n/a	n/a	n/a	n/a	1.3, 1.3
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%R/ECOFF	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Ceftazidime										
Acinetobacter baumannii complex	n	10	7	13	2	9	2	1	1	45
	%I	20.0, –§	n/a	23.1, –§	n/a	n/a	n/a	n/a	n/a	17.8, –§
	%R	0.0, –§	n/a	0.0, –§	n/a	n/a	n/a	n/a	n/a	0.0, –§
Enterobacter cloacae complex	n	142	93	83	24	63	16	8	19	448
	%I	0.0, 2.8	0.0, 2.2	0.0, 2.4	0.0, 4.2	1.6, 1.6	0.0, 18.8	n/a	5.3, 0.0	0.4, 3.1
	%R	23.9, 23.9	26.9, 26.9	20.5, 20.5	33.3, 33.3	19.0, 20.6	6.3, 6.3	n/a	31.6, 36.8	23.2, 23.7
Escherichia coli	n	1,280	1,086	686	471	741	218	224	206	4,912
	%I	1.1, 6.8	0.5, 6.9	0.4, 7.1	1.5, 5.1	0.3, 8.6	0.5, 1.8	0.0, 9.4	0.0, 6.3	0.7, 6.9
	%R	6.7, 7.8	6.1, 6.5	4.4, 4.8	5.1, 6.6	5.8, 6.1	3.7, 4.1	4.5, 4.5	4.9, 4.9	5.6, 6.3
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%I	0.0,	0.0,	16.7,	0.0,	6.3,	n/a	n/a	n/a	3.4, 3.4

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		4.8	6.3	0.0	0.0	0.0				
	%R	35.7, 35.7	37.5, 37.5	33.3, 50.0	50.0, 50.0	18.8, 25.0	n/a	n/a	n/a	32.8, 36.1
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%I	1.3, 0.0	0.0, 3.0	0.0, 3.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 1.5
	%R	0.0, 1.3	1.5, 1.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.8
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%I	1.5, 3.9	1.5, 1.9	0.0, 2.0	0.9, 1.8	1.5, 2.0	0.0, 0.0	3.0, 3.0	0.0, 0.0	1.1, 2.3
	%R	7.4, 8.9	3.1, 4.6	2.0, 2.0	3.5, 4.4	2.5, 3.9	4.5, 4.5	6.1, 9.1	4.3, 4.3	4.2, 5.3
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312
	%I	1.2, 4.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.3, 1.3
	%R	1.2, 2.3	1.2, 1.2	2.3, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	1.0, 1.3
Pseudomonas aeruginosa	n	210	124	141	83	98	20	21	38	735
	%I	5.2, 90.0	4.0, 89.5	0.7, 91.5	6.0, 88.0	2.0, 91.8	10.0, 90.0	4.8, 85.7	2.6, 92.1	3.8, 90.2
	%R	4.8, 10.0	6.5, 10.5	7.8, 8.5	6.0, 12.0	6.1, 8.2	0.0, 10.0	9.5, 14.3	5.3, 7.9	6.0, 9.8
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	6.7, 6.7	n/a	n/a	n/a	n/a	n/a	1.3, 1.3
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%I	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	42	35	15	34	4	1	10	200
	%I	0.0, 0.0	0.0, 0.0	0.0, 2.9	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 0.5
	%R	1.7, 1.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.5, 0.5
Ceftriaxone										
Acinetobacter baumannii complex	n	8	9	13	1	9	3	1	1	45
	%I	n/a	n/a	61.5, –§	n/a	n/a	n/a	n/a	n/a	70.8, –§
	%R	n/a	n/a	7.7, –§	n/a	n/a	n/a	n/a	n/a	2.1, –§
Enterobacter cloacae complex	n	142	93	83	24	63	16	8	19	448
	%I	0.7, 0.7	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	6.3, 6.3	n/a	0.0, 0.0	0.7, 0.7
	%R	27.5, 27.5	29.0, 29.0	20.5, 20.5	37.5, 37.5	19.0, 19.0	18.8, 18.8	n/a	42.1, 42.1	26.3, 26.3
Escherichia coli	n	1,280	1,086	686	471	741	218	224	206	4,912
	%I	0.2, 0.2	0.0, 0.0	0.1, 0.1	0.0, 0.0	0.1, 0.1	0.0, 0.0	0.4, 0.4	0.0, 0.0	0.1, 0.1
	%R	13.6, 13.6	13.0, 13.0	10.3, 10.3	11.0, 11.0	14.2, 14.2	5.5, 5.5	13.4, 13.4	13.1, 13.1	12.5, 12.5
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%I	0.0,	3.1,	0.0,	0.0,	0.0,	n/a	n/a	n/a	0.8, 0.8

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.0	3.1	0.0	0.0	0.0				
	%R	38.1, 38.1	40.6, 40.6	50.0, 50.0	50.0, 50.0	25.0, 25.0	n/a	n/a	n/a	37.8, 37.8
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.6, 3.6	0.0, 0.0	8.3, 8.3	n/a	0.0, 0.0	0.8, 0.8
	%R	3.9, 3.9	13.4, 13.4	0.0, 0.0	7.1, 7.1	5.7, 5.7	0.0, 0.0	n/a	7.1, 7.1	6.8, 6.8
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
	%R	10.7, 10.7	4.6, 4.6	2.5, 2.5	6.1, 6.1	2.9, 2.9	4.5, 4.5	15.2, 15.2	4.3, 4.3	6.1, 6.1
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0
	%R	4.7, 4.7	1.2, 1.2	2.3, 2.3	0.0, 0.0	2.3, 2.3	0.0, 0.0	n/a	n/a	2.2, 2.2
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	6.7, 6.7	n/a	n/a	n/a	n/a	n/a	1.3, 1.3
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%I	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	42	35	15	34	4	1	10	200
	%I	0.0, 0.0	2.4, 2.4	0.0, 0.0	13.3, 13.3	0.0, 0.0	n/a	n/a	0.0, 0.0	1.5, 1.5
	%R	1.7, 1.7	2.4, 2.4	5.7, 5.7	0.0, 0.0	2.9, 2.9	n/a	n/a	10.0, 10.0	3.0, 3.0
Ciprofloxacin										
Acinetobacter baumannii complex	n	10	9	1	2	9	3	1	1	36
	%I	0.0, 100.0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	2.8, 97.2
	%R	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 2.8
Staphylococcus aureus	n	1,100	614	598	225	487	162	119	96	3,401
	%R	9.9, 10.4	7.8, 9.6	3.8, 4.4	7.1, 8.9	5.7, 6.3	3.7, 3.8	5.9, 5.7	7.3, 9.3	7.2, 8.0
Methicillin-resistant *S. aureus*	n	195	79	87	28	81	12	52	12	546
	%R	45.1, 46.2	40.5, 41.8	16.1, 16.1	39.3, 39.3	16.0, 18.5	50.0, 50.0	5.8, 5.8	58.3, 58.3	31.9, 32.8
Methicillin-susceptible *S. aureus*	n	905	535	511	197	406	150	67	84	2,855
	%R	2.3, 2.7	3.0, 3.6	1.8, 2.3	2.5, 3.0	3.7, 3.9	0.0, 0.0	6.0, 6.0	0.0, 2.4	2.5, 2.9
Enterobacter cloacae complex	n	142	93	83	24	63	16	8	19	448
	%I	2.1, 2.1	3.2, 3.2	0.0, 0.0	8.3, 8.3	1.6, 1.6	0.0, 0.0	n/a	0.0, 0.0	2.2, 2.2
	%R	8.5, 8.5	3.2, 3.2	6.0, 6.0	0.0, 0.0	3.2, 3.2	0.0, 0.0	n/a	10.5, 10.5	5.4, 5.4
Escherichia coli	n	1,281	1,085	686	470	740	218	224	206	4,910
	%I	6.0, 6.0	2.9, 2.9	4.5, 4.5	4.5, 4.5	3.6, 3.6	3.7, 3.7	3.6, 3.6	1.9, 1.9	4.2, 4.2

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	12.1, 12.1	13.2, 13.2	8.6, 8.6	8.5, 8.5	16.2, 16.2	10.6, 10.6	17.0, 17.0	13.6, 13.6	12.3, 12.3
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	9.4, 9.4	0.0, 0.0	0.0, 0.0	12.5, 12.5	n/a	n/a	n/a	4.2, 4.2
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%I	1.3, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.6, 3.6	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.8, 0.8
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%I	3.9, 3.9	1.5, 1.5	1.0, 1.0	1.8, 1.8	2.0, 2.0	0.0, 0.0	3.0, 3.0	2.2, 2.2	2.2, 2.2
	%R	8.6, 8.6	7.3, 7.3	8.0, 8.0	9.6, 9.6	3.9, 3.9	4.5, 4.5	6.1, 6.1	4.3, 4.3	7.2, 7.2
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.3, 2.3	0.0, 0.0	n/a	n/a	0.3, 0.3
	%R	7.0, 7.0	9.5, 9.5	2.3, 2.3	3.3, 3.3	2.3, 2.3	0.0, 0.0	n/a	n/a	5.4, 5.4
Pseudomonas aeruginosa	n	210	124	141	83	98	20	21	38	735
	%I	2.9, 92.4	8.1, 87.1	6.4, 92.9	3.6, 92.8	2.0, 93.9	0.0, 100.0	4.8, 95.2	2.6, 89.5	4.4, 92.0
	%R	4.8, 7.6	4.8, 12.9	0.7, 7.1	3.6, 7.2	4.1, 6.1	0.0, 0.0	0.0, 4.8	7.9, 10.5	3.7, 8.0
Salmonella species (non-typhoidal)‡	n	20	22	15	3	7	2	8	4	81
	%I	0.0, –#	4.5, –#	0.0, –#	n/a	n/a	n/a	n/a	n/a	2.5, –#
	%R	0.0, 0.0	0.0, 4.5	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 2.5
Salmonella species (typhoidal)‡	n	1	0	0	0	0	0	0	0	1
	%I	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	42	35	15	34	4	1	10	200
	%I	0.0, 0.0	0.0, 0.0	2.9, 2.9	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.5, 0.5
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	20.0, 20.0	2.9, 2.9	n/a	n/a	0.0, 0.0	2.0, 2.0
Clindamycin (inducible + constitutive resistance)										
Staphylococcus aureus	n	1,099	613	598	225	487	163	119	96	3,400
	%R	14.0, 14.6	10.4, 12.1	19.4, 19.7	8.0, 8.0	12.7, 14.6	12.3, 14.7	19.3, 19.3	11.5, 12.5	13.8, 14.7
Methicillin-resistant *S. aureus*	n	194	79	87	28	81	13	52	12	546
	%R	27.8, 28.9	22.8, 25.3	25.3, 25.3	17.9, 17.9	18.5, 25.9	15.4, 15.4	13.5, 13.5	16.7, 25.0	22.9, 24.9
Methicillin-susceptible *S. aureus*	n	905	534	511	197	406	150	67	84	2,854
	%R	11.0, 11.5	8.6, 10.1	18.4, 18.8	6.6, 6.6	11.6, 12.3	12.0, 14.7	23.9, 23.9	10.7, 10.7	12.0, 12.8
Daptomycin										
Enterococcus faecalis	n	238	166	117	47	114	41	13	25	761
	%R	0.0, –	0.0, –	0.0, –	0.0, –	0.0,	0.0, –	0.0, –	0.0, –	0.0, –#

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW [#]	Vic [#]	Qld [#]	SA [#]	WA [_#]	Tas [#]	NT [#]	ACT [#]	Australia
Enterococcus faecium	n	43	0	0	34	3	0	0	2	82
	%R	0.0, –[#]	n/a	n/a	0.0, –[#]	n/a	n/a	n/a	n/a	0.0, –[#]
Staphylococcus aureus	n	1,101	614	600	229	489	163	119	97	3,412
	%NS[§§]/R	0.3, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2	0.6, 0.6	0.0, 0.0	0.0, 0.0	0.1, 0.1
Methicillin-resistant *S. aureus*	n	196	79	87	30	81	13	52	12	550
	%NS[§§]/R	1.0, 1.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.4, 0.4
Methicillin-susceptible *S. aureus*	n	905	535	513	199	408	150	67	85	2,862
	%NS[§§]/R	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2	0.7, 0.7	0.0, 0.0	0.0, 0.0	0.1, 0.1
Erythromycin										
Staphylococcus aureus	n	1,065	614	598	225	487	163	119	96	3,367
	%R	19.2, 20.2	13.0, 15.1	19.9, 20.7	17.3, 17.8	13.1, 15.2	12.9, 15.3	18.5, 18.5	11.5, 12.5	16.7, 18.0
Methicillin-resistant *S. aureus*	n	187	79	87	28	81	13	52	12	539
	%R	36.4, 36.9	30.4, 32.9	23.0, 25.3	39.3, 39.3	19.8, 27.2	30.8, 30.8	13.5, 13.5	16.7, 16.7	28.2, 30.2
Methicillin-susceptible *S. aureus*	n	878	535	511	197	406	150	67	84	2,828
	%R	15.6, 16.6	10.5, 12.5	19.4, 20.0	14.2, 14.7	11.8, 12.8	11.3, 14.0	22.4, 22.4	10.7, 11.9	14.5, 15.6
Fusidic acid										
Staphylococcus aureus	n	1,064	614	598	225	487	163	119	96	3,366
	%R	–[§], 2.0	–[§], 2.8	–[§], 4.5	–[§], 1.8	–[§], 2.1	–[§], 1.2	–[§], 6.7	–[§], 4.2	–[§], 2.8
Methicillin-resistant *S. aureus*	n	186	79	87	28	81	13	52	12	538
	%R	–[§], 1.1	–[§], 11.4	–[§], 3.4	–[§], 3.6	–[§], 3.7	–[§], 0.0	–[§], 5.8	–[§], 8.3	–[§], 4.1
Methicillin-susceptible *S. aureus*	n	746	523	473	194	422	149	56	106	2,669
	%R	878	535	511	197	406	150	67	84	2,828
Gentamicin										
Acinetobacter baumannii complex	n	10	9	13	2	9	3	1	1	48
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Enterobacter cloacae complex	n	142	93	83	24	63	16	8	19	448
	%R	9.9, 9.9	1.1, 3.2	3.6, 3.6	12.5, 12.5	0.0, 0.0	6.3, 6.3	n/a	10.5, 10.5	5.4, 6.0
Escherichia coli	n	1,281	1,086	686	471	741	218	224	206	4,913
	%R	8.9, 9.4	6.5, 7.2	7.1, 7.4	5.9, 7.9	9.9, 10.3	3.2, 3.2	14.3, 15.2	6.3, 8.7	7.9, 8.6
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%R	0.0, 0.0	6.3, 9.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.7, 2.5
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%R	2.6, 2.6	1.5, 1.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.1, 1.1
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%R	4.2, 4.2	4.2, 4.2	3.0, 3.5	4.4, 4.4	2.0, 2.5	0.0, 0.0	9.1, 9.1	2.2, 2.2	3.6, 3.7
Proteus mirabilis	n	86	84	44	30	44	12	4	8	312

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	4.7, 18.6	2.4, 6.0	0.0, 0.0	0.0, 33.3	2.3, 2.3	0.0, 0.0	n/a	n/a	2.6, 10.6
Serratia marcescens	n	59	42	35	15	34	4	1	10	200
	%R	0.0, 0.0	0.0, 4.8	0.0, 2.9	0.0, 13.3	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 2.5
Staphylococcus aureus	n	1,100	595	598	225	487	163	119	96	3,383
	%R	3.3, 7.5	0.3, 3.5	2.0, 6.4	4.0, 4.9	0.4, 3.3	0.6, 4.3	0.8, 12.6	5.2, 10.4	2.0, 5.9
Methicillin-resistant *S. aureus*	n	195	74	87	28	81	13	52	12	542
	%R	10.8, 21.5	2.7, 8.1	3.4, 8.0	10.7, 10.7	1.2, 3.7	7.7, 30.8	1.9, 5.8	16.7, 33.3	6.3, 13.3
Methicillin-susceptible *S. aureus*	n	905	521	511	197	406	150	67	84	2,841
	%R	1.7, 4.5	0.0, 2.9	1.8, 6.1	3.0, 4.1	0.2, 3.2	0.0, 2.0	0.0, 17.9	3.6, 7.1	1.2, 4.5
Linezolid										
Enterococcus faecalis	n	240	168	122	73	121	56	14	26	820
	%R	0.0, 0.0	1.2, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
Enterococcus faecium	n	193	178	75	56	80	29	17	25	653
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Staphylococcus aureus	n	1,101	614	600	229	489	163	119	97	3,412
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-resistant *S. aureus*	n	194	79	87	30	81	13	52	12	548
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-susceptible *S. aureus*	n	907	535	513	199	408	150	67	85	2,864
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Meropenem										
Acinetobacter baumannii complex	n	10	9	13	2	9	3	1	1	48
	%I	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Enterobacter cloacae complex	n	142	92	83	24	63	16	8	19	447
	%I	1.4, 0.7	0.0, 0.0	1.2, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.7, 0.2
	%R	4.9, 4.2	1.1, 1.1	1.2, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	5.3, 5.3	2.2, 2.0
Escherichia coli	n	1,281	1,085	685	471	741	218	224	206	4,911
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
	%R	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.2, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%I	0.0, 0.0	0.0, 3.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
	%R	0.0, 0.0	9.4, 6.3	8.3, 8.3	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	3.4, 2.5
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%I	1.3, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.0

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	0.0, 0.0	1.5, 1.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
Klebsiella pneumoniae complex	n	337	260	201	114	204	44	33	46	1,239
	%I	0.3, 0.3	0.4, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.1
	%R	0.9, 0.6	0.4, 0.4	0.0, 0.0	0.0, 0.0	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.4, 0.3
Proteus mirabilis	n	86	84	44	29	44	12	4	8	311
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	209	124	141	83	97	20	21	38	733
	%I	3.8, 6.2	4.0, 4.0	2.1, 3.5	2.4, 3.6	5.2, 7.2	0.0, 0.0	4.8, 4.8	0.0, 0.0	3.3, 4.6
	%R	3.8, 1.4	3.2, 3.2	4.3, 2.8	2.4, 1.2	4.1, 2.1	0.0, 0.0	4.8, 4.8	5.3, 5.3	3.7, 2.3
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%I	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	41	35	15	34	4	1	10	199
	%I	0.0, 1.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 0.5
	%R	1.7, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.5, 0.0
Mupirocin (high-level)##										
Staphylococcus aureus	n	606	248	598	225	487	111	1	96	2,372
	%R	1.7, 1.7	0.8, 0.8	4.2, 4.2	0.0, 0.0	1.4, 1.4	0.9, 0.9	n/a, n/a	1.0, 1.0	1.9, 1.9
Methicillin-resistant *S. aureus*	n	104	34	87	28	81	7	1	12	354
	%R	1.0, 1.0	2.9, 2.9	9.2, 9.2	0.0, 0.0	2.5, 2.5	n/a, n/a	n/a, n/a	0.0, 0.0	3.4, 3.4
Methicillin-susceptible *S. aureus*	n	502	214	511	197	406	104	0	84	2,018
	%R	1.8, 1.8	0.5, 0.5	3.3, 3.3	0.0, 0.0	1.2, 1.2	1.0, 1.0	n/a, n/a	1.2, 1.2	1.7, 1.7
Nitrofurantoin										
Enterobacter cloacae complex	n	119	65	83	24	63	16	8	19	397
	%R	11.8, –§	10.8, –§	8.4, –§	16.7, –§	9.5, –§	6.3, –§	n/a	15.8, –§	10.8, –§
Escherichia coli	n	1,281	1,085	686	471	741	218	224	206	4,912
	%R	1.0, 1.0	0.2, 0.2	0.7, 0.7	0.2, 0.2	0.7, 0.7	0.0, 0.0	0.4, 0.4	1.0, 1.0	0.6, 0.6
Klebsiella aerogenes	n	38	23	12	10	16	0	2	5	106
	%R	42.1, –§	52.2, –§	16.7, –§	50.0, –§	37.5, –§	n/a	n/a	n/a	41.5, –§
Klebsiella oxytoca	n	65	55	28	28	35	12	4	14	241
	%R	0.0, –§	0.0, –§	0.0, –§	0.0, –§	0.0, –§	0.0, –§	n/a	0.0, –§	0.0, –§

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Klebsiella pneumoniae complex	n	290	173	201	114	204	44	33	46	1,105
	%R	34.5, –§	39.9, –§	36.8, –§	23.7, –§	45.1, –§	29.5, –§	15.2, –§	43.5, –§	36.2, –§
Proteus mirabilis	n	75	76	44	30	44	12	4	0	285
	%R	94.7, –§	89.5, –§	88.6, –§	93.3, –§	90.9, –§	91.7, –§	n/a	n/a	91.6, –§
Salmonella species (non-typhoidal)	n	14	17	15	3	7	2	8	0	66
	%R	0.0, –§	5.9, –§	0.0, –§	n/a	n/a	n/a	n/a	n/a	1.5, –§
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	42	36	35	15	34	4	1	10	177
	%R	97.6, –§	97.2, –§	100.0, –§	100.0, –§	97.1, –§	n/a	n/a	100.0, –§	98.3, –§
Oxacillin/methicillin										
Staphylococcus aureus	n	1,104	614	607	229	489	163	119	97	3,422
	%R	17.8, 17.8	12.9, 12.9	14.3, 14.3	13.1, 13.1	16.6, 16.6	8.0, 8.0	43.7, 43.7	12.4, 12.4	16.1, 16.1
Piperacillin–tazobactam										
Acinetobacter baumannii complex	n	10	7	13	2	9	2	1	1	45
	%R	10.0, –§	n/a	7.7, –§	n/a	n/a	n/a	n/a	n/a	4.4, –§
Enterobacter cloacae complex	n	141	92	82	24	60	16	7	19	441
	%R	17.7, 31.9	18.5, 30.4	19.5, 24.4	20.8, 25.0	11.7, 20.0	18.8, 25.0	n/a	36.8, 42.1	18.4, 28.1
Escherichia coli	n	1,276	1,083	683	471	725	217	222	206	4,883
	%R	3.1, 6.0	3.3, 7.6	1.3, 6.0	1.5, 3.2	4.3, 9.4	2.3, 4.1	2.7, 8.1	2.4, 3.4	2.8, 6.5
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%R	26.2, 42.9	34.4, 43.8	50.0, 50.0	10.0, 50.0	18.8, 43.8	n/a	n/a	n/a	27.7, 42.9
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%R	5.3, 11.8	13.4, 13.4	0.0, 0.0	17.9, 17.9	11.4, 11.4	8.3, 8.3	n/a	7.1, 7.1	9.1, 11.0
Klebsiella pneumoniae complex	n	337	260	201	114	202	44	33	46	1,237
	%R	4.7, 13.1	4.2, 10.4	1.5, 10.9	1.8, 7.0	1.5, 6.9	0.0, 6.8	0.0, 9.1	2.2, 4.3	2.9, 9.9
Proteus mirabilis	n	86	83	44	30	41	12	4	8	308
	%R	0.0, 0.0	0.0, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.3
Pseudomonas aeruginosa	n	211	123	141	83	92	20	21	38	729
	%R	8.1, 15.2	8.1, 14.6	7.1, 9.2	6.0, 12.0	3.3, 10.9	10.0, 15.0	9.5, 19.0	2.6, 7.9	6.9, 12.8
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	50	41	35	15	5	4	0	10	160
	%R	0.0, 0.0	0.0, 2.4	0.0, 2.9	0.0, 0.0	n/a	n/a	n/a	0.0, 10.0	0.0, 1.9
Rifampicin***										
Staphylococcus aureus	n	1,094	614	598	225	487	163	119	96	3,396

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	0.8, 1.1	0.2, 0.5	0.0, 0.0	0.4, 0.4	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.5
Methicillin-resistant *S. aureus*	n	193	79	87	28	81	13	52	12	545
	%R	2.1, 2.6	1.3, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.9, 1.1
Methicillin-susceptible *S. aureus*	n	901	535	511	197	406	150	67	84	2,851
	%R	0.6, 0.8	0.0, 0.4	0.0, 0.0	0.5, 0.5	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.4
Teicoplanin										
Enterococcus faecalis	n	240	168	122	73	122	56	14	26	821
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Enterococcus faecium	n	187	178	75	56	80	29	17	25	647
	%R	10.2, 19.8	5.6, 6.2	20.0, 21.3	5.4, 7.1	2.5, 3.8	13.8, 24.1	5.9, 23.5	0.0, 0.0	8.3, 12.7
Staphylococcus aureus	n	1,103	614	597	229	489	163	119	97	3,411
	%R	0.0, 0.2	0.0, 0.0	0.0, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1
Tetracycline/doxycycline†‡										
Staphylococcus aureus	n	1,099	614	598	225	487	163	119	96	3,401
	%R	4.3, 5.6	5.0, 5.0	3.8, 4.0	0.4, 2.7	5.7, 6.2	4.9, 4.9	0.8, 0.8	3.1, 3.1	4.2, 4.9
Methicillin-resistant *S. aureus*	n	195	79	87	28	81	13	52	12	547
	%R	15.9, 20.0	16.5, 16.5	10.3, 10.3	0.0, 3.6	11.1, 11.1	7.7, 7.7	0.0, 0.0	16.7, 16.7	11.9, 13.5
Methicillin-susceptible *S. aureus*	n	904	535	511	197	406	150	67	84	2,854
	%R	1.8, 2.5	3.4, 3.4	2.7, 2.9	0.5, 2.5	4.7, 5.2	4.7, 4.7	1.5, 1.5	1.2, 1.2	2.7, 3.2
Ticarcillin–clavulanic acid										
Acinetobacter baumannii complex	n	8	7	13	1	9	2	1	1	42
	%R	n/a	n/a	0.0, –§	n/a	n/a	n/a	n/a	n/a	0.0, –§
Enterobacter cloacae complex	n	95	93	83	11	60	16	8	19	385
	%R	26.3, 32.6	25.8, 31.2	20.5, 22.9	9.1, 9.1	18.3, 21.7	18.8, 31.3	n/a	42.1, 42.1	23.6, 28.1
Escherichia coli	n	815	1,086	686	185	729	218	224	206	4,149
	%R	6.9, 15.0	6.8, 15.7	6.0, 12.8	6.5, 15.1	7.1, 18.0	1.4, 6.0	7.1, 18.8	3.4, 9.2	6.3, 14.8
Klebsiella aerogenes	n	34	32	12	4	16	0	2	5	105
	%R	23.5, 38.2	31.3, 37.5	33.3, 50.0	n/a	31.3, 43.8	n/a	n/a	n/a	26.7, 39.0
Klebsiella oxytoca	n	51	67	28	13	35	12	4	14	224
	%R	5.9, 7.8	11.9, 13.4	0.0, 0.0	15.4, 15.4	11.4, 11.4	8.3, 8.3	n/a	0.0, 0.0	8.0, 8.9
Klebsiella pneumoniae complex	n	213	260	201	46	202	44	33	46	1,045
	%R	6.6, 11.3	4.2, 8.8	3.0, 6.0	4.3, 8.7	2.5, 6.4	0.0, 2.3	3.0, 9.1	0.0, 4.3	3.7, 7.8
Proteus mirabilis	n	65	84	44	14	42	12	4	8	273
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	143	122	141	42	95	20	21	38	622
	%R	18.2, 46.9	15.6, 52.5	9.9, 53.2	16.7, 40.5	11.6, 38.9	15.0, 35.0	19.0, 57.1	13.2, 44.7	14.3, 47.6

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Salmonella species (non-typhoidal)	n	18	22	15	3	7	2	8	4	79
	%R	0.0, 0.0	0.0, 0.0	0.0, 6.7	n/a	n/a	n/a	n/a	n/a	0.0, 1.3
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	27	18	35	5	32	4	1	10	132
	%R	0.0, 0.0	0.0, 0.0	2.9, 5.7	n/a	0.0, 3.1	n/a	n/a	0.0, 0.0	0.8, 2.3
Tobramycin										
Acinetobacter baumannii complex	n	10	9	13	2	9	3	1	1	48
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Enterobacter cloacae complex	n	140	93	83	24	60	16	8	19	443
	%R	5.7, 10.0	1.1, 3.2	3.6, 3.6	0.0, 12.5	0.0, 0.0	0.0, 6.3	n/a	10.5, 10.5	3.2, 6.1
Escherichia coli	n	1,276	1,086	686	471	729	218	224	206	4,896
	%R	2.3, 9.6	2.6, 7.6	1.6, 7.1	1.7, 6.8	5.6, 11.5	0.9, 3.2	3.1, 17.0	1.9, 7.3	2.7, 8.8
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%R	0.0, 0.0	3.1, 9.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.8, 2.5
Klebsiella oxytoca	n	74	67	28	28	35	12	4	14	262
	%R	1.4, 2.7	0.0, 1.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 1.1
Klebsiella pneumoniae complex	n	335	260	201	114	202	44	33	46	1,235
	%R	2.7, 6.0	1.5, 3.8	1.5, 3.5	3.5, 6.1	0.5, 2.0	0.0, 0.0	3.0, 9.1	2.2, 4.3	1.9, 4.3
Proteus mirabilis	n	86	84	44	30	42	12	4	8	310
	%R	4.7, 10.5	1.2, 2.4	0.0, 2.3	0.0, 3.3	0.0, 2.4	0.0, 0.0	n/a	n/a	1.6, 4.5
Pseudomonas aeruginosa	n	210	124	141	83	95	20	21	38	732
	%R	0.5, 1.9	0.0, 0.0	0.7, 0.7	0.0, 0.0	2.1, 2.1	0.0, 5.0	0.0, 0.0	0.0, 2.6	0.5, 1.2
Serratia marcescens	n	58	42	35	15	32	4	1	10	197
	%R	0.0, 39.7	0.0, 31.0	0.0, 28.6	0.0, 60.0	0.0, 15.6	n/a	n/a	0.0, 10.0	0.0, 32.0
Trimethoprim										
Enterobacter cloacae complex	n	142	93	83	24	60	16	8	19	445
	%R	22.5, 22.5	19.4, 19.4	13.3, 14.5	8.3, 8.3	8.3, 8.3	12.5, 12.5	n/a	21.1, 21.1	17.1, 17.3
Escherichia coli	n	1,281	1,086	686	471	729	218	224	206	4,901
	%R	31.4, 31.4	32.2, 32.5	35.0, 35.1	28.9, 28.9	33.9, 33.9	19.3, 19.3	51.3, 51.3	22.8, 22.8	32.2, 32.3
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%R	0.0, 0.0	6.3, 6.3	0.0, 0.0	0.0, 0.0	12.5, 12.5	n/a	n/a	n/a	3.4, 3.4
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%R	9.2, 9.2	1.5, 1.5	10.7, 10.7	0.0, 0.0	2.9, 2.9	0.0, 0.0	n/a	0.0, 0.0	5.3, 5.3
Klebsiella pneumoniae complex	n	337	260	201	114	202	44	33	46	1,237
	%R	23.7, 24.3	15.8, 16.9	14.9, 16.9	15.8, 16.7	10.4, 10.9	4.5, 4.5	18.2, 18.2	6.5, 6.5	16.2, 17.1
Proteus mirabilis	n	86	84	44	30	42	12	4	8	310

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	22.1, 22.1	26.2, 27.4	15.9, 15.9	20.0, 23.3	19.0, 19.0	8.3, 8.3	n/a	n/a	21.3, 21.9
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	42	35	15	32	4	1	10	198
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 6.7	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 0.5
Trimethoprim–sulfamethoxazole										
Acinetobacter baumannii complex	n	10	9	13	2	9	3	1	1	48
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	4.2, 4.2
Enterobacter cloacae complex	n	142	93	83	24	59	16	8	19	444
	%R	22.5, 22.5	16.1, 16.1	14.5, 13.3	4.2, 4.2	8.5, 8.5	12.5, 12.5	n/a	21.1, 21.1	16.2, 16.0
Escherichia coli	n	1,281	1,085	685	471	729	218	224	206	4,899
	%R	29.2, 29.0	29.7, 29.7	31.1, 31.1	24.6, 24.2	31.1, 31.1	17.4, 17.4	49.1, 48.7	22.8, 22.8	29.5, 29.4
Klebsiella aerogenes	n	42	32	12	10	16	0	2	5	119
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	12.5, 12.5	n/a	n/a	n/a	1.7, 1.7
Klebsiella oxytoca	n	76	67	28	28	35	12	4	14	264
	%R	7.9, 7.9	1.5, 1.5	10.7, 10.7	0.0, 0.0	2.9, 2.9	0.0, 0.0	n/a	0.0, 0.0	4.9, 4.9
Klebsiella pneumoniae complex	n	336	260	201	114	202	44	33	46	1,236
	%R	19.0, 18.8	11.9, 10.8	12.4, 11.9	13.2, 12.3	7.4, 7.4	4.5, 4.5	18.2, 18.2	6.5, 6.5	13.0, 12.5
Proteus mirabilis	n	86	84	44	30	42	12	4	8	310
	%R	14.0, 14.0	22.6, 22.6	13.6, 13.6	13.3, 13.3	14.3, 14.3	8.3, 8.3	n/a	n/a	16.1, 16.1
Salmonella species (non-typhoidal)	n	19	22	15	3	7	2	8	4	80
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	1	0	0	0	0	0	0	0	1
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Serratia marcescens	n	59	42	35	15	32	4	1	10	198
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 0.0
Staphylococcus aureus	n	1,083	614	593	224	487	163	119	96	3,379
	%R	1.1, 1.2	0.3, 0.3	1.0, 1.0	1.3, 1.3	0.4, 0.4	0.0, 0.0	1.7, 1.7	1.0, 1.0	0.8, 0.9
Methicillin-resistant *S. aureus*	n	189	79	87	27	81	13	52	12	540
	%R	4.2, 4.2	2.5, 2.5	3.4, 3.4	3.7, 3.7	1.2, 1.2	0.0, 0.0	3.8, 3.8	0.0, 0.0	3.1, 3.1
Methicillin-susceptible *S. aureus*	n	894	535	506	197	406	150	67	84	2,839
	%R	0.4, 0.6	0.0, 0.0	0.6, 0.6	1.0, 1.0	0.2, 0.2	0.0, 0.0	0.0, 0.0	1.2, 1.2	0.4, 0.4
Vancomycin										
Enterococcus faecalis	n	240	168	122	73	122	56	14	26	821
	%R	0.0,	0.0,	0.0,	0.0,	0.0,	0.0,	0.0,	0.0,	0.0,

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Enterococcus faecium	n	195	178	76	56	80	29	17	25	656
	%R	54.9, 55.9	59.6, 60.1	32.9, 32.9	60.7, 62.5	25.0, 25.0	31.0, 31.0	88.2, 88.2	52.0, 52.0	50.2, 50.8
Staphylococcus aureus	n	1,102	614	596	229	489	163	119	97	3,409
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

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

* Category analysed for each organism. If different for CLSI and EUCAST, they are separated by a comma.
† For susceptibility testing purposes, EUCAST fixes the concentration of clavulanic acid at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines
§ No category defined
# No breakpoints defined for indicated species
** Benzylpenicillin resistance including β-lactamase producers
‡ The ciprofloxacin concentration range available on the Vitek® card used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. Results of MIC strips, where available, were provided
§§ Resistance not defined
Mupirocin high-level resistance screen
*** The rifampicin concentration range on the Phoenix™ card and Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility for EUCAST
‡† The doxycycline concentration range available on the Phoenix card used restricts the ability to accurately identify intermediate and resistant (CLSI) categories

Appendix D. Multiple acquired resistance by species and state or territory

The most problematic pathogens are those with multiple acquired resistances. Although there is no agreed benchmark for the definition of multidrug resistance, acquired resistance to at least one agent in three or more antimicrobial categories has been chosen to define multi-drug resistance in this survey.[51] For each species, antimicrobials were excluded from the count if they are affected by natural resistances, and/or neither CLSI nor EUCAST breakpoints were available.

Tables D1 to D10 show multiple acquired resistances for different species. Only isolates for which the full range of antimicrobial agents was tested were included for determination of multi-drug resistance. The agents included for each species are listed in the notes after each table. EUCAST breakpoints were used throughout the analysis.

Table D1: Multiple acquired resistance in *Acinetobacter baumannii* complex, by state and territory, AGAR, 2023

State or territory		Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)		
	Total	0	1	2	%	3	4	%
NSW	10	10	0	0	–*	0	0	–*
Vic	9	9	0	0	–*	0	0	–*
Qld	26	26	0	0	–*	0	0	–*
SA	4	4	0	0	–*	0	0	–*
WA	12	10	2	0	–*	0	0	–*
Tas	6	5	1	0	–*	0	0	–*
NT	13	10	2	1	–*	0	0	–*
ACT	1	1	0	0	–*	0	0	–*
Total	**81**	**75**	**5**	**1**	**100.0**	**0**	**0**	**0.0**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Not applicable, insufficient numbers (<30) to calculate
Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), carbapenems (meropenem), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Acinetobacter baumannii* complex includes *A. nosocomialis* (*n* = 4), *A. pittii* (*n* = 5), and *A. seifertii* (*n* = 2).

Table D2: Multiple acquired resistance in *Citrobacter koseri,* by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	25	22	2	1	–*	0	0	0	0	0	–*
Vic	15	13	1	1	–*	0	0	0	0	0	–*
Qld	14	13	0	1	–*	0	0	0	0	0	–*
SA	6	5	1	0	–*	0	0	0	0	0	–*
WA	5	5	0	0	–*	0	0	0	0	0	–*
Tas	1	1	0	0	–*	0	0	0	0	0	–*
NT	4	3	0	1	–*	0	0	0	0	0	–*
ACT	3	3	0	0	–*	0	0	0	0	0	–*
Total	**73**	**65**	**4**	**4**	**100.0**	**0**	**0**	**0**	**0**	**0**	**0.0**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Not applicable, insufficient numbers (<30) to calculate
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D3: Multiple acquired resistance in *Citrobacter freundii* complex, by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	35	18	3	6	77.1	1	1	0	0	5.7
Vic	28	12	0	3	–*	0	0	0	0	–*
Qld	15	5	0	2	–*	0	0	0	0	–*
SA	7	9	4	0	–*	1	0	0	0	–*
WA	14	2	0	0	–*	0	0	0	0	–*
Tas	2	0	0	2	–*	0	0	0	0	–*
NT	2	3	0	2	–*	1	0	0	0	–*
ACT	6	75	13	17	–*	3	0	0	0	–*
Total	**109**	**75**	**13**	**17**	**96.3**	**3**	**1**	**0**	**0**	**3.7**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups; n/a = not applicable (no isolates)
* Not applicable, insufficient numbers (<30) to calculate
Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Citrobacter freundii* complex includes *C. braakii* (*n* = 16), *C. youngae* (*n* = 2), and *C. werkmanii* (*n* = 1).

Table D4: Multiple acquired resistance in *Klebsiella aerogenes*, by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	56	29	1	24	96.4	1	1	0	0	3.6
Vic	40	23	2	10	87.5	4	1	0	0	12.5
Qld	11	6	1	4	–*	0	0	0	0	–*
SA	9	6	1	2	–*	0	0	0	0	–*
WA	28	17	1	10	–*	0	0	0	0	–*
Tas	5	1	0	4	–*	0	0	0	0	–*
NT	7	7	0	0	–*	0	0	0	0	–*
ACT	8	4	1	2	–*	0	0	0	1	–*
Total	**164**	**93**	**7**	**56**	**95.1**	**5**	**2**	**0**	**1**	**4.9**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Not applicable, insufficient numbers (<30) to calculate
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D5: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	93	73	8	9	96.8	1	0	0	1	1	3.2
Vic	73	59	11	2	98.6	0	0	0	1	0	1.4
Qld	30	27	2	1	100.0	0	0	0	0	0	0.0
SA	34	27	3	4	100.0	0	0	0	0	0	0.0
WA	42	35	4	3	100.0	0	0	0	0	0	0.0
Tas	15	12	1	2	–*	0	0	0	0	0	–*
NT	1	1	0	0	–*	0	0	0	0	0	–*
ACT	21	20	0	0	–*	0	1	0	0	0	–*
Total	**309**	**254**	**29**	**21**	**98.4**	**1**	**1**	**0**	**2**	**1**	**1.6**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Not applicable, insufficient numbers (<30) to calculate
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D6: Multiple acquired resistance in *Morganella morganii*, by state and territory, AGAR, 2023

State or territory	Total	Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)					
		0	1	2	%	3	4	5	6	7	%
NSW	34	14	16	2	94.1	1	1	0	0	0	5.9
Vic	14	6	6	1	–*	1	0	0	0	0	–*
Qld	24	13	10	1	–*	0	0	0	0	0	–*
SA	11	8	3	0	–*	0	0	0	0	0	–*
WA	9	2	5	2	–*	0	0	0	0	0	–*
Tas	2	1	1	0	–*	0	0	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	0	n/a
ACT	5	4	0	0	–*	1	0	0	0	0	–*
Total	**99**	**48**	**41**	**6**	**96.0**	**3**	**1**	**0**	**0**	**0**	**4.0**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Not applicable, insufficient numbers (<30) to calculate
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D7: Multiple acquired resistance in *Proteus mirabilis*, by state and territory, AGAR, 2023

State or territory	Total	Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)						
		0	1	2	%	3	4	5	6	7	8	%
NSW	129	93	10	13	89.9	6	3	4	0	0	0	10.1
Vic	63	46	7	8	96.8	1	1	0	0	0	0	3.2
Qld	48	37	5	6	100.0	0	0	0	0	0	0	0.0
SA	33	22	9	2	100.0	0	0	0	0	0	0	0.0
WA	52	40	4	5	94.2	2	0	1	0	0	0	5.8
Tas	14	9	2	2	–*	0	1	0	0	0	0	–*
NT	7	6	0	1	–*	0	0	0	0	0	0	–*
ACT	4	2	2	0	–*	0	0	0	0	0	0	–*
Total	**350**	**255**	**39**	**37**	**94.6**	**9**	**5**	**5**	**0**	**0**	**0**	**5.4**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups
* Not applicable, insufficient numbers (<30) to calculate
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole), penicillins (ampicillin).

Table D8: Multiple acquired resistance in *Salmonella* species (non-typhoidal), by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	34	25	8	0	97.1	0	1	0	0	2.9
Vic	26	19	7	0	–*	0	0	0	0	–*
Qld	35	31	3	0	97.1	0	1	0	0	2.9
SA	2	2	0	0	–*	0	0	0	0	–*
WA	20	14	4	1	–*	1	0	0	0	–*
Tas	9	8	1	0	–*	0	0	0	0	–*
NT	10	10	0	0	–*	0	0	0	0	–*
ACT	2	2	0	0	–*	0	0	0	0	–*
Total	**138**	**111**	**23**	**1**	**97.8**	**1**	**2**	**0**	**0**	**2.2**

Multi-drug resistant = resistant to at least one agent in three or more antimicrobial groups; n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Note: Antimicrobial categories (agents) are antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins (ampicillin)

Table D9: Multiple acquired resistance in *Salmonella* species (typhoidal), by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	16	0	12	1	–*	2	1	0	0	–*
Vic	30	0	30	0	100.0	0	0	0	0	0.0
Qld	9	0	9	0	–*	0	0	0	0	–*
SA	0	0	0	0	n/a	0	0	0	0	n/a
WA	19	0	18	0	–*	1	0	0	0	–*
Tas	3	0	3	0	–*	0	0	0	0	–*
NT	5	2	3	0	–*	0	0	0	0	–*
ACT	6	0	6	0	–*	0	0	0	0	–*
Total	**88**	**2**	**81**	**1**	**95.5**	**3**	**1**	**0**	**0**	**4.5**

Multi-drug resistant = resistant to at least one agent in three or more antimicrobial groups
* Not applicable (insufficient numbers)
Note: Antimicrobial categories (agents) are antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins (ampicillin).

Table D10: Multiple acquired resistance in *Serratia marcescens*, by state and territory, AGAR, 2023

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	67	21	35	8	95.5	3	0	0	0	0	4.5
Vic	40	18	18	3	97.5	1	0	0	0	0	2.5
Qld	46	13	20	12	97.8	1	0	0	0	0	2.2
SA	8	3	4	1	–*	0	0	0	0	0	–*
WA	12	3	8	1	–*	0	0	0	0	0	–*
Tas	5	2	1	2	–*	0	0	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	0	n/a
ACT	6	1	4	1	–*	0	0	0	0	0	–*
Total	**184**	**61**	**90**	**28**	**97.3**	**5**	**0**	**0**	**0**	**0**	**2.7**

Multidrug-resistant = resistant to at least one agent in three or more antimicrobial groups; n/a = not applicable (no isolates)

* Not applicable (insufficient numbers)
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin and/or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone and/or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Appendix E. Fluoroquinolone resistance determinants

Fluoroquinolone resistance is most commonly due to mutations in DNA gyrase (*gyrA*, *gyrB*) and topoisomerase IV (*parC*, *parE*) genes. Transmissible plasmid-mediated quinolone resistance (PMQR) has emerged in *Enterobacterales*. PMQR determinants include *qnr* genes (*qnrA, qnrB, qnrC, qnrD, qnrE, qnrS, qnrVC); aac(6')-Ib-cr*, coding for a variant aminoglycoside acetyltransferase enzyme, and genes coding for efflux pumps (*qepA*, *oqxAB*).[65, 66]

The fluoroquinolone resistance determinants detected in ciprofloxacin-resistant *Salmonella* species in the 2023 survey are shown in Table E1. The fluoroquinolone resistance mechanisms for the referred *E. coli* and *K. pneumoniae* complex isolates (see Section 2.4) are shown in Table E2 and E3 respectively.

Table E1: Fluroquinolone resistance determinants in ciprofloxacin-resistant *Salmonella* species, AGAR, 2023

	Mutations in QRDR				
Species	***gyrA***	***parC***	**parE**	**PMQR genes**	**Total**
Salmonella (non-typhoidal)					20
	–*	T57S	–*	–*	1
	–*	T57S	–*	*qnrB19* [6], *qnrS1* [1]	7
	D87G	–*	–*	–*	1
	D87N	–*	–*	–*	2
	D87N, S83F	S80I, T57S	–*	–*	1
	D87Y	–*	–*	–*	2
	S83F	–*	–*	–*	2
	S83F	T57S	–*	–*	2
	S83Y	T57S	–*	–*	1
	S83Y	T57S	–*	*qnrS1*	1
Salmonella (typhoidal)					78
S. Typhi (*n* = 56)	D87G	–*	–*	–*	1
	D87G, S83F	–*	–*	–*	1
	D87N, S83F	S80I	–*	–*	12
	D87V, S83F	S80I	–*	–*	1
	S83F	–*	–*	–*	37
	S83F	S80I	–*	–*	1
	S83F	T57S	–*	–*	1
	S83Y	–*	–*	–*	2
S. Paratyphi A (*n* = 21)	S83F	–*	–*	–*	1
	S83F	T57S	–*	–*	15
	S83Y	T57S	–*	–*	5
S. Paratyphi B (*n* = 1)	S83F	–*	–*	–*	1

PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region
* Not detected
Notes:
1. Fluoroquinolone resistant determinants include mutations in either the QRDR of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[101], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*).
2. Mutations in *gyrB* were not detected

Table E2: Fluoroquinolone resistance determinants in *Escherichia coli* (*n* = 883), by ciprofloxacin MIC, AGAR, 2023

QRDR mutations				Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*	PMQR	≤0.25	0.5	>0.5	Total
–*	–*	–*	–*	153	2	2	157
–*	–*	–*	*qnr*	61	34	11	106
–*	–*	I355T	–*	2	0	0	2
–*	–*	I355T	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
–*	–*	I529L	–*	3	0	0	3
–*	–*	I529L	*qnr*	3	1	0	4
–*	S57T	–*	–*	2	0	0	2
–*	S57T	I355T	–*	2	0	0	2
–*	S80I	–*	*qnr*	1	0	0	1
D87G	–*	–*	–*	1	0	0	1
D87G	–*	I529L	–*	1	0	0	1
S83L, D87G	S80I	–*	–*	0	0	2	2
D87N	–*	–*	–*	1	1	0	2
S83L, D87N	S80I, E84G	–*	–*	0	0	2	2
S83L, D87N	E84G	–*	–*	0	0	1	1
S83L, D87N	S80I, E84V	–*	–*	0	0	1	1
S83L, D87N	S80I, E84V	I529L	–*	1	0	111	112
S83L, D87N	S80I, E84V	I529L	*aac(6')-Ib-cr*	0	0	63	63
S83L, D87N	S80I, E84V	I529L	*aac(6')-Ib-cr*, *qnr*	0	0	5	5
S83L, D87N	S80I, E84V	I529L	*qnr*	0	0	8	8
S83L, D87N	S80I, E84V	I529L	*qnr*, *qepA*	0	0	1	1
S83L, D87N	T57S, S80I, E84V	I529L	*aac(6')-Ib-cr*	0	0	1	1
S83L, D87N	S57T, S80I	–*	–*	0	0	1	1
S83L, D87N	S57T, S80I	L416F	–*	0	0	2	2
S83L, D87N	S57T, S80I	S458A	*aac(6')-Ib-cr*	0	0	2	2
S83L, D87N	S57T, S80I	S458A	*qnr*	0	0	1	1
S83L, D87N	S57T, S80I	S458T	–*	0	0	2	2
S83L, D87N	S80I	–*	–*	0	0	6	6
S83L, D87N	S80I	–*	*aac(6')-Ib-cr*	0	0	3	3
S83L, D87N	S80I	–*	*qnr*	0	0	6	6
S83L, D87N	S80I	E460D	–*	0	0	21	21
S83L, D87N	S80I	E460D	*qnr*	0	0	1	1
S83L, D87N	S80I	L416F	–*	0	0	41	41
S83L, D87N	S80I	L416F	*aac(6')-Ib-cr*	0	0	14	14
S83L, D87N	S80I	L416F	*qnr*	0	0	3	3
S83L, D87N	S80I	S458A	–*	0	0	16	16
S83L, D87N	S80I	S458A	*aac(6')-Ib-cr*	0	0	8	8
S83L, D87N	S80I	S458A	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
S83L, D87N	S80I	S458A	QepA	0	0	1	1
S83L, D87N	S80I	S458A	*qnr*	0	0	5	5
S83L, D87N	S80I	S458T	*aac(6')-Ib-cr*	0	0	1	1
S83L, D87Y	S80I, E84G	I355T	–*	0	0	1	1
S83L, D87Y	S80I, E84V	I529L	–*	0	0	4	4
S83L, D87Y	S80I	S458A	–*	0	0	1	1
S83L, D87Y	S80I	S458A	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
S83A	–*	–*	–*	2	0	0	2
S83A	–*	–*	*qnr*	2	0	0	2
S83L	–*	–*	–*	53	30	11	94
S83L	–*	–*	*aac(6')-Ib-cr*	0	0	2	2
S83L	–*	–*	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
S83L	–*	–*	*qnr*	0	6	13	19
S83L	–*	I529L	–*	25	66	26	117
S83L	–*	I529L	*qnr*	0	1	1	2
S83L	–*	L416F	–*	0	1	1	2
S83L	–*	S458A	–*	0	0	1	1
S83L	S80I, E84V	I529L	–*	0	0	3	3
S83L	S80I, E84V	I529L	*qnr*	0	0	1	1
S83L	S57T	–*	–*	3	0	1	4

QRDR mutations			PMQR	Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*		≤0.25	0.5	>0.5	Total
S83L	S80I	–*	–*	0	0	1	1
S83L	S80I	–*	*qnr*	0	0	10	10
S83L	S80R	–*	–*	0	1	0	1
S83L	T57S	I529L	–*	0	0	1	1
Total				316	143	424	883

MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

* Not detected

Notes:

1. Fluoroquinolone resistant determinants include mutations in the QRDR of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[101], and/or PMQR (*qnr* variants, *aac(6')-Ib-cr*, *qepA, oqxAB*) detected by whole genome sequence analysis.
2. Bold formatting highlights **ST131** (blue) and **ST1193** (red) isolates.
3. No mutations in *gyrB* were detected.

Table E3: Fluroquinolone resistance determinants in *Klebsiella pneumoniae* complex (*n* = 153), by ciprofloxacin MIC, AGAR, 2023

QRDR mutations		PMQR	Ciprofloxacin MIC (mg/L)			
gyrA	parC		≤0.25	0.5	>0.5	Total
–*	–*	–*	51	6	6	63
–*	–*	*aac(6')-Ib-cr*	1	0	2	3
–*	–*	*aac(6')-Ib-cr*, *qnr*	0	1	14	15
–*	–*	*qnr*	5	23	30	58
–*	A57G	*qnr*	0	0	1	1
–*	T57S	–*	0	1	0	1
S83Y, D87A	–*	–*	0	0	1	1
S83I	–*	*aac(6')-Ib-cr*	0	0	6	6
S83I	–*	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
S83I	–*	*qnr*	0	0	2	2
S83Y	–*	*aac(6')-Ib-cr*	0	0	1	1
S83Y	–*	*qnr*	0	0	1	1
Total			57	31	65	153

PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

* Not detected

Notes:

1. Fluoroquinolone resistant determinants include mutations in either the QRDR of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[101], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*) detected by whole genome sequence analysis.
2. Mutations in *gyrB* or p*arC* were not detected.

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