AUSTRALIAN COMMISSION ON SAFETY AND QUALITY IN HEALTH CARE

AURA
Antimicrobial Use and Resistance in Australia

D23-53608

AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Surveillance Outcome Programs

Bloodstream infections

2022 report

AGAR

November 2023

Published by the Australian Commission on Safety and Quality in Health Care

Level 5, 255 Elizabeth Street, Sydney NSW 2000
Phone: (02) 9126 3600
Email: mail@safetyandquality.gov.au
Website: www.safetyandquality.gov.au

ISBN: 978-1-922880-68-0

The Commission's preference is that you attribute this publication (and any material sourced from it) using the following citation:

Coombs G, Bell JM, Blyth C, Daley D, Collignon P, Cooley L, Gottlieb T, Iredell J, Warner M, and Robson J on behalf of the Australian Group on Antimicrobial Resistance and Australian Commission on Safety and Quality in Health Care. Australian Group on Antimicrobial Resistance Surveillance Outcomes Programs. Bloodstream infections: 2022 Report. Sydney: ACSQHC; 2023

Disclaimer

The content of this document is published in good faith by the Australian Commission on Safety and Quality in Health Care for information purposes. The document is not intended to provide guidance on particular healthcare choices. You should contact your healthcare provider on particular healthcare choices.

The Commission does not accept any legal liability for any injury, loss or damage incurred by the use of, or reliance on, this document.

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 System. 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 program and AGAR is provided by the Australian Government Department of Health and Aged Care and state and territory health departments.

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

Implications for health care identified by analyses of 2022 AGAR data include:

- A longitudinal trend of increasing 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 was in the community
- Extended lengths of stay for patients with enterococcal and staphylococcal bacteraemias.

To ensure that patients receive the best possible care, the Commission will continue to support states and territories ,the private health sector and primary care to use AGAR and other AURA data to refine and strengthen their approaches to infection prevention and control and antimicrobial stewardship (AMS), and implementation of the National Safety and Quality Health Service (NSQHS) Standards[2] and the National Safety and Quality Primary and Community Healthcare Standards (Primary and Community Healthcare Standards)[3], the Antimicrobial Stewardship Clinical Care Standard[4], and the Sepsis Clinical Care Standard.[5] The Commission also continues to work with Therapeutic Guidelines Limited and other expert guideline development groups to ensure consideration of data such as the rates of gram-negative resistance.

Key findings and implications for health care: 2022 AGAR data

A. Key findings

Enterococcus species

- Between 1 January to 31 December 2022, a total of 1,535 episodes of bacteraemia were reported; the majority (92.8%) of enterococcal bacteraemia episodes were caused by *E. faecalis* or *E. faecium*.
- Twenty-nine *E. lactis* were identified. Prior to 2022 this species was identified as *E. faecium*.
- Approximately two-thirds of *E. faecalis* bacteraemias were community-onset (67.0%), while in *E. faecium* bacteraemias only 25.6% were community-onset.
- The most frequent source of bacteraemia or principal clinical manifestation for *E. faecalis* was urinary tract infection (22.5%); for *E. faecium*, it was febrile neutropenia (19.8%) or intra-abdominal infection other than biliary tract (18.3%).
- The combined 30-day all-cause mortality for *E. faecalis* and *E. faecium* was 21.5%.
- There was a significant difference in 30-day all-cause mortality between *E. faecalis* (17.2%) and *E. faecium* (26.9%) ($P < 0.01$), and between vancomycin-resistant and vancomycin-susceptible *E. faecium* episodes (34.4% and 19.7%, respectively, $P < 0.01$).
- The length of stay in hospital following enterococcal bacteraemia was more than 30 days for 22.3% of patients.
- Of bacteraemias caused by *E. faecium* in 2022, 46.9% were phenotypically vancomycin-resistant. In 2021, 37.9% of *E. faecium* had a vancomycin-resistant phenotype.
- In 2022, 48.8% of *E. faecium* harboured *vanA* and/or *vanB* genes (*vanA* 13.7%; *vanB* 35.1%). In 2021, 42.1% of *E. faecium* harboured *vanA* and/or *vanB* genes.
- Of vancomycin-resistant *E. faecium* (VRE) bacteraemias, 28.3% were due to *vanA*-harbouring isolates. *vanA* was the dominant genotype in New South Wales.
- There were 62 *E. faecium* multi-locus sequence types (STs), of which ST17, ST78, ST1424, ST796, ST80, ST1421, ST555 and ST117 were the most frequently identified.
- v*anA* genes were detected in six STs, and *vanB* genes were detected in 13 STs. The clonal diversity of *E. faecium* harbouring van genes varied across Australia.
- Two linezolid-resistant *E. faecium* were confirmed, one also harboured the *vanB* gene.
- Daptomycin-resistance was confirmed in one *E. faecalis* and one vancomycin-resistant *E. faecium*.
- In 2021, Australia ranked in the top quarter in rates of resistance to vancomycin in *E. faecium* when compared to the World Health Organization (WHO) European region countries. In 2022, the rates of vancomycin resistance rose to 46.9% in Australia.

Staphylococcus aureus

- A total of 3,214 *S. aureus* bacteraemia (SAB) episodes were reported from 1 January to 31 December 2022, 77.5% of which were community-onset. Of all episodes 15.0% were due to methicillin-resistant isolates.
- The 30-day all-cause mortality was 17.5%. There was a significant difference in mortality between methicillin-susceptible *S. aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA) (16.8% and 21.4%, respectively, $P = 0.0246$); and between community-associated MRSA (CA-MRSA) and healthcare-associated MRSA (HA-MRSA) clones (19.9% and 34.5%, respectively, $P = 0.0166$). There was no significant difference in mortality between hospital-onset (19.5%) and community-onset (17.0%) bacteraemia.
- The 30-day all-cause mortality for *S. aureus* was significantly lower among children (<18 years) (5/219, 2.3%) compared to adults (459/2,426, 18.9%) ($P < 0.01$).
- Osteomyelitis/septic arthritis (20.8%) and skin and skin structure infections (19.7%) were the most common principal clinical manifestations.

- The hospital length of stay was more than 30 days in 24.6% of patients (21.5% in MRSA; 25.2% in MSSA).
- Resistance to non-β-lactam antimicrobials in MRSA have continued to decline overall, largely due to the substantial decline in the multi-resistant ST239-III clone.
- Daptomycin resistance was confirmed in one MRSA isolate.
- CA-MRSA strains were the dominant cause of MRSA bacteraemia.
- Two HA-MRSA clones were identified; ST22-IV (EMRSA-15) which was the dominant clone and ST239-III (Aus 2/3 EMRSA). No HA-MRSA isolates harboured the Panton-Valentine leucocidin (PVL)-associated genes.
- The majority of EMRSA-15 bacteraemias were community-onset.
- Sixty-four CA-MRSA clones were identified; the dominant CA-MRSA clone was ST93-IV (Queensland clone).
- Overall, 42.8% of CA-MRSA isolates harboured PVL genes.
- The Queensland clone of CA-MRSA (ST93-IV), which harbours PVL genes, was seen in all states and territories except Tasmania; it is now the most common CA-MRSA clone in all other regions except New South Wales.
- The multi-resistant ST45-V CA-MRSA clone remains prominent in New South Wales and is associated with both community-onset and hospital-onset infections.

Gram-negative species

- From 1 January 2022 to 31 December 2022, a total of 9,739 episodes of gram-negative bacteraemia were reported, including *Enterobacterales* (90.1%), *Pseudomonas aeruginosa* (8.6%) and *Acinetobacter* (1.3%). Of the *Enterobacterales*, three genera – *Escherichia* (60.1%), *Klebsiella* (20.9%) and *Enterobacter* (5.7%) – contributed 86.7% of all *Enterobacterales* bacteraemias.
- The all-cause 30-day mortality rate for gram-negative bacteraemia was 13.0% (12.5% for *Enterobacterales,* 18.4% for *P. aeruginosa*, and 13.0% for *Acinetobacter* species).
- Urinary tract infection was the most frequent source of sepsis or clinical manifestation (*Enterobacterales* 45.1%; *P. aeruginosa* 29.8%). For *Enterobacterales*, device-related urinary tract infections were more common with hospital-onset than community-onset episodes (23.6% versus 9.4%, $P < 0.01$).
- Of all *E. coli* isolates, 82.5% were of community-onset and 12.1% of these were ceftriaxone resistant.
- There was a significant difference in 30-day all-cause mortality between children and adults (3.7% versus 12.9%, $P < 0.01$) with *Enterobacterales* bacteraemia episodes.
- In 2022, 14.4% of *E. coli* (CO 13.8%; HO 17.2%) and 7.5% of *K. pneumoniae* complex isolates (CO 5.3%; HO 12.7%) had an extended-spectrum β-lactamase (ESBL) phenotype.
- Fluoroquinolone resistance in *E. coli* increased to 13.7% in 2022 (up from 12.3% in 2021), most notably in New South Wales (16.4%, up from 12.1% in 2021) and South Australia (14.6%, up from 8.5% in 2021).
- Fluoroquinolone resistance is commonly linked to cephalosporin resistance caused by ESBLs of the CTX-M type. A little over two-thirds (255/358, 71.2%) of *E. coli* that were ciprofloxacin-resistant and also had confirmed ESBL β-lactamase gene(s) belonged to ST131 (n = 198, 55.3%) or ST1193 (n = 57, 15.9%).
- Almost 1 in 4 (23.4%) *E. coli* isolates were classified as multidrug-resistant (MDR), a proportion little changed from the 2021 survey (24.2%). The proportion of MDR *K. pneumoniae* complex isolates was 8.0% in 2022, it was 8.8% in 2021.
- Rates of carbapenemase-producing *Enterobacterales* (CPE) bacteraemic isolates remain low (0.3% overall, mostly carrying $bla_{\text{IMP-4}}$). For *Enterobacter cloacae* complex the figure is higher at 2.1% overall (CO 0.8%; HO 3.5%).
- *mcr-9* or *mcr-10* were the only *mcr* genes detected. Half (8/18, 50.0%) were not linked to other resistance mechanisms.
- The association between the COVID-19 pandemic and the reduction in antimicrobial resistance in 2022 remains unclear, as a number of contributing factors may be involved. These include

reduced antimicrobial use in the community and restrictions limiting movement within Australia and little movement of people into Australia until most restrictions ended in late 2021.

B. Implications of key findings for health care

When interpreting AGAR data, it is important to consider changes in surveillance coverage between 2013 and 2022. The number of hospitals that contribute to AGAR increased from 27 in 2013 to 43 in 2015, and 55 in 2022. In addition, the relative distribution of sites has changed. Paediatric and/or facilities providing specialist obstetric services increased from two in 2013, to five in 2017, six in 2019 and seven in 2020. Since 2015, seven sites have been added and hospitals from north-west regional Western Australia have also been included.

Bacteraemias caused by multidrug-resistant organisms result in increased death rates as well as increased lengths of hospital stay. Overall, 22.3% of patients remained in hospital for more than 30 days after enterococcal bacteraemia and 24.6% after staphylococcal bacteraemia. There are also costs to patients in terms of their length and quality of life, and additional monetary costs to the health system. Hospital-onset *Enterococcus* and *S. aureus* bacteraemias were frequently device-related. This highlights the importance of appropriate infection prevention and control practices and aseptic technique in the management of devices such as urinary catheters, peripheral cannulas, and central lines.

Several other themes, which have implications for the delivery of health care services and the safety of care provided patients, have been also identified from the analyses of AGAR data.

Gram-negative resistance

The percentage resistance in *E. coli* in 2022 was similar to 2021 for all antimicrobial agents tested except for ciprofloxacin, where a 11.1% increase in resistance was observed. The percentage resistance rates in *K. pneumoniae* complex isolates were similar to 2021 for all antimicrobials.

Previous AGAR reports show a longitudinal trend of increasing *E. coli* resistance to key anti-gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin from 2013 to 2020. Resistance to both agents stabilised from 2018 to 2020, declined in 2021 and remained steady in 2022. The steady rise in resistance to fluoroquinolones is 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%.

Increasing resistance to third-generation cephalosporins and fluoroquinolones in *E. coli* strains in the community is of concern, given that access to these agents on the Pharmaceutical Benefits Scheme is quite restricted. It is likely that high community use of unrestricted agents to which these strains are co-resistant such as amoxicillin and cefalexin, is fuelling 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 (most of Asia) from 2020 to 2022 is a likely factor in the changes in percentage rate of resistance during that period.[6, 7]

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.[8-10] It is unclear what is driving the community expansion of CTX-M ESBLs in Australia, as third-generation cephalosporins are not widely used in that 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.[11]

ESBLs in gram-negative organisms have a considerable impact on resistance patterns and limit choices for therapy. Almost 1 in 7 (14.4%) *E. coli* isolates displayed this phenotype in 2022, with

little change since 2018. This phenotype is significantly more common in hospital-onset compared to community-onset *E. coli* infection, with 17.2% demonstrating this pattern in hospital-onset infection compared to 13.8% for community-onset isolates in 2022 ($P < 0.01$). In hospital-onset *K. pneumoniae* complex isolates, this phenotype is also more common than for community-onset isolates (12.7% versus 5.3%, 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, while for *K. pneumoniae* complex, proportions are noticeably higher in the Northern Territory.

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, and OXA-23 either alone or co-produced) were detected in isolates from 18 of the contributing hospitals from six states and territories. $bla_{\text{IMP-4}}$ accounted for 62.1% (18/29) of all carbapenemase-producing *Enterobacterales* (CPE) in 2022. No CPE were found in South Australia or Tasmania.

Notwithstanding low rates of CPE from blood culture isolates reported to AGAR, CARAlert showed increasing rates of CPE in Australian hospitals in 2022 in non-blood isolates.[12] Carbapenemase-producing *Enterobacterales* were the most commonly reported critical antimicrobial resistance (CAR) in 2021 and 2022. There was a 37.4% increase in CPE reports in 2022 compared with 2021. In contrast, 2020 reports decreased 26.6% compared with 2019.

In addition to the *Australian Guidelines for the Prevention and Control of Infection in Healthcare*[13] (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*.[14]

Changing patterns in *Enterococcus* species

Total numbers of enterococcal bacteraemias identified by AGAR, for hospitals participating in both years, increased from 1,300 in 2021 to 1,402 in 2022 (up 7.8%). The increase was mostly in the number of *E. faecium* (493 in 2021; 540 in 2022, up 9.5%) rather than *E. faecalis* (705 in 2021; 757 in 2022, up 7.4%).

The number of vancomycin-resistant *E. faecium* (VRE) isolates increased from 198 in 2021 to 285 in 2022. There was an increase in overall vancomycin resistance rates in *E. faecium* from 40.2% in 2021 to 46.9% ($P = 0.02$). There was an increase in VRE as a proportion of all enterococcal isolates from 15.2% to 18.6%. The overall contribution of *vanA* and *vanB* genes to VRE varied according to state or territory. *vanA*- and *vanB*-harbouring types were in similar proportions in New South Wales, Queensland, and Western Australia, whilst *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.

Methicillin resistance in *Staphylococcus aureus*

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

The total number of *S. aureus* bacteraemia (SAB) identified by AGAR in 2022, excluding isolates from four hospitals that contributed in 2021 or 2022 only, was similar to 2021 (2,947 in 2021; 2,936 in 2022). There was a significant increase in the total number of SAB from Tasmania (115 to 159, $P < 0.01$) due to an increase in the numbers of methicillin-susceptible *S. aureus* (106 to 150, $P < 0.01$). The total number of SAB increased slightly in the Northern Territory, the Australian

Capital Territory, and Queensland; and decreased slightly in New South Wales, Victoria and Western Australia.

Overall, between 2021 and 2022, the proportion of MRSA decreased by 1.5 percentage points, from 16.6% to 15.1%. Over the same period, hospital-onset infections increased from 22.3% to 23.8%. Relative to 2021, there were no significant differences in the proportion of MRSA in all states and territories. The proportion of MRSA decreased in all states and territories except the Northern Territory, which saw a slight increase (40.7% in 2021; 42.9% in 2022).

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

In 2022, CA-MRSA clones accounted for 12.2% (388/3,182) of all *S. aureus*; in 2021 it was 13.7% (401/2,931). ST93-IV was the most prevalent CA-MRSA clone (104/388, 26.8%), and was found in all states and territories except Tasmania. ST45-V continues to dominate in New South Wales. HA-MRSA clones accounted for only 1.9% (61/3,182) of all *S. aureus* in 2022. ST22-IV was the most common HA-MRSA clone (55/61, 90.2%); it was found in all states and territories.

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 2022, febrile neutropenia or intra-abdominal infection other than biliary tract, were the most common clinical manifestations associated with *E. faecium* bacteraemia.

Device-related bacteraemia accounted for 8.2% (1,064/12,949) of bacteraemia across all the AGAR surveillance programs in 2022. The rate was 9.2% in 2021. The decrease was notable for staphylococcal episodes (19.0% in 2021; 16.8% in 2022). Total numbers are dominated by gram-negative (*n* = 370) bacteria and *S. aureus* (*n* = 496) infections.

Gram-negative infections commonly arise from urinary infections associated with the use of indwelling catheters and urinary stents, as well as from biliary stent infections. In contrast, SAB is commonly associated with intra-vascular catheters and/or devices and prosthetic joints. Continuing attention to the requirements of the NSQHS Standards, the Primary and Community Care Standards[3] and the AICGs for optimum medical device management[13] as well as the Commission's *Management of Peripheral Intravenous Catheters Clinical Care Standard*[15] are important for all health service organisations to prevent these type of infections. 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 that is due to be released in mid-2024 will also support prevention of device-related infections.[16]

Variation across states and territories

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

E. coli resistance to third-generation cephalosporins ranged from 5.2% in Tasmania to 28.8% in the Northern Territory; fluoroquinolone resistance ranged from 6.9% in Tasmania to 16.4% in New South Wales; and aminoglycoside resistance ranged from 3.9% in Tasmania to 22.9% in the Northern Territory.

For *K. pneumoniae* complex, resistance to third-generation cephalosporins ranged from 3.5% in Queensland to 21.2% in the Northern Territory; fluoroquinolone resistance ranged from 2.4% in

South Australia to 17.3% in the Northern Territory; and aminoglycoside resistance ranged from 2.0% in Tasmania to 13.5% in the Northern Territory.

Rates of vancomycin resistance in *E. faecium* ranged from 13.0% in Queensland to 65.0% in South Australia. Teicoplanin resistance ranged from 7.1% in the Northern Territory to 20.7% in New South Wales.

Adaptation of national treatment guidelines informed by local antibiograms should be considered in order to minimise the use of broad-spectrum antimicrobials whilst balancing delivery of the most appropriate antimicrobial for severe infections.

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 more commonly hospital-onset (74.4%) than *E. faecalis* (33.0%). Vancomycin-resistant *E. faecium* bacteraemia accounted for 7.2% (55/763) of all community-onset enterococcal bacteraemia, compared to 30.1% (230/763) 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[11, 17, 18] (which are included in the community-onset group in the AGAR data, but not distinguished as such in this report).

International comparisons

Australia had relatively lower rates of resistance in 2022, compared to 2021 data available from the European Union (EU) and European Economic Area (EEA) countries reporting to EARS-Net[19] or the WHO European Region countries (excluding EU/EEA countries) reporting to CAESAR.[20] Australia ranks towards the middle in rates of resistance to methicillin in *S. aureus* compared to all European countries, and in the top quarter in rates of resistance to vancomycin in *E. faecium*. Australia also ranks towards the middle in rates of resistance to third-generation cephalosporins in *E. coli*, but in the bottom quarter in rates of resistance to fluoroquinolones. In *K. pneumoniae* complex isolates, resistance to both fluoroquinolones and third-generation cephalosporins is low (<10.0%) compared to European countries (EU/EEA average 33.6% and 34.3%, respectively).

C. Response

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

- Provide advice for *Therapeutic Guidelines: Antibiotic*[21] and other expert guideline development groups to ensure consideration of data such as the rates of gram-negative resistance
- Work with states and territories and the private laboratory sector to encourage consideration of geographic variation through the use of local antibiograms by antimicrobial stewardship (AMS) services. Antibiograms are tables of antimicrobial susceptibilities that can inform local empiric and therapeutic antimicrobial recommendations and formulary management. APAS contributor laboratory services have ready access to data and functionality to produce antibiograms
- Promote adaption of national prescribing practices to local resistance patterns and regular review of prescribing guidance by local AMS services; this will support the use of broad-spectrum antibiotics where necessary, whilst limiting their use in areas where their use is not justified due to lower rates of resistance
- Promote incorporation of concepts of geographical variation in AMR into clinical practice; particularly to support clinicians who regularly work in a range of settings
- Promote use of the *Priority Antibacterial List for Antimicrobial Resistance Containment*[22] as a

tool to support AMS programs to analyse antimicrobial usage in terms of preferred or optimal prescribing choices
- Support development of guidance for surveillance, prevention and control of specific organisms and resistances
- Advocate for selected resistances to be made nationally notifiable under public health legislation
- Support collaboration and coordination between states and territories, and between hospital and community care settings to explore the drivers of variation and improve local control efforts to help limit progression of AMR
- Contribute to the AURA Surveillance System and promote use of AMR and antimicrobial use data to inform AMS and infection prevention and control programs
- Promote effective infection prevention and control measures, such as those included in the AICGs and the *Recommendations for the control of carbapenemase-producing* Enterobacterales *(CPE). A guide for acute care health service organisations*[14], to limit the transmission of CPE
- Promote effective implementation of systems that address the requirements of the NSQHS Standards relevant to the control of hospital-onset bacteraemia, particularly in relation to invasive medical devices
- Promote effective implementation of systems that address the requirements of the Primary and Community Healthcare Standards, particularly in relation to community-onset infections and community-associated MRSA
- Support submission of AGAR data and Australian Passive AMR Surveillance 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 groups of pathogens: 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)[23], 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 55 hospitals across Australia in 2022.

The 55 hospitals that currently contribute to AGAR, including six private laboratories, are listed in Table 1. In 2022, three additional hospitals contributed data, two from New South Wales and one from Queensland, and one hospital from Queensland was only able to participate for Quarter one, and.

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 System funded and coordinated by the Australian Government Department of Health and Aged Care.

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

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

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

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

Note: In 2022, the Royal Prince Alfred Hospital (NSW) and Queensland Children's Hospital recommenced the survey. Gosford Hospital (NSW), Prince of Wales Hospital (NSW), and the Mater Private Hospital Townsville (Qld) participated for the first time.

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).[31] The term "Sepsis" in the program was changed in 2021 to "Surveillance" to better reflect AGAR's surveillance of episodes of bacteraemia rather than sepsis.

In order to provide data to support improved antimicrobial prescribing and patient care, the objective of AESOP 2022 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.[32] 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.[33]

Despite standardised treatment protocols for SAB, including prolonged antimicrobial therapy and prompt source control[34], mortality can range from as low as 2.5% to as high as 40%.[35-37] Mortality rates are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[38, 39] 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.[40]

AGAR began surveillance of antimicrobial resistance in *S. aureus* in 1986.[41] In 2013, AGAR commenced the Australian *Staphylococcus aureus* Sepsis Outcome Program (ASSOP).[42] The term "Sepsis" in the program was changed in 2021 to "Surveillance" to better reflect AGAR's surveillance of episodes of bacteraemia rather than sepsis.

The primary objective of ASSOP 2022 was to determine the proportion of SAB isolates demonstrating 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.[24, 43] 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.[44-46]

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. 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” in the program 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 the third-generation cephalosporins. Other resistances of interest are to agents that are important for treatment of these serious infections, such as gentamicin and ciprofloxacin, and to reserve agents such as meropenem.

The objectives of the 2022 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-five hospitals, in each state and territory of Australia, were enrolled in the 2022 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, and either all or up to 200 isolates for GnSOP, from 1 January 2022 to 31 December 2022. Approval to conduct the prospective data collection, including de-identified demographic data, was given by the research ethics committees associated with each participating hospital.

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

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

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

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, all-cause or survived) at seven and 30 days (see Appendix A).

2.2. Species identification

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

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 comprises *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–Ed33[47] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v13.1.[48]

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 isolates 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), using the Illumina NextSeq™ 500 platform. Data were analysed using a modified version of the Nullarbor bioinformatic pipeline.[49]

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*). *van* genes (*E. faecium*) were identified using nucleotide sequences from the NCBI database and a BLAST interface. 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.

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 10.0.3 for Windows (GraphPad Software, La Jolla, California).

3. Results

3.1. Isolates recovered

During 2022, a total of 14,488 bloodstream isolates were reported from 55 participating hospitals. Overall, the proportion of isolates from children (<18 years) was 5.5%. The proportion of *S. aureus* isolates from children was 8.6%, *Enterococcus* species 5.9%, *Enterobacterales* 4.3%, *P. aeruginosa* 4.5% and *Acinetobacter* species 7.9%.

A total of 9,739 gram-negative bloodstream isolates (23 genera, 60 species/complexes) were reported. *Enterobacterales* accounted for 90.1%, followed by *P. aeruginosa* (8.6%) and *Acinetobacter* (1.3%). Of the *Enterobacterales*, three genera – *Escherichia* (60.1%), *Klebsiella* (20.9%) and *Enterobacter* (5.7%) – contributed 86.7% of all isolates. Overall, the top 10 ranked species were *E. coli* (54.1%), *K. pneumoniae* complex (14.3%), *P. aeruginosa* (8.6%), *E. cloacae* complex (4.9%), *Proteus mirabilis* (3.3%), *K. oxytoca* (3.0%), *Serratia marcescens* (2.6%), *K. aerogenes* (1.3%), *Morganella morganii* (1.1%), *Salmonella* species (non-typhoidal) and *Citrobacter freundii* complex (1.0%, equal rank). These 11 species comprised 95.5% of all isolates (Table 2).

The proportion of isolates from children was 4.3% (*n* = 423; *Enterobacterales n* = 375, *P. aeruginosa n* = 38, *Acinetobacter* species *n* = 10). *Enterobacter cloacae* complex and *Salmonella* species episodes were more common among children than adults (8.5% versus 4.7% and 8.0% versus 0.7%, respectively) (data not shown).

Of 3,214 SAB episodes, 481 (15.0%; 95% confidence interval [CI]: 13.8-16.2) were methicillin-resistant, ranging from 5.7% (95% CI: 3.0-10.4) in Tasmania to 42.9% (95% CI: 33.5-52.7) in the Northern Territory (Table 2). There was no significant difference in the proportion of MRSA among children (12.2%, 95% CI: 8.9-16.6) and adults (15.2%, 95% CI: 14.0-16.6) (data not shown).

There were 1,535 episodes of enterococcal bloodstream infection. *E. faecalis* and *E. faecium* accounted for 92.8% of all enterococcal isolates (Table 2).

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

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Enterococcus species	494	384	161	123	207	81	33	52	1,535
Enterococcus faecalis	249	180	92	75	118	51	14	33	812
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	215	178	54	41	71	23	14	17	613
Vancomycin-resistant, percent*	49.3	62.4	13.0	65.0	16.9	34.8	57.1	52.9	46.9
Vancomycin-susceptible, percent*	50.7	37.6	87.0	35.0	83.1	65.2	42.9	47.1	53.1
Other enterococcal species	30	26	15	7	18	7	5	2	110
Enterococcus lactis†	9	7	4	1	3	2	2	1	29
Enterococcus casseliflavus	4	4	2	3	5	2	1	0	21
Enterococcus gallinarum	3	6	5	1	2	0	0	0	17
Enterococcus avium	4	4	2	0	3	2	0	1	16
Enterococcus raffinosus	6	2	1	2	1	0	1	0	13
Enterococcus hirae	1	1	1	0	2	0	0	0	5
Enterococcus durans	1	1	0	0	0	1	1	0	4
Enterococcus gilvus	0	0	0	0	2	0	0	0	2
Enterococcus cecorum	1	0	0	0	0	0	0	0	1
Enterococcus dispar	0	1	0	0	0	0	0	0	1
Enterococcus species§	1	0	0	0	0	0	0	0	1

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Staphylococcus aureus	982	593	536	234	497	159	98	115	3,214
Methicillin-resistant, percent	17.8	11.8	11.8	17.1	14.7	5.7	42.9	7.8	15.0
Methicillin-susceptible, percent	82.2	88.2	88.2	82.9	85.3	94.3	57.1	92.2	85.0
Gram-negative species#	3,210	1,960	1,398	785	1,325	426	296	339	9,739
Acinetobacter	23	25	26	12	15	9	12	4	126
Acinetobacter baumannii complex	10	18	22	3	4	3	9	1	70
Acinetobacter lwoffii	4	0	0	4	3	2	2	1	16
Acinetobacter species§	2	6	0	1	5	1	1	0	16
Acinetobacter ursingii	5	0	2	3	1	0	0	1	12
Other *Acinetobacter* (*n* = 7)	2	1	2	1	2	3	0	1	12
Enterobacterales	2,915	1,789	1,218	697	1,197	381	271	305	8,773
Escherichia coli	1,773	1,056	712	441	696	231	174	190	5,273
Klebsiella pneumoniae complex	446	283	227	83	212	50	52	42	1,395
Enterobacter cloacae complex	170	98	88	23	52	19	9	18	477
Proteus mirabilis	113	69	44	31	48	9	4	6	324
Klebsiella oxytoca	87	78	30	28	43	16	5	10	297
Serratia marcescens	105	52	36	7	35	8	4	10	257
Klebsiella aerogenes	39	30	15	13	18	7	3	5	130
Morganella morganii	49	19	12	11	9	7	2	1	110
Citrobacter freundii complex	33	20	7	7	20	5	0	5	97
Salmonella species (non-typhoidal)	21	16	17	0	18	12	10	3	97
Citrobacter koseri	26	12	9	8	14	4	4	3	80
Salmonella species (typhoidal)	9	16	2	1	5	1	1	3	38
Raoultella ornithinolytica	9	3	2	1	7	3	0	3	28
Enterobacter species§	0	0	0	23	0	0	0	0	23
Providencia rettgeri	4	7	3	3	1	0	0	1	19
Providencia stuartii	5	3	1	0	3	0	1	0	13
Pantoea agglomerans	1	4	1	1	3	2	0	0	12
Proteus hauseri	6	2	0	1	1	0	1	0	11
Hafnia alvei	1	2	2	1	4	0	0	0	10
Other *Enterobacterales* (*n* = 29)	18	19	10	14	8	7	1	5	82
Pseudomonas aeruginosa	272	146	154	76	113	36	13	30	840

* Vancomycin susceptibility was not available for five *E. faecalis* (NSW [4], Qld [1]) and five *E. faecium* (NSW [4], SA [1])
† Prior to 2022 *E. lactis* was identified as *E. faecium*
§ Species not determined
# *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*

Note: *Klebsiella pneumoniae* complex Includes *K. variicola* (*n* = 121), and *K. quasipneumoniae* (*n* = 3).

3.2. Place of onset of bacteraemia

Almost all patients with bacteraemia were admitted to hospital (9,562, 98.2% gram-negative species; 1,511, 98.4% *Enterococcus* species; 3,133, 97.5% *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, 74.6% of all episodes were community-onset, with differences seen between *Enterobacterales* (76.5%), *Acinetobacter* species (66.7%) and *P. aeruginosa* (56.4%). The proportion of *Enterobacterales* that were community-onset was significantly lower among paediatrics (67.5%, 253/375) than adults (76.9%, 6,455/8,398) ($P < 0.01$), most notable among *E. coli* (children 74.0%, adults 82.8%) and *K. pneumoniae* complex (children 40.0%, adults 70.4%) (data not shown).

Episodes involving *E. faecalis* and 'other' *Enterococcus* species were predominantly community-onset (*E. faecalis* [67.0%, 95% CI: 63.7-70.1]; other *Enterococcus* species [60.0%, CI: 50.7-68.7]). However, *E. faecium* episodes were predominantly hospital-onset (74.4%; 95% CI: 70.8-77.7). The proportion of *E. faecalis* that were community-onset was significantly lower among paediatrics (43.3%, 29/67) than adults (69.1%, 515/745) ($P < 0.01$).

Most SABs were community-onset (77.5%; 95% CI: 76.0-78.9). The proportion of MRSA episodes that were community-onset was higher among children (85.3%, 29/34) than adults (74.7%, 334/447).

Table 3: Species recovered, by place of onset, AGAR, 2022

Organism	Community-onset % (*n*)	Hospital-onset % (*n*)	Total, 100%
Enterococcus species	50.0 (767)	50.0 (768)	1,535
Enterococcus faecalis	67.0 (544)	33.0 (268)	812
Vancomycin-resistant	–* (0)	–* (0)	0
Vancomycin-susceptible	67.0 (541)	33.0 (266)	807
Enterococcus faecium	25.6 (157)	74.4 (456)	613
Vancomycin-resistant	19.3 (55)	80.7 (230)	285
Vancomycin-susceptible	31.3 (101)	68.7 (222)	323
Other *Enterococcus* species (*n* = 11)	60.0 (66)	40.0 (44)	110
Staphylococcus aureus	77.5 (2,491)	22.5 (723)	3,214
Methicillin-resistant	75.5 (363)	24.5 (118)	481
Methicillin-susceptible	77.9 (2,128)	22.1 (605)	2,733
Gram-negative species	74.6 (7,266)	25.4 (2,473)	9,739
Acinetobacter	66.7 (84)	33.3 (42)	126
Acinetobacter baumannii complex	58.6 (41)	41.4 (29)	70
Acinetobacter lwoffii	81.3 (13)	18.8 (3)	16
Acinetobacter species†	75.0 (12)	25.0 (4)	16
Acinetobacter ursingii	66.7 (8)	33.3 (4)	12
Other *Acinetobacter* species (*n* = 7)	83.3 (10)	16.7 (2)	12
Enterobacterales	76.5 (6,708)	23.5 (2,065)	8,773
Escherichia coli	82.5 (4,349)	17.5 (924)	5,273
Klebsiella pneumoniae complex	69.4 (968)	30.6 (427)	1,395
Enterobacter cloacae complex	52.4 (250)	47.6 (227)	477
Proteus mirabilis	82.4 (267)	17.6 (57)	324
Klebsiella oxytoca	66.0 (196)	34.0 (101)	297
Serratia marcescens	44.4 (114)	55.6 (143)	257
Klebsiella aerogenes	60.8 (79)	39.2 (51)	130
Morganella morganii	70.9 (78)	29.1 (32)	110
Citrobacter freundii complex	74.2 (72)	25.8 (25)	97
Salmonella species (non-typhoidal)	91.8 (89)	8.2 (8)	97
Citrobacter koseri	82.5 (66)	17.5 (14)	80
Salmonella species (typhoidal)	94.7 (36)	5.3 (2)	38
Raoultella ornithinolytica	78.6 (22)	21.4 (6)	28
Enterobacter species†	82.6 (19)	17.4 (4)	23
Providencia rettgeri	84.2 (16)	15.8 (3)	19
Providencia stuartii	92.3 (12)	7.7 (1)	13
Pantoea agglomerans	66.7 (8)	33.3 (4)	12
Proteus hauseri	90.9 (10)	9.1 (1)	11
Hafnia alvei	70.0 (7)	30.0 (3)	10
Other gram-negative species (*n* = 29)	61.0 (50)	39.0 (32)	82
Pseudomonas aeruginosa	56.4 (474)	43.6 (366)	840

* Insufficient numbers (<10) to calculate percentage
† Species not determined

Note: Vancomycin susceptibility was not available for five *E. faecalis* (community-onset [3], hospital-onset [2]) and five *E. faecium* (community-onset [1], hospital-onset [4]).

3.3. Onset versus 30-day all-cause mortality

Information on 30-day all-cause mortality, when place of onset was known, was available for 7,052 (72.4%) episodes involving gram-negative species; 1,281 (83.5%) involving *Enterococcus* and 2,645 (82.3%) involving *S. aureus*.

For gram-negative species, the 30-day all-cause mortality was 12.5% (789/6,318) for *Enterobacterales*, 18.4% (115/626) for *P. aeruginosa*, and 13.0% (14/108) for *Acinetobacter* species. There was no significant difference in 30-day all-cause mortality between CO and HO episodes (Table 4). There was a significant difference in 30-day all-cause mortality between children (3.7%, 11/295) and adults (12.9%, 778/6,023) for *Enterobacterales* ($P < 0.01$). The 30-day all-cause mortality among infants aged 90 days or less was 7.6% (8/105).

The 30-day all-cause mortality for *Enterococcus* species was significantly lower among children (3.9%, 3/77) compared to adults (22.3%, 268/1,204) ($P < 0.01$). There was a significant difference in the 30-day all-cause mortality between *E. faecium* (26.9%, 141/524) and *E. faecalis* (17.2%, 114/664) ($P < 0.01$), and between vancomycin-resistant (34.4%, 88/256) and vancomycin-susceptible (19.7%, 52/264) *E. faecium* episodes ($P < 0.01$).

The 30-day all-cause mortality for *S. aureus* was significantly lower among children (2.3%, 5/219) compared to adults (18.9%, 459/2,426) ($P < 0.01$). There was a significant difference in 30-day all-cause mortality between methicillin-susceptible *S. aureus* (MSSA) and MRSA episodes (16.8% and 21.4%, respectively, $P = 0.0246$), and between community-associated MRSA (CA-MRSA) and healthcare-associated MRSA (HA-MRSA) clones (19.9% and 34.5%, respectively, $P = 0.0166$).

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

Organism	Community-onset		Hospital-onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Enterococcus species	634	19.1 (121)	647	23.2 (150)	1,281	21.2 (271)
Enterococcus faecalis	449	16.3 (73)	215	19.1 (41)	664	17.2 (114)
Vancomycin-resistant	0	–* (0)	0	–* (0)	0	–* (0)
Vancomycin-susceptible	448	16.3 (73)	214	19.2 (41)	662	17.2 (114)
Enterococcus faecium	131	30.5 (40)	393	25.7 (101)	524	26.9 (141)
Vancomycin-resistant	49	40.8 (20)	207	32.9 (68)	256	34.4 (88)
Vancomycin-susceptible	81	24.7 (20)	183	17.5 (32)	264	19.7 (52)
Other enterococcal species (*n* = 10)	54	14.8 (8)	39	20.5 (8)	93	17.2 (16)
Staphylococcus aureus	2,055	17.0 (349)	590	19.5 (115)	2,645	17.5 (464)
Methicillin-resistant	318	20.8 (66)	97	23.7 (23)	415	21.4 (89)
CA-MRSA	261	19.9 (52)	66	19.7 (13)	327	19.9 (65)
HA-MRSA	31	32.3 (10)	27	37.0 (10)	58	34.5 (20)
Methicillin susceptible	1,737	16.3 (283)	493	18.7 (92)	2,230	16.8 (375)
Gram-negative species	5,178	12.4 (642)	1,874	14.7 (276)	7,052	13.0 (918)
Acinetobacter	71	15.5 (11)	37	8.1 (3)	108	13.0 (14)
Acinetobacter baumannii complex	32	12.5 (4)	24	12.5 (3)	56	12.5 (7)
Acinetobacter species†	12	16.7 (2)	4	0.0 (0)	16	12.5 (2)
Acinetobacter lwoffii	10	30.0 (3)	3	0.0 (0)	13	23.1 (3)
Acinetobacter ursingii	7	0.0 (0)	4	0.0 (0)	11	0.0 (0)
Other *Acinetobacter* species (*n* = 7)	10	20.0 (2)	2	0.0 (0)	12	16.7 (2)
Enterobacterales	4,758	11.9 (565)	1,560	14.4 (224)	6,318	12.5 (789)
Escherichia coli	2,998	11.1 (334)	690	13.3 (92)	3,688	11.6 (426)

Organism	Community-onset		Hospital-onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Klebsiella pneumoniae complex	707	12.2 (86)	319	13.8 (44)	1,026	12.7 (130)
Enterobacter cloacae complex	188	10.1 (19)	180	16.1 (29)	368	13.0 (48)
Proteus mirabilis	203	20.7 (42)	44	18.2 (8)	247	20.2 (50)
Klebsiella oxytoca	143	11.9 (17)	74	14.9 (11)	217	12.9 (28)
Serratia marcescens	83	16.9 (14)	106	12.3 (13)	189	14.3 (27)
Klebsiella aerogenes	66	16.7 (11)	36	13.9 (5)	102	15.7 (16)
Morganella morganii	58	20.7 (12)	25	24.0 (6)	83	21.7 (18)
Citrobacter freundii complex	57	15.8 (9)	22	13.6 (3)	79	15.2 (12)
Salmonella species (non-typhoidal)	58	0.0 (0)	7	0.0 (0)	65	0.0 (0)
Citrobacter koseri	48	10.4 (5)	12	25.0 (3)	60	13.3 (8)
Raoultella ornithinolytica	19	10.5 (2)	5	0.0 (0)	24	8.3 (2)
Enterobacter species†	19	5.3 (1)	4	75.0 (3)	23	17.4 (4)
Salmonella species (typhoidal)	22	0.0 (0)	0	n/a	22	0.0 (0)
Providencia rettgeri	14	21.4 (3)	2	100.0 (2)	16	31.3 (5)
Pantoea agglomerans	7	0.0 (0)	4	0.0 (0)	11	0.0 (0)
Providencia stuartii	10	20.0 (2)	0	n/a	10	20.0 (2)
Other *Enterobacterales* species (*n* = 30)	58	13.8 (8)	30	16.7 (5)	88	14.8 (13)
Pseudomonas aeruginosa	349	18.9 (66)	277	17.7 (49)	626	18.4 (115)

CA-MRSA = community-associated methicillin-resistant *Staphylococcus aureus*; HA-MRSA = healthcare-associated methicillin-resistant *S. aureus*; n/a = not applicable (no isolates)

* Insufficient numbers (<10) to calculate percentage
† Species not determined

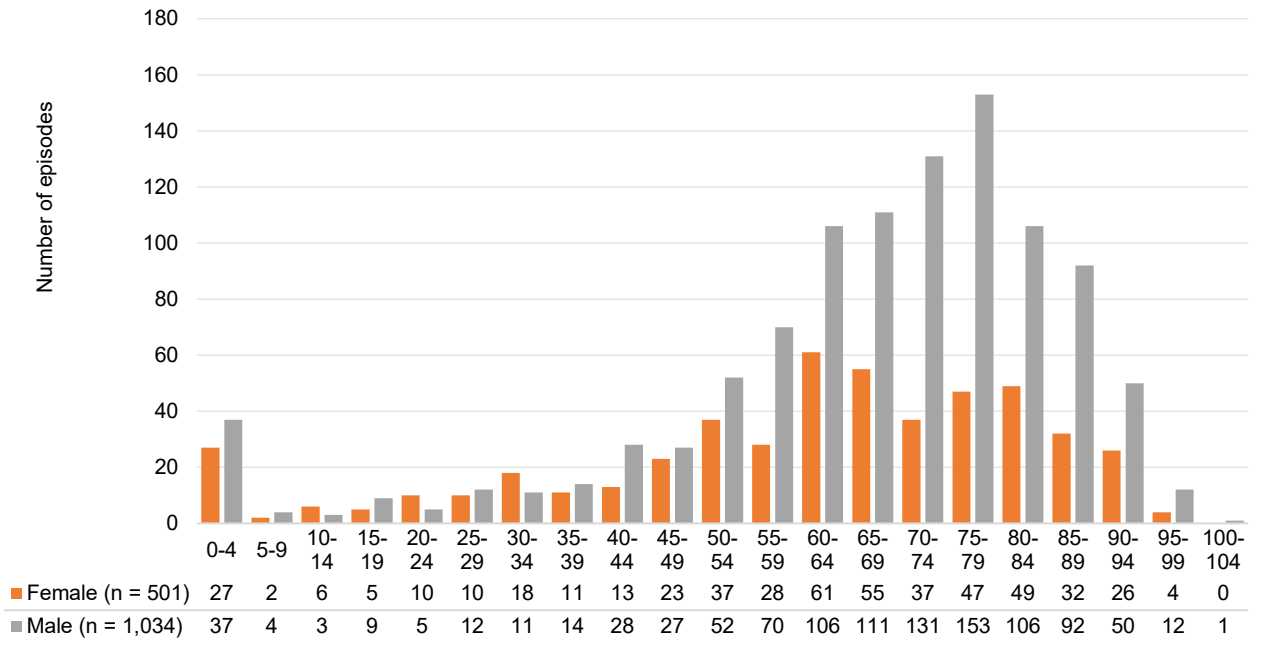
Notes:
1. Thirty methicillin-resistant *Staphylococcus aureus* were not available for whole genome sequencing.
2. Vancomycin susceptibility was not available for two *Enterococcus faecalis* (community-onset [1], hospital-onset [1]) and four *E. faecium* (community-onset [1], hospital-onset [3]).

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 53.7% and females 46.3%. For *Enterococcus* species, 67.4% were male and 32.6% female; for SAB, 66.6% were male and 33.4% female.

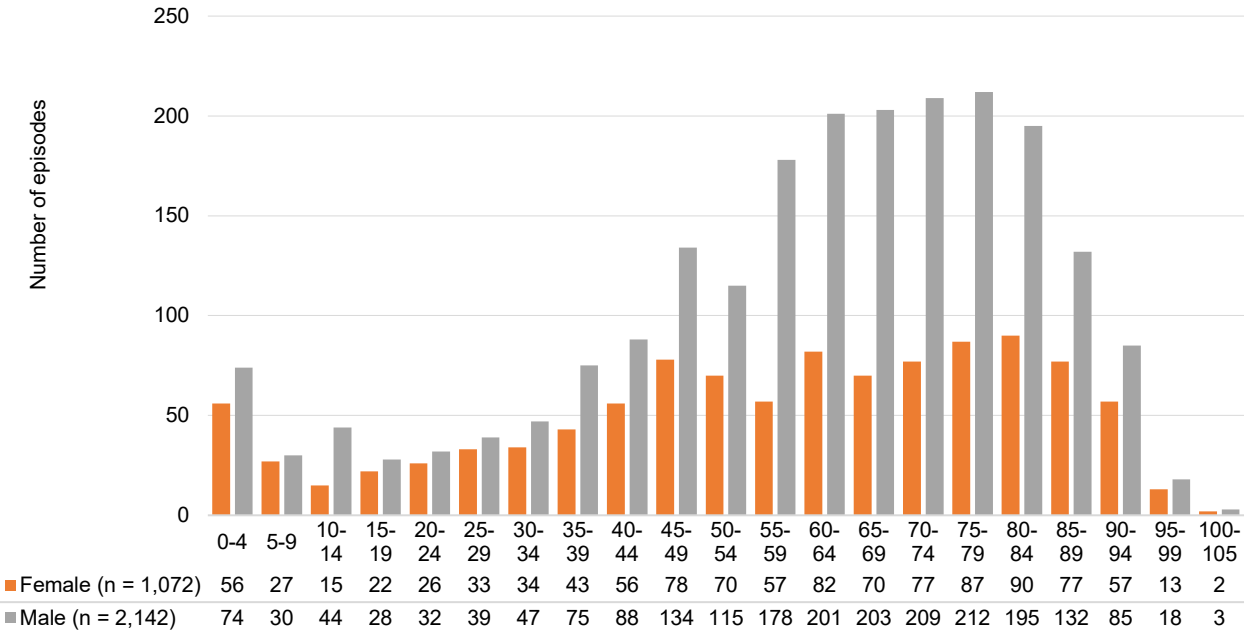
Increasing age was a surrogate risk factor for bacteraemia (Figures 1–3); only 12.0% of *Enterococcus* species episodes,19.4% of *S. aureus* episodes and 12.8% of gram-negative species episodes, were in patients aged less than 40 years. The proportion of patients aged 0–19 years was 6.1% (*n* = 93), 9.2% (*n* = 296) and 4.8% (*n* = 471) 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, 2022



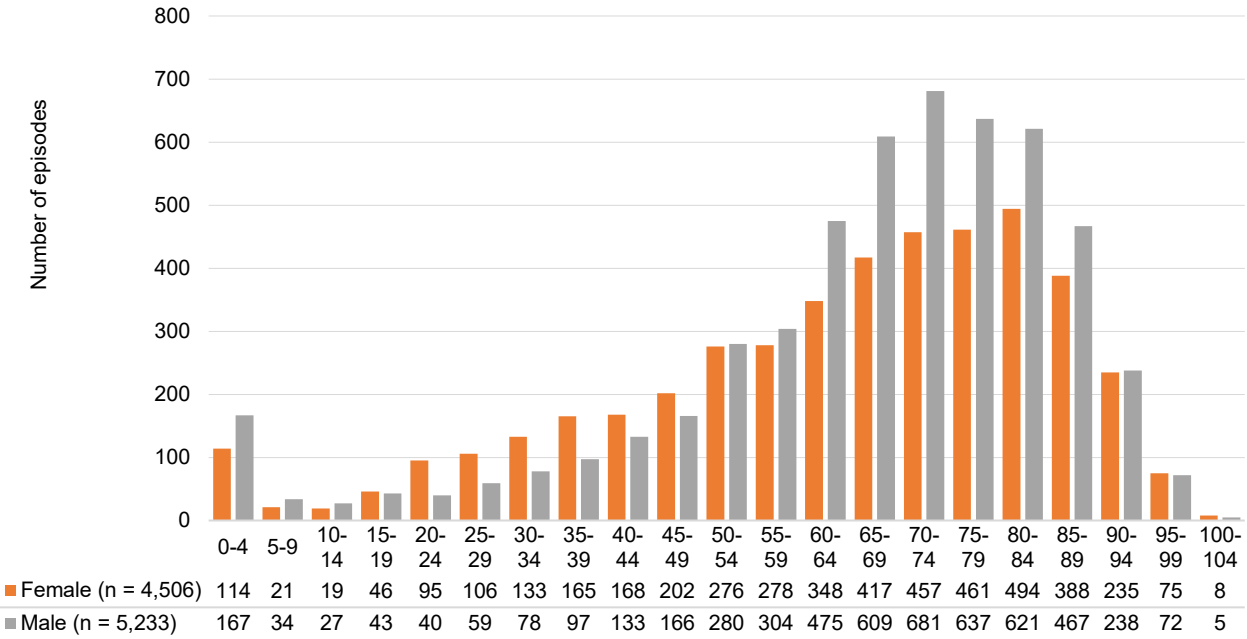
Note: x-axis = age group in years.

Figure 2: Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient age group and sex, AGAR, 2022



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, 2022



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 1,444 (94.1%) patient episodes of enterococcal bacteraemia. Overall, the most frequent principal clinical manifestations were urinary tract infection (14.2%), biliary tract infections (14.0%), intra-abdominal infection other than biliary tract (13.4%), or those with no identifiable focus (13.6%) (Table 5). There was a significant gender difference in terms of principal clinical manifestation for urinary tract infections.

Of the HO episodes where data were available, the most frequent principal clinical manifestations were device-related infection without metastatic focus (18.6%), febrile neutropenia (17.1%), or intra-abdominal infection other than biliary tract (16.9%). Of the CO episodes where data were available, the most frequent principal clinical manifestations were urinary tract infection (20.6%) or biliary tract infections (18.7%) (data not shown).

Table 5: Principal clinical manifestation for enterococcal bacteraemia, by patient sex, AGAR, 2022

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance*
Urinary tract infection	8.8 (42)	16.9 (163)	14.2 (205)	$P < 0.01$
Biliary tract infection (including cholangitis)	16.1 (77)	12.9 (125)	14.0 (202)	ns
No identifiable focus	14.0 (67)	13.4 (130)	13.6 (197)	ns
Intra-abdominal infection other than biliary tract	14.5 (69)	12.8 (124)	13.4 (193)	ns
Device-related infection without metastatic focus	13.0 (62)	11.7 (113)	12.1 (175)	ns
Febrile neutropenia	10.5 (50)	9.2 (89)	9.6 (139)	ns
Other clinical syndrome	9.0 (43)	8.8 (85)	8.9 (128)	ns
Endocarditis left-sided	6.3 (30)	8.1 (78)	7.5 (108)	ns
Skin and skin structure infection	2.3 (11)	2.2 (21)	2.2 (32)	ns
Osteomyelitis/septic arthritis	2.1 (10)	1.6 (15)	1.7 (25)	ns
Device-related infection with metastatic focus	1.9 (9)	1.4 (14)	1.6 (23)	ns
Endocarditis right-sided	1.5 (7)	1.0 (10)	1.2 (17)	ns
Total	477	967	1,444	

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

The principal manifestation was known for 1,340 of the 1,425 (94.0%) *E. faecalis* and *E. faecium* episodes (Table 6). The most common clinical manifestation for *E. faecalis* was urinary tract infection (22.5%), whereas for *E. faecium* it was febrile neutropenia (19.8%) or intra-abdominal infection other than biliary tract (18.3%). 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, 2022

Principal clinical manifestation	*E. faecalis* % (*n*)	*E. faecium* % (*n*)	Total % (*n*)	Significance*
Urinary tract infection	22.5 (171)	5.7 (33)	15.2 (204)	$P < 0.01$
No identifiable focus	16.3 (124)	10.0 (58)	13.6 (182)	$P < 0.01$
Intra-abdominal infection other than biliary tract	9.9 (75)	18.3 (106)	13.5 (181)	$P < 0.01$
Device-related infection without metastatic focus	9.5 (72)	15.9 (92)	12.2 (164)	$P < 0.01$
Biliary tract infection (including cholangitis)	7.9 (60)	17.1 (99)	11.9 (159)	$P < 0.01$
Febrile neutropenia	2.1 (16)	19.8 (115)	9.8 (131)	$P < 0.01$
Other clinical syndrome	8.9 (68)	8.6 (50)	8.8 (118)	ns
Endocarditis left-sided	13.7 (104)	0.7 (4)	8.1 (108)	$P < 0.01$
Skin and skin structure infection	2.6 (20)	1.7 (10)	2.2 (30)	ns
Osteomyelitis/septic arthritis	2.6 (20)	0.9 (5)	1.9 (25)	$0.01 < P < 0.05$
Device-related infection with metastatic focus	1.7 (13)	1.4 (8)	1.6 (21)	ns
Endocarditis right-sided	2.2 (17)	0.0 (0)	1.3 (17)	$P < 0.01$
Total	760	580	1,340	

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 2,960 (92.1%) episodes of SAB (Table 7). Overall, the most frequent principal clinical manifestation was osteomyelitis/septic arthritis (20.8%) followed by skin and skin structure infection (19.7%). Of the clinical manifestations in children a little over one-third (39.8%, 106/266) were due to osteomyelitis/septic arthritis (data not shown).

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

Table 7: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient sex, AGAR, 2022

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

CNS = central nervous system

The most common principal clinical manifestation for MSSA was osteomyelitis/septic arthritis (21.3%, 536/2,521), whereas for MRSA it was skin and skin structure infection (21.9%, 96/439) (Table 8).

Table 8: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, AGAR, 2022

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

CNS = central nervous system

Gram-negative species

The principal clinical manifestation was documented for 8,545 (87.7%) patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations for episodes caused by *Enterobacterales* were urinary tract infection (45.1%) or biliary tract infection (15.0%); for *P. aeruginosa*, urinary tract infections (29.8%) or febrile neutropenia (18.4%) were the most common. For *Acinetobacter*, device-related infection without metastatic focus (23.3%) was the most common while 20.7% had no identifiable focus (Table 9).

Urinary tract infection was the most frequent principal manifestation for community-onset episodes caused by *Enterobacterales* (51.2%) and *P. aeruginosa* (34.7%). For hospital-onset episodes, urinary tract infection (*Enterobacterales* 24.7%, *P. aeruginosa* 23.2%) and febrile neutropenia (*Enterobacterales* 22.5%, *P. aeruginosa* 24.1%) were the most common.

For *Enterobacterales* with urinary tract infection as the principal clinical manifestation, only a small proportion (388/3460, 11.2%) were regarded as a device-related infection. This was higher for hospital-onset than community-onset episodes (hospital-onset 103/447, 23.6%, community-onset 285/3023, 9.4%; $P < 0.01$).

Table 9: Principal clinical manifestation for gram-negative bacteraemia, by patient sex, AGAR, 2022

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Gram-negative species*	3,949	4,596	8,545
Acinetobacter	48	68	116
Device-related infection without metastatic focus	29.2 (14)	19.1 (13)	23.3 (27)
No identifiable focus	20.8 (10)	20.6 (14)	20.7 (24)
Skin and skin structure infection	10.4 (5)	22.1 (15)	17.2 (20)
Other clinical syndrome	14.6 (7)	19.1 (13)	17.2 (20)
Febrile neutropenia	10.4 (5)	5.9 (4)	7.8 (9)
Intra-abdominal infection other than biliary tract	4.2 (2)	4.4 (3)	4.3 (5)
Urinary tract infection	2.1 (1)	4.4 (3)	3.4 (4)
Biliary tract infection (including cholangitis)	4.2 (2)	2.9 (2)	3.4 (4)
Enterobacterales	3,629	4,046	7,675
Urinary tract infection	52.3 (1,897)	38.7 (1,565)	45.1 (3,462)
Biliary tract infection (including cholangitis)	12.9 (468)	16.9 (683)	15.0 (1,151)
Intra-abdominal infection other than biliary tract	8.7 (317)	11.5 (465)	10.2 (782)
Febrile neutropenia	8.0 (291)	10.5 (423)	9.3 (714)
No identifiable focus	7.1 (257)	7.7 (310)	7.4 (567)
Other clinical syndrome	5.0 (180)	6.9 (280)	6.0 (460)
Device-related infection without metastatic focus	3.1 (113)	3.3 (132)	3.2 (245)
Skin and skin structure infection	2.1 (76)	3.2 (128)	2.7 (204)
Osteomyelitis/septic arthritis	0.7 (24)	1.1 (43)	0.9 (67)
Device-related infection with metastatic focus	0.2 (6)	0.4 (17)	0.3 (23)
Pseudomonas aeruginosa	272	482	754
Urinary tract infection	21.7 (59)	34.4 (166)	29.8 (225)
Febrile neutropenia	19.9 (54)	17.6 (85)	18.4 (139)
Other clinical syndrome	12.1 (33)	11.6 (56)	11.8 (89)
Device-related infection without metastatic focus	9.2 (25)	10.0 (48)	9.7 (73)
No identifiable focus	10.3 (28)	8.7 (42)	9.3 (70)
Skin and skin structure infection	11.4 (31)	5.8 (28)	7.8 (59)
Intra-abdominal infection other than biliary tract	8.8 (24)	6.6 (32)	7.4 (56)
Biliary tract infection (including cholangitis)	5.9 (16)	4.1 (20)	4.8 (36)
Osteomyelitis/septic arthritis	0.4 (1)	0.8 (4)	0.7 (5)
Device-related infection with metastatic focus	0.4 (1)	0.2 (1)	0.3 (2)

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

3.6. Length of hospital stay following bacteraemic episode

Information on length of stay following bacteraemia was available for 1,441 (93.9%) episodes involving *Enterococcus* species, 3,002 (93.4%) episodes involving *S. aureus* and 8,894 (91.3%) episodes involving gram-negative species.

Overall, 22.3% of patients remained in hospital for more than 30 days after enterococcal bacteraemia (Table 10) and 24.6% after staphylococcal bacteraemia (Table 11). Over half (3,158/6,067, 52.1%) of patients with a CO gram-negative bacteraemia had a length of hospital stay less than seven days. A little over one-quarter of patients with HO bacteraemia caused by *P. aeruginosa* remained in hospital for more than 30 days (97/342, 28.4%) (Table 12).

Table 10: Length of stay following *Enterococcus* species bacteraemia, by vancomycin resistance and place of onset, AGAR, 2022

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 % days (*n*)	15–30 % days (*n*)	>30 days % (*n*)	
All species	21.8 (314)	28.8 (415)	27.1 (390)	22.3 (322)	1,441
E. faecalis	21.8 (166)	29.6 (226)	26.1 (199)	22.5 (172)	763
Vancomycin-resistant	–* (0)	–* (0)	–* (0)	–* (0)	0
Vancomycin-susceptible	21.5 (163)	29.7 (225)	26.1 (198)	22.7 (172)	758
E. faecium	20.2 (116)	28.3 (163)	29.0 (167)	22.4 (129)	575
Vancomycin-resistant	20.9 (56)	26.1 (70)	32.1 (86)	20.9 (56)	268
Vancomycin-susceptible	19.1 (58)	30.4 (92)	26.7 (81)	23.8 (72)	303
Other *Enterococcus* species (*n* = 10)	31.1 (32)	25.2 (26)	23.3 (24)	20.4 (21)	103
Community-onset					
E. faecalis	24.0 (125)	31.0 (161)	25.6 (133)	19.4 (101)	520
Vancomycin-resistant	–* (0)	–* (0)	–* (0)	–* (0)	0
Vancomycin-susceptible	23.8 (123)	30.9 (160)	25.7 (133)	19.5 (101)	517
E. faecium	30.0 (45)	32.0 (48)	26.0 (39)	12.0 (18)	150
Vancomycin-resistant	22.6 (12)	30.2 (16)	35.8 (19)	11.3 (6)	53
Vancomycin-susceptible	33.3 (32)	33.3 (32)	20.8 (20)	12.5 (12)	96
Hospital-onset					
E. faecalis	16.9 (41)	26.7 (65)	27.2 (66)	29.2 (71)	243
Vancomycin-resistant	–* (0)	–* (0)	–* (0)	–* (0)	0
Vancomycin-susceptible	16.6 (40)	27.0 (65)	27.0 (65)	29.5 (71)	241
E. faecium	16.7 (71)	27.1 (115)	30.1 (128)	26.1 (111)	425
Vancomycin-resistant	20.5 (44)	25.1 (54)	31.2 (67)	23.3 (50)	215
Vancomycin-susceptible	12.6 (26)	29.0 (60)	29.5 (61)	29.0 (60)	207

* Insufficient numbers (<10) to calculate percentage

Note: Vancomycin susceptibility not available for five *E. faecalis* (community-onset [3]; hospital-onset [2]) and four *E. faecium* (community-onset [1]; hospital-onset [3]).

Table 11: Length of stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, AGAR, 2022

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

Table 12: Length of stay following gram-negative bacteraemia, by species and place of onset, AGAR, 2022

Species	Length of stay (days)				Total
	<7, % (*n*)	7–14, % (*n*)	15–30, % (*n*)	>30, % (*n*)	
Gram-negative species	43.3 (3,852)	30.4 (2,708)	15.5 (1,381)	10.7 (953)	8,894
Community-onset	51.1 (3,362)	30.6 (2,012)	12.2 (802)	6.2 (405)	6,581
Hospital-onset	21.2 (490)	30.1 (696)	25.0 (579)	23.7 (548)	2,313
Acinetobacter	39.0 (46)	27.1 (32)	14.4 (17)	19.5 (23)	118
Community-onset	50.6 (39)	32.5 (25)	5.2 (4)	11.7 (9)	77
Hospital-onset	17.1 (7)	17.1 (7)	31.7 (13)	34.1 (14)	41
Enterobacterales	44.7 (3,574)	30.3 (2,427)	14.9 (1,193)	10.0 (803)	7,997
Community-onset	52.1 (3,158)	30.2 (1,833)	11.7 (710)	6.0 (366)	6,067
Hospital-onset	21.6 (416)	30.8 (594)	25.0 (483)	22.6 (437)	1,930
Escherichia coli	49.2 (2,357)	29.1 (1,392)	13.4 (641)	8.4 (400)	4,790
Community-onset	55.1 (2,165)	28.8 (1,132)	10.7 (419)	5.3 (210)	3,926
Hospital-onset	22.2 (192)	30.1 (260)	25.7 (222)	22.0 (190)	864
Klebsiella pneumoniae complex	35.7 (452)	33.6 (426)	18.2 (231)	12.4 (157)	1,266
Community-onset	43.2 (376)	34.0 (296)	15.1 (131)	7.7 (67)	870
Hospital-onset	19.2 (76)	32.8 (130)	25.3 (100)	22.7 (90)	396
Enterobacter cloacae complex	32.7 (147)	34.1 (153)	19.2 (86)	14.0 (63)	449
Community-onset	42.9 (99)	38.5 (89)	12.6 (29)	6.1 (14)	231
Hospital-onset	22.0 (48)	29.4 (64)	26.1 (57)	22.5 (49)	218
Other *Enterobacterales* (*n* = 44)	41.4 (618)	30.6 (456)	15.8 (235)	12.3 (183)	1,492
Pseudomonas aeruginosa	29.8 (232)	32.0 (249)	22.0 (171)	16.3 (127)	779
Community-onset	37.8 (165)	35.2 (154)	20.1 (88)	6.9 (30)	437
Hospital-onset	19.6 (67)	27.8 (95)	24.3 (83)	28.4 (97)	342

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 groups (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, 2022

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Acinetobacter baumannii complex					
Piperacillin–tazobactam	59	6.8 (4)	10.2 (6)	–*	–*
Ceftriaxone	63	71.4 (45)	4.8 (3)	–*	–*
Ceftazidime	59	11.9 (7)	3.4 (2)	–*	–*
Cefepime	40	5.0 (2)	7.5 (3)	–*	–*
Gentamicin	67	0.0 (0)	3.0 (2)	–†	3.0 (2)
Tobramycin	66	0.0 (0)	3.0 (2)	–†	3.0 (2)
Amikacin	52	0.0 (0)	1.9 (1)	–†	3.8 (2)
Ciprofloxacin	65	0.0 (0)	4.6 (3)	95.4 (62)	4.6 (3)
Meropenem	67	0.0 (0)	3.0 (2)	0.0 (0)	3.0 (2)
Enterobacter cloacae complex					
Piperacillin–tazobactam	470	5.7 (27)	18.3 (86)	–†	27.2 (128)
Ceftriaxone	475	0.4 (2)	28.4 (135)	0.4 (2)	28.4 (135)
Ceftazidime	475	1.1 (5)	23.6 (112)	3.6 (17)	24.6 (117)
Cefepime	475	3.6 (17)§	1.9 (9)	8.6 (41)	3.4 (16)
Gentamicin	473	0.0 (0)	5.5 (26)	–†	6.1 (29)
Tobramycin	465	2.4 (11)	3.7 (17)	–†	6.7 (31)
Amikacin	474	0.4 (2)	0.0 (0)	–†	0.6 (3)
Ciprofloxacin	475	1.1 (5)	5.3 (25)	1.1 (5)	5.3 (25)
Meropenem	475	0.2 (1)	2.5 (12)	0.4 (2)	2.1 (10)
Enterococcus faecalis					
Ampicillin	807	–*	0.0 (0)	0.0 (0)	0.0 (0)
Benzylpenicillin	664	–*	0.9 (6)	–†	–†
Daptomycin	745	38.9 (290)	0.1 (1)	–†	–†
Linezolid	804	0.4 (3)	0.0 (0)	–*	0.0 (0)
Teicoplanin	807	0.0 (0)	0.0 (0)	–*	0.0 (0)
Vancomycin	807	0.0 (0)	0.0 (0)	–*	0.0 (0)
Enterococcus faecium					
Ampicillin	606	–*	95.4 (578)	0.5 (3)	95.4 (578)

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Benzylpenicillin	480	–*	94.2 (452)	–†	–†
Daptomycin	58	98.3 (57)§	1.7 (1)	–†	–†
Linezolid	607	0.3 (2)	0.3 (2)	–*	0.3 (2)
Teicoplanin	605	1.5 (9)	8.9 (54)	–*	13.2 (80)
Vancomycin	608	1.0 (6)	45.9 (279)	–*	46.9 (285)
Escherichia coli					
Ampicillin	5,257	1.5 (78)	50.0 (2,628)	–†	51.5 (2,706)
Amoxicillin–clavulanic acid (2:1 ratio)#	4,567	9.9 (452)	7.4 (337)	–*	–*
Piperacillin–tazobactam	5,243	2.3 (121)	2.8 (147)	–†	5.9 (309)
Cefazolin	4,594	–**	22.2 (1,022)	77.8 (3,572)	22.2 (1,022)
Cefuroxime	611	1.6 (10)	16.4 (100)	82.0 (501)	18.0 (110)
Ceftriaxone	5,261	0.1 (6)	12.7 (667)	0.1 (6)	12.7 (667)
Ceftazidime	5,261	0.9 (46)	5.0 (263)	7.3 (384)	5.9 (309)
Cefepime	5,261	2.1 (109)§	2.1 (112)	6.6 (345)	3.1 (162)
Gentamicin	5,259	0.1 (4)	7.9 (415)	–†	8.3 (437)
Tobramycin	5,233	5.8 (301)	2.4 (127)	–†	8.6 (450)
Amikacin	5,260	0.1 (3)	0.0 (2)	–†	0.9 (48)
Ciprofloxacin	5,259	3.7 (196)	13.7 (721)	3.7 (196)	13.7 (721)
Meropenem	5,260	0.0 (1)	0.1 (7)	0.1 (3)	0.1 (4)
Klebsiella aerogenes					
Piperacillin–tazobactam	129	10.1 (13)	20.9 (27)	–†	37.2 (48)
Ceftriaxone	129	0.8 (1)	33.3 (43)	0.8 (1)	33.3 (43)
Ceftazidime	129	3.1 (4)	30.2 (39)	3.9 (5)	33.3 (43)
Cefepime	129	2.3 (3)§	0.0 (0)	3.1 (4)	1.6 (2)
Gentamicin	129	0.0 (0)	2.3 (3)	–†	2.3 (3)
Tobramycin	129	2.3 (3)	0.0 (0)	–†	2.3 (3)
Amikacin	129	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	129	0.8 (1)	3.1 (4)	0.8 (1)	3.1 (4)
Meropenem	129	0.0 (0)	2.3 (3)	1.6 (2)	0.8 (1)
Klebsiella oxytoca					
Amoxicillin–clavulanic acid (2:1 ratio)#	258	4.3 (11)	7.4 (19)	–*	–*
Piperacillin–tazobactam	295	1.7 (5)	8.1 (24)	–†	11.5 (34)
Cefuroxime	35	2.9 (1)	2.9 (1)	94.3 (33)	5.7 (2)
Ceftriaxone	296	0.3 (1)	5.7 (17)	0.3 (1)	5.7 (17)
Ceftazidime	296	0.3 (1)	0.3 (1)	0.3 (1)	0.7 (2)
Cefepime	296	0.0 (0)§	0.3 (1)	0.7 (2)	0.3 (1)
Gentamicin	297	0.0 (0)	1.0 (3)	–†	1.0 (3)
Tobramycin	296	1.0 (3)	0.0 (0)	–†	1.0 (3)
Amikacin	296	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	297	0.3 (1)	0.7 (2)	0.3 (1)	0.7 (2)
Meropenem	295	0.0 (0)	0.7 (2)	0.7 (2)	0.0 (0)
Klebsiella pneumoniae complex					
Amoxicillin–clavulanic acid (2:1 ratio)#	1,230	4.6 (57)	3.2 (39)	–*	–*
Piperacillin–tazobactam	1,386	1.3 (18)	2.9 (40)	–†	8.7 (121)

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Cefazolin	1,235	–**	10.1 (125)	89.9 (1,110)	10.1 (125)
Cefuroxime	138	4.3 (6)	5.8 (8)	89.9 (124)	10.1 (14)
Ceftriaxone	1,392	0.1 (1)	6.6 (92)	0.1 (1)	6.6 (92)
Ceftazidime	1,392	0.9 (13)	4.4 (61)	1.9 (26)	5.3 (74)
Cefepime	1,392	0.9 (13)§	1.7 (24)	3.3 (46)	2.2 (31)
Gentamicin	1,392	0.4 (5)	3.0 (42)	–†	3.4 (47)
Tobramycin	1,383	2.6 (36)	1.4 (20)	–†	4.1 (57)
Amikacin	1,392	0.0 (0)	0.1 (1)	–†	0.2 (3)
Ciprofloxacin	1,391	2.1 (29)	7.8 (109)	2.1 (29)	7.8 (109)
Meropenem	1,392	0.2 (3)	0.6 (8)	0.1 (1)	0.5 (7)
Proteus mirabilis					
Ampicillin	323	0.6 (2)	15.8 (51)	–†	16.4 (53)
Amoxicillin–clavulanic acid (2:1 ratio)#	278	5.8 (16)	3.2 (9)	–*	–*
Piperacillin–tazobactam	322	0.0 (0)	0.0 (0)	–†	0.0 (0)
Cefuroxime	44	0.0 (0)	6.8 (3)	93.2 (41)	6.8 (3)
Ceftriaxone	323	0.6 (2)	1.2 (4)	0.6 (2)	1.2 (4)
Ceftazidime	323	0.3 (1)	0.6 (2)	0.6 (2)	0.9 (3)
Cefepime	323	0.6 (2)§	0.6 (2)	0.9 (3)	0.6 (2)
Gentamicin	323	1.2 (4)	1.9 (6)	–†	5.0 (16)
Tobramycin	323	1.2 (4)	1.9 (6)	–†	3.7 (12)
Amikacin	323	0.0 (0)	0.3 (1)	–†	1.5 (5)
Ciprofloxacin	323	0.6 (2)	4.0 (13)	0.6 (2)	4.0 (13)
Meropenem	323	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin–tazobactam	832	8.5 (71)	6.1 (51)	85.3 (710)	14.7 (122)
Ceftazidime	837	5.5 (46)	5.1 (43)	89.4 (748)	10.6 (89)
Cefepime	838	3.3 (28)	2.9 (24)	93.8 (786)	6.2 (52)
Tobramycin	827	0.2 (2)	0.4 (3)	–†	0.7 (6)
Amikacin	836	0.2 (2)	0.2 (2)	–†	0.5 (4)
Ciprofloxacin	836	5.7 (48)	4.3 (36)	90.0 (752)	10.0 (84)
Meropenem	836	4.5 (38)	5.9 (49)	6.1 (51)	4.3 (36)
Salmonella species (non-typhoidal)					
Ampicillin	96	0.0 (0)	5.2 (5)	–†	5.2 (5)
Amoxicillin–clavulanic acid (2:1 ratio)#	87	1.1 (1)	0.0 (0)	–*	–*
Piperacillin–tazobactam	96	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ceftriaxone	96	0.0 (0)	3.1 (3)	0.0 (0)	3.1 (3)
Ceftazidime	96	0.0 (0)	3.1 (3)	0.0 (0)	3.1 (3)
Cefepime	96	1.0 (1)§	1.0 (1)	2.1 (2)	1.0 (1)
Ciprofloxacin‡	97	3.1 (3)	10.3 (10)	–†	13.4 (13)
Meropenem	96	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	212	0.9 (2)	0.0 (0)	–†	0.9 (2)
Ceftriaxone	257	0.4 (1)	3.1 (8)	0.4 (1)	3.1 (8)
Ceftazidime	257	0.4 (1)	1.6 (4)	0.4 (1)	1.9 (5)
Cefepime	257	0.4 (1)§	0.8 (2)	0.4 (1)	1.2 (3)

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Gentamicin	257	0.0 (0)	1.9 (5)	–†	2.3 (6)
Tobramycin	255	16.1 (41)	1.2 (3)	–†	31.4 (80)
Amikacin	257	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	257	1.6 (4)	2.3 (6)	1.6 (4)	2.3 (6)
Meropenem	257	0.0 (0)	1.6 (4)	0.8 (2)	0.8 (2)
Staphylococcus aureus					
Benzylpenicillin§§	3,199	–†	78.6 (2,516)	–†	78.6 (2,516)
Cefoxitin (methicillin)##	3,214	–†	15.0 (481)	–†	15.0 (481)
Ciprofloxacin	3,203	0.8 (26)	6.3 (202)	92.9 (2,975)	7.1 (228)
Clindamycin (constitutive)	3,201	0.0 (0)	3.2 (101)	0.0 (0)	3.4 (110)
Clindamycin (constitutive + inducible resistance)	3,201	0.0 (0)	12.6 (403)	0.0 (0)	13.4 (428)
Daptomycin	3,209	–†	<0.1 (1)***	–†	<0.1 (1)
Erythromycin	3,147	26.6 (837)	15.5 (488)	–†	16.3 (512)
Fusidic acid	3,147	–*	–*	–†	2.7 (86)
Gentamicin	3,203	1.2 (39)	1.5 (48)	–†	4.6 (148)
Linezolid	3,210	–†	0.0 (0)	–†	0.0 (0)
Mupirocin (high-level)‡†	2,442	–†	1.3 (32)	–†	1.3 (32)
Rifampicin	3,200	0.1 (3)	0.4 (12)	–†	1.8 (22)§§§
Teicoplanin	3,206	0.0 (0)	0.0 (0)	–*	0.1 (2)
Tetracycline/doxycycline)###	3,199	0.1 (2)	3.9 (126)	–†	5.0 (159)
Trimethoprim–sulfamethoxazole****	3,201	0.2 (7)	0.5 (16)	0.2 (5)	0.6 (18)
Vancomycin	3,210	0.0 (0)	0.0 (0)	–†	0.0 (0)

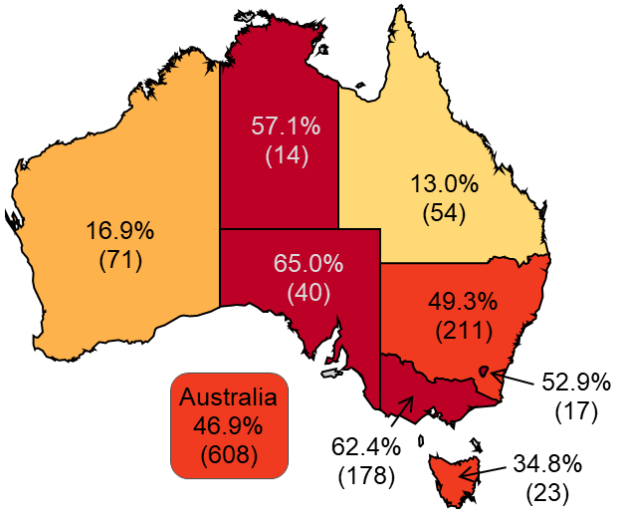
CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing

* 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

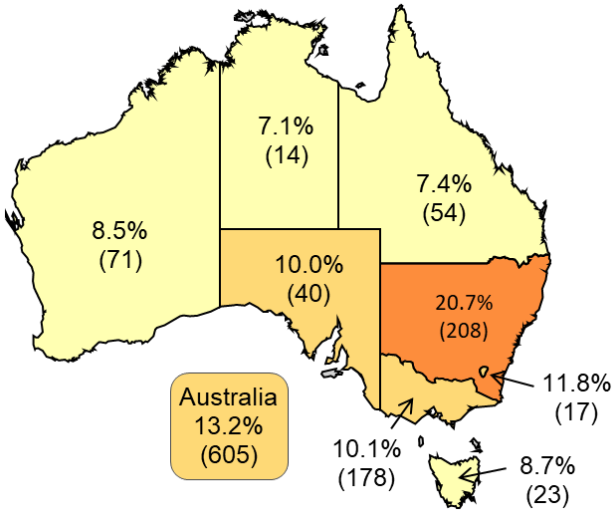
Note: *E. faecium* are usually susceptible dose dependent (CLSI) to daptomycin

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, 2022

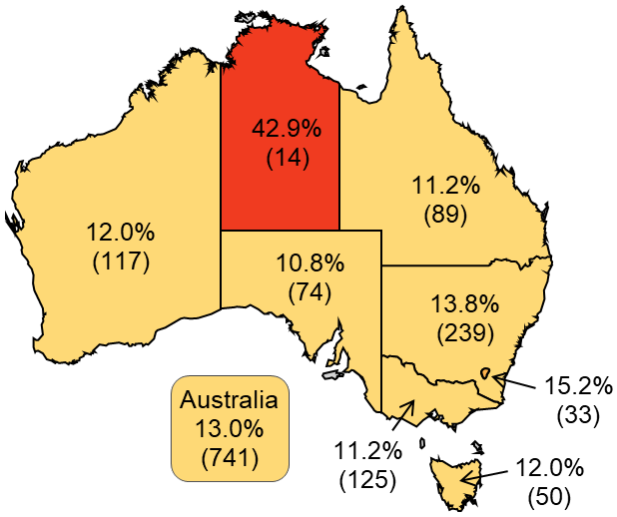
A. Vancomycin

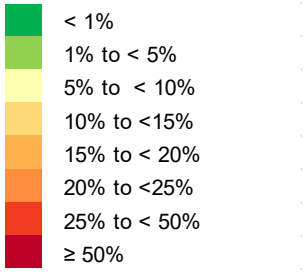


B. Teicoplanin



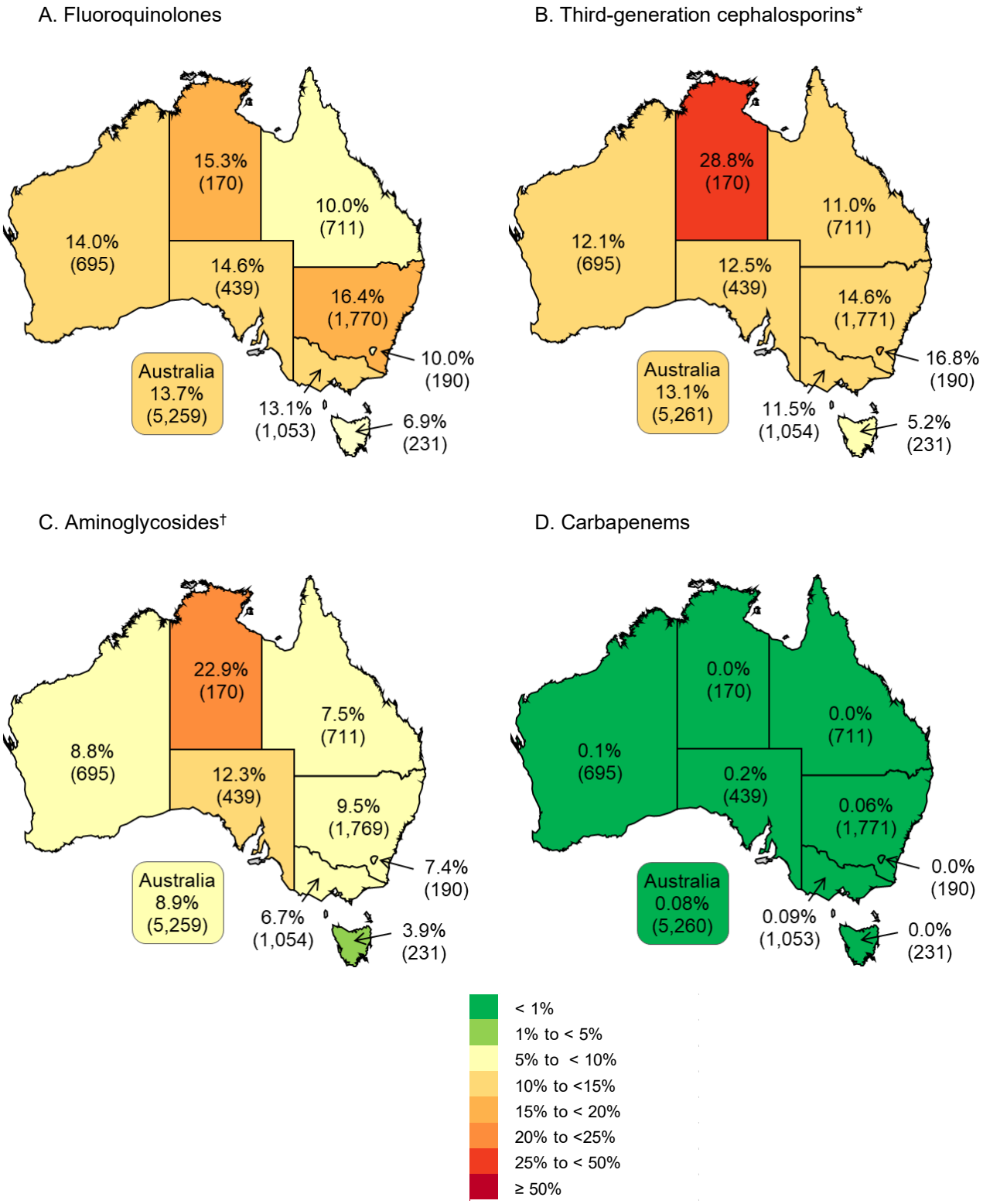
C. High-level gentamicin





EUCAST = European Committee on Antimicrobial Susceptibility Testing

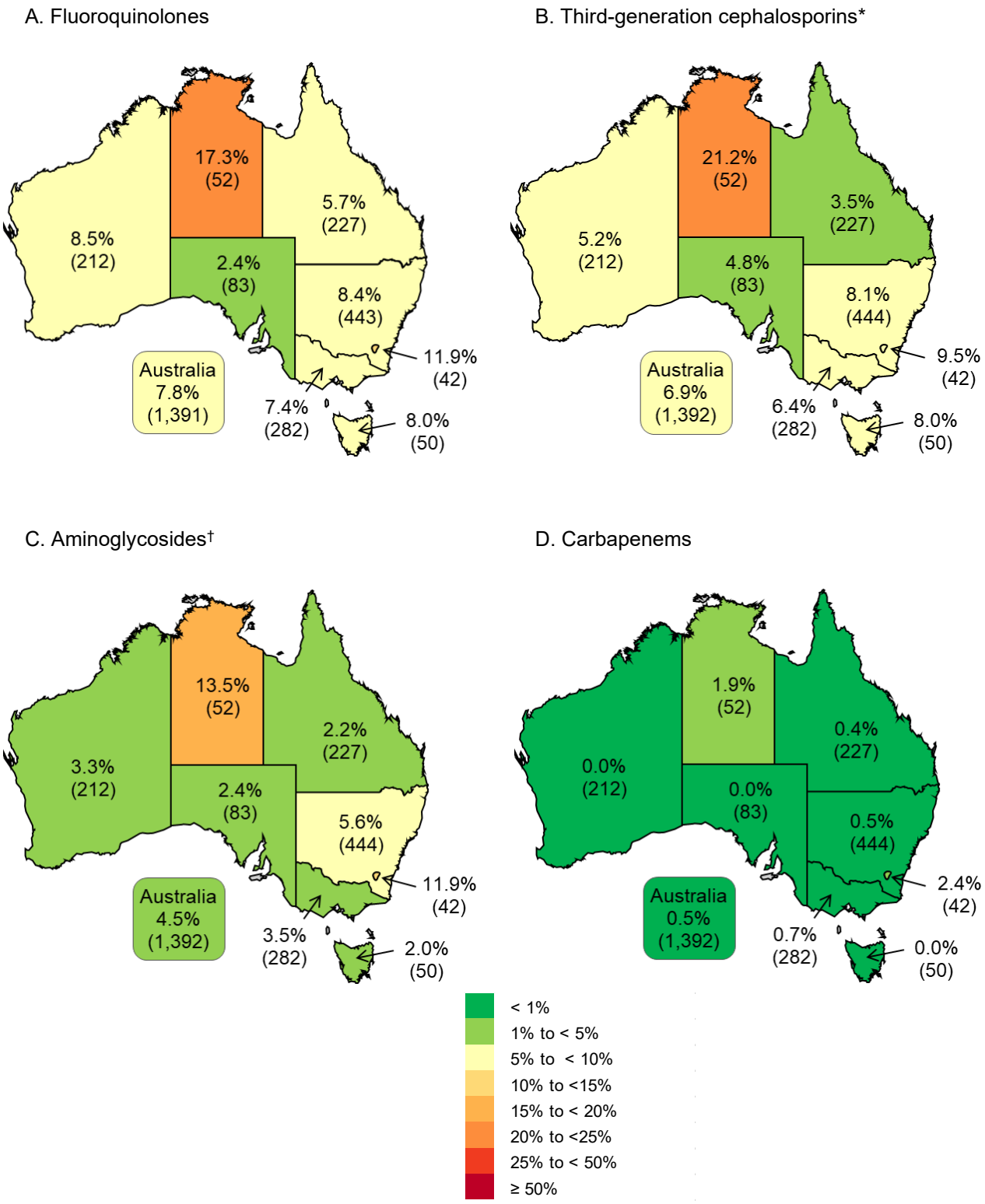
Figure 5: Percentage of *Escherichia coli* from patients with bacteraemia with resistance, as defined by EUCAST, to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, AGAR, 2022



EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Third-generation cephalosporins refers to ceftriaxone and/or ceftazidime
† Aminoglycosides refers to gentamicin or tobramycin

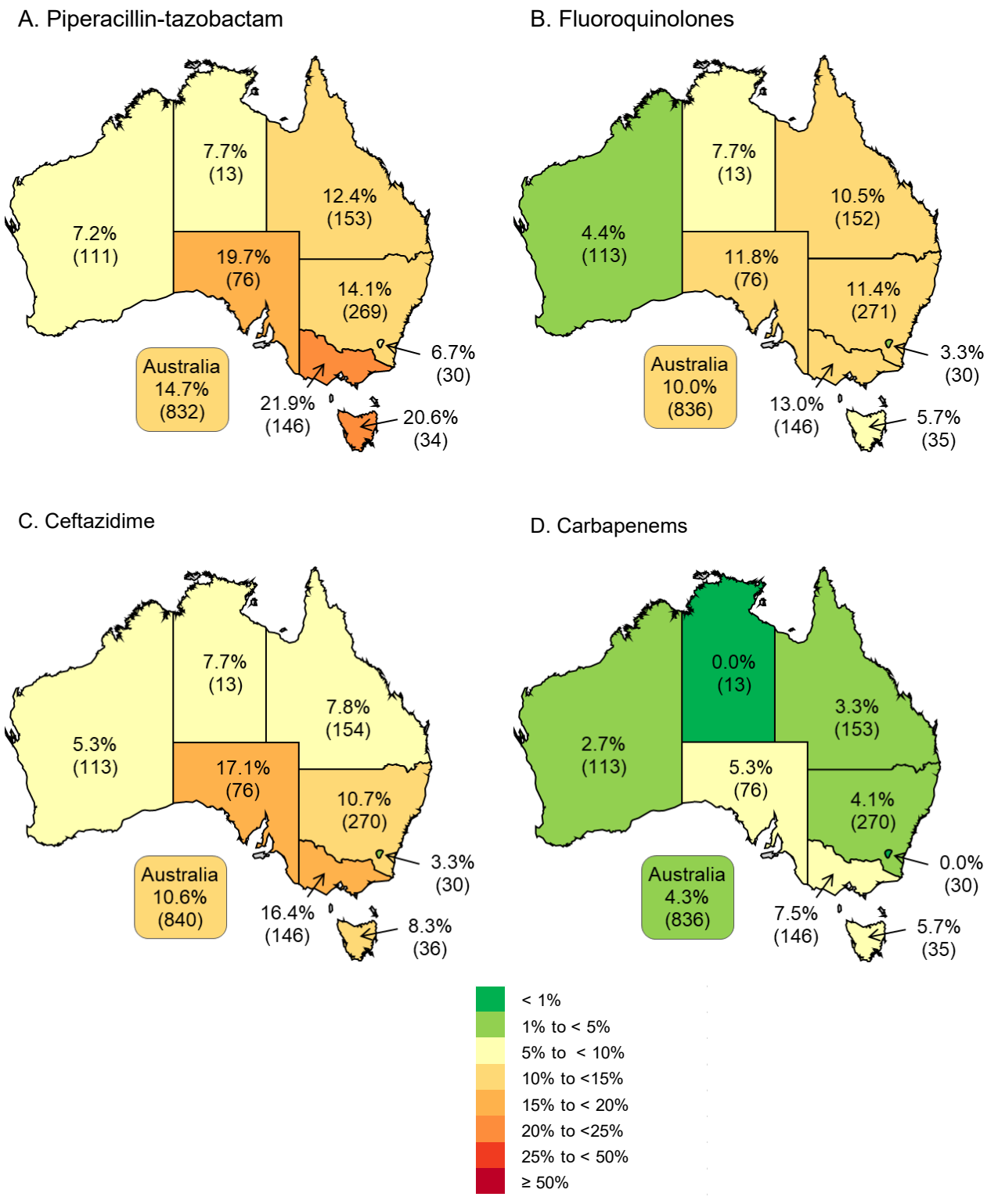
Figure 6: Percentage of *Klebsiella pneumoniae* complex from patients with bacteraemia with resistance, as defined by EUCAST, to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, AGAR, 2022



EUCAST = European Committee on Antimicrobial Susceptibility Testing

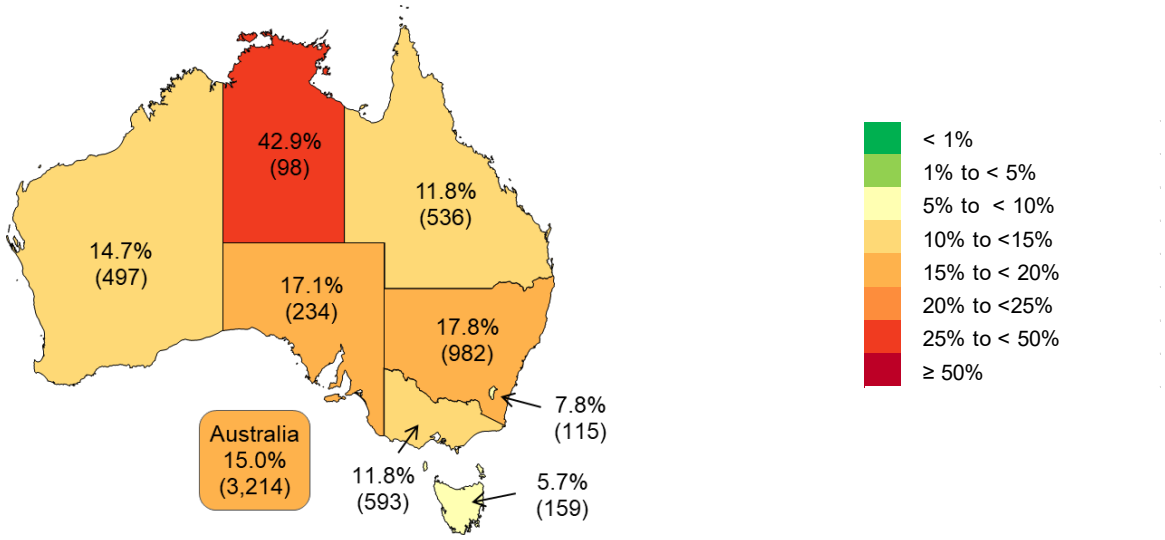
* Third-generation cephalosporins refers to ceftriaxone and/or ceftazidime
† Aminoglycosides refers to gentamicin or tobramycin

Figure 7: Percentage of *Pseudomonas aeruginosa* from patients with bacteraemia with resistance, as defined by EUCAST, to piperacillin–tazobactam (A), fluoroquinolones (B), ceftazidime (C) and carbapenems (D), Australia, AGAR, 2022



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, 2022



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, 2022

	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	30	6.7	10.0	–*	–*	29	6.9	10.3	–*	–*
Ceftriaxone	36	77.8	5.6	–*	–*	27	63.0	3.7	–*	–*
Ceftazidime	31	19.4	3.2	–*	–*	28	3.6	3.6	–*	–*
Cefepime	21	9.5	4.8	–*	–*	19	0.0	10.5	–*	–*
Gentamicin	38	0.0	2.6	–†	2.6	29	0.0	3.4	–†	3.4
Tobramycin	38	0.0	2.6	–†	2.6	28	0.0	3.6	–†	3.6
Amikacin	34	0.0	0.0	–†	0.0	18	0.0	5.6	–†	11.1
Ciprofloxacin	38	0.0	5.3	94.7	5.3	27	0.0	3.7	96.3	3.7
Meropenem	38	0.0	2.6	0.0	2.6	29	0.0	3.4	0.0	3.4
Enterobacter cloacae complex										
Piperacillin–tazobactam	246	5.3	11.8	–†	20.7	224	6.3	25.4	–†	34.4
Ceftriaxone	249	0.4	23.7	0.4	23.7	226	0.4	33.6	0.4	33.6
Ceftazidime	249	1.2	17.3	5.2	18.5	226	0.9	30.5	1.8	31.4
Cefepime	249	2.4§	1.2	7.2	1.6	226	4.9§	2.7	10.2	5.3
Gentamicin	249	0.0	4.0	–†	4.8	224	0.0	7.1	–†	7.6
Tobramycin	242	2.5	2.5	–†	5.4	223	2.2	4.9	–†	8.1
Amikacin	249	0.8	0.0	–†	0.8	225	0.0	0.0	–†	0.4
Ciprofloxacin	249	1.2	3.2	1.2	3.2	226	0.9	7.5	0.9	7.5
Meropenem	249	0.0	0.8	0.0	0.8	226	0.4	4.4	0.9	3.5
Enterococcus faecalis										
Ampicillin	541	–†	0.0	0.0	0.0	266	–†	0.0	0.0	0.0
Benzylpenicillin	451	–†	1.1	–*	–*	213	–†	0.5	–*	–*
Daptomycin	493	37.3	0.0	–*	–*	252	42.1	0.4	–*	–*
Linezolid	538	0.4	0.0	–†	0.0	266	0.4	0.0	–†	0.0
Teicoplanin	541	0.0	0.0	–†	0.0	266	0.0	0.0	–†	0.0
Vancomycin	541	0.0	0.0	–†	0.0	266	0.0	0.0	–†	0.0
Enterococcus faecium										
Ampicillin	155	–†	86.5	0.6	86.5	451	–†	98.4	0.4	98.4
Benzylpenicillin	120	–†	85.0	–*	–*	360	–†	97.2	–*	–*
Daptomycin	14	–*	0.0	–†	–†	44	–*	2.3	–†	–†
Linezolid	156	0.6	0.0	–†	0.0	451	0.2	0.4	–†	0.4
Teicoplanin	155	1.9	8.4	–†	11.0	450	1.3	9.1	–†	14.0
Vancomycin	156	2.6	32.7	–†	35.3	452	0.4	50.4	–†	50.9
Escherichia coli										
Ampicillin	4,338	1.5	48.1	–†	49.6	919	1.4	58.8	–†	60.2
Amoxicillin–clavulanic acid (2:1 ratio)#	3,782	9.5	7.0	–*	–*	785	11.6	9.2	–*	–*
Piperacillin–tazobactam	4,323	2.2	1.8	–†	4.9	920	2.9	7.4	–†	10.7

Species and antimicrobial	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
	No.	I	R	S, IE	R	No.	I	R	S, IE	R
Cefazolin	3,803	–**	21.1	78.9	21.1	791	–**	27.6	72.4	27.6
Cefuroxime	489	2.0	14.9	83.0	17.0	122	0.0	22.1	77.9	22.1
Ceftriaxone	4,340	0.1	12.1	0.1	12.1	921	0.1	15.2	0.1	15.2
Ceftazidime	4,340	0.9	4.6	7.1	5.6	921	0.7	6.7	8.3	7.4
Cefepime	4,340	2.0§	1.9	6.3	2.8	921	2.3§	3.3	7.6	4.5
Gentamicin	4,338	0.0	7.5	–†	7.9	921	0.2	9.6	–†	10.3
Tobramycin	4,316	5.5	2.3	–†	8.2	917	6.9	2.9	–†	10.6
Amikacin	4,339	0.1	0.0	–†	0.9	921	0.0	0.0	–†	1.1
Ciprofloxacin	4,338	3.6	12.8	3.6	12.8	921	4.6	17.8	4.6	17.8
Meropenem	4,339	0.0	0.1	0.0	0.0	921	0.1	0.3	0.1	0.2
Klebsiella aerogenes										
Piperacillin–tazobactam	78	9.0	16.7	–†	33.3	51	11.8	27.5	–†	43.1
Ceftriaxone	78	1.3	29.5	1.3	29.5	51	0.0	39.2	0.0	39.2
Ceftazidime	78	3.8	25.6	6.4	29.5	51	2.0	37.3	0.0	39.2
Cefepime	78	1.3§	0.0	2.6	0.0	51	3.9§	0.0	3.9	3.9
Gentamicin	78	0.0	2.6	–†	2.6	51	0.0	2.0	–†	2.0
Tobramycin	78	2.6	0.0	–†	2.6	51	2.0	0.0	–†	2.0
Amikacin	78	0.0	0.0	–†	0.0	51	0.0	0.0	–†	0.0
Ciprofloxacin	78	1.3	2.6	1.3	2.6	51	0.0	3.9	0.0	3.9
Meropenem	78	0.0	0.0	0.0	0.0	51	0.0	5.9	3.9	2.0
Klebsiella oxytoca										
Amoxicillin–clavulanic acid (2:1 ratio)#	168	3.6	4.8	–*	–*	90	5.6	12.2	–*	–*
Piperacillin–tazobactam	196	1.0	5.6	–†	7.7	99	3.0	13.1	–†	19.2
Ceftriaxone	196	0.0	5.1	0.0	5.1	100	1.0	7.0	1.0	7.0
Ceftazidime	196	0.0	0.0	0.0	0.0	100	1.0	1.0	1.0	2.0
Cefepime	196	0.0§	0.0	0.5	0.0	100	0.0§	1.0	1.0	1.0
Gentamicin	196	0.0	0.5	–†	0.5	101	0.0	2.0	–†	2.0
Tobramycin	196	0.5	0.0	–†	0.5	100	2.0	0.0	–†	2.0
Amikacin	196	0.0	0.0	–†	0.0	100	0.0	0.0	–†	0.0
Ciprofloxacin	196	0.5	0.5	0.5	0.5	101	0.0	1.0	0.0	1.0
Meropenem	196	0.0	0.0	0.0	0.0	99	0.0	2.0	2.0	0.0
Klebsiella pneumoniae complex										
Amoxicillin–clavulanic acid (2:1 ratio)#	859	3.7	2.0	–*	–*	371	6.7	5.9	–*	–*
Piperacillin–tazobactam	962	1.0	1.5	–†	6.3	424	1.9	6.1	–†	14.2
Cefazolin	860	–**	7.6	92.4	7.6	375	–**	16.0	84.0	16.0
Cefuroxime	91	1.1	5.5	93.4	6.6	47	10.6	6.4	83.0	17.0
Ceftriaxone	966	0.1	4.8	0.1	4.8	426	0.0	10.8	0.0	10.8
Ceftazidime	966	0.7	2.9	1.6	3.6	426	1.4	7.7	2.6	9.2
Cefepime	966	0.8§	1.7	2.0	2.1	426	1.2§	1.9	6.3	2.6
Gentamicin	966	0.2	2.6	–†	2.8	426	0.7	4.0	–†	4.7
Tobramycin	961	2.1	1.0	–†	3.1	422	3.8	2.4	–†	6.4
Amikacin	966	0.0	0.1	–†	0.1	426	0.0	0.0	–†	0.5
Ciprofloxacin	965	1.8	6.3	1.8	6.3	426	2.8	11.3	2.8	11.3
Meropenem	966	0.2	0.6	0.1	0.5	426	0.2	0.5	0.0	0.5

	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
Species and antimicrobial	No.	I	R	S, IE	R	No.	I	R	S, IE	R
Proteus mirabilis										
Ampicillin	266	0.4	16.2	–†	16.5	57	1.8	14.0	–†	15.8
Amoxicillin–clavulanic acid (2:1 ratio)#	227	5.7	3.5	–*	–*	51	5.9	2.0	–*	–*
Piperacillin–tazobactam	265	0.0	0.0	–†	0.0	57	0.0	0.0	–†	0.0
Ceftriaxone	266	0.4	1.1	0.4	1.1	57	1.8	1.8	1.8	1.8
Ceftazidime	266	0.4	0.8	0.8	1.1	57	0.0	0.0	0.0	0.0
Cefepime	266	0.4§	0.8	0.4	0.8	57	1.8§	0.0	3.5	0.0
Gentamicin	266	1.1	2.3	–†	4.9	57	1.8	0.0	–†	5.3
Tobramycin	266	1.1	2.3	–†	4.1	57	1.8	0.0	–†	1.8
Amikacin	266	0.0	0.4	–†	1.9	57	0.0	0.0	–†	0.0
Ciprofloxacin	266	0.8	4.9	0.8	4.9	57	0.0	0.0	0.0	0.0
Meropenem	266	0.0	0.0	0.0	0.0	57	0.0	0.0	0.0	0.0
Pseudomonas aeruginosa										
Piperacillin–tazobactam	468	6.6	4.1	89.3	10.7	364	11.0	8.8	80.2	19.8
Ceftazidime	471	3.4	3.0	93.6	6.4	366	8.2	7.9	83.9	16.1
Cefepime	472	1.9	1.5	96.6	3.4	366	5.2	4.6	90.2	9.8
Tobramycin	470	0.2	0.2	–†	0.4	357	0.3	0.6	–†	1.1
Amikacin	471	0.2	0.0	–†	0.2	365	0.3	0.5	–†	0.8
Ciprofloxacin	472	3.6	3.6	92.8	7.2	364	8.5	5.2	86.3	13.7
Meropenem	471	5.1	2.1	6.2	1.1	365	3.8	10.7	6.0	8.5
Salmonella species (non-typhoidal)										
Ampicillin	89	0.0	5.6	–†	5.6	7	n/a	n/a	–†	n/a
Amoxicillin–clavulanic acid (2:1 ratio)#	81	1.2	0.0	–*	–*	6	n/a	n/a	–*	–*
Piperacillin–tazobactam	89	0.0	0.0	–†	0.0	7	n/a	n/a	–†	n/a
Ceftriaxone	89	0.0	3.4	0.0	3.4	7	n/a	n/a	n/a	n/a
Ceftazidime	89	0.0	3.4	0.0	3.4	7	n/a	n/a	n/a	n/a
Cefepime	89	1.1§	1.1	2.2	1.1	7	n/a	n/a	n/a	n/a
Ciprofloxacin‡	89	3.4	11.2	–†	14.6	8	n/a	n/a	–†	n/a
Meropenem	89	0.0	0.0	0.0	0.0	7	n/a	n/a	n/a	n/a
Serratia marcescens										
Piperacillin–tazobactam	85	1.2	0.0	–†	1.2	127	0.8	0.0	–†	0.8
Ceftriaxone	114	0.0	3.5	0.0	3.5	143	0.7	2.8	0.7	2.8
Ceftazidime	114	0.9	1.8	0.9	2.6	143	0.0	1.4	0.0	1.4
Cefepime	114	0.0§	0.9	0.9	0.9	143	0.7§	0.7	0.0	1.4
Gentamicin	114	0.0	1.8	–†	1.8	143	0.0	2.1	–†	2.8
Tobramycin	113	15.9	0.9	–†	30.1	142	16.2	1.4	–†	32.4
Amikacin	114	0.0	0.0	–†	0.0	143	0.0	0.0	–†	0.0
Ciprofloxacin	114	0.9	3.5	0.9	3.5	143	2.1	1.4	2.1	1.4
Meropenem	114	0.0	1.8	0.9	0.9	143	0.0	1.4	0.7	0.7
Staphylococcus aureus										
Benzylpenicillin§§	2,479	–†	78.3	–†	78.3	720	–†	79.9	–†	79.9
Cefoxitin (methicillin)##	2,491	–†	14.6	–†	14.6	723	–†	16.3	–†	16.3
Ciprofloxacin	2,485	0.8	5.5	93.7	6.3	718	1.0	9.1	90.0	10.0

Species and antimicrobial	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
	No.	I	R	S, IE	R	No.	I	R	S, IE	R
Clindamycin (constitutive)	2,483	0.0	3.0	0.0	3.3	718	0.0	3.6	0.0	4.0
Clindamycin (constitutive + inducible resistance)	2,483	0.0	12.1	0.0	12.8	718	0.0	14.2	0.0	15.3
Daptomycin	2,487	0.0***	–†	–†	0.1	722	0.1***	–†	–†	0.1
Erythromycin	2,439	26.0	15.0	–†	15.8	708	28.8	17.1	–†	17.9
Fusidic acid	2,440	–*	–*	–†	2.6	707	–*	–*	–†	3.1
Gentamicin	2,485	1.1	1.3	–†	4.4	718	1.5	2.1	–†	5.3
Linezolid	2,488	–†	0.0	–†	0.0	722	–†	0.0	–†	0.0
Mupirocin (high-level) ‡†	1,902	–†	1.3	–†	1.3	540	–†	1.3	–†	1.3
Rifampicin	2,484	0.0	0.2	–†	1.6§§§	716	0.1	0.6	–†	2.3§§§
Teicoplanin	2,486	0.0	0.0	–†	0.1	720	0.0	0.0	–†	0.0
Tetracycline/doxycycline###	2,481	0.1	3.7	–†	4.7	718	0.0	4.9	–†	5.8
Trimethoprim–sulfamethoxazole****	2,484	0.2	0.3	0.1	0.4	717	0.3	1.1	0.3	1.1
Vancomycin	2,487	0.0	0.0	–†	0.0	722	0.0	0.0	–†	0.0

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate; 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 one or more 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 classes and any additional acquired resistance severely limits the number of treatment options. Range of antimicrobials available on the test panels limits the ability to determine multiple acquired resistance in *E. faecalis* and *E. faecium*. Vancomycin-resistant *enterococcus* are listed as a serious threat to public health[46] and have been identified as a major AMR threat in Australian healthcare facilities.[52]

Table 15: Multiple acquired resistance in *Enterobacter cloacae* complex, by state and territory, AGAR, 2022

State or territory	Total	Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)				
		0	1	2	%	3	4	5	6	%
NSW	169	90	16	42	87.6	6	9	3	3	12.4
Vic	97	61	8	21	92.8	3	2	1	1	7.2
Qld	86	49	17	16	95.3	0	2	1	1	4.7
SA	22	10	2	8	–*	0	1	1	0	–*
WA	51	43	3	3	96.1	2	0	0	0	3.9
Tas	17	12	0	4	–*	1	0	0	0	–*
NT	9	3	2	3	–*	0	0	1	0	–*
ACT	16	11	2	2	–*	0	1	0	0	–*
Total	**467**	**279**	**50**	**99**	**91.6**	**12**	**15**	**7**	**5**	**8.4**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories; * = insufficient numbers (<30) to calculate percentage

Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Enterobacter cloacae* complex includes *E. bugandensis* (*n* = 5), *E. asburiae* (*n* = 4), *E. hormaechei* (*n* = 4), and *E. ludwigii* (*n* = 1).

Table 16: Multiple acquired resistance in *Escherichia coli*, by state and territory, AGAR, 2022

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)							
		0	1	2	%	3	4	5	6	7	8	9	%
NSW	1,738	758	291	239	74.1	135	139	114	36	19	7	0	25.9
Vic	1,051	475	209	144	78.8	87	57	53	18	6	1	1	21.2
Qld	706	327	131	107	80.0	43	39	44	8	6	1	0	20.0
SA	435	188	80	75	78.9	29	26	25	5	5	2	0	21.1
WA	692	267	126	128	75.3	56	58	28	22	5	2	0	24.7
Tas	200	118	35	28	90.5	9	5	4	1	0	0	0	9.5
NT	169	46	16	34	56.8	21	17	25	8	2	0	0	43.2
ACT	190	83	35	27	76.3	20	11	11	2	1	0	0	23.7
Total	**5,181**	**2262**	**923**	**782**	**76.6**	**400**	**352**	**304**	**100**	**44**	**13**	**1**	**23.4**

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

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), non-extended-spectrum cephalosporins (cefazolin or cefuroxime), and penicillins (ampicillin).

Table 17: Multiple acquired resistance in *Klebsiella pneumoniae* complex isolates, by state and territory, AGAR, 2022

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)						
		0	1	2	%	3	4	5	6	7	8	%
NSW	429	324	35	29	90.4	13	9	6	10	3	0	9.6
Vic	282	220	23	21	93.6	7	5	0	3	1	2	6.4
Qld	225	175	26	12	94.7	5	2	2	2	0	1	5.3
SA	82	67	7	3	93.9	2	2	1	0	0	0	6.1
WA	212	175	7	17	93.9	3	5	1	4	0	0	6.1
Tas	43	38	0	0	88.4	1	3	1	0	0	0	11.6
NT	51	33	3	4	78.4	2	2	2	4	0	1	21.6
ACT	42	34	4	0	90.5	0	1	1	1	1	0	9.5
Total	**1,366**	**1066**	**105**	**86**	**92.0**	**33**	**29**	**14**	**24**	**5**	**4**	**8.0**

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

Notes:
1. Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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* = 116) and *K. quasipneumoniae* (*n* = 3).

Table 18: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, AGAR, 2022

State or territory		Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)			
	Total	0	1	2	%	3	4	5	%
NSW	258	199	27	24	96.9	5	2	1	3.1
Vic	146	106	13	13	90.4	9	5	0	9.6
Qld	152	122	15	12	98.0	0	2	1	2.0
SA	76	57	5	9	93.4	2	3	0	6.6
WA	111	99	5	4	97.3	1	2	0	2.7
Tas	34	26	5	1	94.1	1	1	0	5.9
NT	13	11	1	1	–*	0	0	0	–*
ACT	30	27	2	1	100.0	0	0	0	0.0
Total	**820**	**647**	**73**	**65**	**95.7**	**18**	**15**	**2**	**4.3**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories; * = 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, 2022

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	171	66	32	24	71.3	29	4	12	4	0	0	0	0	0	28.7
Vic	70	34	13	5	74.3	10	6	1	1	0	0	0	0	0	25.7
Qld	63	30	10	16	88.9	5	1	1	0	0	0	0	0	0	11.1
SA	40	16	12	6	85.0	5	1	0	0	0	0	0	0	0	15.0
WA	73	53	6	13	98.6	0	0	1	0	0	0	0	0	0	1.4
Tas	9	4	2	2	–*	1	0	0	0	0	0	0	0	0	–*
NT	42	30	2	9	97.6	1	0	0	0	0	0	0	0	0	2.4
ACT	9	4	0	2	–*	1	0	1	1	0	0	0	0	0	–*
Total	477	**237**	**77**	**77**	**82.0**	**52**	**12**	**16**	**6**	0	**0**	**0**	**0**	**0**	**18.0**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories; * = 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, 2022

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

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories

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, 53.8% of all *E. coli* isolates were resistant to at least one of five key antimicrobial groups (aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 21). For *K. pneumoniae* complex, 10.9% were resistant to at least one antimicrobial group (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 22). For *P. aeruginosa,* 21.1% 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, 2022

Resistance pattern	Number	% of total*
Fully susceptible	2,425	46.2
Single resistance	1,801	34.3
Aminopenicillins	1,677	31.9
Fluoroquinolones	107	2.0
Aminoglycosides	16	0.3
Third-generation cephalosporins	1	0.0
Resistance to two antimicrobial groups	456	8.7
Aminopenicillins + third-generation cephalosporins	217	4.1
Aminopenicillins + fluoroquinolones	143	2.7
Aminopenicillins + aminoglycosides	96	1.8
Resistance to three antimicrobial groups	420	8.0
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	214	4.1
Aminopenicillins + third-generation cephalosporins + aminoglycosides	104	2.0
Aminopenicillins + fluoroquinolones + aminoglycosides	102	1.9
Resistance to four antimicrobial groups	150	2.9
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	148	2.8
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + carbapenems	2	<0.1
Resistance to five antimicrobial groups	2	<0.1
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	2	<0.1

Note: Only data from isolates tested against all five antimicrobial groups were included (n = 5,254).

Table 22: Resistance combinations among *Klebsiella pneumoniae* complex tested against fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems, AGAR, 2022

Resistance pattern	Number	% of total
Fully susceptible	1,240	89.1
Single resistance	72	5.2
Fluoroquinolones	40	2.9
Third-generation cephalosporins	23	1.7
Aminoglycosides	9	0.6
Resistance to two antimicrobial groups	41	2.9
Third-generation cephalosporins + fluoroquinolones	26	1.9
Third-generation cephalosporins + aminoglycosides	9	0.6
Fluoroquinolones + aminoglycosides	6	0.4
Resistance to three antimicrobial groups	32	2.3
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	31	2.2
Third-generation cephalosporins + aminoglycosides + carbapenems	1	<0.1
Resistance to four antimicrobial groups	0	0.0
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	6	0.4

Notes:
1. Only data from isolates tested against all four antimicrobial groups are included (*n* = 1,391).
2. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 121) and *K. quasipneumoniae* (*n* = 3).

Table 23: Resistance combinations among *Pseudomonas aeruginosa* tested against piperacillin–tazobactam, ceftazidime, fluoroquinolones, aminoglycosides and carbapenems, AGAR, 2022

Resistance pattern	Number	% of total
Fully susceptible	647	78.9
Single resistance	73	8.9
Fluoroquinolones	39	4.8
Piperacillin–tazobactam	26	3.2
Ceftazidime	5	0.6
Carbapemems	3	0.4
Resistance to two antimicrobial groups	65	7.9
Piperacillin–tazobactam + ceftazidime	47	5.7
Piperacillin–tazobactam + fluoroquinolones	10	1.2
Fluoroquinolones + carbapenems	3	0.4
Ceftazidime + carbapenems	2	0.2
Aminoglycosides + carbapenems	1	0.1
Ceftazidime + fluoroquinolones	1	0.1
Piperacillin–tazobactam + carbapenems	1	0.1
Resistance to three antimicrobial groups	18	2.2
Piperacillin–tazobactam + ceftazidime + fluoroquinolones	8	1.0
Piperacillin–tazobactam + ceftazidime + carbapenems	5	0.6
Piperacillin–tazobactam + fluoroquinolones + carbapenems	4	0.5
Piperacillin–tazobactam + fluoroquinolones + aminoglycosides	1	0.1
Resistance to four antimicrobial groups	15	1.8
Piperacillin–tazobactam + ceftazidime + aminoglycosides + carbapenems	13	1.6
Piperacillin–tazobactam + ceftazidime + fluoroquinolones + carbapenems	2	0.2
Resistance to five antimicrobial groups	2	0.2
Piperacillin–tazobactam + ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	2	0.2

Note: Only data from isolates tested against all five antimicrobial groups are included (*n* = 820).

Table 24: Resistance combinations among *Staphylococcus aureus* tested against methicillin, ciprofloxacin and rifampicin, AGAR, 2022

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

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

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

Multi-drug resistances by onset setting (community or hospital) and 30-day all-cause mortality for the most common species are shown in Table 25. While in general higher mortality rates were associated with multidrug-resistant isolates, there was no significant association between multi-drug resistance and 30-day all-cause mortality or onset setting.

Table 25: Multi-drug resistance, by onset setting and 30-day all-cause mortality, AGAR, 2022

Species	Category	Total		Community-onset		Hospital-onset	
		Number	Deaths, % (n)	Number	Deaths,% (n)	Number	Deaths, % (n)
Enterobacter cloacae complex	Total	360	12.5 (45)	184	9.8 (18)	176	15.3 (27)
	Non-MDR (≤2)	330	12.1 (40)	174	10.3 (18)	156	14.1 (22)
	MDR (>2)	30	16.7 (5)	10	0.0 (0)	20	25.0 (5)
Escherichia coli	Total	3,619	11.5 (415)	2,939	11.1 (325)	680	13.2 (90)
	Non-MDR (≤2)	2,765	11.0 (305)	2,286	10.6 (243)	479	12.9 (62)
	MDR (>2)	854	12.9 (110)	653	12.6 (82)	201	13.9 (28)
Klebsiella pneumoniae complex	Total	1,001	12.8 (128)	688	12.2 (84)	313	14.1 (44)
	Non-MDR (≤2)	922	12.9 (119)	648	11.9 (77)	274	15.3 (42)
	MDR (>2)	79	11.4 (9)	40	17.5 (7)	39	5.1 (2)
Pseudomonas aeruginosa	Total	611	18.5 (113)	343	18.7 (64)	268	18.3 (49)
	Non-MDR (≤2)	581	18.4 (107)	337	18.7 (63)	244	18.0 (44)
	MDR (>2)	30	20.0 (6)	6	16.7 (1)	24	20.8 (5)
Staphylococcus aureus	Total	2,577	17.4 (449)	2,004	16.8 (336)	573	17.9 (113)
	Non-MDR (≤2)	2,080	17.0 (354)	1,623	16.4 (266)	457	17.7 (88)
	MDR (>2)	497	19.1 (95)	381	18.4 (70)	116	18.3 (25)

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

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. bugandensis* (*n* = 5), *E. asburiae* (*n* = 4), *E. hormaechei* (*n* = 3), and *E. ludwigii* (*n* = 1).
3. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 93), *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 2022 dataset. The benefits of this method include increased accuracy in detecting the genetic mechanisms for AMR and clarifying the underlining epidemiology.

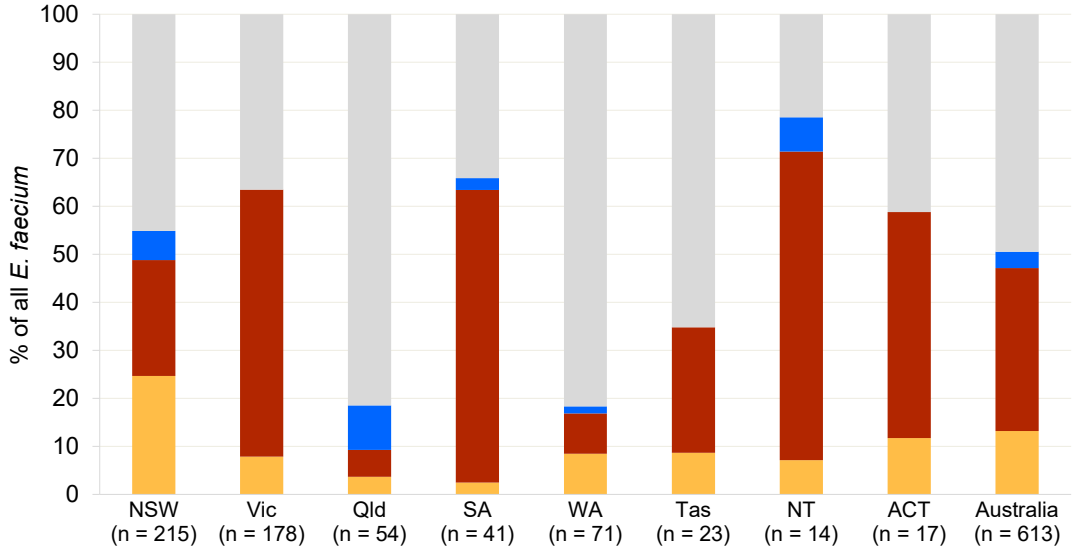
Molecular epidemiology of *Enterococcus faecium*

van genes

Results of PCR testing for *vanA* and *vanB* genes were available for 592 (96.6%) of the 613 *E. faecium* isolates. *van* genes were detected in 289/592 (48.8%) of *E. faecium*; *vanA* in 81 (13.7%), and *vanB* in 208 (35.1%) (Figure 9). No *E. faecium* contained both *vanA* and *vanB* genes.

For vancomycin-resistant *E. faecium* (MIC > 4 mg/L), *vanA* was detected in 79/279 (28.3%), and *vanB* in 199/279 (71.3%). In 9 of 310 (2.9%) vancomycin-susceptible *E. faecium*, *van* genes were detected: eight with *vanB* and one with *vanA*. All nine isolates had vancomycin MIC ≤ 4 mg/L.

Figure 9: Vancomycin genotype of *Enterococcus faecium* isolates, by state and territory, and nationally, AGAR, 2022



	NSW (n = 215)	Vic (n = 178)	Qld (n = 54)	SA (n = 41)	WA (n = 71)	Tas (n = 23)	NT (n = 14)	ACT (n = 17)	Australia (n = 613)
not detected (n = 303)	45.1	36.5	81.5	34.1	81.7	65.2	21.4	41.2	49.4
Not determined (n = 21)	6.0	0.0	9.3	2.4	1.4	0.0	7.1	0.0	3.4
vanB (n = 208)	24.2	55.6	5.6	61.0	8.5	26.1	64.3	47.1	33.9
vanA (n = 81)	24.7	7.9	3.7	2.4	8.5	8.7	7.1	11.8	13.2

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

Multi-locus sequence type

Of the 613 *E. faecium* isolates reported, 560 (91.4%) were available for typing by WGS (Table 26). Based on the MLST, 62 sequence types were identified. Overall, 85.5% of *E. faecium* could be characterised into eight major sequence types (10 or more isolates): ST17 (*n* = 119); ST78 (*n* = 110); ST1424, (*n* = 81); ST796 (*n* = 50); ST80 (*n* = 45); ST1421 (*n* = 44); ST555 (*n* = 20) and ST117 (*n* = 10). There were 40 sequence types with a single isolate.

ST17 was the predominant sequence type in Queensland, Western Australia and Tasmania. ST78 was dominant in the Australian Capital Territory, ST78 and ST555 in the Northern Territory. ST78 and ST796 were detected in equal numbers in Victoria, ST1424 was predominant in New South Wales, and ST555 in South Australia.

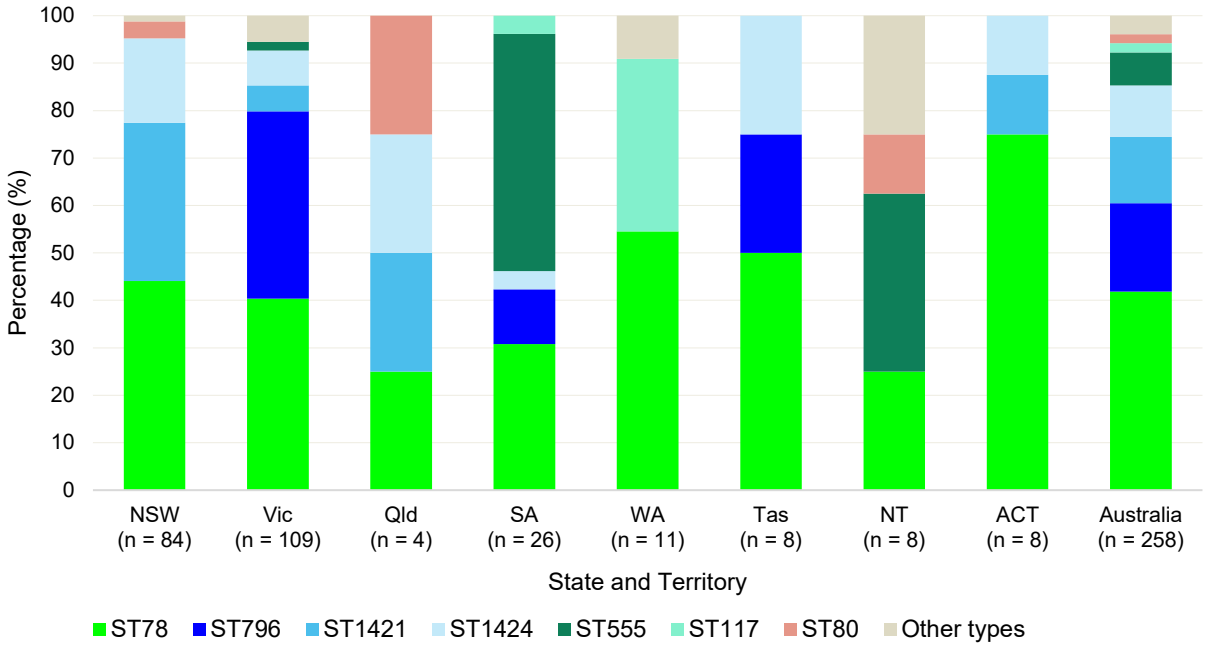
The distribution of vancomycin-resistant *E. faecium* sequence types throughout Australian states and territories are shown in Figure 10.

Table 26: *Enterococcus faecium* MLST, by state and territory, AGAR, 2022

	Percentage, % (*n*)								
MLST	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST17	8.3 (15)	14.9 (26)	52.2 (24)	17.5 (7)	52.2 (36)	40.9 (9)	7.7 (1)	6.3 (1)	21.3 (119)
ST78	21.1 (38)	25.3 (44)	2.2 (1)	20.0 (8)	8.7 (6)	18.2 (4)	23.1 (3)	37.5 (6)	19.6 (110)
ST1424	30.6 (55)	9.2 (16)	6.5 (3)	2.5 (1)	0.0 (0)	18.2 (4)	0.0 (0)	12.5 (2)	14.5 (81)
ST796	0.6 (1)	25.3 (44)	0.0 (0)	7.5 (3)	0.0 (0)	9.1 (2)	0.0 (0)	0.0 (0)	8.9 (50)
ST80	5.6 (10)	5.7 (10)	21.7 (10)	2.5 (1)	10.1 (7)	4.5 (1)	7.7 (1)	31.3 (5)	8.0 (45)
ST1421	18.3 (33)	4.0 (7)	6.5 (3)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	6.3 (1)	7.9 (44)
ST555	0.6 (1)	1.1 (2)	0.0 (0)	32.5 (13)	1.4 (1)	0.0 (0)	23.1 (3)	0.0 (0)	3.6 (20)
ST117	1.1 (2)	0.0 (0)	0.0 (0)	2.5 (1)	10.1 (7)	0.0 (0)	0.0 (0)	0.0 (0)	1.8 (10)
Other types (*n* = 54)	13.9 (25)	14.4 (25)	10.9 (5)	15.0 (6)	17.4 (12)	9.1 (2)	38.5 (5)	6.3 (1)	14.5 (81)
Total	**180**	**174**	**46**	**40**	**69**	**22**	**13**	**16**	**560**

MLST = multi-locus sequence type

Figure 10: Distribution of vancomycin-resistant *Enterococcus faecium* sequence types, by state and territory, AGAR, 2022



MLST and *van* genes

The *vanA* gene alone was detected in six sequence types; ST1421 (*n* = 36), ST1424 (*n* = 28), ST117 (*n* = 4), ST80 (*n* = 3), ST17 (*n* = 1) and ST18 (*n* = 1).

The *vanB* gene alone was detected in 13 sequence types: ST78 (*n* = 110), ST796 (*n* = 50), ST555 (*n* = 18), ST17 (*n* = 3), ST203 (n = 3), ST80 (*n* = 2), ST2217 (*n* = 2), and one each of ST117, ST341, ST612, ST1424, ST2430 and ST2439 (Table 27).

Table 27: *Enterococcus faecium* MLST harbouring *van* genes, AGAR, 2022

	Percentage* (*n*)			
MLST	*vanA*	*vanB*	*van* genes not detected	Total, *n*
ST17	0.8 (1)	2.5 (3)	96.6 (115)	119
ST78	0.0 (0)	100.0 (110)	0.0 (0)	110
ST1424	34.6 (28)	1.2 (1)	64.2 (52)	81
ST796	0.0 (0)	100.0 (50)	0.0 (0)	50
ST80	6.7 (3)	4.4 (2)	88.9 (40)	45
ST1421	81.8 (36)	0.0 (0)	18.2 (8)	44
ST555	0.0 (0)	90.0 (18)	10.0 (2)	20
ST117	40.0 (4)	10.0 (1)	50.0 (5)	10
Other types (*n* =54)	1.2 (1)	11.1 (9)	87.7 (71)	81
Total	13.0 (73)	34.6 (194)	52.3 (293)	560

MLST = multi-locus sequence type

* Percentage of total with *van* genes

Linezolid resistance

Two linezolid-resistant *E. faecium* from Victoria were confirmed. Both harboured the G2576T 23S rRNA mutation. One isolate with a linezolid MIC > 256 mg/L was ST2217, vancomycin resistant and harboured the *vanB* gene. The second isolate with a linezolid MIC = 8 mg/L was ST1424 and vancomycin susceptible.

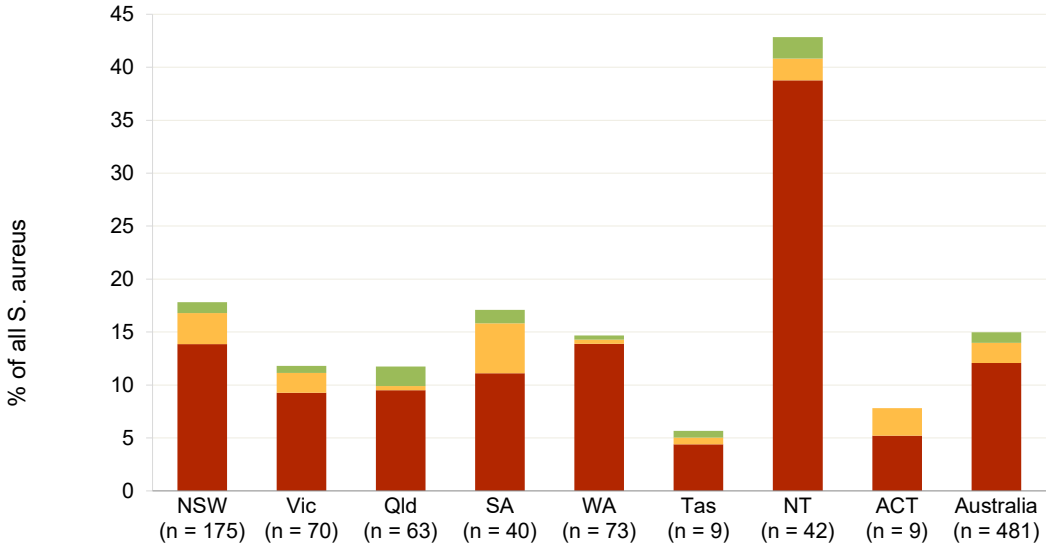
Daptomycin resistance

Two daptomycin-resistant isolates from NSW, one *E. faecalis* and one *E. faecium* were confirmed. The *E. faecalis* with a daptomycin MIC = 8 mg/L was ST16 and harboured the F478L GdpD mutation.[53] The *E. faecium* with a daptomycin MIC = 24 mg/L was ST78 and harboured the A20D Cls mutation.[54] The daptomycin-resistant *E. faecium* was also vancomycin-resistant and harboured the *vanB* gene.

Molecular epidemiology of methicillin-resistant *Staphylococcus aureus*

Of the 481 MRSA reported, 449 (93.3%) 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 5.7% (9/159) in Tasmania to 42.9% (42/98) in the Northern Territory (Figure 11).

Figure 11: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, AGAR, 2022



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

MRSA = methicillin-resistant *Staphylococcus aureus*

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

Healthcare-associated MRSA

Based on the MLST and SCC*mec* type, two HA-MRSA clones were identified: ST22-IV (EMRSA-15) and ST239-III (Aus 2/3 EMRSA) (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 identified in three states or territories, New South Wales, Victoria, and the Australian Capital Territory (Table 29).

Community-associated MRSA

Based on the MLST and SCC*mec* type, 64 CA-MRSA clones were identified. There were 35 sequence types with a single isolate. PVL was detected in 13 CA-MRSA clones. Overall, 42.8% (166/388) 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 except Tasmania.

Four PVL positive ST22-IV isolates were identified: two in Victoria, one each in Queensland and Western Australia (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.[55]

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

Table 28: MRSA clones, association, place of onset and PVL carriage, AGAR, 2022

Clone	Clonal complex	Total, *n*	Community-onset, % (*n*)*	Hospital-onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)	CC22	55	54.5 (30)	45.5 (25)	0.0 (0)
ST239-III (Aus2/3 EMRSA)	CC8	6	–† (2)	–† (4)	–† (0)
Total HA-MRSA		61	52.5 (32)	47.5 (29)	0.0 (0)
Community-associated					
ST93-IV (Qld CA-MRSA)	CC93	104	88.5 (92)	11.5 (12)	99.0 (103)
ST5-IV	CC5	48	81.3 (39)	18.8 (9)	45.8 (22)
ST45-V	CC45	38	71.1 (27)	28.9 (11)	0.0 (0)
ST1-IV (WA1 MRSA)	CC1	25	68.0 (17)	32.0 (8)	4.0 (1)
ST30-IV (SWP MRSA)	CC30	21	85.7 (18)	14.3 (3)	61.9 (13)
ST97-IV	CC97	21	61.9 (13)	38.1 (8)	0.0 (0)
ST953-IV	CC97	11	90.9 (10)	9.1 (1)	0.0 (0)
ST8-IV	CC8	11	81.8 (9)	18.2 (2)	72.7 (8)
ST6-IV	CC6	8	–† (4)	–† (4)	–† (0)
ST78-IV (WA2 MRSA)	CC78	6	–† (4)	–† (2)	–† (0)
ST5-V	CC6	6	–† (3)	–† (3)	–† (0)
ST45-IV	CC45	5	–† (2)	–† (3)	–† (0)
ST872-IV	CC1	5	–† (3)	–† (2)	–† (0)
Other (*n* = 51)		79	79.7 (63)	20.3 (16)	24.1 (19)
Total CA-MRSA		388	78.4 (304)	21.6 (84)	42.8 (166)
MRSA		449	74.8 (336)	25.2 (113)	37.0 (166)

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

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

Table 29: Healthcare-associated MRSA clones, by state and territory, AGAR, 2022

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

MRSA = methicillin-resistant *Staphylococcus aureus*

* Insufficient numbers (<10) to calculate percentage

Table 30: Major community-associated MRSA clones (>10 isolates) by state and territory and PVL carriage, AGAR, 2022

	Percentage (*n*)								
Clone	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST93-IV (Qld CA-MRSA)	15.4 (21)	20.0 (11)	37.3 (19)	42.3 (11)	24.6 (17)	–* (0)	60.5 (23)	–* (2)	26.8 (104)
Number PVL positive	21	11	19	10	17	0	23	2	103
Number PVL negative	0	0	0	1	0	0	0	0	1
ST5-IV	7.4 (10)	7.3 (4)	9.8 (5)	15.4 (4)	20.3 (14)	–* (1)	26.3 (10)	–* (0)	12.4 (48)
Number PVL positive	0	1	0	2	11	0	8	0	22
Number PVL negative	10	3	5	2	3	1	2	0	26
ST45-V	20.6 (28)	12.7 (7)	2.0 (1)	0.0 (0)	0.0 (0)	–* (0)	2.6 (1)	–* (1)	9.8 (38)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	28	7	1	0	0	0	1	1	38
ST1-IV	6.6 (9)	0.0 (0)	5.9 (3)	11.5 (3)	13.0 (9)	–* (1)	0.0 (0)	–* (0)	6.4 (25)
Number PVL positive	1	0	0	0	0	0	0	0	1
Number PVL negative	8	0	3	3	9	1	0	0	24
ST30-IV	8.8 (12)	7.3 (4)	3.9 (2)	3.8 (1)	1.4 (1)	–* (0)	0.0 (0)	–* (1)	5.4 (21)
Number PVL positive	7	2	1	1	1	0	0	1	13
Number PVL negative	5	2	1	0	0	0	0	0	8
ST97-IV	6.6 (9)	3.6 (2)	9.8 (5)	0.0 (0)	4.3 (3)	–* (1)	0.0 (0)	–* (1)	5.4 (21)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	9	2	5	0	3	1	0	1	21
ST953-IV	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	15.9 (11)	–* (0)	0.0 (0)	–* (0)	2.8 (11)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	0	0	0	0	11	0	0	0	11
ST8-IV	5.9 (8)	3.6 (2)	2.0 (1)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	–* (0)	2.8 (11)
Number PVL positive	5	2	1	0	0	0	0	0	8
Number PVL negative	3	0	0	0	0	0	0	0	3
Other clones (*n* = 56)	28.7 (39)	45.5 (25)	29.4 (15)	26.9 (7)	20.3 (14)	–* (4)	10.5 (4)	–* (1)	28.1 (109)
Number PVL positive	4	8	4	1	2	0	0	0	19
Number PVL negative	35	17	11	6	12	4	4	1	90
Total	**136**	**55**	**51**	**26**	**69**	**7**	**38**	**6**	**388**
PVL positive	38	24	25	14	31	0	31	3	166
PVL negative	98	31	26	12	38	7	7	3	222

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

* Insufficient numbers (<10) to calculate percentage

Daptomycin resistance

One MRSA from NSW was confirmed to have a daptomycin MIC = 2 mg/L. This isolate was an ST93-IV and carried the A302V MprF mutation and the A23V Cls2 mutation.[56, 57]

Gram-negative species

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

Third-generation cephalosporin resistance

Extended-spectrum β-lactamases

Resistances conferred by ESBL-containing gram-negative organisms are important internationally, especially in hospital practice. 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.[8-10] It is unclear what is driving the community expansion of CTX-M ESBLs in Australia, as third-generation cephalosporins are not widely used in that 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.[11] Returning travellers and visitors from high prevalence areas such as Asia, is also likely a factor.[6, 7]

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.

Most ESBL-producing isolates will be detected using the CLSI/EUCAST ceftriaxone ‘susceptible’ breakpoint of 1 mg/L. The CLSI ‘susceptible’ breakpoint of 4 mg/L for ceftazidime is less reliable for ESBL detection. Isolates with either ceftriaxone or ceftazidime MICs above 1 mg/L were referred and underwent sequencing.

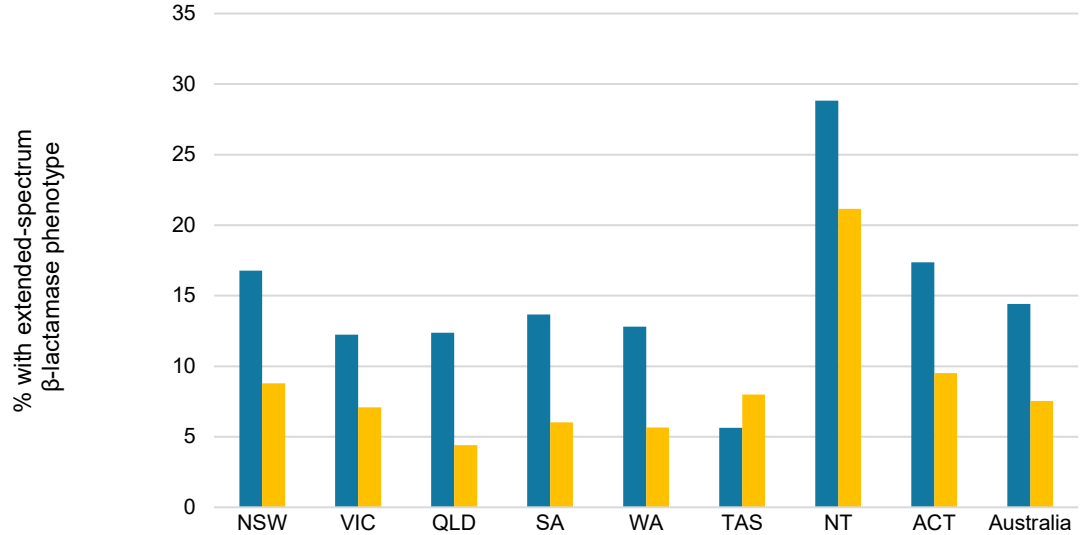
Neither ceftriaxone nor ceftazidime testing will identify ESBL production in *Enterobacter* species because of their intrinsic chromosomal AmpC β-lactamase. In *Enterobacter*, cefepime MICs of greater than 0.25 mg/L suggest that an isolate of this genus harbours an ESBL.[58] However, due to the cefepime 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.

The percentage of *E. coli* with an ESBL phenotype was highest in the Northern Territory (28.8%, 49/170) and lowest in Tasmania (5.6%, 13/231). The percentage of *K. pneumoniae* complex with an ESBL phenotype ranged from 21.2% (11/52) in the Northern Territory, to 4.4% (10/227) in Queensland.

Figure 12: Percentage of *Escherichia coli* and *Klebsiella pneumoniae* complex with extended-spectrum β-lactamase phenotype, by state and territory, and nationally, AGAR, 2022



	NSW	VIC	QLD	SA	WA	TAS	NT	ACT	Australia
E. coli, %	16.8	12.2	12.4	13.7	12.8	5.6	28.8	17.4	14.4
K. pneumoniae complex, %	8.8	7.1	4.4	6.0	5.7	8.0	21.2	9.5	7.5
E. coli (n = 5,261)	297	129	88	60	89	13	49	33	758
K. pneumoniae complex (n = 1,392)	39	20	10	5	12	4	11	4	105

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* (158/921 [17.2%] vs 600/4340 [13.8%], $P < 0.01$) and *K. pneumoniae* complex bacteraemia (54/426 [12.7%] vs 51/966 [5.3%], $P < 0.01$).

An ESBL phenotype was more common among *E. coli* (758/5261, 14.4%) than *K. pneumoniae* complex isolates (105/1392, 7.5%) (Figure 11). For 57 *E. cloacae* complex isolates with cefepime MIC >1 mg/L, 24 (42.1%; 4.4% overall) contained a non-intrinsic β-lactamase gene(s): ESBL only (*n* = 14), ESBL + carbapenemase (*n* = 8), or carbapenemase only (*n* = 2) (Table 31).

The vast majority (17/18, 94.4%) of *K. oxytoca* isolates with a ceftriaxone-resistant phenotype were 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).[59, 60] This pattern is not typical of other types of gram-negative β-lactamases.

Plasmid-borne AmpC and/or carbapenemase genes were also detected in isolates that had an ESBL phenotype but no ESBL genes.

Table 31: β-lactamase genes detected in *Enterobacterales* with extended-spectrum β-lactamase phenotype, AGAR, 2022

β-lactamase mechanism	*Escherichia coli*	*Klebsiella pneumoniae* complex	*Enterobacter cloacae* complex	*Klebsiella oxytoca*	*Proteus mirabilis*	*Salmonella* spp.†
Total	5,261	1,392	475	323	296	133
ESBL phenotype*, % (n)	14.4 (758)	7.5 (105)	12.0 (57)	2.5 (8)	6.1 (18)	4.5 (6)
β-lactamase genes confirmed/number tested (%)	683/723 (94.5)	91/103 (88.3)	24/57 (42.1)	4/6 (66.7)	1/14 (7.1)	6/6 (100.0)
ESBL	560	75	14	3	0	6
ESBL, AmpC	17	1	0	0	0	0
ESBL, AmpC, Carb	0	1	0	0	0	0
ESBL, Carb	4	3	8	0	0	0
AmpC	99	7	0	1	1	0
AmpC, Carb	1	1	0	0	0	0
Carb	2	3	2	0	0	0
Not detected	40	12	33	2	13	0
Not determined§	35	2	0	2	4	0

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* = 96), typhoidal (*n* = 37)
§ Isolate not available for confirmation

The β-lactamase genes confirmed in *Enterobacterales* with an ESBL phenotype are shown in Table 32. *bla*$_{\text{CTX-M}}$ types continue to be the dominant β-lactamase genes in *E. coli*. Of 683 with confirmed β-lactamase gene(s), 578 (84.6%) had one or more *bla*$_{\text{CTX-M}}$ genes, either *bla*$_{\text{CTX-M}}$ group 1 (*n* = 295), *bla*$_{\text{CTX-M}}$ group 9 (*n* = 282), or a CTX-M group 1/9/1 hybrid (*n* = 1). CTX-M group 1 types were dominant in Victoria, South Australia, and the Australian Capital Territory. CTX-M group 9 types were more prevalent in Queensland, Western Australia, and Tasmania.

Among *K. pneumoniae* complex isolates with confirmed β-lactamase genes, 73 of 91 (80.2%) contained a *bla*$_{\text{CTX-M}}$ gene: *bla*$_{\text{CTX-M}}$ group 1 (*n* = 65), *bla*$_{\text{CTX-M}}$ group 9 (*n* = 6) or *bla*$_{\text{CTX-M}}$ group 1 + *bla*$_{\text{CTX-M}}$ group (*n* = 1) (Table 32).

Table 32: β-lactamase genes among *Enterobacterales* with extended-spectrum β-lactamase phenotype, by state and territory, AGAR, 2022

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,771	1,054	711	439	695	231	170	190	5,261
ESBL phenotype*, % (*n*)	16.8 (297)	12.2 (129)	12.4 (88)	13.7 (60)	12.8 (89)	5.6 (13)	28.8 (49)	17.4 (33)	14.4 (758)
Confirmed β-lactamase genes/number tested	251/ 270	120/ 128	82/ 86	53/ 58	85/ 87	12/ 13	48/ 48	32/ 33	683/ 723
ESBL types	198	113	61	48	75	12	46	28	581
CTX-M-types	197	112	60	48	75	12	46	28	578
group 1	96	61	24	29	35	4	25	21	295
group 9	101	50	36	19	40	8	21	7	282
group 1/9/1 hybrid	0	1	0	0	0	0	0	0	1
SHV (ESBL types)	1	1	0	0	0	0	0	0	2
TEM (ESBL types)	0	0	1	0	0	0	0	0	1
Plasmid-borne AmpC	62	8	23	6	11	1	3	3	117
CMY-2-like	31	5	10	0	3	0	1	2	52
DHA-1	31	3	13	6	7	1	2	1	64
CMY-2-like + DHA	0	0	0	0	1	0	0	0	1
Carbapenemases	4	1	0	0	1	0	0	1	7
NDM-5	2	1	0	0	1	0	0	0	4
NDM-5 + OXA-181	1	0	0	0	0	0	0	0	1
IMP-4	0	0	0	0	0	0	0	1	1
OXA-181	1	0	0	0	0	0	0	0	1
Klebsiella pneumoniae complex	444	282	227	83	212	50	52	42	1,392
ESBL phenotype*, % (*n*)	8.8 (39)	7.1 (20)	4.4 (10)	6.0 (5)	5.7 (12)	8.0 (4)	21.2 (11)	9.5 (4)	7.5 (105)
Confirmed β-lactamase genes/number tested	33/37	18/20	7/10	4/5	10/12	4/4	11/11	4/4	91/103
ESBL types	26	18	6	3	9	4	11	3	80
CTX-M-types	25	15	6	2	9	4	10	2	73
group 1	24	11	5	2	9	4	10	0	65
group 9	1	4	1	0	0	0	0	0	6
group 1 + group 9	0	0	0	0	0	0	0	2	2
SHV (ESBL types)	2	3	1	1	0	1	1	3	12
PER	0	1	0	0	0	0	0	0	1
Plasmid-borne AmpC	6	1	1	1	1	0	0	0	10
DHA-1	5	0	1	1	1	0	0	0	8
CMY-2-like	1	1	0	0	0	0	0	0	2
Carbapenemases	2	3	1	0	0	0	1	1	8
IMP-4	2	1	0	0	0	0	1	1	5
NDM-1	0	1	1	0	0	0	0	0	2
NDM-1 + OXA-181	0	1	0	0	0	0	0	0	1

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Enterobacter cloacae complex	170	98	88	22	51	19	9	18	475
ESBL phenotype*, % (*n*)	15.3 (26)	13.3 (13)	6.8 (6)	31.8 (7)	2.0 (1)	10.5 (2)	11.1 (1)	5.6 (1)	12.0 (57)
Confirmed β-lactamase genes/number tested (%)	13/26	5/13	2/6	1/7	1/1	1/2	1/1	0/1	24/57
ESBL types	11	5	2	1	1	1	1	0	22
CTX-M-types	5	3	1	1	1	0	1	0	12
group 1	5	3	1	1	0	0	1	0	11
group 9	0	0	0	0	1	0	0	0	1
SHV (ESBL types)	4	2	2	0	0	1	0	0	9
VEB	2	0	0	0	0	0	0	0	2
Carbapenemases	7	1	2	0	0	0	0	0	10
IMP-4	7	1	1	0	0	0	0	0	9
NDM-1	0	0	1	0	0	0	0	0	1

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 79.9% (578/723) of *E. coli* with an ESBL phenotype (Table 33). In the *bla*$_{\text{CTX-M-1}}$ group, *bla*$_{\text{CTX-M-15}}$ accounted for 89.2% (263/295). 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 78.4% (221/282) and 18.1% (51/282), respectively.

Table 33: *Escherichia coli*, CTX-M variants, ESBL phenotype, sequence type, AGAR, 2022

		Phenotype		Sequence type						
CTX-M variant	Number	ESBL	Non-ESBL	131	1193	69	-*	73	38	Other types (*n* = 93)
Not detected	221	145	76	13	14	35	12	10	8	129
CTX-M-1 group	296	295	2	120	23	12	18	33	7	84
CTX-M-15	261	260	1	114	16	9	13	33	7	69
CTX-M-55	22	21	1	5	6	2	2	0	0	7
CTX-M-3	7	7	0	0	0	0	3	0	0	4
CTX-M-1	2	2	0	0	1	0	0	0	0	1
CTX-M-15-like†	2	2	0	0	0	1	0	0	0	1
CTX-M-15, CTX-M-189	1	1	0	1	0	0	0	0	0	0
CTX-M-62	1	1	0	0	0	0	0	0	0	1
CTX-M-182	1	1	0	0	0	0	0	0	0	1
CTX-M-9 group	283	282	1	171	27	5	22	5	27	26
CTX-M-27	221	220	1	146	24	3	21	1	14	12
CTX-M-14a	47	47	0	19	2	2	1	4	6	13
CTX-M-24	7	7	0	5	0	0	0	0	2	0
CTX-M-14b	4	4	0	0	0	0	0	0	4	0
CTX-M-27-like§	1	1	0	0	0	0	0	0	1	0
CTX-M-65	1	1	0	0	0	0	0	0	0	1
CTX-M-134	1	1	0	1	0	0	0	0	0	0
CTX-M-240	1	1	0	0	1	0	0	0	0	0
CTX-M group 1/9/1 hybrid	1	1	0	0	1	0	0	0	0	0
CTX-M-64	1	1	0	0	1	0	0	0	0	0
	802	723	79	304	65	52	52	48	42	239

ESBL = extended-spectrum β-lactamase

* Not available
† CTX-M-15-like (*n* = 2): one has 2 SNPs at 214T to A (Cys to Ser) and 239C to T (Ala to Val); and another with 2 SNPs at 208G to C (Ala to Pro) and 724G to A (Gly to Ser)
§ CTX-M-27-like: 1 SNP. 352G to A (Gly to Ser)

In the *bla*$_{\text{CTX-M}}$-positive isolates, *bla*$_{\text{SHV}}$- or *bla*$_{\text{TEM}}$-type ESBL genes were not detected. Among 145 *bla*$_{\text{CTX-M}}$-negative isolates with an ESBL phenotype, 99 harboured one or more pAmpC type genes only (*bla*$_{\text{DHA-1}}$ [56], *bla*$_{\text{DHA-27}}$ [1], *bla*$_{\text{CMY-2}}$ [38], *bla*$_{\text{CMY-4}}$ [1], *bla*$_{\text{CMY-42}}$ [1], *bla*$_{\text{CMY-141}}$ [1], *bla*$_{\text{CMY-42}}$ + *bla*$_{\text{DHA-1}}$ [1]). Three harboured only a *bla*$_{\text{SHV}}$ or *bla*$_{\text{TEM}}$ ESBL gene (*bla*$_{\text{SHV-12}}$ [2], *bla*$_{\text{TEM-207}}$ [1]); two harboured only carbapenemase gene(s) alone (*bla*$_{\text{IMP-4}}$ [1]; *bla*$_{\text{NDM-5}}$ + *bla*$_{\text{OXA-181}}$ [1]); and one harboured both pAmpC and carbapenemase gene (*bla*$_{\text{CMY-146}}$ + *bla*$_{\text{OXA-181}}$). β-lactam resistance mechanisms were not detected in the remaining 40 isolates.

Half (49.9%, 290/581) of the ESBL-producing *E. coli* with confirmed ESBL genes belong to sequence type 131 (ST131) (Table 34). The fluoroquinolone-resistant subclade, H30R, was the most prevalent subclade of ST131 (52.4%, 152/290). Within ST131, all isolates that identified as H30Rx (subclade C2) (*n* = 87) carried *bla*$_{\text{CTX-M-15}}$, a finding reported globally.[61-63] Two-thirds (65.9%, 145/220) of isolates with *bla*$_{\text{CTX-M-27}}$ were ST131; 86 belonged to H41 subclade A; 45 belonged to H30R subclade C1-M27, 11 belonged to H99 and 3 to other *fimH* alleles.

ST1193 has recently been identified as an emerging MDR type.[64, 65] In the 2022 survey, ST1193 was the second most prevalent ST among *E. coli* with an ESBL phenotype (57/723, 7.9%). All 57 ST1193 isolates were ciprofloxacin resistant, and harboured either ESBL (*bla*$_{\text{CTX-M}}$ [49]), pAmpC (*bla*$_{\text{DHA-1}}$ [6] or (*bla*$_{\text{CMY-42}}$ [1]) alone, or both ESBL + pAmpC (*bla*$_{\text{CTX-M-27}}$ + *bla*$_{\text{CMY-2}}$ [1]) genes.

Table 34: ESBL-producing *Escherichia coli* subset, *fimH* allele, H30Rx, AGAR, 2022

ESBL type	ST131								Non-ST131
			H30						
	Number	All	H41*	H30Rx	H30R	H99	H89	Others†	
CTX-M-15	260	114	20	87	3	1	0	3	146
CTX-M-27	220	145	86	0	45	11	0	3	75
CTX-M-14a	47	19	4	0	14	0	0	1	28
CTX-M-55	21	5	2	0	2	0	0	1	16
CTX-M-3	7	0	0	0	0	0	0	0	7
CTX-M-24	7	5	0	0	0	0	5	0	2
CTX-M-14b	4	0	0	0	0	0	0	0	4
CTX-M-1	2	0	0	0	0	0	0	0	2
CTX-M-15-like	2	0	0	0	0	0	0	0	2
CTX-M-15, CTX-M-189	1	1	1	0	0	0	0	0	0
CTX-M-27-like	1	0	0	0	0	0	0	0	1
CTX-M-62	1	0	0	0	0	0	0	0	1
CTX-M-64	1	0	0	0	0	0	0	0	1
CTX-M-65	1	0	0	0	0	0	0	0	1
CTX-M-134	1	1	0	0	1	0	0	0	0
CTX-M-182	1	0	0	0	0	0	0	0	1
CTX-M-240	1	0	0	0	0	0	0	0	1
SHV-12	2	0	0	0	0	0	0	0	2
TEM-207	1	0	0	0	0	0	0	0	1
	581	290	113	87	65	12	5	8	291

ESBL = extended-spectrum β-lactamase

* Includes H41-like (*n* = 1)
† H22 (*n* = 4), H54 (*n* = 2), unknown (*n* = 2)

Plasmid-borne AmpC β-lactamases

Plasmid-borne *ampC* β-lactamase genes have emerged internationally as a potential gram-negative resistance problem. They are the result of mobilisation of natural chromosomally located genes from common 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. *Enterobacter* species naturally possess a chromosomally encoded AmpC enzyme.

All referred isolates were examined for the presence of plasmid-borne *ampC* (bla_{CMY-2}-like, bla_{DHA}, bla_{FOX}, bla_{MOX}, $bla_{ACT/MIR}$, bla_{ACC}) genes using WGS 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 (5.3% and 5.0% respectively) (Table 35). A little over one-third (108/265, 40.8%) of *E. coli* and 15.6% (10/64) of *K. pneumoniae* complex isolates with cefoxitin MIC > 8 mg/L that were available for confirmation contained one or more plasmid-borne *ampC* genes. In most cases the plasmid-borne *ampC* gene type was bla_{DHA}, found in 57.4% (62/108) of *E. coli* and 80.0% (8/10) of *K. pneumoniae* complex isolates.

Table 35: Numbers of isolates with presumptive plasmid-borne AmpC β-lactamase production, by state and territory, AGAR, 2022

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Escherichia coli	1,771	1,053	711	439	695	231	170	190	5,260
Cefoxitin MIC > 8 mg/L (%)	123 (6.9)	47 (4.5)	39 (5.5)	17 (3.9)	31 (4.5)	6 (2.6)	5 (2.9)	10 (5.3)	278 (5.3)
Confirmed/number tested	54/115	6/46	23/37	6/15	11/31	1/6	3/5	4/10	108/265
bla$_{DHA-1}$*	27	2	14	6	7	1	1	2	60
bla$_{DHA-6}$	0	0	0	0	0	0	1	0	1
bla$_{DHA-27}$	1	0	0	0	0	0	0	0	1
bla$_{CMY-2}$	21	4	9	0	2	0	1	2	39
bla$_{CMY-4}$	2	0	0	0	0	0	0	0	2
bla$_{CMY-42}$	1	0	0	0	0	0	0	0	1
bla$_{CMY-141}$	1	0	0	0	0	0	0	0	1
bla$_{CMY-146}$	1	0	0	0	0	0	0	0	1
Other *bla*$_{CMY-2}$-like	0	0	0	0	1	0	0	0	1
bla$_{CMY-42}$ + $_{DHA-1}$	0	0	0	0	1	0	0	0	1
Klebsiella pneumoniae complex	444	282	227	83	212	50	52	42	1,392
Cefoxitin MIC > 8 mg/L (%)	24 (5.4)	17 (6.0)	8 (3.5)	4 (4.8)	12 (5.7)	0 (0.0)	3 (5.8)	1 (2.4)	69 (5.0)
Confirmed/number tested	6/23	1/16	1/6	1/3	1/12	0/0	0/3	0/1	10/64
bla$_{DHA-1}$	5	0	1	1	1	0	0	0	8
bla$_{CMY-6}$	0	1	0	0	0	0	0	0	1
bla$_{CMY-13}$	1	0	0	0	0	0	0	0	1

MIC = minimum inhibitory concentration

* Includes DHA-1-like (*n* = 1): 1 SNP, 721G to T (Gly to Cys)

Of cefoxitin non-wild type (MIC > 8 mg/L) isolates that did not have a plasmid-encoded *ampC* gene, one or more carbapenemase genes were detected in six of 157 (3.8%) *E. coli* (*bla*$_{IMP-5}$ [4], *bla*$_{NDM-5}$ + *bla*$_{OXA-181}$ [1], *bla*$_{IMP-4}$ [1]), and six of 54 (11.1%) *K. pneumoniae* complex (*bla*$_{IMP-4}$ [5], *bla*$_{NDM-7}$ [1]). Eleven *E. coli* with a wild type cefoxitin MIC (≤ 8 mg/L) contained pAmpC types (*bla*$_{CMY-2}$ [5], *bla*$_{CMY-4}$ [2], *bla*$_{DHA-1}$ [4]), and one *K. pneumoniae* complex with cefoxitin MIC ≤ 8 mg/L contained *bla*$_{CMY-70}$ (data not shown).

Carbapenem resistance

Only 0.4% (37/8,742) of *Enterobacterales* had a meropenem MIC > 2 mg/L; an additional 28 had meropenem MIC between 1 and 2 mg/L. Meropenem resistance (MIC > 8 mg/L) was at 4.3% (36/836) for *P. aeruginosa*, and 1.9% (2/106) for *Acinetobacter* species (Table 36).

Among meropenem-resistant (MIC >8 mg/L) isolates that were available, carbapenemase genes were found in 91.7% (22/24) of *Enterobacterales*, 2.9% (1/34) *P. aeruginosa*, and all (2/2) *Acinetobacter* species (Table 36). Carbapenemase genes were found in two *Enterobacterales* with meropenem MIC of 2 mg/L, *K. pneumoniae* (*bla*$_{NDM-1}$ + *bla*$_{OXA-181}$), and *E. coli* (*bla*$_{OXA-244}$), and one *E. coli* (*bla*$_{OXA-181}$), with MIC of 0.5 mg/L.

Table 36: Number of isolates with carbapenemase genes, organism group, meropenem MIC, AGAR, 2022

	Acinetobacter (*n* = 106)			*Enterobacterales* (*n* = 8,742)				*Pseudomonas* (*n* = 836)		
	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	104	0	2	8,677	28	12	25	749	51	36
Confirmed/number tested	0/0	–*	2/2	1/1,142	2/27	4/11	22/24	0/3	0/11	1/34
Carbapenemase type†										
Class B	0	0	0	0	0	3	22	0	0	1
bla$_{IMP-4}$	0	0	0	0	0	2	16	0	0	0
bla$_{NDM-1}$	0	0	0	0	0	0	3	0	0	1
bla$_{NDM-5}$	0	0	0	0	0	1	3	0	0	0
Class D	0	0	2	1	1	0	0	0	0	0
bla$_{OXA-23}$	0	0	2	0	0	0	0	0	0	0
bla$_{OXA-181}$	0	0	0	1	0	0	0	0	0	0
bla$_{OXA-244}$	0	0	0	0	1	0	0	0	0	0
Class B + class D	0	0	0	0	1	1	0	0	0	0
bla$_{NDM-1}$ + *bla*$_{OXA-181}$	0	0	0	0	1	0	0	0	0	0
bla$_{NDM-5}$ + *bla*$_{OXA-181}$	0	0	0	0	0	1	0	0	0	0

MIC = minimum inhibitory concentration

* not applicable
† Carbapenemase molecular class: class B (metallo-β-lactamases - IMP, NDM); class D (oxacillinases – OXA-23, OXA-181, OXA-244)

Note: No Class A carbapenemases (KPC) were detected in 2022

Thirty-two (0.3%) isolates from 31 patients were found to harbour a carbapenemase gene (Table 37). Overall prevalence of carbapenemase genes among *Enterobacterales* was 0.3% (29/8773), although for *E. cloacae* complex isolates it was 2.1% (10/477). *bla*$_{IMP-4}$ accounted for 62.1% (18/29) of all CPE in 2022. Half of the *bla*$_{IMP-4}$ genes were found in *E. cloacae* complex isolates (9/18, 50.0%). Other types detected in *Enterobacterales* were *bla*$_{NDM}$ (*n* = 7), *bla*$_{NDM}$ + *bla*$_{OXA-181}$ (*n* = 2), *bla*$_{OXA-181}$ (*n* = 1), and *bla*$_{OXA-244}$ (*n* = 1) genes.

In the 2022 survey among *Acinetobacter* species isolates only 1.6% (2/126), both *Acinetobacter baumannii* complex, harboured a carbapenemase gene; *bla*$_{OXA-23}$. Only one of 840 (0.1%) *P. aeruginosa* isolates carried a carbapenemase gene (*bla*$_{NDM-1}$).

Table 37: Carbapenemase-producing organisms, carbapenemase genes, AGAR, 2022

Species	Total	Carbapenemase type, number								
		IMP-4	NDM-1	NDM-5	OXA-23	OXA-181	OXA-244	NDM-1, OXA-181	NDM-5, OXA-181	% (*n*)
Enterobacterales	8,773	18	3	4	0	1	1	1	1	0.3 (29)
Escherichia coli	5,273	1	0	4	0	1	1	0	1	0.2 (8)
Klebsiella pneumoniae complex*	1,395	5	2	0	0	0	0	1	0	0.6 (8)
Enterobacter cloacae complex†	477	9	1	0	0	0	0	0	0	2.1 (10)
Serratia marcescens	257	3	0	0	0	0	0	0	0	1.2 (3)
Pseudomonas aeruginosa	840	0	1	0	0	0	0	0	0	0.1 (1)
Acinetobacter	126	0	0	0	2	0	0	0	0	1.6 (2)
Acinetobacter baumannii complex	70	0	0	0	2	0	0	0	0	2.8 (2)
All species	9,739	18	4	4	2	1	1	1	1	0.3 (32)

* *K. pneumoniae* (*n* = 7: bla_{IMP-4} [5], bla_{NDM-1} [1], bla_{NDM-1} + $bla_{OXA-181}$ [1]); *K. variicola* (*n* = 1: bla_{NDM-1})
† *E. hormaechei* (*n* = 9: bla_{IMP-4} [8], bla_{NDM-1} [1]); *E. cloacae* (*n* = 1, bla_{IMP-4})

Isolates carrying carbapenemase genes were detected in 18 hospitals from six states and territories. CPE infections are particularly notable in New South Wales (15/2195, 0.5%) and Victoria (7/1789, 0.4%), compared to other states and territories (Table 38). A little over one-half (10/18, 55.6%) of the hospitals had one carbapenemase-producing isolate only.

Table 38: Carbapenemase genes, organism group, state and territory, AGAR, 2022

Organism group and carbapenemase	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Total species, *n*	3,210	1,960	1,398	785	1,325	426	296	339	9,739
Acinetobacter	23	25	26	12	15	9	12	4	126
Carbapenemase, % (*n*)	0.0 (0)	0.0 (0)	3.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	8.3 (1)	0.0 (0)	1.6 (2)
bla_{OXA-23}	0	0	1	0	0	0	1	0	2
Enterobacterales	2,915	1,789	1,218	697	1,197	381	271	305	8,773
Carbapenemase, % (*n*)	0.5 (15)	0.4 (7)	0.3 (3)	0.0 (0)	0.1 (1)	0.0 (0)	0.7 (1)	0.6 (2)	0.3 (29)
bla_{IMP-4}	10	4	1	0	0	0	1	2	18
bla_{NDM-5}	2	1	0	0	1	0	0	0	4
bla_{NDM-1}	0	1	2	0	0	0	0	0	3
bla_{NDM-1} + $bla_{OXA-181}$	0	1	0	0	0	0	0	0	1
bla_{NDM-5} + $bla_{OXA-181}$	1	0	0	0	0	0	0	0	1
$bla_{OXA-181}$	1	0	0	0	0	0	0	0	1
$bla_{OXA-244}$	1	0	0	0	0	0	0	0	1
Pseudomonas aeruginosa	272	146	154	76	113	36	13	30	840
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_{NDM-1}	1	0	0	0	0	0	0	0	1
Overall prevalence, % (n)	0.5 (16)	0.4 (7)	0.3 (4)	0.0 (0)	0.1 (1)	0.0 (0)	0.7 (2)	0.6 (2)	0.3 (32)

Fluoroquinolone resistance

Multiple resistance mechanisms against quinolones have been described. Resistance is most commonly due to mutations in the quinolone resistance-determining region (QRDR) of DNA gyrase (*gyrA*, *gyrB*) and/or topoisomerase IV (*parC*, *parE*). 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 or genes coding for efflux pumps (*qepA*, *oqxAB*).[66, 67] *oqxAB* genes are intrinsic in *Klebsiella* and *Enterobacter*.

Salmonella species

Ciprofloxacin resistance (MIC > 0.06 mg/L) among non-typhoidal species was 13.4% (13/97 confirmed). For the typhoidal species, 84.2% (32/38) were resistant, comprising 28/34 (82.4%) *S*. Typhi and all *S*. Paratyphi A (*n* = 4) (Table 39).

Table 39: *Salmonella* species, ciprofloxacin minimum inhibitory concentrations, AGAR, 2022

	Ciprofloxacin minimum inhibitory concentration (mg/L)							
Organism	≤0.06	0.125	0.25	0.5	1	2	≥4	Total
Salmonella species (non-typhoidal)	84	1	1	3	3	3	2	99
Salmonella species (typhoidal)	6	0	6	8	12	0	6	36
S. Typhi	6	0	6	7	9	0	6	34
S. Paratyphi A	0	0	0	1	3	0	0	4
Total	90	1	7	11	15	3	8	135

Notes:
1. MICs 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* = 30) or codon 87 (*n* = 1), known mutations conferring quinolone resistance (refer to Appendix E1).[68]

ESBL genes were also confirmed in six *Salmonella* isolates with QRDR mutations: $bla_{\text{CTX-M-15}}$ (*n* = 3, typhoidal species) $bla_{\text{CTX-M-55}}$ (*n* = 3, non-typhoidal species).

Escherichia coli

Nationally, 17.4% (917/5,259) of *E. coli* had a ciprofloxacin MIC >0.25 mg/L, ranging from 8.2% (19/231) in Tasmania to 24.7% in the Northern Territory (42/170). A subset of 801 *E. coli* (15.2% of total) was referred and underwent WGS. This included 723 with an ESBL phenotype and 494 with ciprofloxacin MIC >0.25 mg/L (Table 40).

Table 40: *Escherichia coli*, ciprofloxacin susceptibility, ESBL phenotype, AGAR, 2022

		Ciprofloxacin MIC (mg/L)				
Subset	Phenotype	≤0.25	0.5	>0.5	Total	% of total
Total	ESBL	35.0 (265)	14.6 (111)	50.4 (382)	758	14.4
	non-ESBL	90.6 (4,077)	1.9 (85)	7.5 (339)	4,501	85.6
	Total	82.6 (4,342)	3.7 (196)	13.7 (721)	5,259	
WGS	ESBL	254	105	364	723	
	non-ESBL	53	0	25	78	
	Total	307	105	389	801	

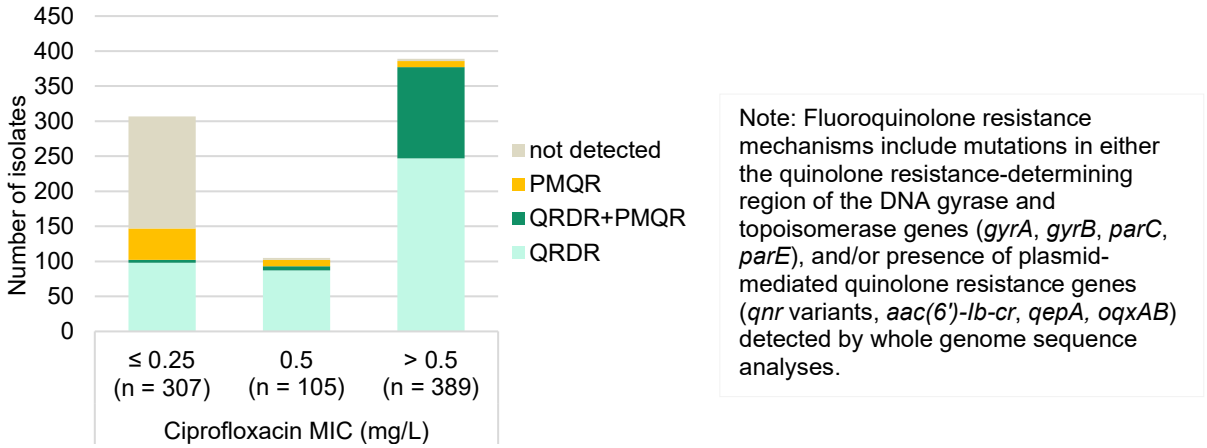
ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; n/a = not applicable; WGS = whole genome sequencing

Note: ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L.

Almost all (488/494, 98.8%) of the *E. coli* subset that had ciprofloxacin MIC > 0.25 mg/L harboured fluoroquinolone resistance determinants (Figure 13). The vast majority (93.4%, 456/488) of this group harboured a QRDR mutation in codon 83 of *gyrA*. A substantial majority (82.5%, 311/377) of isolates resistant to ciprofloxacin (MIC >0.5 mg/L) also had a second mutation in *gyrA* (codon 87), and 88.6% (334/377) showed at least one mutation in *parC* (refer to Appendix E1).

PMQR genes (*qnr* variants) alone were more common in ciprofloxacin-susceptible isolates. Of 63 *E. coli* with confirmed *qnr*, most had *qnrB* (*n* = 40, 63.5%), while some had *qnrS* (*n* = 21, 33.3%) or *qnrB* + *qnrS* (*n* = 2) (data not shown).

Figure 13: *Escherichia coli* (*n* = 801), fluoroquinolone resistance mechanisms, ciprofloxacin MIC, AGAR, 2022



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

A substantial majority (68.4%, 266/389) of the ciprofloxacin-resistant *E. coli* belonged to either ST131 (*n* = 202, 51.9%) or ST1193 (*n* = 64, 16.5%), both with reported distinguishing *parE* mutations (I529L and L416F, respectively).[69, 70]

Almost one-quarter (94/389, 24.2%) harboured *aac(6')-Ib-cr*, almost all (90/94, 95.7%) of which harboured $bla_{\text{CTX-M-15}}$ (*n* = 89) or $bla_{\text{CTX-M-65}}$ (*n* = 1) (data not shown). Just over one half (87/165, 52.7%) of the ciprofloxacin-resistant isolates with $bla_{\text{CTX-M-15}}$ belonged to the ST131-H30Rx clone (data not shown).

Klebsiella pneumoniae complex

Nationally, 9.9% (139/1,401) of *K. pneumoniae* complex isolates had a ciprofloxacin MIC >0.25 mg/L, ranging from 4.8% in South Australia (4/83) to 23.1% in the Northern Territory (12/52). A subset of 147 *K. pneumoniae* complex (10.6% of total) was referred and underwent WGS. This included 103 with an ESBL phenotype and 85 with ciprofloxacin MIC >0.25 mg/L (Table 41).

Table 41: *Klebsiella pneumoniae* complex, ciprofloxacin susceptibility, ESBL phenotype, AGAR, 2022

Subset	Phenotype	Ciprofloxacin MIC (mg/L)			Total	% of total
		≤0.25	0.5	>0.5		
Total	ESBL	26.7 (28)	11.4 (12)	61.9 (65)	105	7.5
	non-ESBL	95.3 (1,225)	1.3 (17)	3.4 (44)	1,286	92.5
	Total	90.1 (1,253)	2.1 (29)	7.8 (109)	1,391	
WGS	ESBL	27	12	64	103	
	non-ESBL	35	4	5	44	
	Total	62	16	69	147	

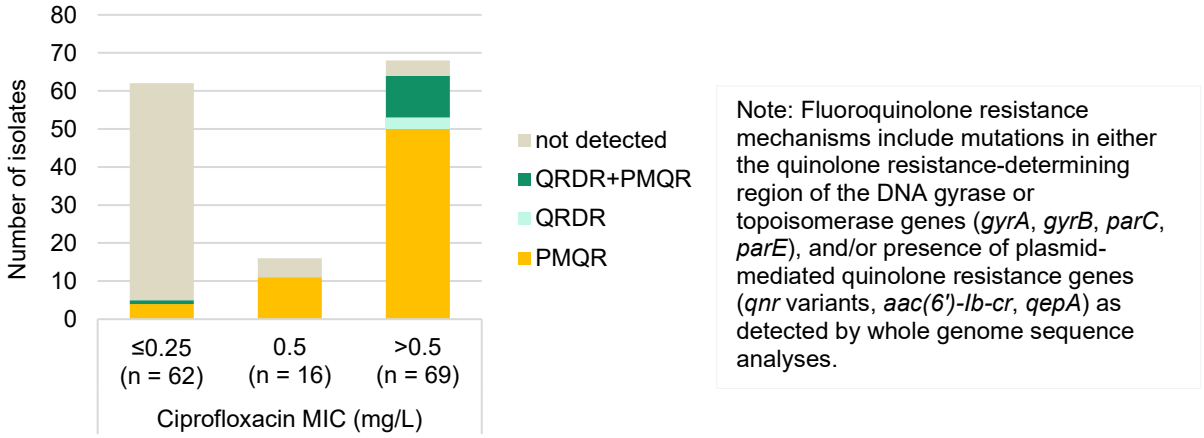
ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; n/a = not applicable; WGS = whole genome sequencing

Note: ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L.

Of the *K. pneumoniae* complex subset that had ciprofloxacin MIC > 0.25 mg/L, 89.4% (76/85) harboured fluoroquinolone resistance determinants (Figure 14) PMQR genes either alone (71.8%, 61/85) or in combination with QRDR mutations in codon 83 of *gyrA* (14.1%, 12/85) were prevalent; only 3/85 had *gyrA* mutations alone. One *K. pneumoniae* complex harboured a *parE* mutation (ciprofloxacin MIC > 0.5 mg/L (refer to Appendix Table E2).

In *K. pneumoniae* complex isolates, when PMQR genes (*qnr* variants) were found alone (39/65, 60.0%) they were usually in isolates with ciprofloxacin MIC >0.25 mg/L (37/39, 94.9%). In 39 *K. pneumoniae* complex isolates with confirmed *qnr*, most had *qnrS* (*n* = 27, 69.2%), while some had *qnrB* (*n* = 11) or *qnrA* (*n* = 1).

Figure 14: *Klebsiella pneumoniae* complex (*n* = 147), fluoroquinolone resistance mechanisms, ciprofloxacin MIC, AGAR, 2022



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

Pseudomonas aeruginosa

Of 49 *P. aeruginosa* isolates referred for sequencing eight harboured QRDR mutations, in codon 83 of *gyrA* (T83I, *n* = 6; T83A, *n* = 1). One isolate with a T83I mutation also had a second mutation in codon 87 (S87L). The ciprofloxacin MIC for all these isolates was ≥ 2 mg/L. No PMQR genes were detected.

Plasmid-mediated colistin determinants

Four *E. cloacae* complex isolates with the bla_{IMP-4} carbapenemase gene (*E. hormaechei*, *n* = 3; *E. cloacae*, *n* = 1) also harboured *mcr-9.1*.

Fourteen additional isolates (*E. cloacae* complex, *n* = 13; *K. pneumoniae*, *n* = 1) that did not carry a carbapenemase gene had either *mcr-9* (*n* = 8) or *mcr-10* (*n* = 6). *mcr-9* has recently been found among several species of *Enterobacterales*. It is not associated with a resistant phenotype[71], but is typically carried on HI2 plasmids.[72, 73]

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.[74, 75]

In the 2022 survey, three *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 all three; one *E. coli* with *rmtB1*, one *E. coli* with *armA* and one *K. pneumoniae* complex isolate with *rmtC*. All also carried a bla_{CTX-M} gene.

Two *A. baumannii* complex isolates that carried bla_{OXA-23} also harboured *armA*. One *P. aeruginosa* that carried bla_{NDM-1} also harboured *rmtB4*.

3.10. Trend analysis (2013–2022)

Trend data were available for *Enterococcus* species, *S. aureus* and *Enterobacterales,* for the ten-year period 2013 to 2022. *Acinetobacter* species and *P. aeruginosa* were introduced to the program in 2015.

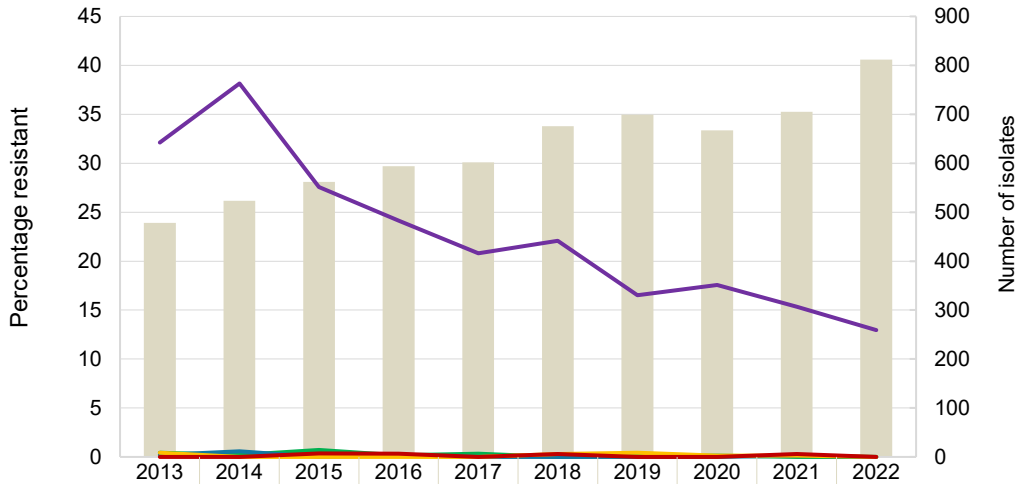
Enterococcus species

The 2022 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 2013 to 2022 are described below.

Enterococcus faecalis

National
Resistance (EUCAST) to key antimicrobial agents for *E. faecalis* over the ten-year period from 2013 to 2022 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, 2013–2022



	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Number of isolates	478	523	562	594	602	676	699	667	705	812
Gentamicin (high-level)	32.1	38.2	27.6	24.1	20.8	22.1	16.5	17.6	15.3	13.0
Vancomycin	0.4	0.2	0.7	0.2	0.3	0.0	0.1	0.2	0.0	0.0
Ampicillin	0.2	0.6	0.0	0.2	0.0	0.0	0.0	0.0	0.1	0.0
Teicoplanin	0.4	0.0	0.0	0.0	0.0	0.3	0.4	0.2	0.1	0.0
Linezolid	0.0	0.0	0.4	0.3	0.0	0.3	0.0	0.0	0.3	0.0

EUCAST = European Committee on Antimicrobial Susceptibility Testing

Notes:
1. Percentage resistance determined using EUCAST 2023 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2013 and 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.

State and territory

There were no significant changes in antimicrobial resistances among *E. faecalis* in 2022, compared to 2021.

From 2018 to 2022, there was a significant decreasing trend in high-level gentamicin resistance in Victoria (X^2 for linear trend = 7.167, $P < 0.01$), the Australian Capital Territory (X^2 for linear trend = 6.370, $P = 0.0116$), and New South Wales (X^2 for linear trend = 4.256, $P = 0.0391$) (Table 42).

Table 42: *Enterococcus faecalis*, percentage resistant to gentamicin (high-level) (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
South Australia	31.6 (19)	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)	↔
Victoria	34.0 (106)	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)**	▼
Queensland	27.6 (87)	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)	↔
Western Australia	28.2 (71)	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)	↔
Tasmania	18.2 (11)	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)	↔
New South Wales	40.0 (85)	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)	▼§
Australian Capital Territory	30.4 (23)	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)**	▼
Northern Australia	–† (6)	–† (6)	40.0 (10)	–† (7)	10.0 (10)	18.2 (11)	–† (7)	–† (5)	–† (8)	42.9 (14)	↔
Australia	32.1 (408)	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)**	▼

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P < 0.01$), ▼ ($0.01 < P < 0.05$), ↔ no significant difference

† Not applicable, insufficient numbers (<10) to calculate percentage

§ Significant trend in the overall data, which was not observed when only data from institutions consistently reporting for all five years were included

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

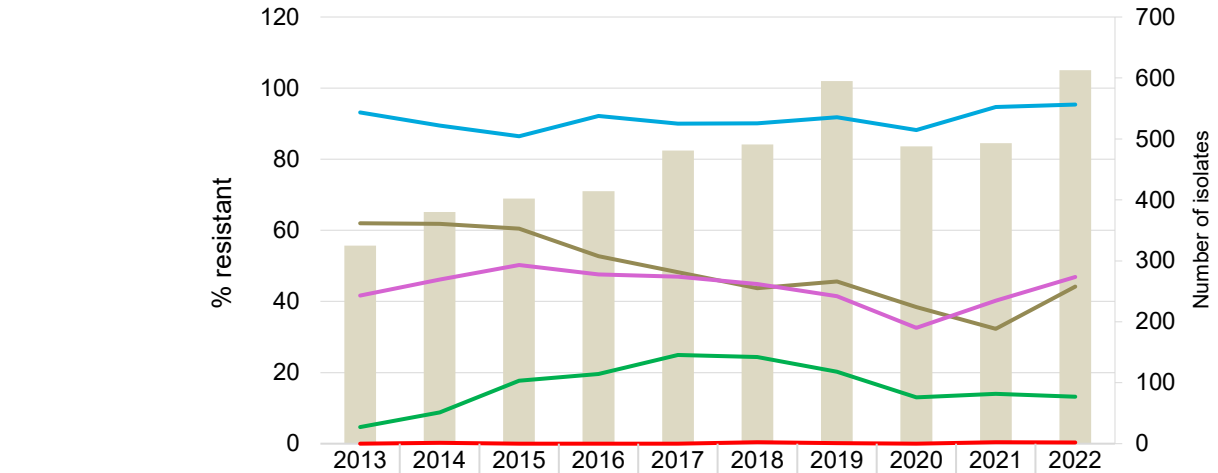
Enterococcus faecium

National

The total number of *E. faecium* isolated from patients with bacteraemia increased 17.2% in 2021 compared to 2020 (*n* = 523 in 2021; *n* = 613 in 2022) (Figure 16). There was a significant increase in the proportion of *E. faecium* isolates resistant to vancomycin (198/492, 40.2% in 2021; 285/608, 46.9% in 2022 P = 0.0280), but no significant change in teicoplanin resistance (69/492. 14.0% in 2021; 80/605, 13.2% in 2022).

There was a significant increase in the proportion of *E. faecium* isolates resistant to gentamicin (high-level) (146/452, 32.3% in 2021; 245/554, 44.2% in 2022, $P < 0.01$). The increase was seen in both vancomycin-resistant (52.0% in 2021, 64.6% in 2022, P < 0.01), and vancomycin-susceptible (19.6% in 2021, 26.8% in 2022, P = 0.0484) *E. faecium* isolates (Figure 17).

Figure 16: *Enterococcus faecium*, antimicrobial resistance (EUCAST), AGAR, 2013–2022

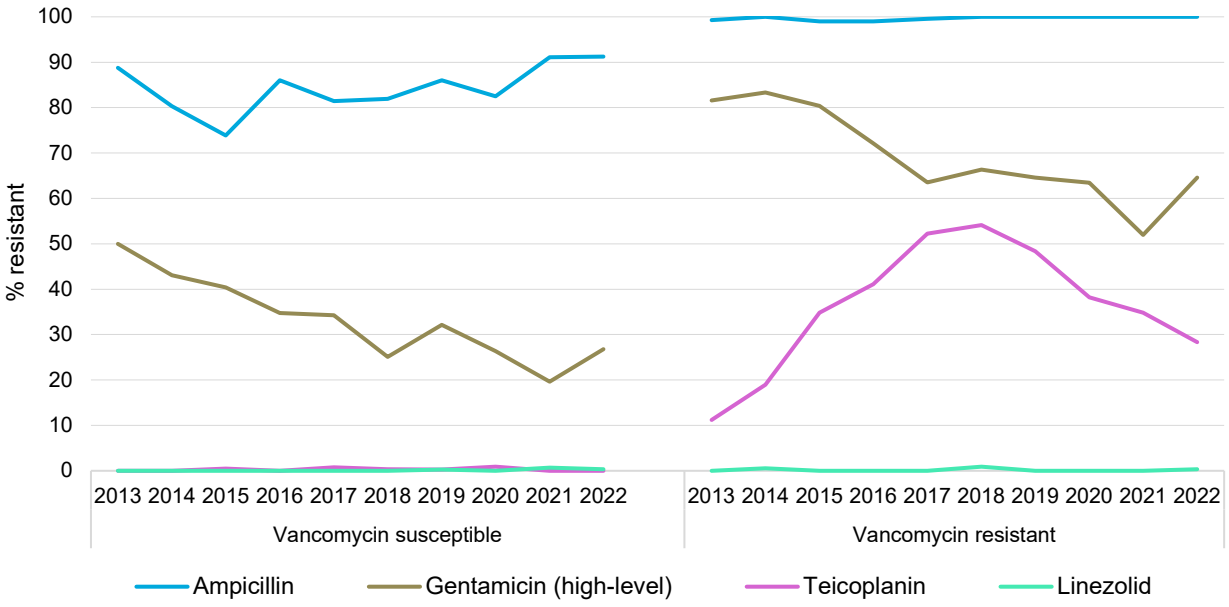


	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Total, n	325	380	402	414	481	491	595	488	493	613
Ampicillin	93.1	89.4	86.5	92.2	90.0	90.1	91.9	88.2	94.7	95.4
Gentamicin (high-level)	62.0	61.8	60.5	52.7	48.2	43.7	45.6	38.4	32.3	44.2
Vancomycin	41.7	46.2	50.2	47.6	47.0	44.9	41.5	32.6	40.2	46.9
Teicoplanin	4.7	8.8	17.7	19.6	24.9	24.4	20.2	13.0	14.0	13.2
Linezolid	0.0	0.3	0.0	0.0	0.0	0.4	0.2	0.0	0.4	0.3

EUCAST = European Committee on Antimicrobial Susceptibility Testing

Notes:
1. Percentage resistance determined using EUCAST 2023 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2013 and 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.

Figure 17: *Enterococcus faecium,* antimicrobial resistance (EUCAST), by vancomycin susceptibility, AGAR, 2013–2022



EUCAST = European Committee on Antimicrobial Susceptibility Testing

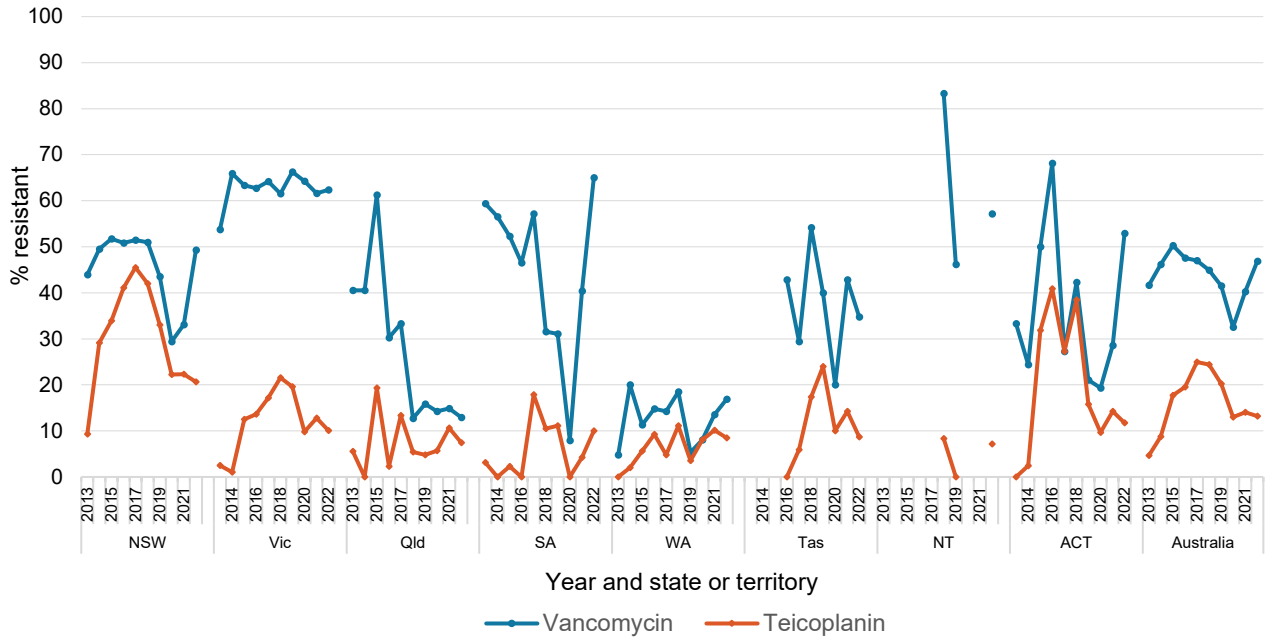
Notes:
1. Percentage resistance determined using EUCAST 2023 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2013 and 2014; *n* = 43 in 2015; *n* = 44 in 2016; *n* = 48 in 2017 and 2018; *n* = 51 in 2019, 2020 and 2021; *n* = 55 in 2022.

State and territory

The proportion of glycoside-resistant *E. faecium* by state and territory is shown in Figure 18. There was an increase in the proportion of vancomycin-resistant *E. faecium* in New South Wales (46/139, 33.1% in 2021; 104/211, 49.3% in 2022, $P < 0.01$), and South Australia (19/47, 40.0% in 2021; 26/40, 65.0% in 2022, $P < 0.0312$). There was little change in teicoplanin resistance in *E. faecium* in 2022 compared to 2021.

The overall increase in high-level gentamicin resistance in *E. faecium* isolates (32.3% in 2021, 44.2% in 2022) (Figure 16) was most notable in New South Wales (49/134, 36.6% in 2021; 123/210, 58.6% in 2022, $P < 0.01$), and South Australia (12/46, 26.1% in 2021; 19/39, 48.7% in 2022, $P < 0.0421$) (data not shown).

Figure 18: *Enterococcus faecium*, glycopeptide resistance (EUCAST), by state and territory, and nationally, AGAR, 2013–2022



Notes:

1. Percentage resistance determined using EUCAST 2023 breakpoints for all years.
2. Number of contributors per year: *n* = 27 in 2013 and 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.
3. Insufficient numbers (<10) to calculate percentage for Tasmania (2013–2015) and the Northern Territory (2013–2017, 2020, 2021).

Over the past five years (2018–2022), the only significant trend in vancomycin resistance in *E. faecium* was an increasing trend in South Australia (X^2 for linear trend = 10.29, $P < 0.01$) (Table 43). Over the same period, teicoplanin resistance in *E. faecium* decreased significantly nationally (X^2 for linear trend = 29.94, $P < 0.01$); notably in New South Wales (X^2 for linear trend = 23.11, $P < 0.01$), Victoria (X^2 for linear trend = 10.57, $P < 0.01$); and the Australian Capital Territory (X^2 for linear trend = 5.306, $P = 0.0213$) (Table 44).

Table 43: *Enterococcus faecium*, percentage resistant to vancomycin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Queensland	40.5 (37)	40.5 (37)	61.3 (31)	69.8 (43)	33.3 (45)	12.7 (55)	15.9 (63)	14.3 (35)	14.9 (47)	13.0 (54)	↔
Western Australia	4.8 (42)	20.0 (50)	11.3 (53)	85.2 (54)	14.3 (63)	18.5 (54)	5.4 (56)	8.1 (62)	13.6 (59)	16.9 (71)	↔
Tasmania	–† (5)	–† (7)	–† (8)	57.1 (14)	29.4 (17)	54.2 (24)	40.0 (25)	20.0 (10)	42.9 (14)	34.8 (23)	↔
New South Wales	43.9 (107)	49.5 (103)	51.7 (116)	49.2 (124)	51.5 (167)	51.0 (151)	43.5 (209)	29.4 (180)	33.1 (139)	49.3 (211)	↔
Australian Capital Territory	33.3 (18)	24.4 (41)	50.0 (22)	31.8 (22)	27.3 (22)	42.3 (26)	21.1 (19)	19.4 (31)	28.6 (14)	52.9 (17)	↔
Northern Territory	–† (3)	–† (1)	–† (8)	–† (4)	–† (5)	83.3 (12)	46.2 (13)	–† (6)	–† (8)	57.1 (14)	↔
Victoria	53.8 (80)	66.0 (94)	63.3 (120)	37.3 (110)	64.2 (134)	61.5 (130)	66.3 (163)	64.2 (123)	61.6 (164)	62.4 (178)	↔
South Australia	59.4 (32)	56.5 (46)	52.3 (44)	53.5 (43)	57.1 (28)	**31.6 (38)**	**31.1 (45)**	**7.9 (38)**	**40.4 (47)**	**65.0 (40)**	▲
Australia	41.7 (324)	46.2 (379)	50.2 (402)	52.4 (414)	47.0 (481)	44.9 (490)	41.5 (593)	32.6 (485)	40.2 (492)	46.9 (608)	↔

* Chi-square test for trend for past five years (2018–2022), bold text significant increase ▲ ($P < 0.01$), ↔ no significant difference
† Not applicable, insufficient numbers (<10) to calculate percentage

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

Table 44: *Enterococcus faecium*, percentage resistant to teicoplanin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Northern Territory	–† (3)	–† (1)	–† (8)	–† (4)	–† (5)	8.3 (12)	0.0 (13)	–† (6)	–† (8)	7.1 (14)	↔
Queensland	5.6 (36)	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)	↔
Western Australia	0.0 (42)	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)	↔
Tasmania	–† (5)	–† (7)	–† (8)	0.0 (14)	5.9 (17)	17.4 (23)	24.0 (25)	10.0 (10)	14.3 (14)	8.7 (23)	↔
South Australia	3.1 (32)	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)	↔
Victoria	2.5 (80)	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)**	▼
Australian Capital Territory	0.0 (16)	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)**	▼
New South Wales	9.3 (107)	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)**	▼§
Australia	4.7 (321)	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)**	▼

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P < 0.01$), ↔ no significant difference
† Not applicable, insufficient numbers (<10) to calculate percentage
§ Significant trend in the overall data, which was not observed when only data from hospitals consistently reporting for all five years (2018–2022) were included

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

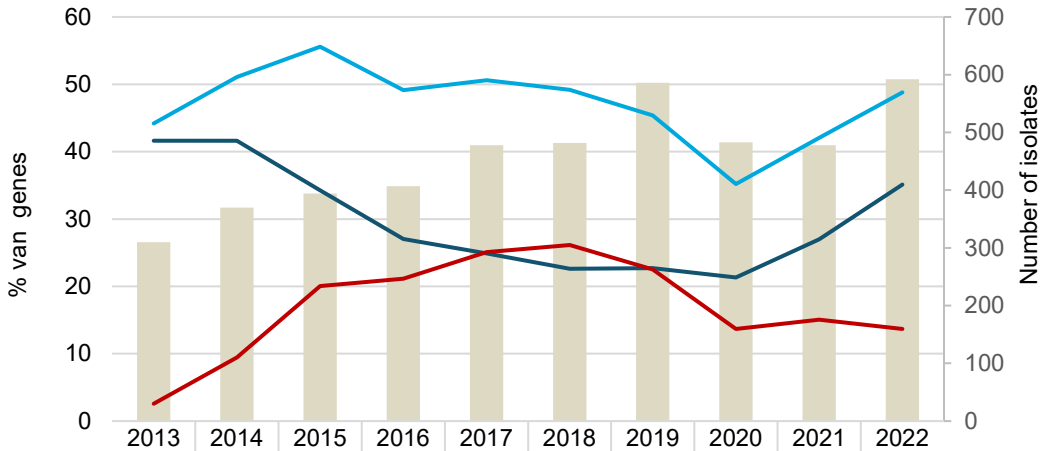
Glycopeptide-resistance and *van* genes in *Enterococcus faecium*

National

In 2022, glycopeptide resistance in *E. faecium* was predominantly due to *vanB* genes. Overall, the proportion of *vanB E. faecium* increased from 27.0% in 2021 to 35.1% in 2022 (P < 0.01), and the proportion of *vanA E. faecium* remained stable (Figure 19).

Over the past five-years (2018-2022), there was a significantly increasing trend in the proportion of *E. faecium* with *vanB* genes (X^2 for linear trend = 26.36, $P < 0.01$), and a significantly decreasing trend in the proportion of *vanA* genes (X^2 for linear trend = 36.41, $P < 0.01$).

Figure 19: Ten-year trend in percent *Enterococcus faecium* with *van* genes, AGAR, 2013–2022



	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
E. faecium, n	310	370	394	407	478	482	586	483	478	592
Any van gene, %	44.2	51.1	55.6	49.1	50.6	49.2	45.4	35.2	42.1	48.8
vanB, %	41.6	41.6	34.3	27.0	24.9	22.6	22.7	21.3	27.0	35.1
vanA,%	2.6	9.5	20.1	21.1	25.1	26.1	22.5	13.7	15.1	13.7

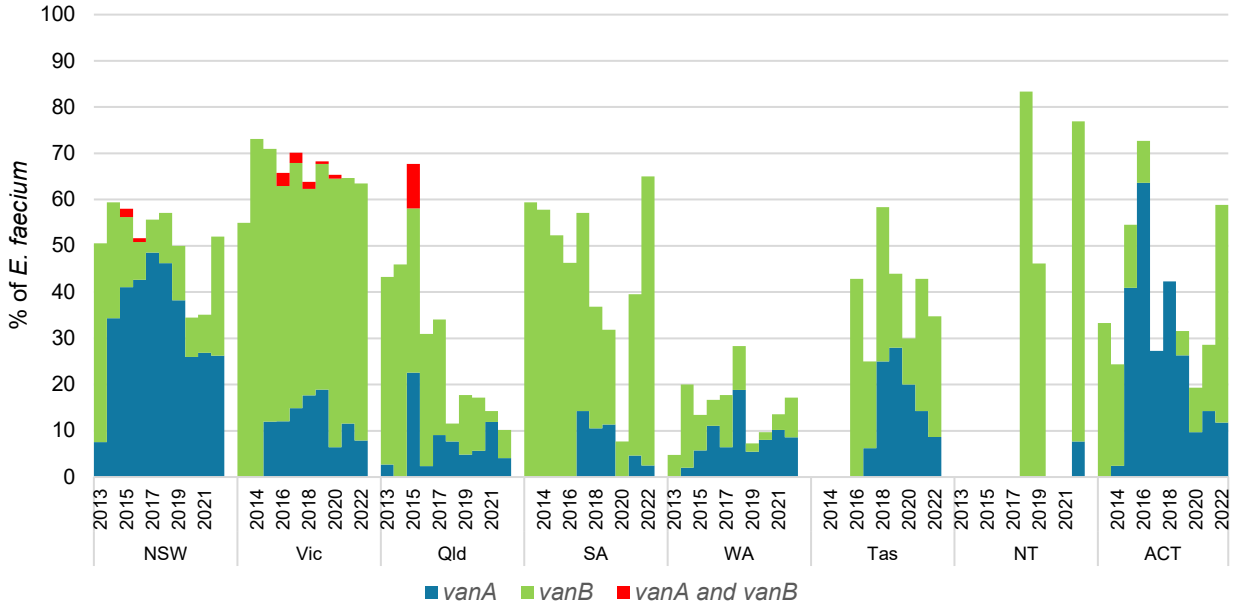
State and territory

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

In 2022, there was a notable increase in *vanB E. faecium* in NSW (11/134, 8.2% in 2021; 52/205, 25.7% in 2022, $P < 0.01$) (note one hospital did not participate in 2021), and South Australia (15/43, 34.9% in 2021; 25/40, 62.5% in 2022, $P = 0.0159$).

Over the past five-years (2018-2022), there was a significantly increasing trend in the proportion of *E. faecium* with *vanB* genes, notably in South Australia (X^2 for linear trend = 14.59, $P < 0.01$), New South Wales (X^2 for linear trend = 14.03, $P < 0.01$) and Victoria (X^2 for linear trend = 3.933, $P = 0.0473$). Over the same period, there was a significantly decreasing trend in the proportion of *vanA* genes in New South Wales (X^2 for linear trend = 19.01, $P < 0.01$), Victoria (X^2 for linear trend = 10.42, $P < 0.01$) and the Australian Capital Territory (X^2 for linear trend = 7.636, $P < 0.01$).

Figure 20: Proportion of *van* genes in *Enterococcus faecium* by state and territory, AGAR, 2013–2022



Note: Insufficient number of *E. faecium* isolates (<10) to calculate percentage for Tasmania 2013-2015) and the Northern Territory (2013-2017, 2020, 2021).

Staphylococcus aureus

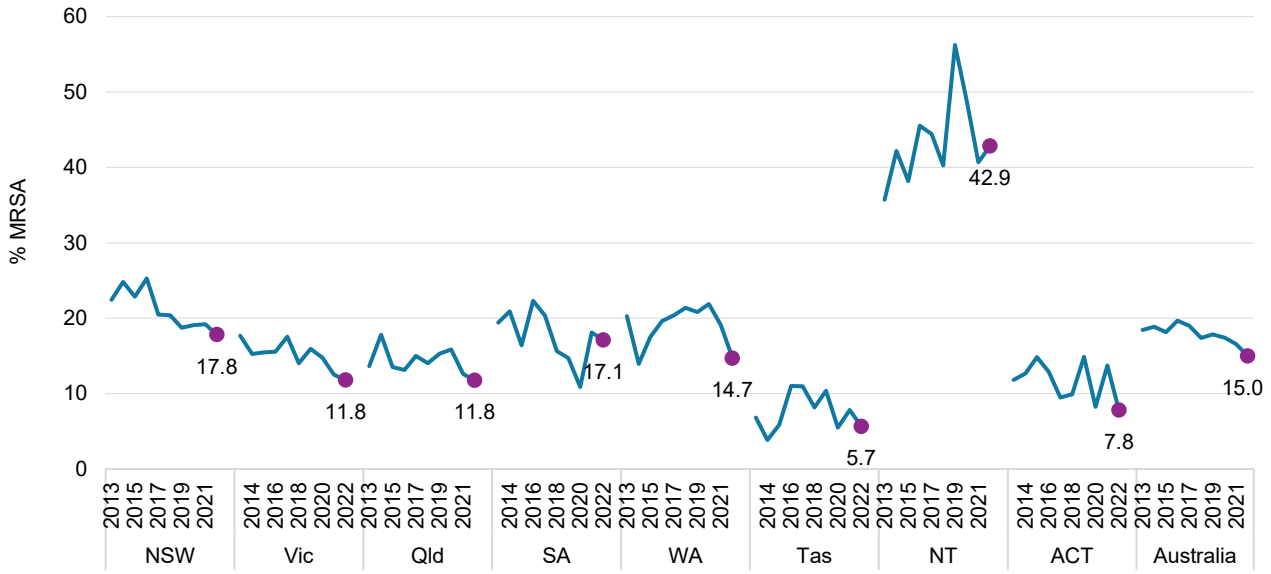
A primary objective of the ASSOP 2022 survey was to determine the proportion of SAB isolates demonstrating resistance to methicillin and other important anti-staphylococcal agents. The following sections describe the major trends observed for the period 2013 to 2022.

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 2021, there were no significant differences in the proportion of MRSA in the states and territories.

From 2018 to 2022, there was a significantly decreasing trend in MRSA in Australia (X^2 for linear trend = 8.677, $P < 0.01$), notably in Western Australia ((X^2 for linear trend = 7.168, $P < 0.01$) (Table 45).

Figure 21: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, AGAR, 2013–2022



MRSA = methicillin-resistant *Staphylococcus aureus*

Notes:

1. Percentage resistance determined using EUCAST 2023 breakpoints for all years. Filled circles indicate values for 2022.
2. Number of contributors per year: *n* = 27 in 2013 and 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.

Table 45: *Staphylococcus aureus*, percentage resistant to methicillin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

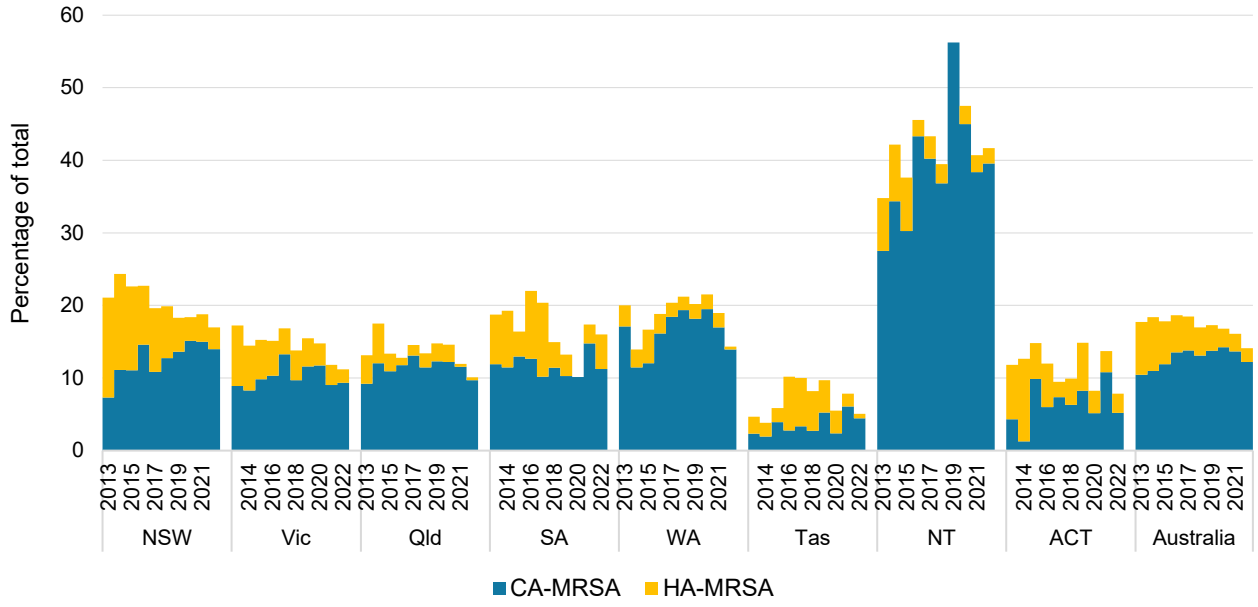
	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tasmania	6.8 (44)	3.8 (52)	5.9 (51)	11.0 (109)	11.0 (91)	8.2 (110)	10.4 (135)	5.5 (127)	7.8 (115)	5.7 (159)	↔
Australian Capital Territory	11.8 (93)	12.7 (79)	14.8 (81)	12.9 (101)	9.5 (95)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

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P < 0.01$), ↔ no significant difference

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

Since 2013, there were significant increases in the proportion of CA-MRSA clones nationally (X^2 for linear trend = 8.729, $P < 0.01$); notably in New South Wales (Figure 22). The proportion of HA-MRSA clones declined nationally (X^2 for linear trend = 190.1, $P < 0.01$), in all states and territories with the exception of Tasmania.

Figure 22: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory and association, AGAR, 2013–2022

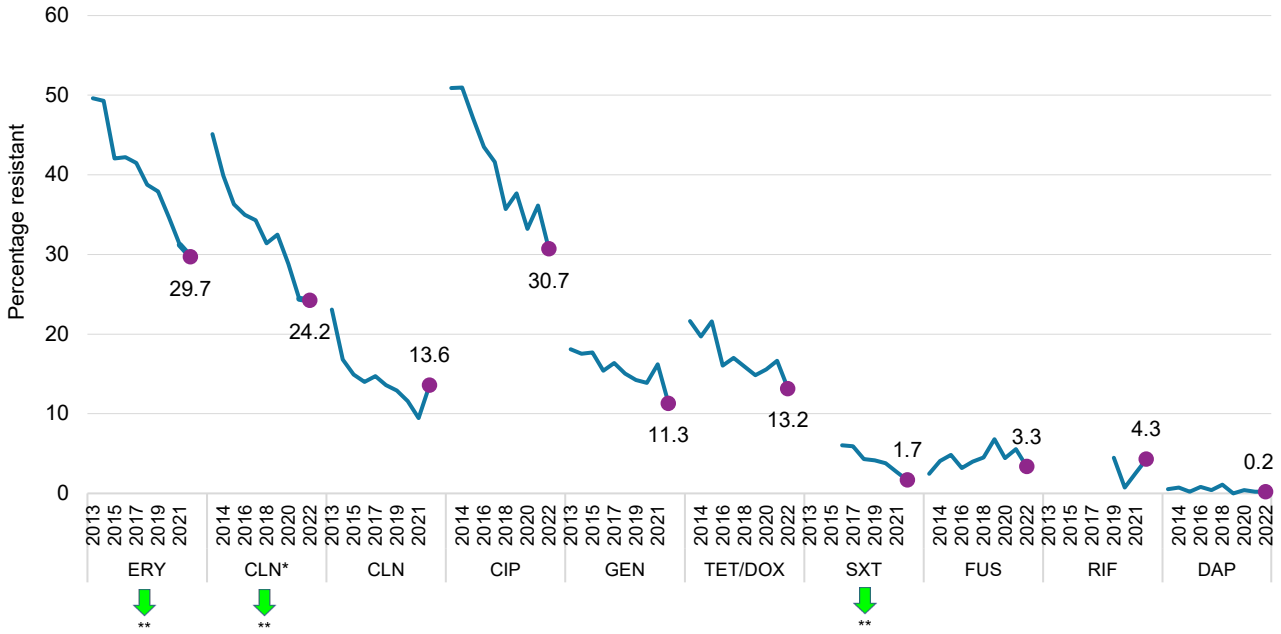


MRSA = methicillin-resistant *Staphylococcus aureus*; CA-MRSA = community-associated MRSA; HA-MRSA = healthcare-associated MRSA

Relative to 2021, the percentage resistance to antimicrobial agents tested against MRSA in 2022 remained stable, except for gentamicin (16.2% 2021, 11.3% in 2022, $P = 0.0315$).

Rates of resistance in MRSA from 2018 to 2022 decreased for erythromycin (χ^2 for linear trend = 13.22, $P = < 0.01$), clindamycin (inducible + constitutive resistance [χ^2 for linear trend = 12.37, $P < 0.01$], and trimethoprim–sulfamethoxazole (χ^2 for linear trend = 6.815, $P < 0.01$) (Figure 23).

Figure 23: Methicillin-resistant *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



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

Notes:

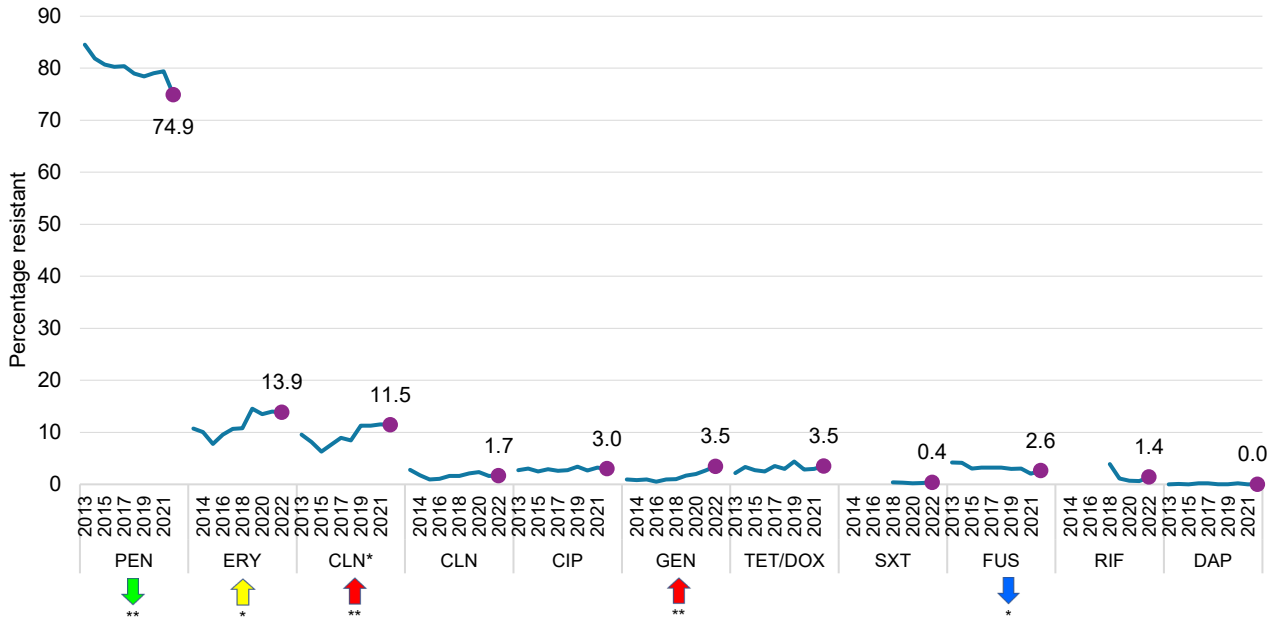
1. Percentage resistance determined using EUCAST 2023 breakpoints for all years
2. Down arrows indicate antimicrobial agents with significant decrease ↓** ($P < 0.01$) over the past five years (2018–2022).
3. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek® or Phoenix™) was not confirmed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

Methicillin-susceptible *Staphylococcus aureus*

The percentage resistance for MSSA in 2022 was similar to 2021 for the antimicrobial agents tested, except for benzylpenicillin (79.4% in 2021, 74.9% in 2022, $P < 0.01$) (Figure 24).

Rates of resistance in MSSA over the past five years increased for gentamicin (χ^2 for linear trend = 39.18, $P < 0.01$); clindamycin (inducible + constitutive) (χ^2 for linear trend = 8.811, $P < 0.01$) and erythromycin (χ^2 for linear trend = 5.278, $P = 0.0216$), and decreased for benzylpenicillin (χ^2 for linear trend = 8.632, $P < 0.01$) and fusidic acid (χ^2 for linear trend = 3.874, $P = 0.0491$) (Figure 24).

Figure 24: Methicillin-susceptible *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



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

Notes:

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

Gram-negative species

The following sections describe the major trends observed for key gram-negative species for the period 2013 to 2022.

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.

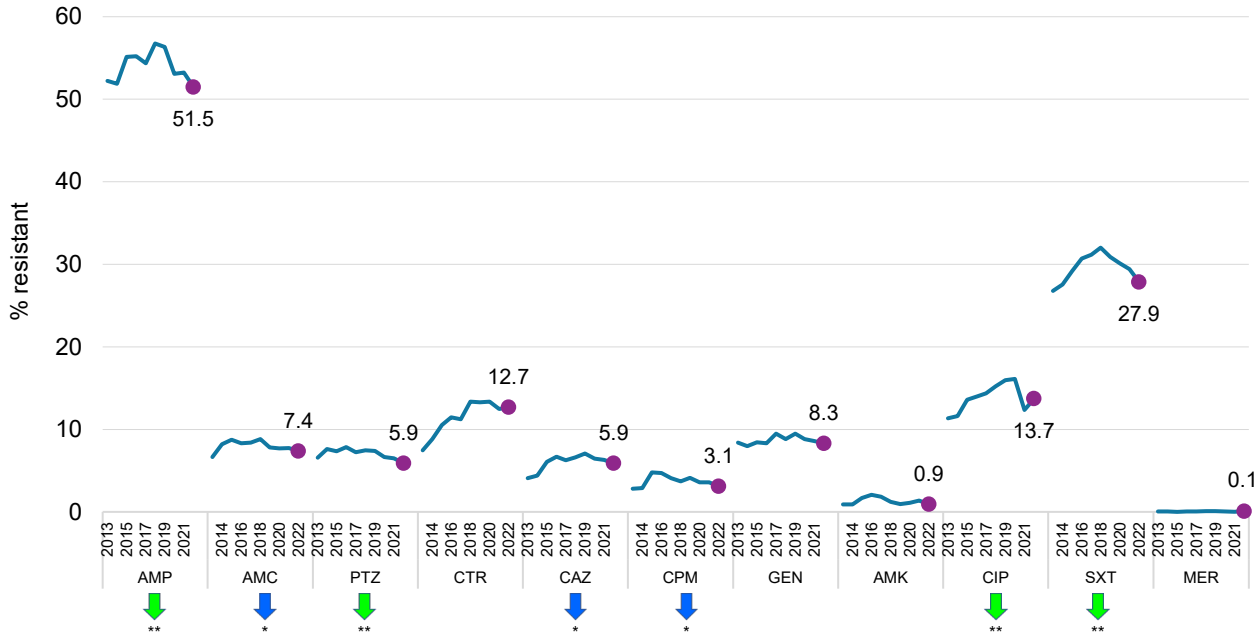
Escherichia coli

National

The percentage of resistant *E. coli* in 2022 was similar to 2021 for all antimicrobial agents tested, except for ciprofloxacin, where a 11.1% increase in resistance was seen relative to 2021 (606/4910, 12.3% in 2021, 721/5259, 13.7% in 2022; $P = 0.0421$) (Figure 25).

Rates of resistance to key antimicrobial agents over the past five years (2018–2022) decreased for ampicillin (X^2 for linear trend = 36.82, $P < 0.01$), trimethoprim–sulfamethoxazole (X^2 for linear trend = 22.48, $P < 0.01$), ciprofloxacin (X^2 for linear trend = 17.47, $P < 0.01$), and piperacillin–tazobactam (X^2 for linear trend = 12.91, $P < 0.01$) (Figure 25).

Figure 25: *Escherichia coli* resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



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 2023 breakpoints for all years. Numbers adjacent to filled circles are those for 2022.
2. Number of contributors per year: $n = 24$ in 2013; $n = 26$ in 2014; $n = 44$ in 2015 and 2016; $n = 48$ in 2017 and 2018; $n = 51$ in 2019, 2020 and 2021; $n = 20$ in 2021; $n = 55$ in 2022.
3. Down arrows indicate antimicrobial agents for which there was a significant decrease in resistance over the past five years (2018 and 2022), ↓** ($P < 0.01$); ↓* ($0.01 < P < 0.05$).

By state and territory

In 2022, ciprofloxacin resistance in *E. coli* increased in three states and territories relative to 2021, most notably in New South Wales (2021, 12.1%; 2022, 16.4%, up 35.4%, $P < 0.01$) and South Australia (2021, 8.5%; 2022, 14.6%, up 71.3%, $P < 0.01$) (Table 46). There was an increase in third-generation cephalosporin resistance in the Northern Territory (2021, 13.4%; 2022, 28.8%, up 115%, $P < 0.01$) (Table 47), and an increase in aminoglycoside resistance in South Australia (2021, 8.1%; 2022, 12.3%, up 52.5%, $P = 0.0368$) (Table 48).

There were significantly decreasing trends in ciprofloxacin resistance in *E. coli* over the past five years (2018-2022) in Victoria (X^2 for linear trend = 17.05, $P = <0.01$), Western Australian (X^2 for linear trend = 10.45, $P = 0.0012$) and the Australian Capital Territory (X^2 for linear trend = 7.438, $P = 0.0064$) (Table 46).

Over the past five years (2018-2022), Victoria was the only state with significantly decreasing trends in third-generation cephalosporin (X^2 for linear trend = 16.91, $P < 0.01$) (Table 47), and aminoglycoside (X^2 for linear trend = 19.74, $P < 0.01$) resistance in *E. coli* isolates (Table 48).

Table 46: *Escherichia coli*, percentage resistant to ciprofloxacin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	6.3 (79)	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)	↔
Qld	8.1 (652)	7.1 (742)	8.7 (691)	9.0 (811)	12.9 (858)	10.3 (868)	10.4 (817)	11.6 (628)	8.6 (686)	10.0 (711)	↔
ACT	13.6 (118)	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)	▼**
Vic	11.7 (530)	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)	▼**
WA	13.9 (524)	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)	▼**
SA	10.6 (379)	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)	↔
NT	10.3 (78)	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)	↔
NSW	13.2 (555)	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)	↔
Australia	11.3 (2,915)	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** (4,910)	**13.7** (5,259)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P < 0.01$, **), ↔ no significant difference

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

Table 47: *Escherichia coli*, percentage resistant to ceftriaxone and/or ceftazidime (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	1.3 (80)	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)	↔
Qld	5.4 (652)	7.1 (742)	6.1 (691)	8.1 (811)	9.4 (858)	11.5 (868)	8.4 (817)	8.9 (628)	10.6 (686)	11.0 (711)	↔
Vic	11.1 (530)	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)	▼**
WA	6.3 (524)	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)	↔
SA	5.5 (379)	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)	↔
NSW	11.2 (555)	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 (1,281)	14.6 (1,771)	↔
ACT	5.1 (118)	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)	↔
NT	9.0 (78)	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)	↔
Australia	7.7 (2,916)	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 (4,913)	13.1 (5,261)	↔

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P < 0.01$, **), ↔ no significant difference

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

Table 48: *Escherichia coli*, percentage resistant to gentamicin and/or tobramycin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	2.5 (80)	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)	↔
Vic	11.9 (530)	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)	▼**
ACT	14.4 (118)	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)	↔
Qld	7.2 (652)	8.1 (742)	7.7 (691)	8.1 (811)	9.7 (858)	7.7 (868)	8.4 (817)	8.3 (628)	7.6 (686)	7.5 (711)	↔
WA	9.2 (524)	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)	↔
NSW	11.0 (555)	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)	↔
SA	6.9 (378)	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)	↔
NT	14.1 (78)	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)	↔
Australia	9.4 (2,915)	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)	9.3 (4,913)	8.9 (5,259)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P<0.01$, **), ↔ no significant difference

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

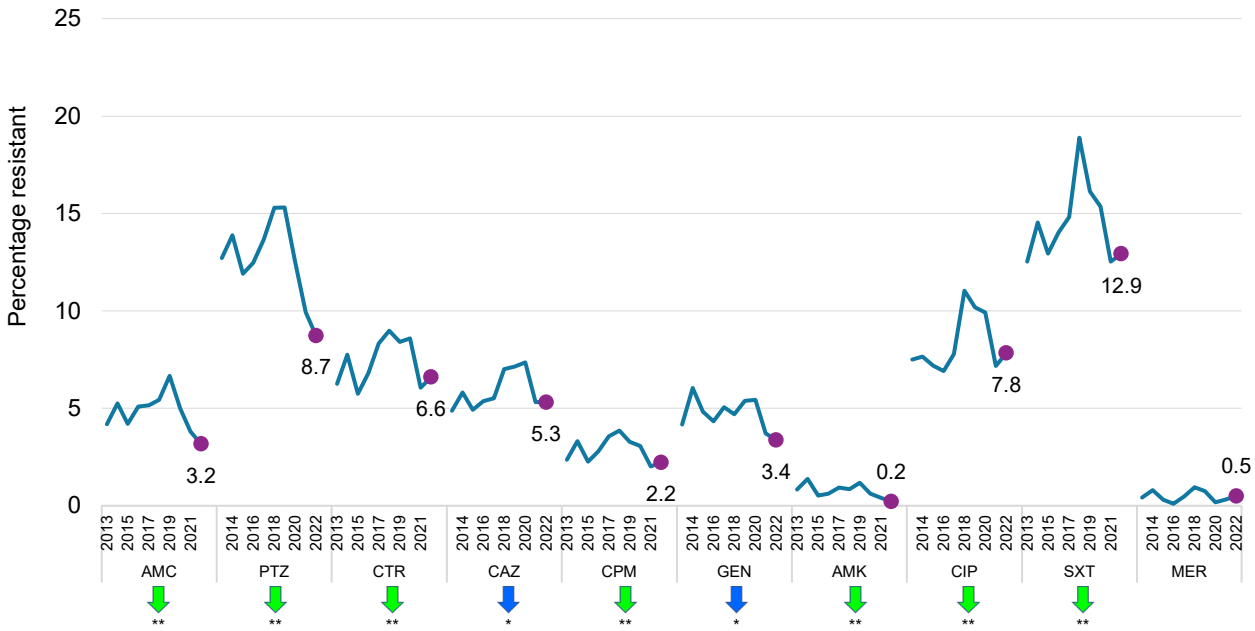
Klebsiella pneumoniae complex

National

The percentage of resistance among *K. pneumoniae* complex isolates in 2022 was similar to that seen in 2021 (Figure 26).

Over the past five years (2018–2022), there was a significant decreasing trend in resistance to piperacillin-tazobactam (X^2 for linear trend = 40.27, $P < 0.01$), amoxicillin–clavulanic acid (X^2 for linear trend = 13.66, $P < 0.01$), trimethoprim–sulfamethoxazole (X^2 for linear trend = 23.00, $P < 0.01$), ciprofloxacin (X^2 for linear trend = 13.08, $P < 0.01$), cefepime (X^2 for linear trend = 8.994, $P < 0.01$), ceftriaxone (X^2 for linear trend = 8.848, $P < 0.01$), and amikacin (X^2 for linear trend = 8.553, $P < 0.01$) (Figure 26).

Figure 26: *Klebsiella pneumoniae* complex resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



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 2023 breakpoints for all years. Numbers adjacent to filled circles are those for 2022.
2. Number of contributors per year: *n* = 24 in 2013; *n* = 26 in 2014; *n* = 44 in 2015 and 2016; *n* = 48 in 2017 and 2018; *n* = 51 in 2019, 2020 and 2021; *n* = 20 in 2021; *n* = 55 in 2022.
3. Down arrows indicate antimicrobial agents for which there was a significant decrease in resistance over the past five years (2018 and 2022), ↓** ($P < 0.01$); ↓* ($0.01 < P < 0.05$).

By state and territory

Four states and territories (Western Australia, Tasmania, Northern Territory and the Australian Capital Territory) had an increase in fluoroquinolone (Table 49), third-generation cephalosporin (Table 50), and aminoglycoside resistance (Table 51) in *K. pneumoniae* complex isolates in 2022, relative to 2021. The only notable change was a decline in fluoroquinolone resistance in South Australia (2021, 9.6%; 2022, 2.4%; down 75.0%; $P = 0.047$).

Over the past five years (2018-2022), Victoria was the only state with significantly decreasing trends in fluoroquinolone (X^2 for linear trend = 37.54, $P < 0.01$), third generation cephalosporin (X^2 for linear trend = 30.99, $P < 0.01$), and aminoglycoside (X^2 for linear trend = 43.07, $P < 0.01$) resistance in *K. pneumoniae* complex isolates (Tables 49-51).

Table 49: *Klebsiella pneumoniae* complex, percentage resistant to ciprofloxacin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
SA	13.3 (75)	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)	↔
Qld	5.8 (207)	5.3 (208)	6.3 (189)	4.2 (189)	6.1 (246)	5.6 (270)	5.2 (249)	6.5 (185)	8.0 (201)	5.7 (227)	↔
Vic	12.4 (145)	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)	▼**
Tas	7.1 (14)	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)	↔
NSW	3.5 (113)	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)	↔
WA	4.8 (124)	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)	↔
ACT	4.5 (22)	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)	↔
NT	10.5 (19)	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)	↔
Australia	7.5 (719)	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)	**7.2** (1,239)	**7.8** (1,391)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P<0.01$, **), ↔ no significant difference

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

Table 50: *Klebsiella pneumoniae* complex, percentage resistant to ceftriaxone and/or ceftazidime (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Qld	6.3 (207)	4.3 (208)	3.7 (189)	3.7 (189)	3.3 (246)	5.9 (270)	4.4 (249)	3.8 (185)	2.5 (201)	3.5 (227)	↔
SA	2.7 (75)	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)	↔
WA	4.0 (124)	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)	↔
Vic	13.1 (145)	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)	▼**
Tas	7.1 (14)	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)	↔
NSW	2.7 (113)	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)	↔
ACT	0.0 (22)	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)	↔
NT	15.8 (19)	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)	↔
Australia	6.4 (719)	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** (1,239)	**6.9** (1,392)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ (P<0.01, **), ↔ no significant difference

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

Table 51: *Klebsiella pneumoniae* complex, percentage resistant to gentamicin and/or tobramycin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	7.1 (14)	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)	↔
Qld	3.9 (207)	4.3 (208)	4.2 (189)	3.7 (189)	3.3 (246)	3.0 (270)	2.4 (249)	2.7 (185)	3.5 (201)	2.2 (227)	↔
SA	5.3 (75)	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)	↔
WA	3.2 (124)	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)	↔
Vic	11.0 (145)	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)	▼**
NSW	2.7 (113)	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)	↔
ACT	0.0 (22)	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)	↔
NT	15.8 (19)	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)	↔
Australia	5.4 (719)	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** (1,239)	**4.5** (1,392)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ (P<0.01, **), ↔ no significant difference

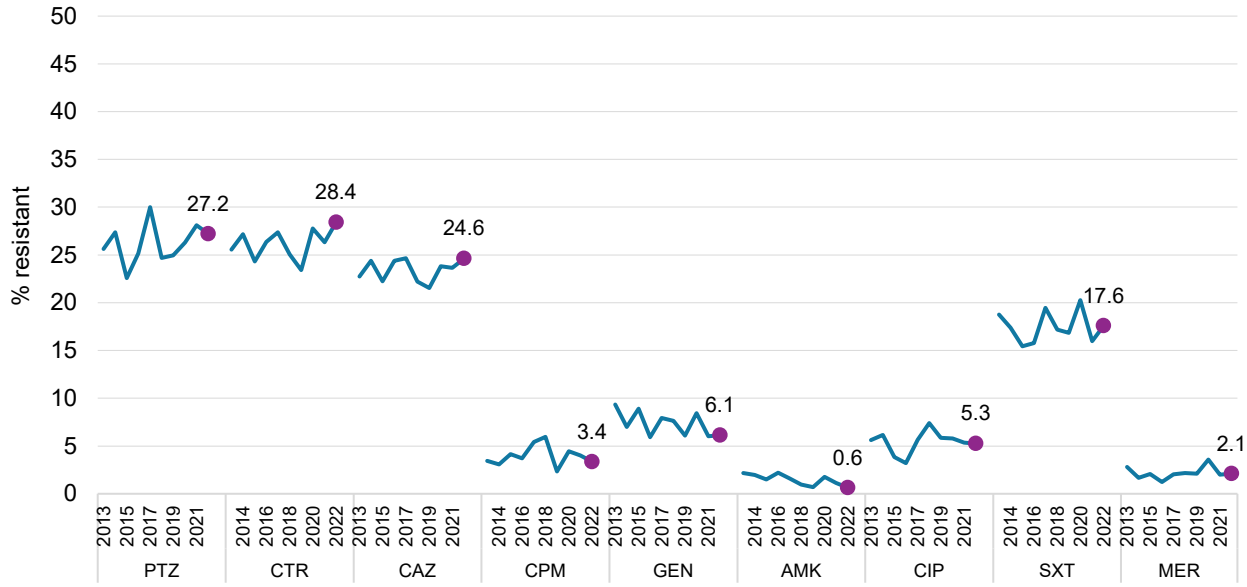
Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years

Enterobacter cloacae complex

National

For *E. cloacae* complex isolates, the percentage resistance to all key antimicrobials in 2022 was similar to 2021. There were no significant trends of increasing or decreasing resistance in *E. cloacae* complex isolates over the five-year period (2018–2022) (Figure 27).

Figure 27: *Enterobacter cloacae* complex resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



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

Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years. Filled circles indicate values for 2022.

Extended-spectrum β-lactamases

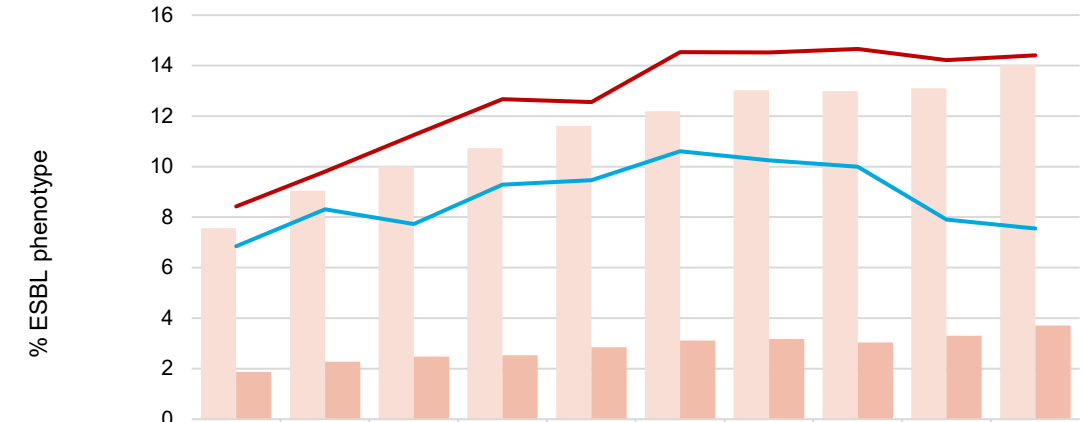
The frequency of *E. coli* with an ESBL phenotype increased from 8.4% in 2013 to 14.5% in 2018 and has remained at steady at 14% since 2019 (Figure 28). For *K. pneumoniae* complex isolates, the frequency of ESBL phenotypes was lower than that observed among *E. coli* and increased from 6.8% in 2013 to 10% in 2018 to 2020, decreasing to 7.9% in 2021 and 7.5% in 2022.

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 2022 survey, there was little change in the proportion of *E. coli* with confirmed ESBL genes relative to 2021 (2021: 524/4873, 10.8%; 2022: 581/5226, 11.1%). However, in the Northern Territory, the proportion of confirmed ESBL genes doubled (2021,12.9%; 2022, 27.2%, $P < 0.01$) (Figure 29). In *K. pneumoniae* complex isolates, the proportion of confirmed ESBL genes overall in 2022 increased by 24.7% relative to 2021 (2021: 57/1235, 4.6%; 2022: 80/1390, 5.8%) (Figure 30).

Over the past five years (2018-2022), a significantly decreasing trend ($P < 0.01$) in the proportion of *E. coli* (X_2 for linear trend = 10.39) (Figure 29), and *K. pneumoniae* complex isolates (X_2 for linear trend = 21.95) with confirmed ESBL-genes was seen in Victoria (Figure 30). Over the same period, there was an increasing trend seen in the proportion of *E. coli* with confirmed ESBL-genes in the Northern Territory (X_2 for linear trend = 4.143, $P = 0.0418$).

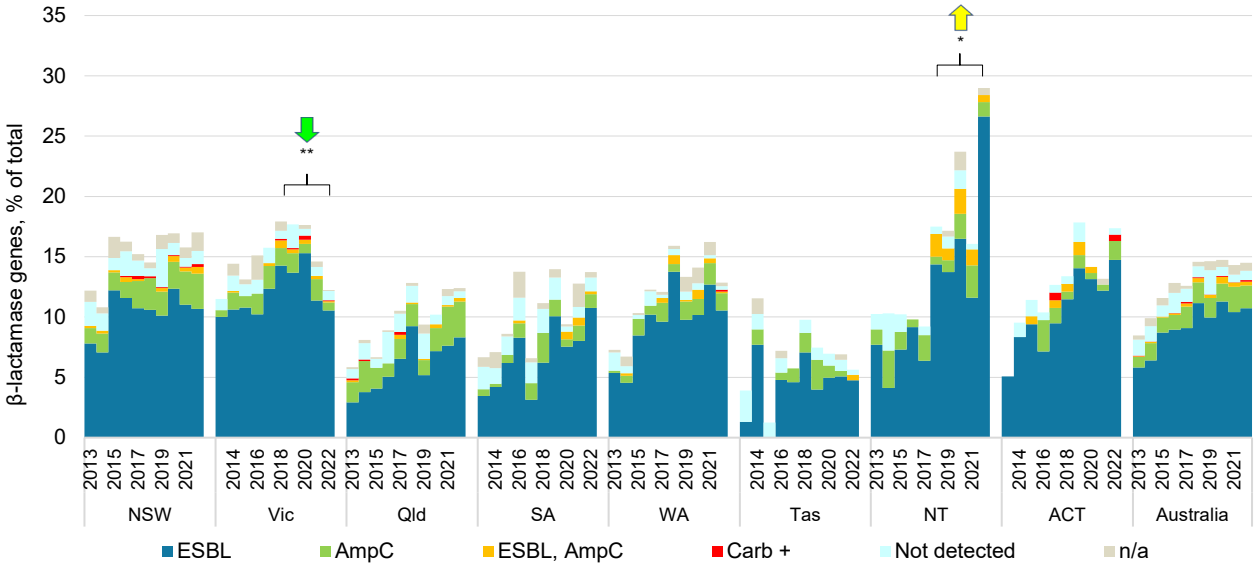
Figure 28: *Escherichia coli* and *Klebsiella pneumoniae* complex isolates with extended spectrum β-lactamase phenotype, AGAR, 2013–2022



	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
E. coli, n	2,837	3,394	3,753	4,024	4,355	4,569	4,884	4,871	4,912	5,261
K. pneumoniae complex, n	701	855	932	948	1,068	1,169	1,190	1,141	1,239	1,392
E. coli, % ESBL	8.4	9.8	11.2	12.7	12.6	14.5	14.5	14.7	14.2	14.4
K. pneumoniae, % ESBL	6.8	8.3	7.7	9.3	9.5	10.6	10.3	10.0	7.9	7.5

ESBL = extended-spectrum β-lactamase

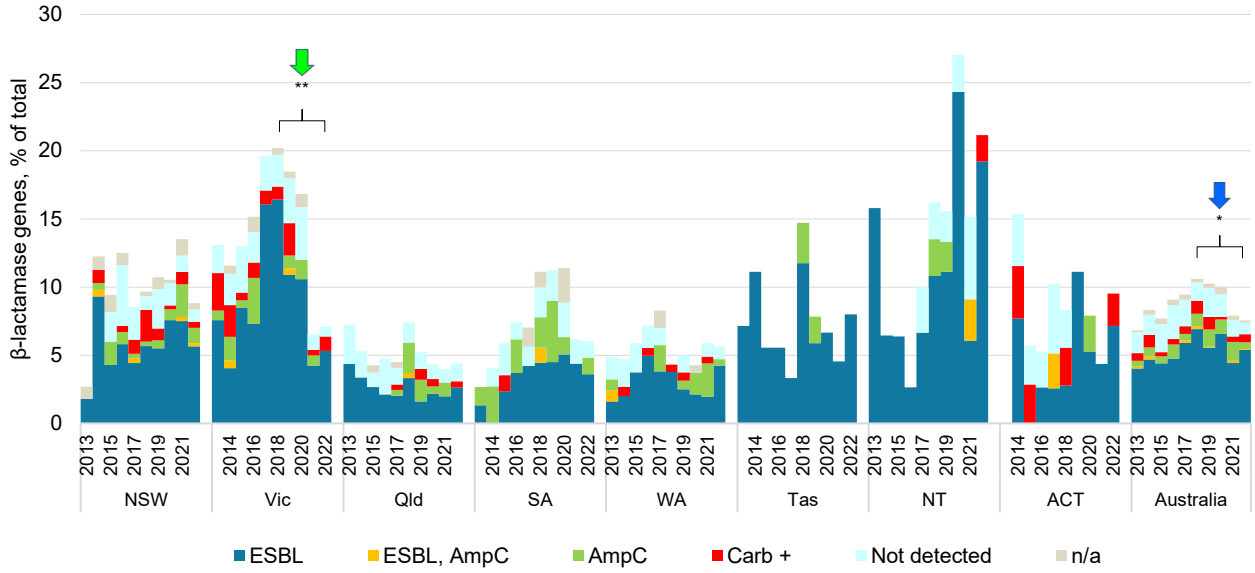
Figure 29: β-lactamase genes in *Escherichia coli*, by state and territory, and nationally, AGAR, 2013–2022



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 WGS

Notes:
1. β-lactamase genes (ESBL-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Down arrow indicates a significant decrease (*P* < 0.01) over the past five years (2018 to 2022) seen in Victoria.
3. Up arrow indicates a significant increase (P^{*} < 0.01 < *P* < 0.05) over the past five years (2018 to 2022) seen in the Northern Territory.

Figure 30: β-lactamase genes in *Klebsiella pneumoniae* complex isolates by state and territory, and nationally, AGAR, 2013–2022



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 WGS

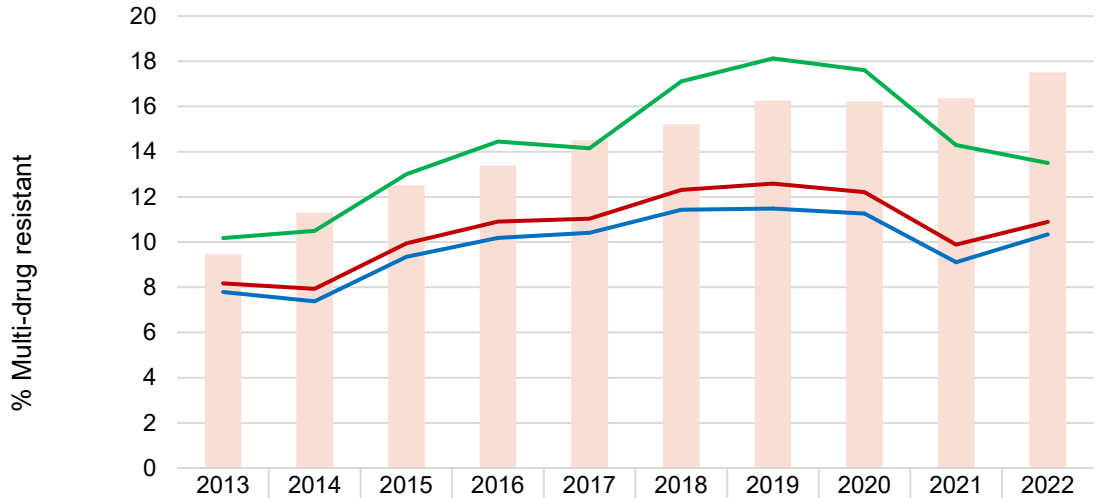
Notes:
1. β-lactamase genes (ESBL-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Down arrows indicate states and territories where there was a significant decrease (**)($P < 0.01$), (*)($0.01 < P < 0.05$) in proportion of β-lactamase genes over the past five years (2013 to 2022).

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 8.2% in 2013 to 11.0% in 2017, remained steady at 12% from 2018 to 2020, and decreased to 9.9% in 2021 and 10.9% in 2022. It was highest among HO isolates (Figure 31). Although the rate of MDR among CO isolates increased in 2022 (10.3%) compared to 2021 (9.1%), the increase was not statistically significant.

For *K. pneumoniae* complex isolates, the frequency of MDR to fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems was more variable (Figure 32). For HO isolates, the highest frequency was observed from 2018 and 2019 (10.6%–11.2%). It fell sharply in 2020 to 5.4% and was 4.2% in 2021 and 4.0% in 2022. There was little change in frequency among CO isolates; the lowest rate was observed in 2021 (2.0%), down from 4.6% in 2018. It was 2.2% in 2022.

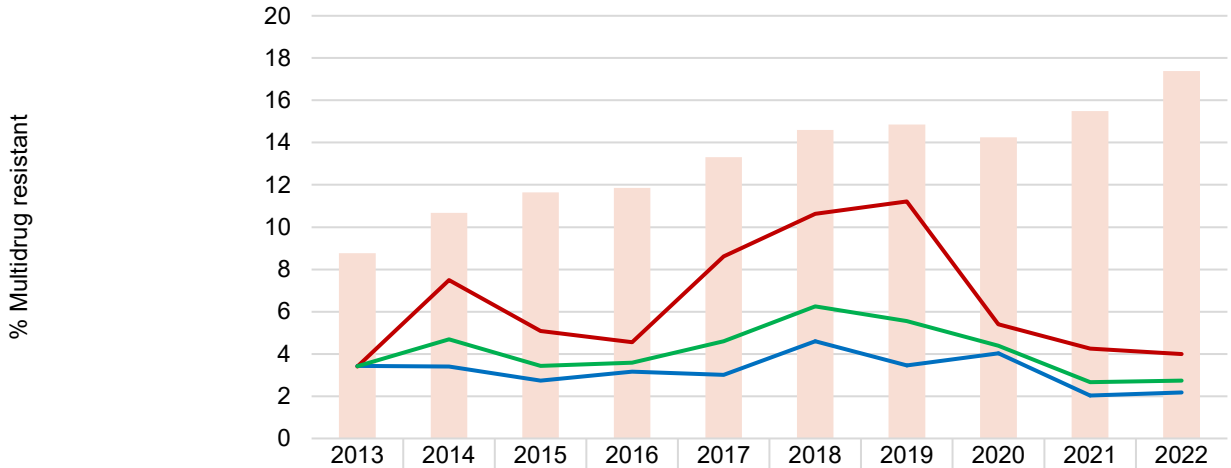
Figure 31: Trends in multi-drug resistance among *Escherichia coli*, by onset, AGAR, 2013 to 2022



	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Isolates, n	2,838	3,392	3,751	4,016	4,352	4,566	4,878	4,865	4,907	5,254
Community-onset, %	7.8	7.4	9.3	10.2	10.4	11.4	11.5	11.3	9.1	10.3
Hospital-onset, %	10.2	10.5	13.0	14.5	14.1	17.1	18.1	17.6	14.3	13.5
Overall, %	8.2	7.9	9.9	10.9	11.0	12.3	12.6	12.2	9.9	10.9

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

Figure 32: Trends in multi-drug resistance among *Klebsiella pneumoniae* complex isolates by onset, AGAR, 2013 to 2022



	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Isolates, n	701	854	932	948	1,065	1,168	1,189	1,140	1,239	1,391
Community-onset, %	3.4	3.4	2.7	3.2	3.0	4.6	3.5	4.0	2.0	2.2
Hospital-onset, %	3.4	7.5	5.1	4.6	8.6	10.6	11.2	5.4	4.2	4.0
Overall, %	3.4	4.7	3.4	3.6	4.6	6.3	5.6	4.4	2.7	2.7

Notes:
1. Multi-drug resistance was defined as resistance to one or more agent in three or more antimicrobial categories.
2. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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)[23] and the Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network. 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.[20]

Data from AGAR can be compared with data from the EARS-Net program, and the CAESAR network, as all these surveillance programs examine resistance in bacterial pathogens found in bloodstream infection.

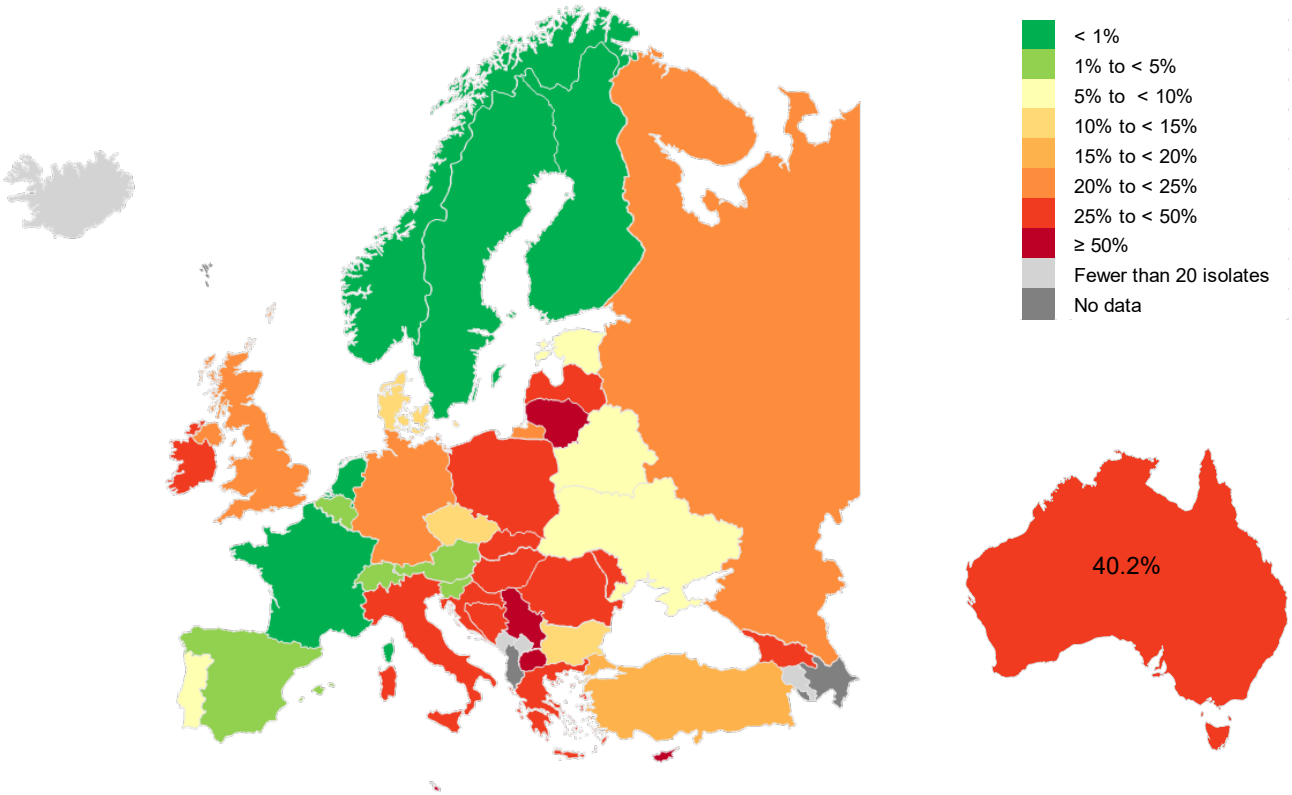
Data for 2022 were not available from either EARS-Net or CAESAR at the time of this report.

Enterococcus faecium

Australia ranks in the top quarter in rates of resistance to vancomycin in *E. faecium* compared to the WHO European Region countries (Figure 32). The rate of vancomycin resistance in *E. faecium* in Australia increased from 40.2% in 2021 to 46.9% in 2022 (*P* = 0.0280).

In 2021, for the European countries, percentages of below 1% resistance to vancomycin in *E. faecium* were reported by six (14%) of 44 countries providing data on this microorganism (Finland, France, Luxembourg, the Netherlands, Norway and Sweden). AMR percentages equal to or above 25% were found in 17 (39%) countries, five of which (11% of 44 countries) reported percentages equal to or above 50% (Cyprus, Lithuania, Malta, North Macedonia and Serbia).

Figure 32: Comparison of *Enterococcus faecium* rates of resistance to vancomycin in Australia (AGAR) and European countries, blood culture isolates, 2021



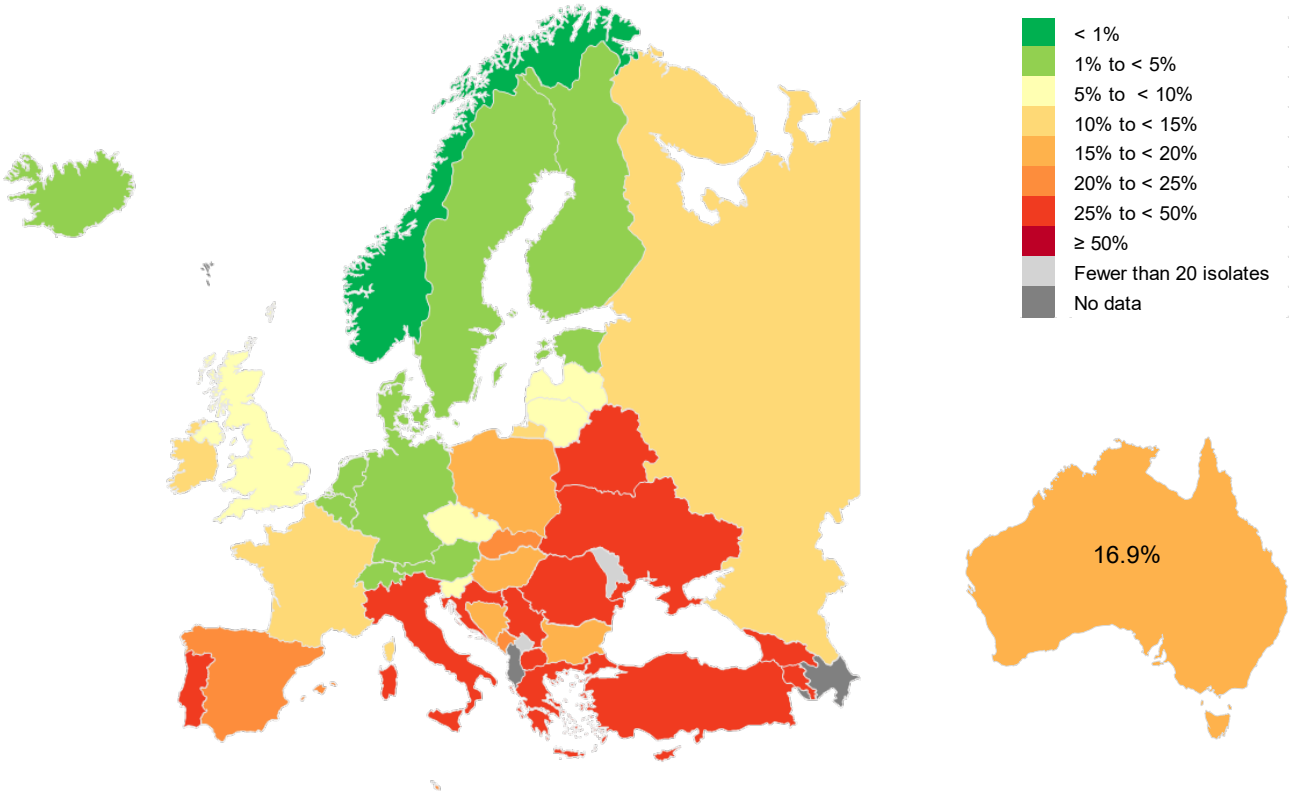
Source: Antimicrobial resistance surveillance in Europe[20]

Staphylococcus aureus

Australia ranks towards the middle in rates of resistance to methicillin in *S. aureus* compared to the WHO European Region countries (Figure 33). The rate of methicillin resistance in *S. aureus* in Australia decreased from 16.9% in 2021 to 15.0% in 2022.

In 2021, 11 (25%) of 44 European countries reporting data on *S. aureus* had MRSA percentages below 5%. MRSA percentages equal to or above 25% were found in 13 (30%) countries.

Figure 33: Comparison of *Staphylococcus aureus* rates of resistance to methicillin in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2021



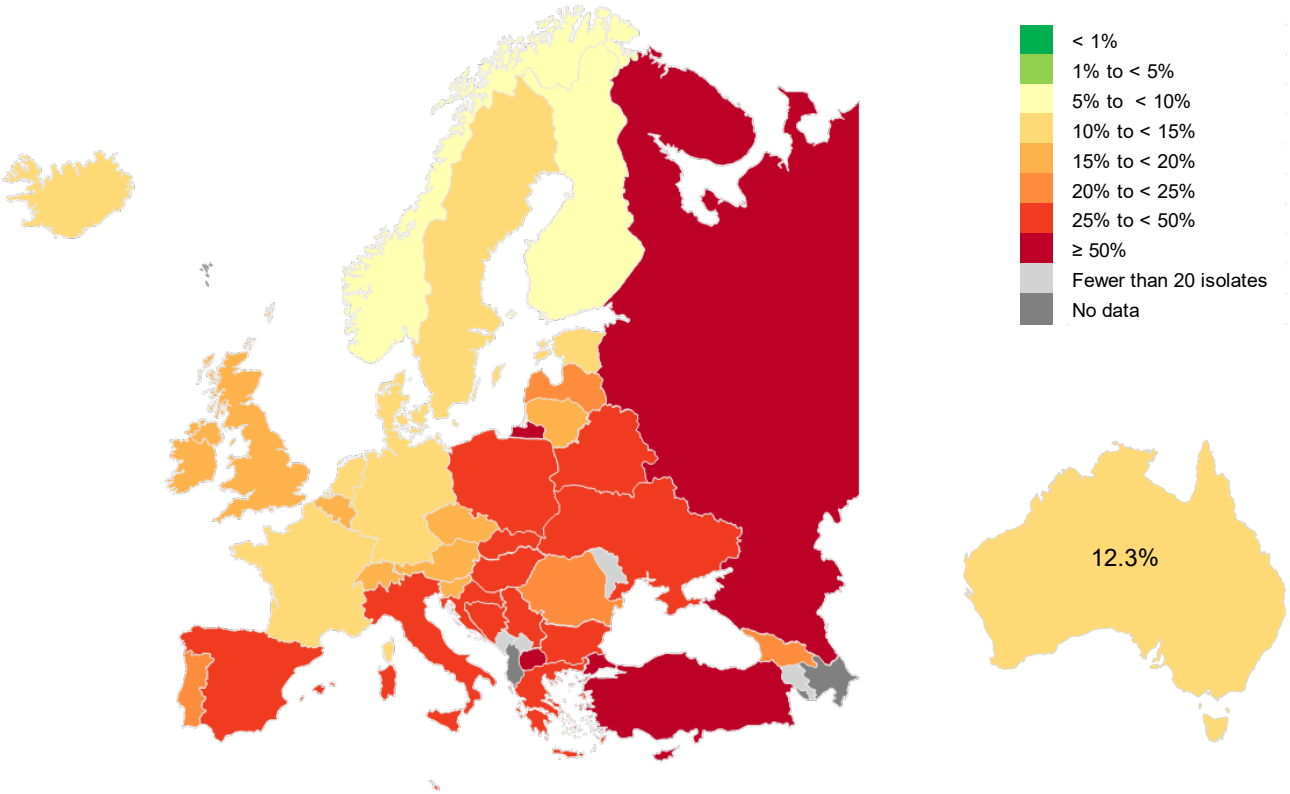
Source: Antimicrobial resistance surveillance in Europe[20]

Escherichia coli

Australia ranks in the bottom quarter in rates of resistance to ciprofloxacin in *E. coli* compared to the WHO European Region countries (Figure 34). The rate of ciprofloxacin resistance in *E. coli* in Australia increased from 12.3% in 2021 to 13.7% in 2022 (*P* = 0.0421).

In the European countries, in 2021, resistance to fluoroquinolones in *E. coli* was generally lowest in the northern and western parts of the WHO European Region and highest in southern and eastern parts (Figure 34). A resistance percentage below 10% was observed in two (4%) of 45 countries (Finland and Norway) reporting data on this microorganism. Seventeen countries (38%) reported a percentage of 25% or above. AMR percentages of 50% or above were observed in four (9%) countries (Cyprus, North Macedonia, Russia, and Türkiye).

Figure 34: Comparison of *Escherichia coli* rates of resistance to ciprofloxacin in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2021

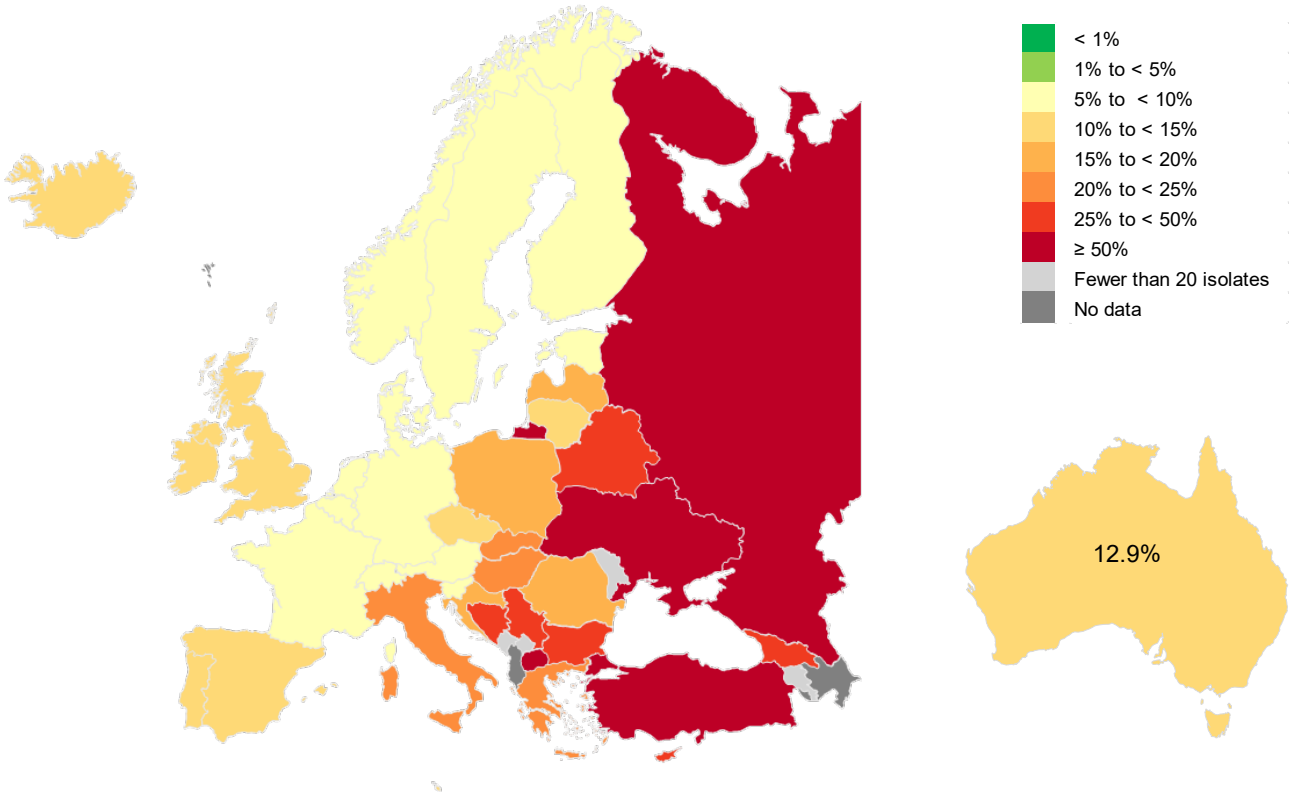


Source: Antimicrobial resistance surveillance in Europe[20]

Australia ranks towards the middle in resistance rates to third-generation resistance in *E. coli* compared to WHO European Region countries (Figure 35). The rate of third-generation cephalosporin resistance in *E. coli* in Australia has remained steady (12.9% in 2021; 13.1% in 2022).

For third-generation cephalosporin resistance in *E. coli,* 12 (27%) of the 45 European countries reported percentages below 10% in 2021, whereas AMR percentages equal to or above 50% were observed in four (9%) countries (North Macedonia, Russia, Türkiye and Ukraine) (Figure 35).

Figure 35: Comparison of *Escherichia coli* rates of resistance to third-generation cephalosporins in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2021



Source: Antimicrobial resistance surveillance in Europe[20]

Klebsiella pneumoniae complex

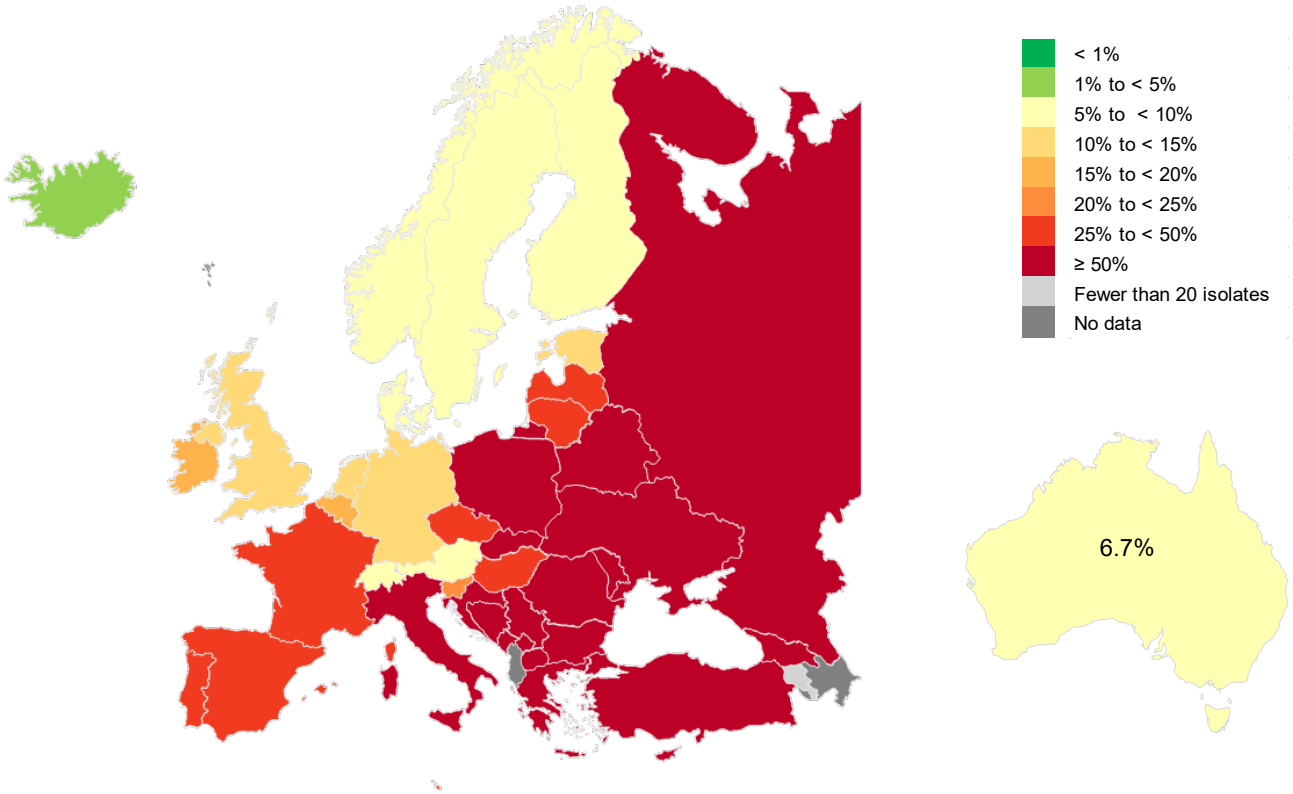
Rates of resistance to third-generation cephalosporins in *K. pneumoniae* complex are low (< 10%) in Australia compared with most of the WHO European Region countries (Figures 36). The rate of third-generation cephalosporin resistance in *K. pneumoniae* in Australia has remained steady (6.7% in 2021; 6.9% in 2022).

Third-generation cephalosporin resistance in *K. pneumoniae* has become quite widespread in the WHO European Region. In 2021, AMR percentages below 10% were observed in seven (16%) of 45 countries reporting data on this microorganism (Austria, Denmark, Finland, Iceland, Norway, Sweden, and Switzerland), while 19 (42%), particularly in the southern and eastern parts of the Region, reported AMR percentages of 50% or above (Figure 36).

The rate of carbapenem resistance in *K. pneumoniae* in Australia was very low (0.3% in 2021; 0.5% in 2022).

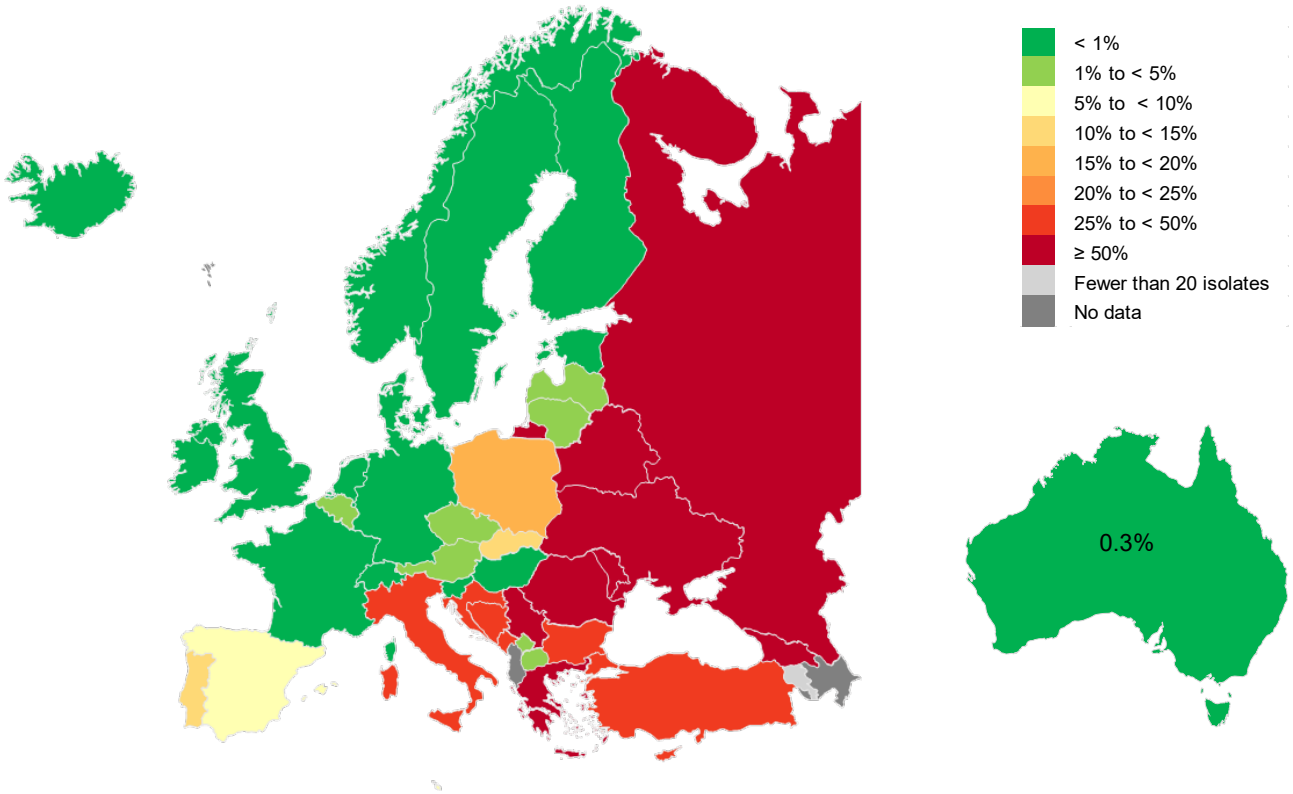
In 2021, in the European countries, percentages were generally low in northern and western parts of the WHO European Region; 14 (31%) of 45 countries reported AMR percentages below 1% (Figure 37). However, fifteen (33%) countries reported percentages equal to or above 25%, eight of which (18% of 45 countries) reported AMR percentages equal to or above 50% (Belarus, Georgia, Greece, Moldova, Romania, Russia, Serbia and Ukraine)

Figure 36: Comparison of *Klebsiella pneumoniae* complex rates of resistance to third-generation cephalosporins in Australia (AGAR) WHO European Region countries, blood culture isolates, 2021



Source: Antimicrobial resistance surveillance in Europe[20]

Figure 37: Comparison of *Klebsiella pneumoniae* complex rates of resistance to carbapenems in Australia (AGAR) and WHO European Region countries, blood culture isolates, 2021



Source: Antimicrobial resistance surveillance in Europe[20]

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 42 large hospitals and 13 regional or district hospitals from north-west Western Australia, it is not yet clear how representative the sample is of Australia as a whole, because the proportion of the population that is served by the laboratories that participate in AGAR is not accurately known. Further, it is likely that the proportion of the population served differs in each state and territory
- 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 12% 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; healthcare-associated community-onset infections may be included in the community-onset group
- Association with relevant mobile genetic element/s (for example, plasmid/s) is not included in this report.

6. Discussion and conclusions

AGAR data show that in 2022, episodes of bacteraemia in Australia had their onset overwhelmingly in the community, for *S. aureus* (77.5%), *E. faecalis* (67.0%), and *Enterobacterales* (76.5%) episodes.

In 2022, febrile neutropenia, intra-abdominal infections, biliary tract infections, or device-related infections were the most common clinical manifestations associated with *E. faecium*. However, episodes where there was no detected focus and setting also contributed to high proportions of presentations for enterococcal bacteraemia overall, and for each of *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 take this information on clinical manifestation (sources of bloodstream infection) into account. In hospital-onset and other healthcare-associated infections, intravascular devices remain a common source for bloodstream infection. In 2022, 11.0% of all *E. coli* bloodstream infections were associated with indwelling urinary devices such as urinary catheters; it was 23.6% for hospital-onset episodes.

Previous AGAR reports had shown a longitudinal trend of increasing *E. coli* resistance to key anti-gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin.[41, 76] Resistance to both agents stabilised in 2018 to 2020 (ceftriaxone 13.3%–13.4%, ciprofloxacin 15.2%–16.1%); the level of resistance declined to 12.5% and 12.3%, respectively in 2021. In 2022, the level of resistance remained stable (12.7% and 13.7%). The steady rise in resistance to fluoroquinolones is 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 to 21.8% in 2020. In 2021 the level of resistance fell to 16.7%, and it increased slightly to 17.8% in 2022. In *K. pneumoniae* complex, rates of resistance to ciprofloxacin were lower than for *E. coli*. Resistance in this species peaked in 2018–2019 at 11.0%–10.2%, falling to 7.2% in 2021, and was 7.8% in 2022.

A little over a decade ago, ciprofloxacin resistance rates were very low and consistently between 1% and 4%.[41, 76] Despite the concerning recent increase (16.7% in 2021), the percentage of fluoroquinolone-resistant *E. coli* in Australia remains low in comparison to most European countries.[19, 20] 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.

The proportion of *E. coli* with an ESBL phenotype in 2022 was similar to 2021 (2021 14.2%; 2022 14.4%). For *K. pneumoniae* complex, the proportion with an ESBL phenotype was also similar to the previous year (2021 7.9%; 2022 7.5%). A substantial majority (79.2%) of ESBL-producing *E. coli* bloodstream infections were community-onset. This indicates that a substantial reservoir of resistance exists in the community, known to be in the elderly population and in long-term residential care settings particularly.[17] Current Australian guidelines recommend third-generation cephalosporins for empirical treatment for many conditions, partly to minimise prescribing of even broader-spectrum antimicrobials, especially carbapenems. The AGAR data suggest that customised patient risk assessment may be required in empirical treatment decisions. In *E. coli* rates of resistance to ceftriaxone in hospital-onset bacteraemia rose from 13.0% in 2016 to 20.2% in 2019. Rates fell to 18.8% in 2020, 17.8% in 2021, and to 15.2% in 2022. The rate of community-onset ceftriaxone resistance has remained steady since 2016 (11.1% in 2016, 11.9% in 2019, 12.4% in 2020, 11.5% in 2021, and 12.1% in 2022).

To date, carbapenemase-producing *Enterobacterales* (CPE) remain relatively uncommon in patients with bacteraemia (0.2% in *E. coli* and 0.5% in *K. pneumoniae* complex). The overall low rates of CPE bloodstream infection are encouraging; however, some organisms harbour them more commonly; namely 2.1% of *E. cloacae* complex infections harboured a carbapenemase (3.5% HO; 0.8% CO) in 2022. Examining previous and current AGAR surveys, most CPEs are endemic in origin.[50, 77] Eighteen of the 29 (62.1%) CPEs had $bla_{\text{IMP-4}}$, with reports predominately from New South Wales (10/18, 55.6%). Eighteen of the participating hospitals 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.[14] There were no reports of *bla*$_{KPC-2}$.

No mobile colistin resistance genes other than *mcr-9* or *mcr-10* were detected in any isolates referred for WGS (*n* = 1,233). *mcr-9* has recently been found among several species of *Enterobacterales*. It is not associated with a colistin resistant phenotype[71], but is typically found on IncHI2 plasmids that may carry a carbapenemase gene.[72, 73]

E. faecium bacteraemia has significant clinical consequences and resource implications, due to increased length of hospital stay. Bacteraemia episodes contributed to increased length of hospital stay; the average length of stay in all Australian public hospitals in 2020–21 was 5.0 days without a hospital-acquired complication (HAC), and 20.6 days with a HAC.[78] In 2022, where data were available for episodes of bacteraemia caused by GnSOP isolates, a little over one-half (56.6%) had a length of stay seven days or more. For episodes of enterococcal bacteraemia, almost one-quarter (22.3%) had a length of stay >30 days; for staphylococcal bacteraemia.it was 24.6%

Thirty-day all-cause mortality due to *E. faecium* in 2022 was 26.9% (community-onset 30.5%; hospital-onset 25.7%); there was a significant difference in 30-day all-cause mortality between vancomycin-susceptible and resistant episodes (19.7% and 34.4%, respectively, $P < 0.01$). The 30-day all-cause mortality associated with *E. coli* and methicillin-resistant *S. aureus* hospital-onset infections (13.3% and 23.7%, respectively) exceeds community-onset infections (11.1% and 20.8% respectively).

In the 2022 survey, 48.8% of *E. faecium* harboured *vanA* or *vanB* genes; in 2021 it was 42.1%. Vancomycin, which until recently was the mainstay of therapy for *E. faecium*, can no longer be recommended empirically; agents with less certain efficacy but much lower resistance rates, such as linezolid, are the alternative.

For almost two decades, and unlike in most other countries where vancomycin resistance is a problem, 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 35.7% in 2020 and 36.4% in 2021. In the 2022 survey 28.3% 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 most European countries. Australia ranks in the top quarter in rates of resistance to vancomycin in *E. faecium*.[20] The rate of vancomycin resistance in *E. faecium* in Australia increased from 40.2% in 2021 to 46.9% in 2022.

The percentage of high-level gentamicin resistance in *E. faecium* has increased significantly from 32.3% in 2021 to 44.2% in 2022 ($P < 0.01$). This increase was seen in both vancomycin-susceptible and vancomycin-resistant isolates ($P = 0.0484$ and $P < 0.01$ respectively).

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 as an empiric therapeutic choice for MRSA, and 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 fell from 16.6% in 2021[79] to 15.0% in the 2022 study. This compares with the 2021 EU/EEA population-weighted mean MRSA percentage of 15.8%.[19, 20]

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

The rapidly changing picture of MRSA in Australia, drawing from 15 years of AGAR surveillance, was further explored in *Methicillin-resistant* Staphylococcus aureus *in Australia. MRSA bacteraemia – 2013 to 2018*.[55] This technical paper will be updated as appropriate by AGAR and the Commission to provide further information on the issue.

In this survey, multi-drug resistance did not appear to play a contributory role in 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 MDR organisms 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 assessed with other sources of information to provide broader insights into antimicrobial resistance in Australia. The AURA Surveillance System enables these assessments via Australian Passive AMR Surveillance (APAS) and National Alert System for Critical Antimicrobial Resistances (CARAlert) data, which complement AGAR data.

The association between COVID-19 and rates of antimicrobial resistance remains unclear and may be influenced by a number of contributing factors. A combination of COVID-19-related travel restrictions on incoming travellers throughout much of 2020 and 2021, and implementation of AMS programs to meet the requirements of the NSQHS Standards[2], may have reduced some resistance, particularly for ESBLs and fluoroquinolone resistance in *E. coli*.

Pharmaceutical Benefits Scheme (PBS) and Repatriation PBS data indicate that the fall in antimicrobial use that was observed in 2020 compared with previous years, most likely due to changes in healthcare practice and infection risk related to the COVID-19 pandemic, was maintained in 2021. The level of use rose in 2022 but has not returned to pre-2020 levels.[50, 80]

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.

AGAR surveillance remains core to informing Australia's response to the problem of increasing AMR and contribute 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
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
SA	South Australia

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

Acknowledgements

Participating members of AGAR in 2022:

Hospitals	AGAR members
Alfred Hospital, Vic	Adam Jenney and Jacqueline Williams
Alice Springs Hospital, NT	James McLeod
Austin Hospital, Vic	Marcel Leroi and Elizabeth Grabsch
Canberra Hospital, ACT	Peter Collignon and Susan Bradbury
Children's Hospital Westmead, NSW	Alison Kesson and Andrew Jarrett
Concord Hospital, NSW	Thomas Gottlieb and John Huynh
Dandenong Hospital, Vic	Tony Korman and Kathryn Cisera
Fiona Stanley Hospital, WA	Denise Daley
Flinders Medical Centre, SA	Kelly Papanaoum and Xiao Chen,
Gold Coast University Hospital, Qld	Petra Derrington and Cheryl Curtis
Gosford Hospital, NSW	Gabrielle O'Kane and Nola Hitchick
Greenslopes Private Hospital, Qld	Jennifer Robson and Marianne Allen
John Hunter Hospital, NSW	Hemalatha Varadhan and Bree Harris
Joondalup Hospital, WA	Shalinie Perera and Ian Meyer
Launceston General Hospital, Tas	Pankaja Kalukottege and Brooke Woolley
Liverpool Hospital, NSW	Michael Maley and Helen Ziochos
Mater Private Hospital, Townsville, Qld	Jennifer Robson and Marianne Allen
Monash Children's Hospital, Vic	Tony Korman and Despina Kotsanas
Monash Medical Centre, Vic	Tony Korman and Despina Kotsanas
Nepean Hospital, NSW	James Branley and Linda Douglass
North-west regional WA	Michael Leung and Jacinta Bowman
Pathology Queensland Central Laboratory, Qld	Claire Heney and Narelle George
Perth Children's Hospital, WA	Chris Blyth and Jacinta Bowman
Prince Charles Hospital, Qld	Robert Horvath and Laura Martin
Prince of Wales Hospital, NSW	Monica Lahra and Peter Huntington
Princess Alexandra Hospital, Qld	Naomi Runnegar and Joel Douglas
Queensland Children's Hospital, Qld	Clare Nourse and Narelle George
Royal Adelaide Hospital, SA	Morgyn Warner and Kija Smith
Royal Darwin Hospital, NT	Rob Baird and Jann Hennessy
Royal Hobart Hospital, Tas	Louise Cooley and David Jones
Royal Melbourne Hospital, Vic	Katherine Bond and Rose Cotronei
Royal North Shore Hospital, NSW	Angela Wong
Royal Perth Hospital, WA	Owen Robinson and Geoffrey Coombs
Royal Prince Alfred Hospital, NSW	Sebastiaan van Hal and Thomas Le
Royal Women's Hospital, Vic	Andrew Daley and Gena Gonis
Sir Charles Gairdner Hospital, WA	Ronan Murray and Jacinta Bowman
St John of God Hospital, Murdoch, WA	Sudha Pottumarthy-Boddu and Alicia Robinson
St Vincent's Hospital, Melbourne, Vic	Amy Crowe and Lisa Brenton
St Vincent's Hospital, Sydney, NSW	David Lorenz
Sydney Children's Hospital, NSW	Monica Lahra and Peter Huntington
Westmead Hospital, NSW	Jon Iredell and Elena Martinez
Wollongong Hospital, NSW	Peter Newton and Melissa Hoddle
Women's and Children's Hospital, SA	Morgyn Warner and Kija Smith

Reference laboratories

AGAR gratefully acknowledges the Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, Centre for Infectious Diseases and Microbiology Laboratory Services (CIDMLS), Institute of Clinical Pathology and Medical Research (ICPMR), Westmead Hospital [Jenny Draper, Elena Martinez and Andrew Ginn] for performing whole genome sequencing on the referred isolates.

AGAR also gratefully acknowledges Dr Shakeel Mowlaboccus and Princy Shoby at the Antimicrobial Resistance and Infectious Disease Research Laboratory, Murdoch University, Western Australia for performing the whole genome sequencing and bioinformatics analyses on *E. faecium* and MRSA isolates.

Funding

The AGAR Surveillance Outcome Programs are funded by the Australian Government Department of Health and Aged Care (the Department) and the Department funded the Australian Commission on Safety and Quality in Health Care to prepare this report.

References

1. World Health Organization. Global Antimicrobial Resistance and Use Surveillance System (GLASS). [Internet] Geneva: WHO; 2023 [cited 2023 Oct] Available from: https://www.who.int/initiatives/glass.
2. Australian Commission on Safety and Quality in Health Care. National Safety and Quality Health Service Standards. 2nd ed. – version 2. Sydney: ACSQHC; 2021.
3. Australian Commission on Safety and Quality in Health Care. National Safety and Quality Primary and Community Healthcare Standards. Sydney: ACSQHC; 2021.
4. Australian Commission on Safety and Quality in Health Care. Antimicrobial Stewardship Clinical Care Standard. Sydney: ACQSC; 2020.
5. Australian Commission on Safety and Quality in Health Care. Sepsis Clinical Care Standard. Sydney: ACQSC; 2022.
6. Furuya-Kanamori L, Mills DJ, Trembizki E, Robson JM, Jennison AV, Whiley DM, et al. High rate of asymptomatic colonization with antimicrobial-resistant *Escherichia coli* in Australian returned travellers. J Travel Med. 2022;29(1).
7. Furuya-Kanamori L, Stone J, Yakob L, Kirk M, Collignon P, Mills DJ, et al. Risk factors for acquisition of multidrug-resistant Enterobacterales among international travellers: a synthesis of cumulative evidence. J Travel Med. 2020;27(1).
8. Chen LF, Freeman JT, Nicholson B, Keiger A, Lancaster S, Joyce M, et al. Widespread dissemination of CTX-M-15 genotype extended-spectrum-β-lactamase-producing enterobacteriaceae among patients presenting to community hospitals in the southeastern United States. Antimicrob Agents Chemother. 2014;58(2):1200-1202.
9. Woodford N, Ward ME, Kaufmann ME, Turton J, Fagan EJ, James D, et al. Community and hospital spread of *Escherichia coli* producing CTX-M extended-spectrum β-lactamases in the UK. J Antimicrob Chemother. 2004;54(4):735-743.
10. Xia S, Fan X, Huang Z, Xia L, Xiao M, Chen R, et al. Dominance of CTX-M-type extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* isolated from patients with community-onset and hospital-onset infection in China. PLoS One. 2014;9(7):e100707.
11. Stuart RL, Kotsanas D, Webb B, Vandergraaf S, Gillespie EE, Hogg GG, et al. Prevalence of antimicrobial-resistant organisms in residential aged care facilities. Med J Aust. 2011;195(9):530-533.
12. Australian Commission on Safety and Quality in Health Care. AURA 2023: fifth Australian report on antimicrobial use and resistance in human health. Sydney: ACSQHC, 2023.
13. National Health and Medical Research Council. Australian Guidelines for the Prevention and Control of Infection in Healthcare (2019). Canberra: NHMRC; 2019.
14. Australian Commission on Safety and Quality in Health Care. Recommendations for the control of carbapenemase-producing *Enterobacterales* (CPE). A guide for acute care health service organisations. Sydney: ACSQHC, 2021.
15. Australian Commission on Safety and Quality in Health Care. Management of Peripheral Intravenous Catheters Clinical Care Standard. Sydney: ACSQHC, 2021.
16. Australian Commission on Safety and Quality in Health Care. Aged Care Quality Standards - Clinical Care. Sydney: ACQSC; 2022.
17. Australian Commission on Safety and Quality in Health Care. Australian Passive Antimicrobial Resistance Surveillance. First report: multi-resistant organisms. Sydney: 2018.
18. Australian Commission on Safety and Quality in Health Care. Australian Passive Antimicrobial Resistance Surveillance - third-generation cephalosporin resistance in *Escherichia coli* and *Klebsiella pneumoniae*: prevalence of extended-spectrum β-lactamase (ESBL) phenotype. Sydney: 2022.
19. European Centre for Disease Prevention and Control. Antimicrobial resistance in the EU/EEA (EARS-Net) - Annual epidemiological report for 2021. [Internet] Stockholm: ECDC; 2022 [updated 17 Nov 2022] Available from: https://www.ecdc.europa.eu/en/publications-data/surveillance-antimicrobial-resistance-europe-2021.
20. European Centre for Disease Prevention and Control and World Health Organisation. Antimicrobial resistance surveillance in Europe 2023 - 2021 data. [Internet] Stockholm:

ECDC; 2023 [updated 14 April 2023] Available from: https://www.ecdc.europa.eu/en/publications-data/antimicrobial-resistance-surveillance-europe-2023-2021-data.
21. Antibiotic Expert Groups. Antibiotic. In: Therapeutic Guidelines [Internet]. Melbourne: Therapeutic Guidelines Limited. Available from: https://tgldcdp.tg.org.au/etgcomplete.
22. Australian Commission on Safety and Quality in Health Care. Priority Antibacterial List for antimicrobial resistance containment: a stewardship resource for human health. [Internet] Sydney: ACSQHC; 2020 [cited 2023 Oct 5] Available from: https://www.safetyandquality.gov.au/publications-and-resources/resource-library/priority-antibacterial-list-antimicrobial-resistance-containment.
23. European Centre for Disease Prevention and Control. European Antimicrobial Resistance Surveillance Network (EARS-Net). [Internet] Stockholm: ECDC; 2023 [cited 05 Oct 2023] Available from: https://www.ecdc.europa.eu/en/about-us/networks/disease-networks-and-laboratory-networks/ears-net-data.
24. Diekema DJ, Hsueh PR, Mendes RE, Pfaller MA, Rolston KV, Sader HS, et al. The microbiology of bloodstream infection: 20-year trends from the SENTRY Antimicrobial Surveillance Program. Antimicrob Agents Chemother. 2019;63(7):63:e00355-00319.
25. Pinholt M, Ostergaard C, Arpi M, Bruun NE, Schonheyder HC, Gradel KO, et al. Incidence, clinical characteristics and 30-day mortality of enterococcal bacteraemia in Denmark 2006-2009: a population-based cohort study. Clin Microbiol Infect. 2014;20(2):145-151.
26. Murray BE. The life and times of the Enterococcus. Clin Microbiol Rev. 1990;3(1):46-65.
27. Simonsen GS, Smabrekke L, Monnet DL, Sorensen TL, Moller JK, Kristinsson KG, et al. Prevalence of resistance to ampicillin, gentamicin and vancomycin in *Enterococcus faecalis* and *Enterococcus faecium* isolates from clinical specimens and use of antimicrobials in five Nordic hospitals. J Antimicrob Chemother. 2003;51(2):323-331.
28. Treitman AN, Yarnold PR, Warren J, Noskin GA. Emerging incidence of *Enterococcus faecium* among hospital isolates (1993 to 2002). J Clin Microbiol. 2005;43(1):462-463.
29. Boucher HW, Talbot GH, Bradley JS, Edwards JE, Gilbert D, Rice LB, et al. Bad bugs, no drugs: no ESKAPE! An update from the Infectious Diseases Society of America. Clin Infect Dis. 2009;48(1):1-12.
30. Christiansen KJ, Turnidge JD, Bell JM, George NM, Pearson JC, Australian Group on Antimicrobial Resistance. Prevalence of antimicrobial resistance in Enterococcus isolates in Australia, 2005: report from the Australian Group on Antimicrobial Resistance. Commun Dis Intell Q Rep. 2007;31(4):392-397.
31. Coombs GW, Daley D, Pearson JC, Ingram PR. A change in the molecular epidemiology of vancomycin resistant enterococci in Western Australia. Pathology. 2014;46(1):73-75.
32. Laupland KB. Incidence of bloodstream infection: a review of population-based studies. Clin Microbiol Infect. 2013;19(6):492-500.
33. Johnson AP, Pearson A, Duckworth G. Surveillance and epidemiology of MRSA bacteraemia in the UK. J Antimicrob Chemother. 2005;56(3):455-462.
34. Thwaites GE, Edgeworth JD, Gkrania-Klotsas E, Kirby A, Tilley R, Torok ME, et al. Clinical management of *Staphylococcus aureus* bacteraemia. Lancet Infect Dis. 2011;11(3):208-222.
35. Benfield T, Espersen F, Frimodt-Moller N, Jensen AG, Larsen AR, Pallesen LV, et al. Increasing incidence but decreasing in-hospital mortality of adult *Staphylococcus aureus* bacteraemia between 1981 and 2000. Clin Microbiol Infect. 2007;13(3):257-263.
36. Collignon P, Nimmo GR, Gottlieb T, Gosbell IB, Australian Group on Antimicrobial Resistance. *Staphylococcus aureus* bacteremia, Australia. Emerg Infect Dis. 2005;11(4):554-561.
37. Frederiksen MS, Espersen F, Frimodt-Moller N, Jensen AG, Larsen AR, Pallesen LV, et al. Changing epidemiology of pediatric *Staphylococcus aureus* bacteremia in Denmark from 1971 through 2000. Pediatr Infect Dis J. 2007;26(5):398-405.
38. Kaasch AJ, Barlow G, Edgeworth JD, Fowler VG, Jr., Hellmich M, Hopkins S, et al. *Staphylococcus aureus* bloodstream infection: a pooled analysis of five prospective, observational studies. J Infect. 2014;68(3):242-251.
39. van Hal SJ, Jensen SO, Vaska VL, Espedido BA, Paterson DL, Gosbell IB. Predictors of mortality in *Staphylococcus aureus* Bacteremia. Clin Microbiol Rev. 2012;25(2):362-386.

40. Turnidge JD, Kotsanas D, Munckhof W, Roberts S, Bennett CM, Nimmo GR, et al. *Staphylococcus aureus* bacteraemia: a major cause of mortality in Australia and New Zealand. Med J Aust. 2009;191(7):368-373.
41. Nimmo GR, Bell JM, Collignon PJ, Australian Group for Antimicrobial R. Fifteen years of surveillance by the Australian Group for Antimicrobial Resistance (AGAR). Commun Dis Intell Q Rep. 2003;27 Suppl:S47-54.
42. Coombs GW, Nimmo GR, Daly DA, Le TT, Pearson JC, Tan HL, et al. Australian *Staphylococcus aureus* Sepsis Outcome Programme annual report, 2013. Commun Dis Intell Q Rep. 2014;38(4):E309-319.
43. Sader HS, Mendes RE, Fuhrmeister AS, Shortridge D, Huband MD, Duncan LR, et al. Bloodstream Infections in Europe and United States: Aetiology and Antimicrobial Susceptibility Results from the SENTRY Antimicrobial Surveillance Program (2019–2021). ECCMID 2023; April 15–18; Copenhagen, Denmark2023.
44. GBD 2019 Antimicrobial Resistance Collaborators. Global mortality associated with 33 bacterial pathogens in 2019: a systematic analysis for the Global Burden of Disease Study 2019. Lancet. 2022;400(10369):2221-2248.
45. Goto M, Al-Hasan MN. Overall burden of bloodstream infection and nosocomial bloodstream infection in North America and Europe. Clin Microbiol Infect. 2013;19(6):501-509.
46. Centers for Disease Control and Prevention. Antibiotic resistance threats in the United States, 2019. Atlanta, GA: CDC, 2019.
47. CLSI. Performance standards for antimicrobial susceptibility testing. 33rd ed. CLSI supplement M100. Wayne, PA: Clinical and Laboratory Standards Institute; 2023.
48. European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 13.1, valid from 2022-06-29. 2023.
49. Seemann T, Goncalves da Silva A, Bulach DM, Schultz MB, Kwong JC, Howden BP. *Nullarbor* Github. [Internet] 2020 Available from: https://github.com/tseemann/nullarbor.
50. Australian Commission on Safety and Quality in Health Care. AURA 2021: fourth Australian report on antimicrobial use and resistance in human health. Sydney: ACSQHC, 2021.
51. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012;18(3):268-281.
52. Williamson DA, Howden BP, Paterson DL. The risk of resistance: what are the major antimicrobial resistance threats facing Australia? Med J Aust. 2019;211(3):103-105 e101.
53. Rozman V, Mohar Lorbeg P, Treven P, Accetto T, Janezic S, Rupnik M, et al. Genomic insights into antibiotic resistance and mobilome of lactic acid bacteria and bifidobacteria. Life Sci Alliance. 2023;6(4).
54. Lellek H, Franke GC, Ruckert C, Wolters M, Wolschke C, Christner M, et al. Emergence of daptomycin non-susceptibility in colonizing vancomycin-resistant *Enterococcus faecium* isolates during daptomycin therapy. Int J Med Microbiol. 2015;305(8):902-909.
55. Coombs G, Daley D, Nimmo G, Collignon P, Bell JM, Daveson K. Methicillin-resistant *Staphylococcus aureus* in Australia: MRSA bacteraemia - 2013 to 2018. Sydney: Australian Group on Antimicrobial Resistance (AGAR) and the Australian Commission on Safety and Quality in Health Care, 2020.
56. Berti AD, Baines SL, Howden BP, Sakoulas G, Nizet V, Proctor RA, et al. Heterogeneity of genetic pathways toward daptomycin nonsusceptibility in *Staphylococcus aureus* determined by adjunctive antibiotics. Antimicrob Agents Chemother. 2015;59(5):2799-2806.
57. Peleg AY, Miyakis S, Ward DV, Earl AM, Rubio A, Cameron DR, et al. Whole genome characterization of the mechanisms of daptomycin resistance in clinical and laboratory derived isolates of *Staphylococcus aureus*. PLoS One. 2012;7(1):e28316.
58. Bell JM, Turnidge JD, Jones RN, SENTRY Asia-Pacific Participants. Prevalence of extended-spectrum β-lactamase-producing *Enterobacter cloacae* in the Asia-Pacific region: results from the SENTRY Antimicrobial Surveillance Program, 1998 to 2001. Antimicrob Agents Chemother. 2003;47(12):3989-3993.
59. Livermore DM. β-lactamases in laboratory and clinical resistance. Clin Microbiol Rev. 1995;8(4):557-584.

60. Potz NA, Colman M, Warner M, Reynolds R, Livermore DM. False-positive extended-spectrum β-lactamase tests for *Klebsiella oxytoca* strains hyperproducing K1 β-lactamase. J Antimicrob Chemother. 2004;53(3):545-547.
61. Johnson JR, Porter S, Thuras P, Castanheira M. The pandemic H30 subclone of sequence type 131 (ST131) as the leading cause of multidrug-resistant *Escherichia coli* infections in the United States (2011-2012). Open Forum Infect Dis. 2017;4(2):ofx089.
62. Merino I, Hernandez-Garcia M, Turrientes MC, Perez-Viso B, Lopez-Fresnena N, Diaz-Agero C, et al. Emergence of ESBL-producing *Escherichia coli* ST131-C1-M27 clade colonizing patients in Europe. J Antimicrob Chemother. 2018;73(11):2973-2980.
63. Pitout JD, DeVinney R. *Escherichia coli* ST131: a multidrug-resistant clone primed for global domination. F1000Res. 2017;6:195.
64. Flament-Simon SC, Garcia V, Duprilot M, Mayer N, Alonso MP, Garcia-Menino I, et al. High prevalence of ST131 subclades C2-H30Rx and C1-M27 among extended-spectrum β-lactamase-producing *Escherichia coli* causing human extraintestinal infections in patients from two hospitals of Spain and France during 2015. Front Cell Infect Microbiol. 2020;10:125.
65. Johnson JR, Johnston BD, Porter SB, Clabots C, Bender TL, Thuras P, et al. Rapid emergence, subsidence, and molecular detection of *Escherichia coli* sequence type 1193-*fimH64*, a new disseminated multidrug-resistant commensal and extraintestinal pathogen. J Clin Microbiol. 2019;57(5):e01664-01618.
66. Albornoz E, Tijet N, De Belder D, Gomez S, Martino F, Corso A, et al. *qnrE1*, a member of a new family of plasmid-located quinolone resistance genes, originated from the chromosome of *Enterobacter* species. Antimicrob Agents Chemother. 2017;61(5):e02555-02516.
67. Hooper DC, Jacoby GA. Mechanisms of drug resistance: quinolone resistance. Ann N Y Acad Sci. 2015;1354:12-31.
68. Cuypers WL, Jacobs J, Wong V, Klemm EJ, Deborggraeve S, Van Puyvelde S. Fluoroquinolone resistance in *Salmonella*: insights by whole-genome sequencing. Microb Genom. 2018;4(7):e000195.
69. Paltansing S, Kraakman ME, Ras JM, Wessels E, Bernards AT. Characterization of fluoroquinolone and cephalosporin resistance mechanisms in Enterobacteriaceae isolated in a Dutch teaching hospital reveals the presence of an *Escherichia coli* ST131 clone with a specific mutation in parE. J Antimicrob Chemother. 2013;68(1):40-45.
70. Zeng Q, Xiao S, Gu F, He W, Xie Q, Yu F, et al. Antimicrobial Resistance and Molecular Epidemiology of Uropathogenic Escherichia coli Isolated From Female Patients in Shanghai, China. Front Cell Infect Microbiol. 2021;11:653983.
71. Tyson GH, Li C, Hsu CH, Ayers S, Borenstein S, Mukherjee S, et al. The *mcr-9* gene of *Salmonella* and *Escherichia coli* Is not associated with colistin resistance in the United States. Antimicrob Agents Chemother. 2020;64(8).
72. Kieffer N, Royer G, Decousser JW, Bourrel AS, Palmieri M, Ortiz De La Rosa JM, et al. *mcr-9*, an inducible gene encoding an acquired phosphoethanolamine transferase in *Escherichia coli*, and its origin. Antimicrob Agents Chemother. 2019;63(9):e00965-00919.
73. Li Y, Dai X, Zeng J, Gao Y, Zhang Z, Zhang L. Characterization of the global distribution and diversified plasmid reservoirs of the colistin resistance gene *mcr-9*. Sci Rep. 2020;10(1):8113.
74. Doi Y, Arakawa Y. 16S ribosomal RNA methylation: emerging resistance mechanism against aminoglycosides. Clin Infect Dis. 2007;45(1):88-94.
75. Doi Y, Wachino JI, Arakawa Y. Aminoglycoside resistance: the emergence of acquired 16S ribosomal RNA methyltransferases. Infect Dis Clin North Am. 2016;30(2):523-537.
76. Pearson J, Turnidge J, Franklin C, Bell J, Australian Group on Antimicrobial Resistance. Prevalence of antimicrobial resistances in common pathogenic Enterobacteriaceae in Australia, 2004: report from the Australian Group on Antimicrobial Resistance. Commun Dis Intell Q Rep. 2007;31(1):106-112.
77. Australian Group for Antimicrobial Resistance. The evolution of carbapenemases in major gram-negative bacteria in Australia. [Internet] 2016 Available from: https://agargroup.org.au/agar-reports/.

78. Australian Institute of Health and Welfare. Australia's hospitals at a glance. [Internet] Canberra: AIHW; 2022 [updated 7/12/2022; cited 02 October 2023] Available from: https://www.aihw.gov.au/reports/hospitals/australias-hospitals-at-a-glance/contents/hospital-safety-and-quality.
79. Coombs GW, Daley DA, Shoby P, Mowlaboccus S. Australian Group on Antimicrobial Resistance (AGAR) Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP). Commun Dis Intell (2018). 2022;46.
80. Gadzhanova S, Roughead E, on behalf of the Australian Commission on Safety and Quality in Health Care. Analysis of 2015–2022 PBS and RPBS antimicrobial dispensing data. Sydney: ACSQHC, 2023.
81. Australian Institute of Health and Welfare. Australia's hospital peer groups. [Internet] Canberra: AIHW; 2015 [updated 7/08/2017 v1.0; cited 14 July 2023] Available from: https://www.aihw.gov.au/reports/hospitals/australian-hospital-peer-groups/data.
82. Coombs GW, Mowlaboccus S, Daley D, Lee T, Pearson J, Pang S, et al. Sulfamethoxazole/trimethoprim resistance overcall by VITEK(R) 2 and BD Phoenix in community-associated MRSA and MSSA. J Antimicrob Chemother. 2019;74(12):3639-3641.
83. Harris TM, Bowen AC, Holt DC, Sarovich DS, Stevens K, Currie BJ, et al. Investigation of trimethoprim/sulfamethoxazole resistance in an emerging sequence type 5 methicillin-resistant *Staphylococcus aureus* clone reveals discrepant resistance reporting. Clin Microbiol Infect. 2018;24(9):1027-1029.
84. Weber RE, Layer F, Klare I, Werner G, Strommenger B. Comparative evaluation of VITEK$^{(R)}$ 2 and three commercial gradient strip assays for daptomycin susceptibility testing of *Staphylococcus aureus*. J Antimicrob Chemother. 2017;72(11):3059-3062.
85. Seemann T. *Abricate*, Github. [Internet] 2020 Available from: https://github.com/tseemann/abricate.
86. National Center for Biotechnology Information. AMRFinder. [Internet]: NCBI; 2020 Available from: https://ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/AMRFinder/
87. Hunt M, Mather AE, Sanchez-Buso L, Page AJ, Parkhill J, Keane JA, et al. ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. Microb Genom. 2017;3(10):e000131.
88. Alcock BP, Raphenya AR, Lau TTY, Tsang KK, Bouchard M, Edalatmand A, et al. CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. Nucleic Acids Res. 2020;48(D1):D517-D525.
89. Zankari E, Allesoe R, Joensen KG, Cavaco LM, Lund O, Aarestrup FM. PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens. J Antimicrob Chemother. 2017;72(10):2764-2768.
90. Roer L, Tchesnokova V, Allesoe R, Muradova M, Chattopadhyay S, Ahrenfeldt J, et al. Development of a web tool for *Escherichia coli* subtyping based on *fimH* alleles. J Clin Microbiol. 2017;55(8):2538-2543.
91. Price LB, Johnson JR, Aziz M, Clabots C, Johnston B, Tchesnokova V, et al. The epidemic of extended-spectrum-β-lactamase-producing *Escherichia coli* ST131 is driven by a single highly pathogenic subclone, H30-Rx. mBio. 2013;4(6):e00377-00313.

Appendix A. Study design

Fifty-five hospitals participated in the 2022 survey, 48 adult and seven children's hospitals. All states and territories were represented. The hospital peer group/type[81] represented were:

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

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

The 33 laboratories that serviced the hospitals participating in AGAR collected all 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 community-onset if the first positive blood culture was collected 48 hours or less after admission, and as hospital-onset if collected greater than 48 hours after admission.

All laboratories that participated in AGAR obtained basic laboratory information for each patient episode plus varying demographic information, depending on the level at which they are enrolled in the program, 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 2022, three additional hospitals contributed data, two from New South Wales and one from Queensland, and one hospital from Queensland was only able to participate for Quarter one.

Table A1: Level of participation of laboratories that contributed data on gram-negative* bacteraemia, by state and territory, 2022

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	13	2	11
Victoria	8	0	8
Queensland	7†	0	7†
South Australia	3	0	3
Western Australia	19§	2	17§
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	55	5	50

* *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
† One hospital participated for Quarter 1 only
§ Includes 13 regional and district hospitals from north-west Western Australia

Table A2: Level of participation of laboratories that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2022

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

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

Table A3: Level of participation of laboratories that contributed data on enterococcal bacteraemia, by state and territory, 2022

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	13	2	11
Victoria	8	0	8
Queensland	7	0	7
South Australia	3	0	3
Western Australia	19*	2	17*
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	55	5	50

* 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[47] and the EUCAST v13.1[48] breakpoints from January 2023 were used in the analysis.

S. aureus were classified as MRSA if cefoxitin screen positive (Vitek®) or cefoxitin MIC > 4 mg/L (Phoenix™) and *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.[47, 48]

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.[82-84]

- 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, 2022

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

Length of hospital stay following bacteraemia

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

All-cause mortality

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

Antimicrobials tested

The antimicrobials tested 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 v12.0†		
	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 v12.0†		
	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	0.002–1	>1
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 v12.0†		
	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 2022.

* The breakpoints selected to identify resistance are described in the *Performance Standards for Antimicrobial Susceptibility Testing.* 33rd *ed. CLSI supplement* M100, 2023
† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 13.1, 2023 (www.eucast.org)
§ No category defined
# No guidelines for indicated species
** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanate 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* species, *Proteus* species and *Salmonella* species 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 whole genome sequencing (WGS).

For GnSOP WGS was performed by the Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, CIDMLS, ICPMR, Westmead Hospital using the Illumina NextSeq™ 500 platform. Data were analysed using a modification of the Nullarbor bioinformatic pipeline[49], incorporating searching contigs against the NCBI AMRFinder database (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA313047) using ABRicate[85] and AMRFinder[86], followed by a custom AMR-specific pipeline which includes a read-based search using ARIBA[87] against the CARD[88] 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 Prime 2022.1 (https://www.geneious.com). 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[89] potentially contributing to resistance were also examined manually. *fimH* type was predicted by FimTyper[90]. Detection of *H30-Rx* specific SNPs were carried out by *in silico* PCR.[91]

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[49] was used to identify the multi-locus sequence type, *van* gene (*E. faecium*), and Panton-Valentine leucocidin (MRSA). For MRSA SCC*mec* was determined using KmerFinder v3.2 and the SCCmec database curated from the Center for Genomic Epidemiology database (www.genomicepidemiology.org).

Quality control

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

Data validation

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

- Null values in the mandatory fields
- Missing MIC data
- Patient age if ≥100 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[22] 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, 2022

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, –§

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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, –§
	%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	245	180	91	75	118	51	14	33	807
	%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	210	178	54	40	71	23	13	17	606
	%R	95.7, 95.7	96.1, 96.1	98.1, 98.1	90.0, 90.0	91.5, 91.5	100.0, 100.0	100.0, 100.0	94.1, 94.1	95.4, 95.4
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	223	101	89	74	118	12	14	33	664
	%R	1.3, –#	1.0, –#	1.1, –#	0.0, –#	0.8, –#	0.0, –#	0.0, –#	0.0, –#	0.9, –#

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	199	81	54	39	70	7	13	17	480
	%R	94.5, –[#]	96.3, –[#]	98.1, –[#]	84.6, –[#]	92.9, –[#]	n/a	92.3, –[#]	94.1, –[#]	94.2, –[#]
Staphylococcus aureus	n	974	592	535	234	493	158	98	115	3,199
	%R**	81.2, 81.2	77.5, 77.5	75.9, 75.9	80.8, 80.8	80.5, 80.5	69.0, 69.0	88.8, 88.8	67.8, 67.8	78.6, 78.6
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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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 aeruginosa	n	210	124	141	83	98	20	21	38	735
	%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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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, 4.8	0.0, 6.3	16.7, 0.0	0.0, 0.0	6.3, 0.0	n/a	n/a	n/a	3.4, 3.4
	%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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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, 0.0	3.1, 3.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
	%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	974	593	536	234	495	158	98	115	3,203
	%R	10.0, 10.7	7.6, 8.4	2.1, 3.4	8.5, 9.0	3.6, 4.2	1.9, 3.2	3.1, 4.1	4.3, 4.3	6.3, 7.1
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	42.8, 43.9	41.4, 41.4	11.1, 14.3	37.5, 37.5	8.2, 8.2	n/a, n/a	7.1, 7.1	n/a, n/a	29.4, 30.7
Methicillin-susceptible *S. aureus*	n	801	523	473	194	422	149	56	106	2,724
	%R	2.9, 3.5	3.1, 4.0	0.8, 1.9	2.6, 3.1	2.8, 3.6	0.7, 0.7	0.0, 1.8	0.0, 0.0	2.2, 3.0

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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
	%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	974	593	535	234	494	158	98	115	3,201
	%R	12.8, 13.4	11.8, 12.1	14.8, 15.3	6.0, 6.0	10.3, 12.8	12.0, 12.7	26.5, 26.5	16.5, 17.4	12.6, 13.4

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	24.9, 26.6	24.3, 24.3	33.3, 34.9	17.5, 17.5	12.3, 15.1	n/a, n/a	19.0, 19.0	n/a, n/a	23.0, 24.2
Methicillin-susceptible *S. aureus*	n	801	523	472	194	421	149	56	106	2,722
	%R	10.2, 10.6	10.1, 10.5	12.3, 12.7	3.6, 3.6	10.0, 12.4	11.4, 12.1	32.1, 32.1	15.1, 16.0	10.8, 11.5
Daptomycin										
Enterococcus faecalis	n	246	179	91	44	117	22	14	32	745
	%R	0.4, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.1, –[#]
Enterococcus faecium	n	39	0	0	17	2	0	0	0	58
	%R	2.6, –[#]	n/a	n/a	0.0, –[#]	n/a	n/a	n/a	n/a	1.7, –[#]
Staphylococcus aureus	n	978	593	536	233	497	159	98	115	3,209
	%NS[§§]/R	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-resistant *S. aureus*	n	151	78	65	42	98	9	37	14	494
	%NS[§§]/R	0.0, 0.0	0.0, 0.0	1.5, 1.5	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0, 0.0	0.0, 0.0	0.2, 0.2
Methicillin-susceptible *S. aureus*	n	618	537	430	189	415	106	49	88	2,432
	%NS[§§]/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Erythromycin										
Staphylococcus aureus	n	919	593	536	233	495	158	98	115	3,147
	%R	16.2, 17.0	15.9, 16.2	15.5, 15.7	17.2, 17.2	11.5, 13.5	12.0, 12.7	26.5, 26.5	17.4, 20.0	15.5, 16.3
Methicillin-resistant *S. aureus*	n	172	70	63	40	73	9	42	9	478
	%R	29.7, 31.4	31.4, 31.4	36.5, 36.5	40.0, 40.0	16.4, 19.2	n/a, n/a	19.0, 19.0	n/a, n/a	28.7, 29.7
Methicillin-susceptible *S. aureus*	n	747	523	473	193	422	149	56	106	2,669
	%R	13.1, 13.7	13.8, 14.1	12.7, 12.9	12.4, 12.4	10.7, 12.6	11.4, 12.1	32.1, 32.1	16.0, 18.9	13.2, 13.9
Fusidic acid										
Staphylococcus aureus	n	918	593	536	234	495	158	98	115	3,147
	%R	–[§], 3.7	–[§], 1.9	–[§], 3.4	–[§], 3.4	–[§], 1.8	–[§], 1.9	–[§], 2.0	–[§], 0.9	–[§], 2.7
Methicillin-resistant *S. aureus*	n	172	70	63	40	73	9	42	9	478
	%R	–[§], 5.2	–[§], 2.9	–[§], 3.2	–[§], 7.5	–[§], 0.0	–[§], n/a	–[§], 0.0	–[§], n/a	–[§], 3.3
Methicillin-susceptible *S. aureus*	n	746	523	473	194	422	149	56	106	2,669
	%R	–[§], 3.4	–[§], 1.7	–[§], 3.4	–[§], 2.6	–[§], 2.1	–[§], 2.0	–[§], 3.6	–[§], 0.9	–[§], 2.6
Gentamicin										
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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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
	%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	974	593	536	234	495	158	98	115	3,203
	%R	2.6, 6.3	0.3, 4.9	1.5, 3.4	2.6, 2.6	0.6, 2.8	0.6, 1.3	0.0, 12.2	2.6, 5.2	1.5, 4.6
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	10.4, 20.8	2.9, 7.1	3.2, 4.8	5.0, 5.0	2.7, 4.1	n/a, n/a	0.0, 4.8	n/a, n/a	5.8, 11.3
Methicillin-susceptible *S. aureus*	n	801	523	473	194	422	149	56	106	2,724
	%R	0.9, 3.1	0.0, 4.6	1.3, 3.2	2.1, 2.1	0.2, 2.6	0.7, 1.3	0.0, 17.9	0.9, 2.8	0.7, 3.5
Linezolid										
Enterococcus faecalis	n	244	179	90	75	118	51	14	33	804
	%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	211	177	54	40	71	23	14	17	607
	%R	0.0, 0.0	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.3
Staphylococcus aureus	n	978	593	536	234	497	159	98	115	3,210
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-resistant *S. aureus*	n	174	70	63	40	73	9	42	9	480
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0, 0.0	n/a, n/a	0.0, 0.0
Methicillin-susceptible *S. aureus*	n	804	523	473	194	424	150	56	106	2,730
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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
	%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	528	408	536	234	493	115	13	115	2,442
	%R	2.1, 2.1	1.0, 1.0	2.6, 2.6	1.3, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.3, 1.3
Methicillin-resistant *S. aureus*	n	96	53	63	40	73	8	4	9	346
	%R	3.1, 3.1	1.9, 1.9	4.8, 4.8	0.0, 0.0	0.0, 0.0	n/a, n/a	n/a, n/a	n/a, n/a	2.0, 2.0
Methicillin-susceptible *S. aureus*	n	432	355	473	194	420	107	9	106	2,096
	%R	1.9, 1.9	0.8, 0.8	2.3, 2.3	1.5, 1.5	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0, 0.0	1.2, 1.2

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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, –§
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	982	593	536	234	497	159	98	115	3,214
	%R	17.8, 17.8	11.8, 11.8	11.8, 11.8	17.1, 17.1	14.7, 14.7	5.7, 5.7	42.9, 42.9	7.8, 7.8	15.0, 15.0
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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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	769	615	495	226	513	114	86	102	2,920
	%R	0.1, 1.0	0.0, 1.1	0.4, 0.4	0.0, 1.2	n/a, n/a	0.0, 0.0	0.0, 0.0	1.0, 1.0	0.2, 0.4
Methicillin-resistant *S. aureus*	n	152	78	65	41	98	9	37	14	494
	%R	0.7, 1.3	0.0, 0.0	1.5, 1.5	0.0, 0.0	0.0, 1.0	n/a, n/a	0.0, 0.0	0.0, 0.0	0.4, 0.8
Methicillin-susceptible *S. aureus*	n	617	537	430	185	415	105	49	88	2,426
	%R	0.0, 0.2	0.0, 0.2	0.2, 0.2	0.0, 0.5	0.2, 0.2	0.0, 0.0	0.0, 0.0	1.1, 1.1	0.1, 0.2
Teicoplanin										
Enterococcus faecalis	n	245	180	91	75	118	51	14	33	807
	%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	208	178	54	40	71	23	14	17	605
	%R	13.0, 20.7	6.7, 10.1	5.6, 7.4	7.5, 10.0	7.0, 8.5	4.3, 8.7	7.1, 7.1	11.8, 11.8	8.9, 13.2
Staphylococcus aureus	n	977	593	533	234	497	159	98	115	3,206
	%R	0.0, 0.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1
Tetracycline/doxycycline†‡										
Staphylococcus aureus	n	974	593	536	234	495	158	98	115	3,203
	%R	6.0, 7.5	4.6, 4.9	2.6, 3.0	0.9, 4.7	3.8, 4.0	1.3, 1.3	1.0, 2.0	2.6, 5.2	3.9, 5.0
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	19.1, 23.7	15.7, 15.7	6.3, 6.3	0.0, 0.0	4.1, 4.1	n/a, n/a	0.0, 2.4	n/a, n/a	10.9, 13.2
Methicillin-susceptible *S. aureus*	n	801	523	473	194	422	149	56	106	2,724
	%R	3.1, 4.0	3.1, 3.4	2.1, 2.5	1.0, 5.7	3.8, 4.0	1.3, 1.3	1.8, 1.8	1.9, 2.8	2.7, 3.5
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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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
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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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
	%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

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
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	972	593	536	234	495	158	98	115	3,201
	%R	0.8, 1.0	0.3, 0.3	0.4, 0.4	0.4, 0.4	0.2, 0.2	0.0, 0.0	1.0, 1.0	0.9, 0.9	0.5, 0.6
Methicillin-resistant *S. aureus*	n	172	70	63	40	73	9	42	9	478
	%R	2.9, 2.9	1.4, 1.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a, n/a	2.4, 2.4	n/a, n/a	1.7, 1.7
Methicillin-susceptible *S. aureus*	n	800	523	473	194	422	149	56	106	2,723
	%R	0.4, 0.6	0.2, 0.2	0.4, 0.4	0.5, 0.5	0.2, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.4
Vancomycin										
Enterococcus faecalis	n	245	180	91	75	118	51	14	33	807
	%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	211	178	54	40	71	23	14	17	608
	%R	48.8, 49.3	60.1, 62.4	13.0, 13.0	65.0, 65.0	16.9, 16.9	30.4, 34.8	57.1, 57.1	52.9, 52.9	45.9, 46.9
Staphylococcus aureus	n	978	593	536	234	497	159	98	115	3,210
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

CLSI = Clinical and Laboratory Standards Institute; 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 one or more 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, 2022

State or territory		Number of categories (non-multidrug-resistant)				Number of categories (multidrug-resistant)		
	Total	0	1	2	%	3	4	%
NSW	9	9	0	0	–*	0	0	–*
Vic	18	17	1	0	–*	0	0	–*
Qld	19	17	1	0	–*	1	0	–*
SA	3	3	0	0	–*	0	0	–*
WA	4	3	1	0	–*	0	0	–*
Tas	3	3	0	0	–*	0	0	–*
NT	8	7	0	0	–*	0	1	–*
ACT	1	1	0	0	–*	0	0	–*
Total	**65**	**60**	**3**	**0**	**96.9**	**1**	**1**	**3.1**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), carbapenems (meropenem), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Acinetobacter baumannii* complex includes *A. nosocomialis* (*n* = 6) and *A. pittii* (*n* = 5).

Table D2: Multiple acquired resistance in *Citrobacter koseri,* by state and territory, AGAR, 2022

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	26	22	3	1	–*	0	0	0	0	0	–*
Vic	12	11	0	0	–*	1	0	0	0	0	–*
Qld	9	8	0	1	–*	0	0	0	0	0	–*
SA	8	8	0	0	–*	0	0	0	0	0	–*
WA	14	13	1	0	–*	0	0	0	0	0	–*
Tas	4	4	0	0	–*	0	0	0	0	0	–*
NT	4	4	0	0	–*	0	0	0	0	0	–*
ACT	3	3	0	0	–*	0	0	0	0	0	–*
Total	**80**	**73**	**4**	**2**	**98.8**	**1**	**0**	**0**	**0**	**0**	**1.3**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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, 2022

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	31	14	2	3	61.3	0	0	0	0	0.0
Vic	19	6	1	0	–*	0	0	0	0	–*
Qld	7	0	3	2	–*	0	0	0	0	–*
SA	6	16	2	2	–*	0	1	0	0	–*
WA	20	3	0	1	–*	0	0	0	0	–*
Tas	4	0	0	0	–*	0	0	0	0	–*
NT	0	3	1	1	n/a	0	0	0	0	n/a
ACT	5	71	10	10	–*	0	0	0	0	–*
Total	**92**	**71**	**10**	**10**	**98.9**	**0**	**1**	**0**	**0**	**1.1**

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

* Not applicable, insufficient numbers (<30) to calculate

Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Citrobacter freundii* complex includes *C. braakii* (*n* = 7), *C. youngae* (*n* = 2).

Table D4: Multiple acquired resistance in *Klebsiella aerogenes*, by state and territory, AGAR, 2022

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	39	23	3	11	94.9	2	0	0	0	5.1
Vic	29	17	1	11	–*	0	0	0	0	–*
Qld	15	11	1	3	–*	0	0	0	0	–*
SA	13	6	1	5	–*	1	0	0	0	–*
WA	18	14	2	2	–*	0	0	0	0	–*
Tas	7	3	1	2	–*	0	1	0	0	–*
NT	3	1	0	1	–*	0	1	0	0	–*
ACT	5	1	0	4	–*	0	0	0	0	–*
Total	**129**	**76**	**9**	**39**	**96.1**	**3**	**2**	**0**	**0**	**3.9**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D5: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, AGAR, 2022

	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	85	70	6	7	97.6	1	1	0	0	0	2.4
Vic	78	63	11	4	100.0	0	0	0	0	0	0.0
Qld	30	27	3	0	100.0	0	0	0	0	0	0.0
SA	28	25	2	1	–*	0	0	0	0	0	–*
WA	43	36	5	2	100.0	0	0	0	0	0	0.0
Tas	16	11	2	3	–*	0	0	0	0	0	–*
NT	5	2	0	3	–*	0	0	0	0	0	–*
ACT	10	8	1	1	–*	0	0	0	0	0	–*
Total	**295**	**242**	**30**	**21**	**99.3**	**1**	**1**	**0**	**0**	**0**	**0.7**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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, 2022

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	47	25	17	2	93.6	1	2	0	0	0	6.4
Vic	19	12	6	1	–*	0	0	0	0	0	–*
Qld	11	6	4	1	–*	0	0	0	0	0	–*
SA	11	5	4	1	–*	1	0	0	0	0	–*
WA	9	4	4	1	–*	0	0	0	0	0	–*
Tas	7	3	3	0	–*	1	0	0	0	0	–*
NT	1	0	1	0	–*	0	0	0	0	0	–*
ACT	1	0	1	0	–*	0	0	0	0	0	–*
Total	**106**	**55**	**40**	**6**	**95.3**	**3**	**2**	**0**	**0**	**0**	**4.7**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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, 2022

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)						
	Total	0	1	2	%	3	4	5	6	7	8	%
NSW	113	84	12	10	93.8	3	2	2	0	0	0	6.2
Vic	69	53	10	4	97.1	1	1	0	0	0	0	2.9
Qld	42	36	4	1	97.6	1	0	0	0	0	0	2.4
SA	31	23	3	4	96.8	0	1	0	0	0	0	3.2
WA	48	37	4	6	97.9	0	1	0	0	0	0	2.1
Tas	9	5	1	3	–*	0	0	0	0	0	0	–*
NT	4	4	0	0	–*	0	0	0	0	0	0	–*
ACT	6	5	1	0	–*	0	0	0	0	0	0	–*
Total	**322**	**247**	**35**	**28**	**96.3**	**5**	**5**	**2**	**0**	**0**	**0**	**3.7**

Multidrug-resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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, 2022

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	21	16	3	1	–*	1	0	0	0	–*
Vic	16	11	3	1	–*	0	1	0	0	–*
Qld	16	16	0	0	–*	0	0	0	0	–*
SA	0	0	0	0	n/a	0	0	0	0	n/a
WA	18	16	1	0	–*	0	1	0	0	–*
Tas	12	12	0	0	–*	0	0	0	0	–*
NT	10	9	1	0	–*	0	0	0	0	–*
ACT	3	2	1	0	–*	0	0	0	0	–*
Total	**96**	**82**	**9**	**2**	**96.9**	**1**	**2**	**0**	**0**	**3.1**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories; 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 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, 2022

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	9	1	4	0	–*	3	0	1	0	–*
Vic	15	3	12	0	–*	0	0	0	0	–*
Qld	2	1	0	0	–*	1	0	0	0	–*
SA	1	0	1	0	–*	0	0	0	0	–*
WA	5	0	4	0	–*	1	0	0	0	–*
Tas	1	0	1	0	–*	0	0	0	0	–*
NT	1	0	1	0	–*	0	0	0	0	–*
ACT	3	0	2	0	–*	0	1	0	0	–*
Total	**37**	**5**	**25**	**0**	**81.1**	**5**	**1**	**1**	**0**	**18.9**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable (insufficient numbers)

Note: Antimicrobial categories (agents) are antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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, 2022

State or territory	Number of categories (non-multidrug-resistant)					Number of categories (multidrug-resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	95	22	53	15	94.7	3	2	0	0	0	5.3
Vic	52	21	20	7	92.3	2	2	0	0	0	7.7
Qld	36	11	23	2	100.0	0	0	0	0	0	0.0
SA	7	1	6	0	–*	0	0	0	0	0	–*
WA	4	2	1	1	–*	0	0	0	0	0	–*
Tas	8	2	5	0	–*	0	1	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	0	n/a
ACT	10	5	5	0	–*	0	0	0	0	0	–*
Total	**212**	**64**	**113**	**25**	**95.3**	**5**	**5**	**0**	**0**	**0**	**4.7**

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

* Not applicable (insufficient numbers)

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone 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 the quinolone resistance-determining region (QRDR) of DNA gyrase (*gyrA*, *gyrB*) and/or topoisomerase IV (*parC*, *parE*). 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 or genes coding for efflux pumps (*qepA*, *oqxAB*).[66, 67]

The fluoroquinolone resistance determinants detected in ciprofloxacin-resistant *Salmonella* species in the 2022 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, 2022

Species	Mutations in QRDR			PMQR genes	Total
	gyrA	*parC*	parE		
Salmonella (non-typhoidal)					11
	–*	T57S	–*	*qnrB19*	3
	S83Y	–*	–*	–*	2
	S83Y	T57S	–*	*qnrS1*	2
	S83F	T57S	–*	–*	1
	D87Y	–*	–*	–*	1
	S83F, D87N	S80I	–*	–*	1
	S83F, D87Y	T57S, S80I	–*	–*	1
Salmonella (typhoidal)					31
S. Typhi (*n* = 28)	S83F	–*	–*	–*	19
	S83F	–*	–*	*qnrS1*	3
	S83F, D87N	S80I	–*	–*	2
	D87N	–*	L416F	–*	1
	S83F	S80I	–*	–*	1
	S83Y	–*	–*	–*	1
	S83Y	E84G	–*	–*	1
S. Paratyphi A (*n* = 3)	S83F	T57S	–*	–*	3

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[89], 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* = 801), by ciprofloxacin MIC, AGAR, 2022

QRDR mutations				Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*	*PMQR*	≤0.25	0.5	>0.5	Total
–*	–*	–*	–*	159	3	3	165
–*	–*	–*	*qnr*	45	9	9	63
–*	–*	I355T	–*	1	0	0	1
–*	–*	I355T	*qnr*	1	0	0	1
–*	–*	I529L	–*	12	0	0	12
–*	–*	I529L	*aac(6')–*Ib–*cr, qnr*	0	0	1	1
–*	–*	I529L	*qnr*	1	0	0	1
–*	S57T	I355T	–*	1	0	0	1
–*	S80I	L416F	–*	0	0	3	3
–*	S80I	S458A	–*	0	0	1	1
–*	S80I, E84V	–*	–*	0	0	4	4
–*	S80I, E84V	–*	*aac(6')–*Ib–*cr*	0	0	4	4
–*	T57S	–*	–*	1	0	0	1
D87N	–*	–*	–*	2	0	0	2
D87Y	–*	–*	–*	1	0	1	2
D87Y	S57T	–*	–*	3	0	0	3
S83A	–*	–*	*qnr*	2	1	1	4
S83L	–*	–*	–*	1	0	0	1
S83L	–*	–*	–*	44	23	7	74
S83L	–*	–*	*aac(6')–*Ib–*cr*	0	0	1	1
S83L	–*	–*	*qnr*	0	5	11	16
S83L	–*	D476N	–*	1	0	0	1
S83L	–*	I529L	–*	29	61	12	102
S83L	–*	I529L	*qnr*	0	0	1	1
S83L	–*	I529L, S458A	–*	1	0	1	2
S83L	–*	I529L	–*	0	2	2	4
S83L	–*	S458A	–*	0	0	5	5
S83L	E84G	–*	–*	0	0	1	1
S83L	S57T	–*	–*	1	0	0	1
S83L	S80I	–*	–*	0	0	5	5
S83L	S80I	–*	*qnr*	0	0	3	3
S83L	S80I, E84V	I529L	–*	0	0	1	1
S83L	S80R	–*	–*	0	0	1	1
S83L, D87G	S80I	–*	–*	0	0	1	1
S83L, D87N	S57T, S80I	–*	–*	0	0	1	1
S83L, D87N	S57T, S80I	S458A	–*	0	0	1	1
S83L, D87N	S57T, S80I	S458A	*aac(6')–*Ib–*cr*	0	0	2	2
S83L, D87N	S80I	–*	–*	1	0	5	6
S83L, D87N	S80I	–*	*qnr*	0	0	2	2
S83L, D87N	S80I	E460D	–*	0	0	6	6
S83L, D87N	S80I	L416F	–*	0	0	51	51
S83L, D87N	S80I	L416F	*aac(6')–*Ib–*cr*	0	0	12	12
S83L, D87N	S80I	L416F	*qnr*	0	0	6	6
S83L, D87N	S80I	L445H	–*	0	0	1	1
S83L, D87N	S80I	S458A	–*	0	1	16	17
S83L, D87N	S80I	S458A	*aac(6')–*Ib–*cr*	0	0	12	12

QRDR mutations				Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*	*PMQR*	≤0.25	0.5	>0.5	Total
S83L, D87N	S80I	S458A	*qnr*	0	0	3	3
S83L, D87N	S80I, E84G	–*	–*	0	0	1	1
S83L, D87N	S80I, E84V	–*	–*	0	0	2	2
S83L, D87N	S80I, E84V	I529L	–*	0	0	113	113
S83L, D87N	S80I, E84V	I529L	*aac(6')–*Ib–*cr*	0	0	60	60
S83L, D87N	S80I, E84V	I529L	*qnr*	0	0	6	6
S83L, D87N	S80R	–*	*qnr*	0	0	1	1
S83L, D87V	S80I	–*	*qnr*	0	0	1	1
S83L, D87Y	S80I	–*	–*	0	0	1	1
S83L, D87Y	S80I	–*	*aac(6')–*Ib–*cr*	0	0	1	1
S83L, D87Y	S80I	S458A	–*	0	0	2	2
S83L, D87Y	S80I	S458A	*aac(6')–*Ib–*cr*	0	0	1	1
S83L, D87Y	S80I	S458A	*qnr*	0	0	1	1
S83L, D87Y	S80I, E84V	I529L	–*	0	0	2	2
Total				307	105	389	801

MIC = minimum inhibitory concentration; 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[89], and/or presence of plasmid-mediated quinolone resistance genes (*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* = 147), by ciprofloxacin MIC, AGAR, 2022

QRDR mutations			Ciprofloxacin MIC (mg/L)			
gyrA	parE	PMQR	≤0.25	0.5	>0.5	Total
–*	–*	–*	57	5	4	66
–*	–*	*aac(6')-Ib-cr*	2	0	1	3
–*	–*	*aac(6')-Ib-cr*, *qnr*	0	0	23	23
–*	–*	qnr	2	11	26	39
–*	I529L	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
D87Y	–*	–*	0	0	1	1
S83F	–*	*qnr*	0	0	1	1
S83F, D87A	–*	*aac(6')-Ib-cr*, *qnr*	0	0	2	2
S83I	–*	–*	0	0	1	1
S83I	–*	*aac(6')-Ib-cr*	0	0	2	2
S83I	–*	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
S83I	–*	*qnr*	0	0	1	1
S83Y	–*	–*	0	0	1	1
S83Y	–*	*aac(6')-Ib-cr*	1	0	4	5
Total			62	16	69	147

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[89], 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.

This page is left intentionally blank

AUSTRALIAN COMMISSION
ON SAFETY AND QUALITY IN HEALTH CARE

Level 5, 255 Elizabeth Street, Sydney NSW 2000
GPO Box 5480, Sydney NSW 2001

Phone: (02) 9126 3600

Email: mail@safetyandquality.gov.au
Website: www.safetyandquality.gov.au