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AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Sepsis Outcome Programs

2020 report

AGAR

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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. AGAR is a longstanding collaboration of clinicians and scientists from major microbiology laboratories across Australia. The Group has grown to involve 30 laboratories servicing 49 institutions across Australia, including four private institutions and 11 regional or district hospitals from north-west Western Australia (Table 1).

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 state and territory health departments.

Antimicrobial resistance continues to be one of the greatest threats to human and animal health, and to food safety. This level of concern is recognised by the World Health Organization and, the Australian Government through the *Australia's National Antimicrobial Resistance Strategy – 2020 and Beyond* (the National AMR Strategy)[1] and has been reported on in a series of publications by the Commission as part of the AURA Surveillance System. Overuse, and inappropriate use, of antimicrobials is one of the key factors in driving resistance. The other major factor is the spread of resistant bacteria and their resistance genes, and the need for improved infection control and prevention both in healthcare facilities and in the community. Antimicrobial resistance is a risk to patient safety, because it reduces the number of antimicrobials available to treat infections; increases treatment times and costs; increases the potential for hospitalisation for conditions usually managed in the community; and, increases overall morbidity and mortality.

Antimicrobial-resistant bacteria can spread rapidly between people across all settings: primary care services, hospitals, residential aged care homes and in the community. The spread of these bacteria has the potential to not only significantly affect individuals, but also their communities, the health services where they receive care, and the health system as a whole. Enhanced surveillance programs such as AGAR play a critical role in identifying, monitoring and reporting on rates of resistant bacteria with the highest risk of causing harm to humans.

The AURA Surveillance System supports monitoring and reporting on Australia's antimicrobial use and resistance patterns. In 2020, AURA data were submitted to the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) for the first time, following a change in the GLASS requirements to allow receipt of aggregated data without a denominator. Data from the AGAR 2019 Sepsis Outcome programs were submitted on five pathogens from blood (*Staphylococcus aureus*, *Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter* species and *Salmonella* species). Annual submission of AGAR data to GLASS will continue, and from 2021, AGAR data will be complemented by APAS data.

AGAR 2020 data show that episodes of bacteraemia in Australia had their onset overwhelmingly in the community. For the Gram-negative Sepsis Outcome Program (GNSOP) and the Australian Enterococcal Sepsis Outcome Program (AESOP), the most frequent predisposing clinical manifestations were urinary tract infection and biliary tract infection. 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 the Australian Staphylococcal Sepsis Outcome Program (ASSOP), the most frequent principal clinical manifestations were osteomyelitis/septic arthritis and skin and skin structure infections. Strategies to reduce blood stream infections should take this information on clinical manifestation (sources of bacteraemia) into account.

AGAR data show a longitudinal trend of increasing *E. coli* resistance to key anti-gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin. The steady rise in resistance to fluoroquinolones is more striking in hospital-onset bacteraemia, with a change from 13.7% to 21.3% between 2013 and 2019; it was 21.8% in 2020. Increasing fluoroquinolone resistance in Australia remains a concern.

This data continues to be used to inform clinical and public health policy and practice. While AMR continues to be a challenge to delivery of safe and effective health care, the data and information provided by AURA, including from AGAR, is a substantial resource to inform effective responses to reduce the impact of AMR. The AURA Surveillance System also supports the implementation and assessment of the impact of the antimicrobial stewardship and infection prevention and control requirements of National Safety and Quality Health Service (NSQHS) Standards[2] and the National AMR Strategy.[1]

To ensure that patients receive the best possible care, the Commission will continue to support states and territories and the private health sector in utilising AGAR and other AURA data to refine and strengthen their approaches to infection prevention and control and antimicrobial stewardship. The Commission also continues to work with Therapeutic Guidelines: Antibiotic 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; 2020

A. Key findings

Gram-negative species

- A total of 8,752 episodes of gram-negative bacteraemia were reported, including *Enterobacterales* (89.9%), *Pseudomonas aeruginosa* (8.8%) and *Acinetobacte*r species (1.3%). Of the *Enterobacterales*, three genera – *Escherichia* (62.1%), *Klebsiella* (19.8%) and *Enterobacter* (5.9%) – contributed 87.8% of all *Enterobacterales* bacteraemias
- The all-cause 30-day mortality rate for gram-negative bacteraemia was 11.4% (9.7% for *E. coli*, 15.5% for *P. aeruginosa*)
- Urinary tract infection was the most frequent source of sepsis or clinical manifestation (*Enterobacterales* 44.5%; *P. aeruginosa* 25.9%)
- Of *E. coli* isolates causing community-onset (CO) bacteraemia, which accounted for 85% of all *E. coli* bacteraemia cases, 12.4% were ceftriaxone resistant
- There was a significant difference in 30-day all-cause mortality between CO and hospital-onset (HO) (8.6% versus 14.9%, P < 0.01) *E. coli* bacteraemia episodes
- In 2020, an extended-spectrum β-lactamase (ESBL) phenotype was found in 14.7% of *E. coli* (CO 13.5%, HO 21.3%) and 10.0% of *Klebsiella pneumoniae* complex (CO 9.1%, HO 12.5%), and this was more common in isolates from patients defined as HO
- Fluoroquinolone resistance in *E. coli* is a continuing concern; and is most striking in HO bacteraemia, with a change from 13.7% to 21.3% between 2013 and 2019; it was 21.8%in 2020
- The low rates of carbapenemase-producing *Enterobacterales* (CPE) bacteraemia are encouraging (0.3% overall, mostly carrying $bla_{\text{IMP-4}}$). For *Enterobacter cloacae* complex the figure is higher at 3.5% overall (CO 2.9%, HO 4.3%)
- The rate of colistin resistance – when tested for but excluding species with intrinsic resistance – was 0.4% (4/1,035). Among all sequenced isolates, one *E. coli* isolate was found to carry *mcr-1.* The patient attended an institution in South Australia.

Enterococcus species

- A total of 1,230 episodes of enterococcal bacteraemia were reported; the majority (93.9%) of enterococcal bacteraemia episodes were caused by *Enterococcus faecalis* or *E. faecium*
- The majority of *E. faecalis* bacteraemias were CO (71.4%), while in *E. faecium* bacteraemias only 33.2% were CO
- The most frequent source of sepsis or clinical manifestation for *E. faecalis* was urinary tract infection (25.3%); for *E. faecium*, it was biliary tract infection (including cholangitis) (21.7%)
- The combined 30-day all-cause mortality for *E. faecalis* and *E. faecium* was 18.3%; the 30-day all-cause mortality for *E. faecium* bacteraemia was higher, particularly in HO vancomycin-susceptible (24.2%) isolates
- There was no significant difference in 30-day all-cause mortality between *E. faecalis* (17.3%) and *E. faecium* (19.6%), or between vancomycin-resistant and vancomycin-susceptible *E. faecium* episodes
- The length of hospital stay following enterococcal bacteraemia was more than 30 days for 22.8% of patients
- Of bloodstream infections caused by *E. faecium*, 32.6% were phenotypically vancomycin resistant, and 35.2% of *E. faecium* harboured *vanA* and/or *vanB* genes (*vanA* 13.7%, *vanB* 21.3%, both 0.2%). In 2019 45.2% of *E. faecium* harboured *vanA* and/or *vanB* genes
- Of vancomycin-resistant *E. faecium* (VRE) bacteraemias, 36.3% were due to *vanA*-harbouring isolates. This type of vancomycin resistance has emerged steadily in the past eight years and is now the dominant genotype in New South Wales, Western Australia, and Tasmania.

- There were 71 *E. faecium* multi-locus sequence types (STs), of which ST17, ST1424, ST80, ST796, ST78, ST1421, ST555, and ST117 were the most frequently identified
- *vanA* genes were detected in seven STs, and *vanB* genes were detected in 10 STs; one ST harboured *vanA* and *vanB* genes. The clonal diversity of *E. faecium* harbouring *van* genes varied across Australia
- Compared to European countries for rates of resistance to vancomycin in *E. faecium,* Australia was ranked 10th in 2020 and in 2019 was ranked fourth.

Staphylococcus aureus

- A total of 2,734 *Staphylococcus aureus* bacteraemia episodes were reported, 79.7% of which were CO. Of all episodes 17.6% were methicillin resistant
- The 30-day all-cause mortality was 13.5%. Mortality for methicillin-resistant *S. aureus* (MRSA) (14.2%) and methicillin-susceptible *S. aureus* (MSSA) (13.3%) were similar; and was higher in HO (15.9%) than CO (12.8%) bacteraemia
- The 30-day all-cause mortality for *S. aureus* was significantly lower among children (1.5%, 4/265) compared to adults (15.1%, 292/1,935) ($P < 0.01$)
- Osteomyelitis/septic arthritis (22.8%) and skin and skin structure infections (19.2%) were the most common principal clinical manifestations
- The hospital length of hospital stay was more than 30 days in 24.7% of patients (28.2% in MRSA, 23.9%in MSSA)
- In MRSA, resistance to erythromycin and clindamycin has continued to decline overall, largely due to the substantial decline in the multi-resistant ST239-III clone
- Community-associated methicillin-resistant *S. aureus* (CA-MRSA) strains were the dominant cause of MRSA bacteraemia
- Five healthcare-associated methicillin-resistant *S. aureus* (HA-MRSA) clones were identified; the dominant HA-MRSA clone was ST22-IV (EMRSA-15). No HA-MRSA isolates harboured the Panton-Valentine leucocidin (PVL) associated genes
- The majority of EMRSA-15 bacteraemias were in the community, which is consistent with the prevalence of this clone in aged care homes in Australia
- Forty-eight CA-MRSA clones were identified; the dominant CA-MRSA clone was ST93-IV (Queensland clone)
- Overall, 43.9% of CA-MRSA isolates harboured the PVL associated genes
- The Queensland clone of CA-MRSA (ST93-IV), which harbours the PVL associated genes, was seen in all states and territories except Tasmania and the Australian Capital Territory; it is now the most common CA-MRSA clone in all states and territories except New South Wales
- The ST45-V MRSA clone remains prominent in New South Wales and is associated with both CO and HO infections.

B. Implications of key findings for health care

When interpreting AGAR data, it is important to consider changes in surveillance coverage between 2013 and 2020. AGAR has increased the number of institutions from 26 in 2013 to 46 in 2018 and 49 in 2020. In addition, the relative distribution of sites has changed with the addition of three more paediatric and/or facilities providing specialist obstetric services, from 2017, and one additional site in 2019 and another in 2020 and the inclusion of hospitals from north-west regional Western Australia from 2015.

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

Gram-negative resistance

The percentage resistance in *E. coli* in 2020 was similar to 2019 for all antimicrobial agents tested except for ampicillin, where a decrease in resistance was seen. Resistance in *K. pneumoniae* complex was also similar or slightly less, although there was a slight increase in the percentage of resistance to the third-generation cephalosporins.

AGAR data show a longitudinal trend of increasing *E. coli* resistance to key anti-gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin. The steady rise in resistance to fluoroquinolones is more striking in hospital-onset bacteraemia, with a change from 13.7% to 21.3% between 2013 and 2019; it was 21.8% in 2020.

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.

Prevalence of extended spectrum beta-lactamases

Two additional trends have become apparent: extended spectrum beta-lactamases (ESBLs) in *Enterobacter* species, and the emergence of specific types of ESBLs (CTX-M enzymes) in *E. coli* from the community. The latter is part of a global epidemic.[3-5] 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.

ESBLs in gram-negative organisms have a considerable impact on resistance patterns and limit choices for therapy. Almost one in seven (14.7%) *E. coli* isolates displayed this phenotype in 2020, with little change since 2018. This phenotype is significantly more common in hospital-onset compared to community-onset *E. coli* infection, with 1 in 5 (21.3%) demonstrating this pattern in hospital-onset infection compared to 13.5% for community-onset isolates. In hospital-onset *K. pneumoniae* complex isolates, this phenotype is also more common than for community-onset isolates (12.5% versus 9.1%), although the difference was not significant. The prevalence of ESBLs also varies by state and territory. These variations are small for *E. coli* but for *K. pneumoniae,* proportions are noticeably higher in Victoria and the Northern Territory. Whilst CTX-M-type enzymes occur in community-acquired infections, the different rates in hospital-onset infection suggest opportunities for further control.

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, OXA-23, GES-5, and IMI) were detected in isolates from just over one-third (17/38, 45%) of the contributing institutions from non-remote/very remote regions. $bla_{\text{IMP-4}}$ accounted for 68% (19/28) of all CPE.

Invasive CPE infections are particularly notable in Victoria (13/1,460, 0.9%) and New South Wales (9/2,473, 0.4%), compared to other states and territories. Nine of 13 (69.2%) CPE from Victoria were from one institution. No CPE were found in South Australia, Tasmania, and the Northern Territory.

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*.[6]

Changing patterns in *Enterococcus* species

Total numbers of enterococcal bacteraemias identified by AGAR, excluding those from two institutions that contributed in 2019 or 2020 only, decreased in 2020 compared to 2019 (2019: 1,340; 2020: 1,212, down 9.6%). The decrease was mostly in the number of *E. faecium* (2019: 591; 2020: 480, down 18.8%) rather than *E. faecalis* (2019: 684; 2020: 658, down 3.8%).

The number of VRE isolates decreased; 158 in 2020, compared to 247 in 2019. There was a reduction in overall vancomycin resistance rates in *E. faecium* from 41.6% to 32.6%, down 21.7% ($P < 0.01$). There was a significant decrease in VRE as a proportion of all enterococcal isolates at 12.8%, it was 18.1% in 2019. The overall contribution of *vanA* and *vanB* genes to VRE varied according to jurisdiction. *vanA*-harbouring types are dominant in New South Wales, Western Australia, and Tasmania, whilst *vanB*-harbouring types are dominant in Victoria, Queensland, South Australia, and the Northern Territory.

The gradual shift to *vanA*-harbouring *E. faecium* creates the potential for the loss of a valuable treatment choice, namely teicoplanin, which is active only against *vanB*-harbouring types. 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 was methicillin resistant throughout Australia remained stable over the years 2013–2020, although there were notable variations at state and territory level.

The total number of *S. aureus* bacteraemias identified by AGAR, excluding isolates from two institutions that contributed in 2019 or 2020 only, decreased in 2020 compared to 2019 (2019: 3,044; 2020: 2,700, down 11.3%). This trend was seen in all states and territories except in the Northern Territory, where there was a 28.1% increase (64 to 82). Overall, the proportion of MRSA decreased by 0.7 percentage points, from 18.3% to 17.6% (down 4.2%), HO infections decreased from 22.9% to 19.7%, whilst community MRSA rates remained stable at 17%.

Relative to 2019, there were no significant differences in the proportion of MRSA in the states and territories, however there was a decrease in the proportion of MRSA in South Australia (15.1% in 2019, 10.9% in 2020, down 28%), Tasmania (11.9% in 2019, 5.5% in 2020, down 53%), and the Australian Capital Territory (16.5% in 2019, 8.2% in 2020, down 50%).

Since 2013, there have been significant increases in the proportion of CA-MRSA clones nationally, notably in New South Wales, Western Australia and the Northern Territory. The proportion of HA-MRSA clones declined nationally, notably in New South Wales, Victoria, Queensland, South Australia, and the Northern Territory

In 2020, CA-MRSA clones accounted for 14.2% (387/2,734) of all *S. aureus*; in 2019, it was 13.7% (433/3,157). ST93-IV was the most prevalent CA-MRSA clone (100/387, 25.8%), and was found in all states and territories except New South Wales, where ST45-V continued to dominate. In Victoria, ST93-IV accounted for 25.0% (17/68) of all MRSA, up from 14.3% (12/84) in 2019.

Hospital-associated MRSA clones accounted for 2.5% (69/2,734) of all *S. aureus* in 2020. ST22-IV was the most common HA-MRSA clone (59/69, 85.5%), found in all states and territories except for South Australia, where only CA-MRSA clones were detected.

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 blood stream infection in *Enterobacterales*, *P. aeruginosa*, and *E. faecalis* episodes. In 2020, biliary and non-biliary intra-abdominal infections were the most common clinical manifestations associated with *E. faecium*.

Device-related bacteraemia accounted for 8.2% (906/11,048) of bacteraemia across all the AGAR surveillance programs in 2020. The rate was 9.1% in 2019. The decrease was notable for staphylococcal episodes (16.3% versus 18.9%). Total numbers are dominated by gram-negative (*n* = 377) bacteria and *S. aureus* (*n* = 405) 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, *S. aureus* bacteraemia is commonly associated with intra-vascular catheters and/or devices and prosthetic joints. Continuing attention to the NSQHS Standards requirements for optimum medical device management[7] and the Commission's *Management of Peripheral Intravenous Catheters Clinical Care Standard*[8] are important for all health service organisations to prevent these types of infections.

Variation across states and territories

Resistance rates vary considerably across states and territories. Methicillin resistance in *S. aureus* ranged from 5.5% in Tasmania to 48.8% in the Northern Territory. *E. coli* resistance to third-generation cephalosporins, aminoglycosides and fluoroquinolone was lowest is Tasmania (6.0%, 4.5%, 8.0%, respectively) and highest in the Northern Territory (19.8%, 20.8% 20.8%). For *K. pneumoniae* complex, the lowest resistance for the same antimicrobial classes was in Western Australia (3.7%, 2.1%, 2.6%). The highest resistance to third-generation cephalosporins and aminoglycosides in this species was in the Northern Territory (27.0%, 24.3%, respectively), and for fluoroquinolones, in Victoria (17.7%). Rates of vancomycin resistance in *E. faecium* ranged from 7.9% in South Australia to 83.3% in the Northern Territory. Teicoplanin resistance was more common in New South Wales (22.2%), although down from 32.5% in 2019.

Appropriate adaptation of national treatment guidelines 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. *Enterococcus faecium* (66.8%) was more commonly hospital onset than *E. faecalis* (28.6%). Vancomycin-resistant *E. faecium* bacteraemia accounted for 5.1% (35/688) of all community-onset enterococcal bacteraemia, compared to 22.9% (124/542) 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 (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 2020, compared to European data available at the time of publication, for fluoroquinolone resistance in *E. coli* (16.1% versus 23.5%) and *K. pneumoniae* (9.9% versus 33.6%), and for third-generation cephalosporin resistance in *K. pneumoniae* (9.1% versus 33.5%). Australia's ranking for resistance to third-generation cephalosporins in *E. coli* (13.6%) was however similar to the EU/EEA average (15.2%).

C. Response

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

- Provide advice for the Therapeutic Guidelines: Antibiotic[9] 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 are used to inform local empirical and therapeutic antimicrobial recommendations and formulary management
- 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*[10] 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 ensure that AMR and antimicrobial use data are readily available to inform antimicrobial stewardship and infection prevention and control programs
- Promote effective infection prevention and control measures, such as those included in the *Recommendations for the control of carbapenemase-producing* Enterobacterales *(CPE). A guide for acute care health service organisations*[6], 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 blood stream infections, particularly in relation to invasive medical devices.

1. Background and objectives

This fifth amalgamated report on sepsis outcome programs operated by the Australian Group on Antimicrobial Resistance (AGAR) presents analyses of antimicrobial resistance (AMR) associated with episodes of bacteraemia (blood stream infection) that were reported by 49 participating Australian public and private institutions across Australia in 2020.

AGAR currently focuses on bloodstream infections and has three major programs: the Gram-negative Sepsis Outcome Program (GNSOP), the Australian Enterococcal Sepsis Outcome Program (AESOP) and the Australian Staphylococcal Sepsis Outcome Program (ASSOP). AGAR's focus on bacteraemia allows examination of laboratory-confirmed, invasive infections and comparison of rates over time for hospitals, states and territories. AGAR compares Australian data with the European Antimicrobial Resistance Surveillance Network, enabling benchmarking and trend projections. AGAR has collected ongoing data on the prevalence of antimicrobial resistance in Australia over a long period using standardised methods.

The 49 institutions across Australia that currently contribute to AGAR, including five private institutions, are listed in Table 1.

Historically, the main focus of AGAR was antimicrobial resistance in *Staphylococcus aureus*. The scope broadened over time to include studies on *Escherichia coli*, *Enterobacter* species, *Klebsiella* species, *Haemophilus influenzae, Streptococcus pneumoniae* and *Enterococcus* species. It now concentrates on the three groups of pathogens within the listed programs.

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

Table 1 Hospitals that contributed to AGAR, by state and territory, 2020

State or territory	Hospital
New South Wales	Children's Hospital Westmead
	Concord Repatriation General Hospital
	John Hunter Hospital
	Liverpool Hospital
	Nepean Hospital
	Royal North Shore Hospital
	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 Women's and Children's Hospital
	St Vincent's Hospital
Queensland	Gold Coast Hospital
	Queensland Children's Hospital†
	Prince Charles Hospital†
	Princess Alexandra Hospital†
	Royal Brisbane and Women's Hospital
	Greenslopes Private Hospital§
South Australia	Flinders Medical Centre
	Royal Adelaide Hospital
	Women's and Children's Hospital#
Western Australia	Fiona Stanley Hospital
	Joondalup Hospital
	North-west regional Western Australia (Broome, Derby, Fitzroy Crossing, Halls Creek, Karratha, Kununurra, Newman, Onslow, Port Hedland 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

* Microbiology services provided by Monash Medical Centre (Monash Health)
† Microbiology services provided by Pathology Queensland Central Laboratory
§ Microbiology services provided by Sullivan Nicolaides Pathology
# Microbiology services provided by SA Pathology, Royal Adelaide Hospital
** Microbiology services provided by PathWest Laboratory Medicine WA, Sir Charles Gairdner Hospital
†† Microbiology services provided by PathWest Laboratory Medicine WA, Fiona Stanley Hospital

1.1. Gram-negative Sepsis Outcome Program

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.

In 2004, another genus of gram-negative pathogens in which resistance can be of clinical importance – *Enterobacter* – was added. *E. coli* is the most common cause of community-onset urinary tract infection, whereas *Klebsiella* species are less common but are known to harbour important resistance mechanisms. *Enterobacter* species are less common in the community, but of high importance because of their intrinsic resistance to first-line antimicrobials used in the community. Taken together, the three groups of species surveyed are valuable sentinels for multi-drug resistance and emerging resistance in enteric gram-negative bacilli. In 2013, AGAR began the ongoing *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).

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

The objectives of the 2020 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 multi-drug resistance in the major species
- Detect emerging resistance to newer last-line agents such as carbapenems and colistin
- Examine the molecular basis of resistance to third-generation cephalosporins, quinolones and carbapenems.

1.2. Australian Enterococcal Sepsis 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.[11, 12] 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.[13-15] 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 (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, P. aeruginosa,* and *Enterobacter* species) pathogens requiring new therapies.[16]

AGAR began surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[17] In 2011, AGAR commenced the Australian Enterococcal Sepsis Outcome Program (AESOP).[18]

In order to provide data to support improved antimicrobial prescribing and patient care, the objective of AESOP 2020 was to determine the proportion of *E. faecalis* and *E. faecium* bacteraemia isolates demonstrating antimicrobial resistance with particular emphasis on:

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

1.3. Australian Staphylococcal Sepsis Outcome Program

Globally *Staphylococcus aureus* is one of the most frequent causes of hospital-acquired and community-acquired blood stream infections.[19] 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.[20]

Despite standardised treatment protocols for SAB, including prolonged antimicrobial therapy and prompt source control[21], mortality can range from as low as 2.5% to as high as 40%.[22-24] Mortality rates are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[25, 26] A prospective study of SAB conducted by 27 laboratories in Australia and New Zealand found a 30-day all-cause mortality of 20.6%. On univariate analysis, increased mortality was significantly associated with older age, European ethnicity, methicillin resistance, infections not originating from a medical device, sepsis syndrome, pneumonia/empyema and treatment with a glycopeptide or other non-β-lactam antibiotic.[27]

AGAR began surveillance of antimicrobial resistance in *S. aureus* in 1986.[28] In 2013, AGAR commenced the Australian Staphylococcal Sepsis Outcome Program (ASSOP).[29]

The primary objective of ASSOP 2020 was to determine the proportion of SAB isolates demonstrating antimicrobial resistance with particular emphasis on:

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

2. Summary of methods

Forty-nine institutions, in each state and territory of Australia, were enrolled in the 2020 AGAR programs. The AGAR laboratories collected all isolates from unique patient episodes of bacteraemia for ASSOP and AESOP, or either all or up to 200 isolates for GNSOP, from 1 January 2020 to 31 December 2020. Approval to conduct the prospective data collection, including de-identified demographic data, was given by the research ethics committees associated with each participating hospital.

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

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

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

2.1. Data fields

Laboratory data collected for each episode included an accession number, the date the blood culture was collected, the organism isolated (genus and species), and the antimicrobial susceptibility test results (minimum inhibitory concentrations) for each species. The patient's date of birth, sex and postcode of residence were also provided. If the patient was admitted to hospital, the dates of admission and discharge were recorded. Depending on the level of participation, limited clinical and outcome data were also provided. These included the principal clinical manifestation, 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, *Acinetobacter baumannii* complex comprises *A. calaoaceticus*, *A. baumannii*, *A. dijkshoorniae*, *A. nosocomialis*, *A. pittii*, and *A. seifertii*; *Enterobacter cloacae* complex comprises *E. cloacae, E. asburiae, E. kobei, E. ludwigii, E. hormaechei* and *E. nimipressuralis*; *Klebsiella pneumoniae* complex comprises *K. pneumoniae*, *K. quasipneumoniae* and *K. variicola*; and *Citrobacter freundii* comprises all species of the *C. freundii* complex (*C. freundii, C. braakii, C. gillenii, C. murliniae, C. rodenticum, C. sedlakii, C. werkmanii* and *C. youngae*). *Klebsiella aerogenes* was previously known as *Enterobacter aerogenes*.

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–A31[30] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v11.0.[31]

2.4. PCR screening and whole genome sequencing

E. coli, *Klebsiella* spp., *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone MIC >1 mg/L, or cefoxitin MIC >8 mg/L; any other *Enterobacterales* with cefepime MIC >1 mg/L; all *Enterobacterales* with meropenem MIC >0.25 mg/L; all *Acinetobacter* species or *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) and underwent PCR to detect selected resistance genes (Centre for Infectious Diseases & Microbiology Laboratory Services, ICPMR, Westmead Hospital) or whole genome sequencing (WGS) (Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, CIDMLS, ICPMR, Westmead Hospital).

The following isolates were subjected to WGS:

- all isolates with meropenem MIC >0.25 mg/L (*Enterobacterales*) or MIC >4 mg/L (*P. aeruginosa* and *Acinetobacter* species)
- all referred isolates of *P. aeruginosa*
- all referred isolates of *Acinetobacter* species
- all referred *Salmonella* and *Shigella* species
- selected *E. coli* and *K. pneumoniae,* based on phenotype (ceftriaxone, ceftazidime, and ciprofloxacin) and state and territory.

All *E. faecium* and methicillin-resistant *S. aureus* (MRSA) were subjected to WGS using the Illumina NextSeq™ 500 platform. Data were analysed using the Nullarbor bioinformatic pipeline.[32] The pipeline was used to identify the multi-locus sequence type, *van* gene (*E. faecium*), SCC*mec* (MRSA) and Panton-Valentine leucocidin (MRSA).

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

3. Results

3.1. Isolates recovered

During 2020, a total of 12,716 bloodstream isolates were reported from 49 participating institutions. Overall, the proportion of isolates from children (<18 years) was 6.4%. The proportion of *S. aureus* isolates from children was 10.9%, *Enterococcus* spp. 7.6%, *Enterobacterales* 4.6%, *P. aeruginosa* 4.0% and *Acinetobacter* spp. 24.5%.

A total of 8,752 gram-negative bloodstream isolates (51 species/complex, 20 genera) were reported. *Enterobacterales* accounted for 89.9%, followed by *P. aeruginosa* (8.8%) and *Acinetobacter* species (1.3%). Of the *Enterobacterales*, three genera – *Escherichia* (62.1%), *Klebsiella* (19.8%) and *Enterobacter* (5.9%) – contributed 87.8% of all isolates. Overall, the top 10 species by rank were *E. coli* (55.8%), *K. pneumoniae* complex (13.1%), *P. aeruginosa* (8.8%), *E. cloacae* complex (5.2%), *Proteus mirabilis* (3.2%), *K. oxytoca* (2.9%), *Serratia marcescens* (2.2%), *K. aerogenes* (1.4%), *Salmonella* species (non- typhoidal) (1.1%), and *Morganella morganii* (0.9%). These 10 species comprised 94.6% of all isolates (Table 2).

Enterobacter cloacae complex and *Salmonella* spp. episodes were more common among children than adults (14.4% versus 4.7% and 8.9% versus 1.2%, respectively).

Of 2,734 SAB episodes, 481 (17.6%; 95% confidence interval [CI] 16.2-19.1) were methicillin resistant, ranging from 5.5% (95% CI 2.7-10.9) in Tasmania to 48.8% (95% CI: 38.3-59.4) in the Northern Territory (Table 2). There was little difference in the proportion of MRSA among children (14.4%, 95% CI: 10.9-18.9) and adults (18.0%, 95% CI: 16.5-19.6)

There were 1,230 episodes of enterococcal bacteraemia. *E. faecalis* and *E. faecium* accounted for 93.9% of all enterococcal isolates (Table 2).

Table 2: Number of each species recovered, by state and territory, 2020

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Gram-negative species*	2,769	1,583	1,271	792	1,368	358	290	321	8,752
Escherichia coli	1,500	899	624	482	780	202	197	198	4,882
Klebsiella pneumoniae complex	373	210	186	81	192	30	37	38	1,147
Pseudomonas aeruginosa	264	100	162	72	102	27	12	32	771
Enterobacter cloacae complex	165	88	83	23	59	19	6	10	453
Proteus mirabilis	101	55	39	23	45	8	6	6	283
Klebsiella oxytoca	72	54	36	23	41	20	2	10	258
Serratia marcescens	74	33	32	17	24	8	0	7	195
Klebsiella aerogenes	33	27	24	4	25	6	1	4	124
Salmonella species (non-typhoidal)	27	7	19	2	19	5	11	3	93
Citrobacter freundii complex	27	11	12	9	12	8	0	3	82
Morganella morganii	32	13	8	10	14	2	0	1	80
Citrobacter koseri	23	5	10	6	16	6	5	2	73
Acinetobacter baumannii complex	20	11	9	4	6	2	7	1	60
Salmonella species (typhoidal)	16	12	6	0	2	3	0	1	40
Klebsiella species	2	19	1	4	0	0	0	0	26
Raoultella ornithinolytica	3	4	1	2	5	2	0	2	19
Acinetobacter species	2	8	0	4	3	0	0	0	17
Enterobacter species	2	0	0	12	0	0	0	0	14
Acinetobacter lwoffii	5	1	2	1	3	1	0	0	13
Proteus vulgaris	1	2	3	0	5	0	0	0	11
Providencia rettgeri	3	1	3	0	3	0	0	0	10

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Pantoea agglomerans	2	5	1	0	2	0	0	0	10
Other species (*n* = 29)	22	18	10	13	10	9	6	3	91
Enterococcus species	428	274	142	101	164	44	14	63	1,230
Enterococcus faecalis	224	134	97	59	89	27	6	31	667
vancomycin resistant, percent§	0.0	0.0	0.0	0.0	1.1	0.0	0.0	0.0	0.2
vancomycin susceptible, percent§	100.0	100.0	100.0	100.0	98.9	100.0	100.0	100.0	99.8
Enterococcus faecium	180	124	35	39	63	10	6	31	488
vancomycin resistant, percent§	29.4	64.2	14.3	7.9	8.1	20.0	83.3	19.4	32.6
vancomycin susceptible, percent§	70.6	35.8	85.7	92.1	91.9	80.0	16.7	80.6	67.4
Other enterococcal species	24	16	10	3	12	7	2	1	75
Enterococcus gallinarum	5	3	6	1	3	1	0	1	20
Enterococcus casseliflavus	6	6	2	0	3	1	1	0	19
Enterococcus raffinosus	6	3	0	1	1	0	1	0	12
Enterococcus avium	4	2	1	0	4	1	0	0	12
Enterococcus hirae	1	2	1	1	1	2	0	0	8
Enterococcus durans	1	0	0	0	0	1	0	0	2
Enterococcus species	0	0	0	0	0	1	0	0	1
Enterococcus cecorum	1	0	0	0	0	0	0	0	1
Staphylococcus aureus	807	461	473	239	448	127	82	97	2,734
methicillin resistant, percent	19.5	15.0	15.9	10.9	22.1	5.5	48.8	8.2	17.6
methicillin susceptible, percent	80.5	85.0	84.1	89.1	77.9	94.5	51.2	91.8	82.4

* *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
† *Klebsiella pneumoniae* complex Includes *K. variicola* (*n* = 76)
§ Vancomycin susceptibility was not available for three *E. faecium* (one each from Vic, SA, and WA) and one *E. faecalis* from NT

3.2. Place of onset of bacteraemia

Almost all patients with bacteraemia were admitted to hospital (8,625, 98.5% gram-negative species; 1,219, 99.1% *Enterococcus* species; 2,694, 98.5% *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, 77.7% of all episodes were community onset, with differences seen between *Enterobacterales* (79.5%), *Acinetobacter* species (61.8%) and *P. aeruginosa* (61.1%). The proportion of *Enterobacterales* that were community onset was significantly lower among children (66.6%, 239/359) than adults (80.1%, 6,020/7,512) (P < 0.01), most notable among *K. pneumoniae* complex (children 50.8%, adults 75.4%), and *E. coli* (children 74.5%, adults 85.4%).

Episodes involving *E. faecalis* and 'other' *Enterococcus* species were predominantly community onset (71.4%, 95% CI: 67.8-74.7 for *E. faecalis*). However, *E. faecium* episodes were predominantly hospital onset (66.8%; 95% CI: 62.5-70.8). The proportion of *E. faecalis* that were community onset was lower among children (61.7%, 37/60) than adults (72.3%, 439/607).

Most SABs were community onset (79.7%; 95% CI 78.2-81.2). The proportion of MRSA episodes that were community onset was lower among children (72.1%, 31/43) than adults (77.4%, 339/438).

Table 3: Species recovered, by place of onset, 2020

Organism	Community onset % (*n*)	Hospital onset % (*n*)	Total, 100%
Enterococcus species	55.9 (688)	44.1 (542)	1,230
Enterococcus faecalis	71.4 (476)	28.6 (191)	667
Vancomycin resistant	–* (1)	–* (0)	1
Vancomycin susceptible	71.3 (474)	28.7 (191)	665
Enterococcus faecium	33.2 (162)	66.8 (326)	488
Vancomycin resistant	22.0 (35)	78.0 (124)	159
Vancomycin susceptible	38.3 (125)	61.7 (201)	326
Other *Enterococcus* species (*n* = 8)	66.7 (50)	33.3 (25)	75
Gram-negative species†	77.7 (6,798)	22.3 (1,954)	8,752
Escherichia coli	85.0 (4,151)	15.0 (731)	4,882
Klebsiella pneumoniae complex	74.1 (850)	25.9 (297)	1,147
Pseudomonas aeruginosa	61.1 (471)	38.9 (300)	771
Enterobacter cloacae complex	53.9 (244)	46.1 (209)	453
Proteus mirabilis	85.2 (241)	14.8 (42)	283
Klebsiella oxytoca	73.3 (189)	26.7 (69)	258
Serratia marcescens	56.9 (111)	43.1 (84)	195
Klebsiella aerogenes	56.5 (70)	43.5 (54)	124
Salmonella species (non-typhoidal)	90.3 (84)	9.7 (9)	93
Citrobacter freundii complex	52.4 (43)	47.6 (39)	82
Morganella morganii	66.3 (53)	33.8 (27)	80
Citrobacter koseri	83.6 (61)	16.4 (12)	73
Acinetobacter baumannii complex	56.7 (34)	43.3 (26)	60
Salmonella species (typhoidal)	100.0 (40)	0.0 (0)	40
Klebsiella species	73.1 (19)	26.9 (7)	26
Raoultella ornithinolytica	84.2 (16)	15.8 (3)	19
Acinetobacter species	58.8 (10)	41.2 (7)	17
Enterobacter species	64.3 (9)	35.7 (5)	14
Acinetobacter lwoffii	69.2 (9)	30.8 (4)	13
Proteus vulgaris	81.8 (9)	18.2 (2)	11
Providencia rettgeri	70.0 (7)	30.0 (3)	10
Pantoea agglomerans	60.0 (6)	40.0 (4)	10
Other gram-negative species (*n* = 29)	78.0 (71)	22.0 (20)	91
Staphylococcus aureus	79.7 (2,180)	20.3 (554)	2,734
Methicillin resistant	76.9 (370)	23.1 (111)	481
Methicillin susceptible	80.3 (1,810)	19.7 (443)	2,253

* Insufficient numbers (<10) to calculate percentage
† *Enterobacterales, Acinetobacter* species and *Pseudomonas aeruginosa*

Note: Vancomycin susceptibility was not available for three *Enterococcus faecium* (community onset [2], hospital onset [1]) and one *E. faecalis* (community onset).

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 6,141 (70.2%) episodes involving gram-negative species; 962 (78.2%) involving *Enterococcus* species and 2,200 (80.5%) involving *S. aureus*.

For gram-negative species, the 30-day all-cause mortality rate was 11.0% for *Enterobacterales*, 15.5% for *P. aeruginosa* and 9.2% for *Acinetobacter* species. The only species for which a significant difference was seen in the 30-day all-cause mortality between community-onset and hospital-onset episodes were *E. coli* ($P < 0.01$) (Table 4). There was a significant difference in 30-day all-cause mortality between children and adults among *Enterobacterales* (5.0% versus 10.2%, $P < 0.01$), and *P. aeruginosa* (0.0% versus 1.5%, $P < 0.01$).

The 30-day all-cause mortality for *Enterococcus* species was significantly lower among children (4.5%, 4/88) compared to adults (19.5%, 170/874) ($P < 0.01$). There was no significant difference in the 30-day all-cause mortality between *E. faecium* (19.6%) and *E. faecalis* (17.3%), or between vancomycin-resistant and vancomycin-susceptible *E. faecium* episodes.

The 30-day all-cause mortality for *S. aureus* was significantly lower among children (1.5%, 4/265) compared to adults (15.1%, 292/1,935) ($P < 0.01$). There was no significant difference in 30-day all-cause mortality between methicillin-susceptible *S. aureus* (MSSA) (13.3%) and MRSA (14.2%) episodes, or between healthcare-associated MRSA (HA-MRSA) (11.1%) and community-associated MRSA (CA-MRSA) (14.0%) clones.

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), 2020

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Enterococcus species	533	15.9 (85)	429	20.7 (89)	962	18.1 (174)
Enterococcus faecalis	365	17.3 (63)	148	17.6 (26)	513	17.3 (89)
Vancomycin resistant	1	–* (0)	0	–* (0)	1	–* (0)
Vancomycin susceptible	363	17.4 (63)	148	17.6 (26)	511	17.4 (89)
Enterococcus faecium	130	13.8 (18)	262	22.5 (59)	392	19.6 (77)
Vancomycin resistant	31	19.4 (6)	100	20.0 (20)	131	19.8 (26)
Vancomycin susceptible	97	11.3 (11)	161	24.2 (39)	258	19.4 (50)
Other enterococcal species (*n* = 8)	38	10.5 (4)	19	21.1 (4)	57	14.0 (8)
Gram-negative species†	4,662	10.4 (483)	1,479	14.7 (218)	6,141	11.4 (701)
Escherichia coli	2,767	8.6 (239)	549	14.9 (82)	3,316	9.7 (321)
Klebsiella pneumoniae complex	595	11.6 (69)	224	14.7 (33)	819	12.5 (102)
Pseudomonas aeruginosa	328	15.9 (52)	235	14.9 (35)	563	15.5 (87)
Enterobacter cloacae complex	196	11.7 (23)	166	15.1 (25)	362	13.3 (48)
Klebsiella oxytoca	146	11.6 (17)	51	17.6 (9)	197	13.2 (26)
Proteus mirabilis	163	16.0 (26)	28	14.3 (4)	191	15.7 (30)
Serratia marcescens	78	16.7 (13)	60	16.7 (10)	138	16.7 (23)
Klebsiella aerogenes	50	14.0 (7)	35	25.7 (9)	85	18.8 (16)
Citrobacter freundii complex	32	9.4 (3)	30	10.0 (3)	62	9.7 (6)
Salmonella species (non-typhoidal)	56	0.0 (0)	2	0.0 (0)	58	0.0 (0)
Citrobacter koseri	47	14.9 (7)	10	10.0 (1)	57	14.0 (8)
Morganella morganii	34	17.6 (6)	22	4.5 (1)	56	12.5 (7)
Acinetobacter baumannii complex	23	13.0 (3)	20	10.0 (2)	43	11.6 (5)
Klebsiella species	17	17.6 (3)	5	0.0 (0)	22	13.6 (3)

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Acinetobacter species[§]	10	10.0 (1)	7	0.0 (0)	17	5.9 (1)
Salmonella species (typhoidal)	17	0.0 (0)	0	n/a	17	0.0 (0)
Raoultella ornithinolytica	12	16.7 (2)	3	33.3 (1)	15	20.0 (3)
Proteus vulgaris	9	33.3 (3)	2	0.0 (0)	11	27.3 (3)
Enterobacter species	8	12.5 (1)	3	0.0 (0)	11	9.1 (1)
Acinetobacter lwoffii	6	16.7 (1)	4	0.0 (0)	10	10.0 (1)
Pantoea agglomerans	6	0.0 (0)	4	25.0 (1)	10	10.0 (1)
Other gram-negative species (*n* = 29)	62	11.3 (7)	19	10.5 (2)	81	11.1 (9)
Staphylococcus aureus	1,740	12.8 (223)	460	15.9 (73)	2,200	13.5 (296)
Methicillin resistant	302	14.6 (44)	93	12.9 (12)	395	14.2 (56)
CA-MRSA	246	13.8 (34)	75	14.7 (11)	321	14.0 (45)
HA-MRSA	39	12.8 (5)	15	6.7 (1)	54	11.1 (6)
Methicillin susceptible	1,438	12.4 (179)	367	16.6 (61)	1,805	13.3 (240)

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
[†] *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
[§] Species not determined

Notes:

1. Twenty methicillin-resistant *Staphylococcus aureus* were not available for whole genome sequencing.
2. Vancomycin susceptibility was not available for two *Enterococcus faecium* (community onset) and one *E. faecalis* (hospital onset).

3.4. Patient age and sex

Age and sex were available for all patients with gram-negative, enterococcal or staphylococcal bacteraemia. For gram-negative bacteraemia, the proportion of males was 52.9%. For *Enterococcus* species and SAB, 65.1% and 66.7%, respectively, were male.

Increasing age was a surrogate risk factor for bacteraemia (Figures 1-3); only 12.9% of gram-negative species episodes, 14.1% of *Enterococcus* species episodes and 24.4% of *S. aureus* episodes were in patients aged less than 40 years. The proportion of patients aged 0-19 years was 5.1% (*n* = 449), 7.7% (*n* = 95) and 11.6% (*n* = 316) among gram-negative episodes, enterococcal episodes and *S. aureus* episodes, respectively.

Figure 1: Number of episodes of bacteraemia due to gram-negative species, by patient age group and sex, 2020

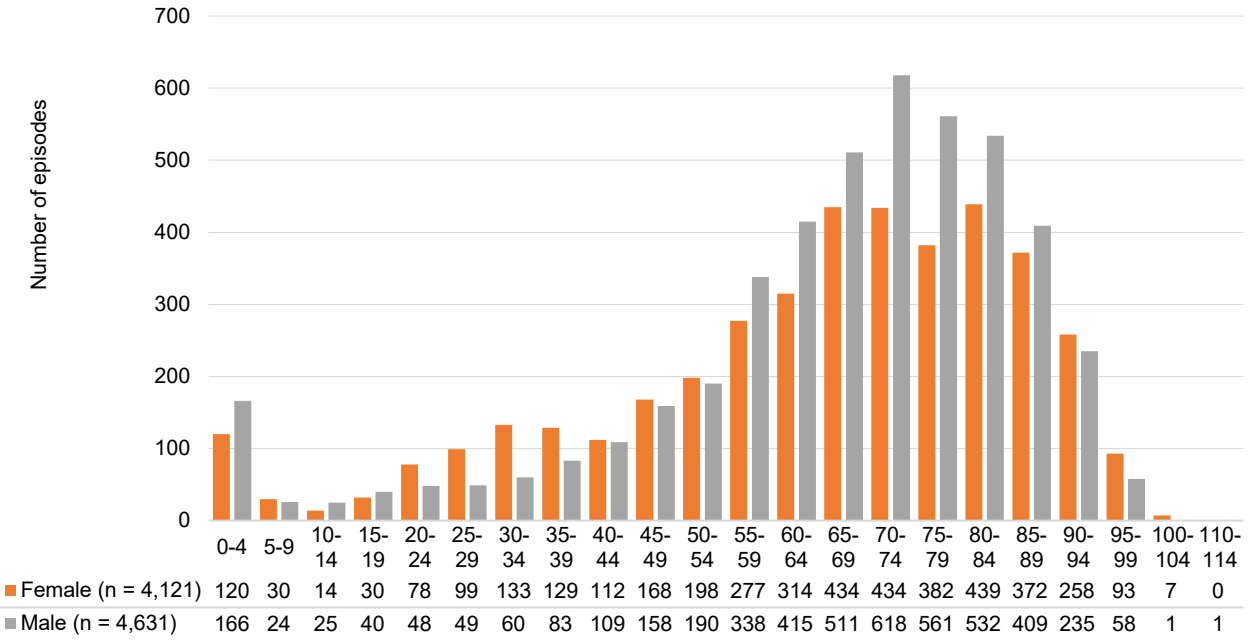


Figure 2: Number of episodes of bacteraemia due to *Enterococcus* species, by patient age group and sex, 2020

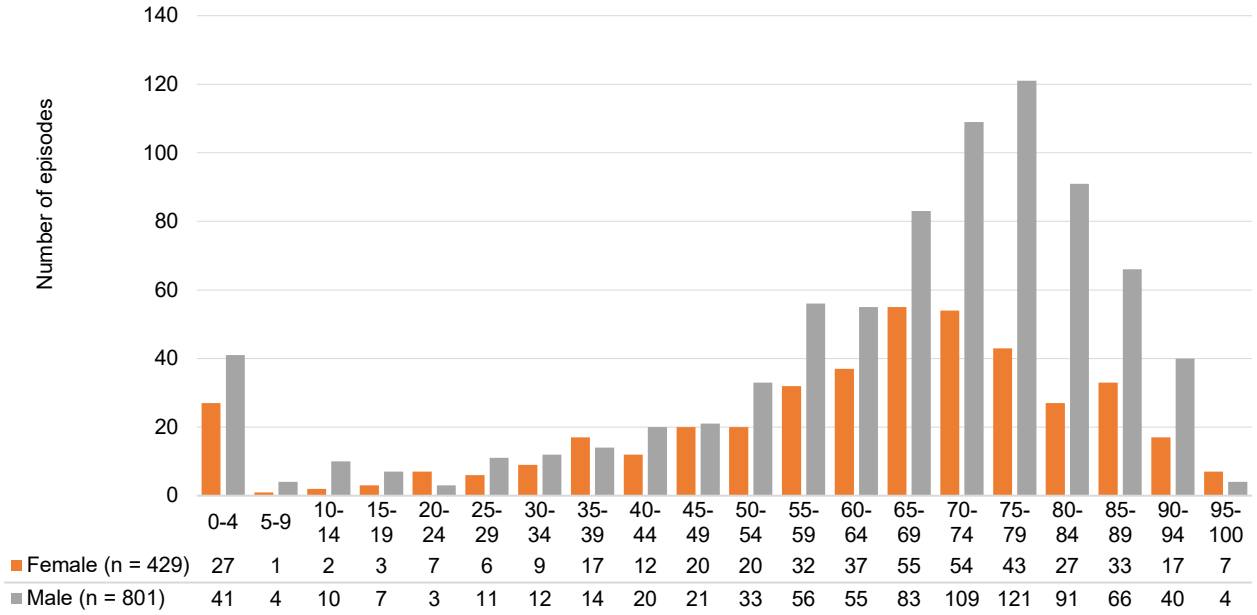
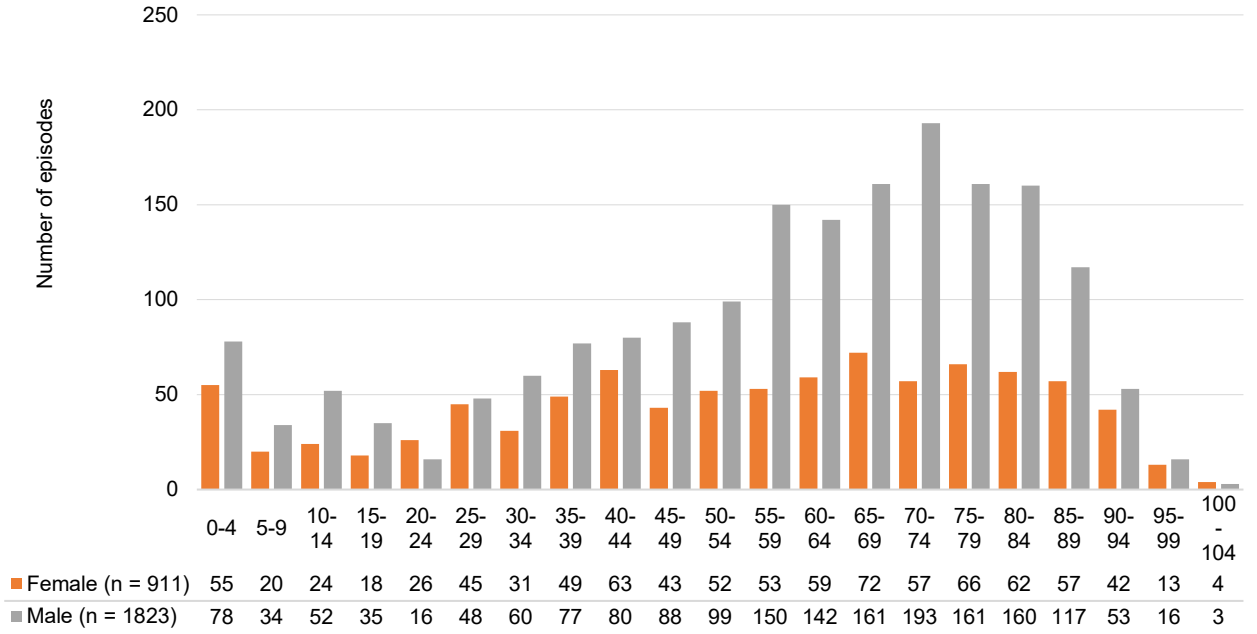


Figure 3: Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient age group and sex, 2020



3.5. Principal clinical manifestation

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

Gram-negative bacteria

The principal clinical manifestation was documented for 7,415 (84.7%) patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations for episodes caused by *Enterobacterales* were urinary tract infection (44.5%) and biliary tract infection (17.1%); for *P. aeruginosa*, urinary tract infections (25.9%) and febrile neutropenia (where known) (17.4%) were the most common (Table 5).

Urinary tract infection was the most frequent principal manifestation for both community-onset (50.2%) and hospital-onset (22.4%) episodes caused by *Enterobacterales*. For *P. aeruginosa*, urinary tract infection was most common for community onset (27.7%). For hospital-onset episodes urinary tract infection (23.0%) and febrile neutropenia (where known) (20.6%) were the most common.

Table 5: Principal clinical manifestation for gram-negative bacteraemia, by patient sex, 2020

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Gram-negative species*	3,474	3,941	7,415
Acinetobacter species	42	54	96
No focus	11.9 (5)	33.3 (18)	24.0 (23)
Device-related infection without metastatic focus	33.3 (14)	16.7 (9)	24.0 (23)
Other clinical syndrome	26.2 (11)	18.5 (10)	21.9 (21)
Skin and skin structure infection	7.1 (3)	16.7 (9)	12.5 (12)
Intra-abdominal infection other than biliary tract	7.1 (3)	7.4 (4)	7.3 (7)
Febrile neutropenia (where known)	7.1 (3)	3.7 (2)	5.2 (5)
Urinary tract infection	7.1 (3)	1.9 (1)	4.2 (4)
Biliary tract infection (including cholangitis)	0.0 (0)	1.9 (1)	1.0 (1)
Enterobacterales	3,187	3,465	6,652
Urinary tract infection	53.5 (1,706)	36.2 (1,253)	44.5 (2,959)
Biliary tract infection (including cholangitis)	13.8 (439)	20.2 (699)	17.1 (1,138)
Intra-abdominal infection other than biliary tract	8.3 (266)	11.5 (400)	10.0 (666)
Febrile neutropenia (where known)	7.3 (233)	9.2 (319)	8.3 (552)
No focus	6.2 (197)	8.7 (301)	7.5 (498)
Other clinical syndrome	4.7 (149)	5.9 (204)	5.3 (353)
Device-related infection without metastatic focus	3.5 (113)	4.3 (148)	3.9 (261)
Skin and skin structure infection	1.9 (59)	2.4 (83)	2.1 (142)
Osteomyelitis/septic arthritis	0.4 (12)	1.3 (45)	0.9 (57)
Device-related infection with metastatic focus	0.4 (13)	0.4 (13)	0.4 (26)
Pseudomonas aeruginosa	245	422	667
Urinary tract infection	18.4 (45)	30.3 (128)	25.9 (173)
Febrile neutropenia (where known)	21.6 (53)	14.9 (63)	17.4 (116)
No focus	15.5 (38)	11.1 (47)	12.7 (85)
Other clinical syndrome	10.2 (25)	11.4 (48)	10.9 (73)
Device-related infection without metastatic focus	10.2 (25)	9.5 (40)	9.7 (65)
Intra-abdominal infection other than biliary tract	6.1 (15)	10.2 (43)	8.7 (58)

Skin and skin structure infection	10.2 (25)	7.1 (30)	8.2 (55)
Biliary tract infection (including cholangitis)	6.1 (15)	3.8 (16)	4.6 (31)
Osteomyelitis/septic arthritis	1.2 (3)	1.2 (5)	1.2 (8)
Device-related infection with metastatic focus	0.4 (1)	0.5 (2)	0.4 (3)

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

Enterococcus species

The principal clinical manifestation was known for 1,146 (93.2%) patient episodes of enterococcal bacteraemia. Overall, the most frequent principal clinical manifestations were those with no identifiable focus of infection (16.7%), urinary tract (16.3), and biliary tract infections (15.9%) (Table 6). There were some significant gender differences in terms of principal clinical manifestation.

Of the hospital-onset episodes where data were available, the most frequent principal clinical manifestations were no focus (14.9%) and intra-abdominal infection other than biliary tract (14.5%). Of the community-onset episodes where data were available, the most frequent principal clinical manifestations was urinary tract infection (23.6%).

The principal manifestation was known for 1,077 of the 1,155 (93.2%) *E. faecalis* and *E. faecium* episodes (Table 7). The most common clinical manifestation for *E. faecalis* was urinary tract infection (25.3%), whereas for *E. faecium* it was biliary tract infection (including cholangitis) (21.7%). Significant differences were seen between *E. faecalis* and *E. faecium* for a number of clinical manifestations.

Table 6: Principal clinical manifestation for enterococcal bacteraemia, by patient sex, 2020

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance*
No focus	18.4 (72)	15.8 (119)	16.7 (191)	ns
Urinary tract infection	13.0 (51)	18.0 (136)	16.3 (187)	0.01 < P < 0.05
Biliary tract infection (including cholangitis)	13.8 (54)	17.0 (128)	15.9 (182)	ns
Intra-abdominal infection other than biliary tract	15.1 (59)	11.0 (83)	12.4 (142)	ns
Device-related infection without metastatic focus	12.0 (47)	8.9 (67)	9.9 (114)	ns
Febrile neutropenia (where known)	8.9 (35)	7.7 (58)	8.1 (93)	ns
Endocarditis left-sided	3.8 (15)	8.6 (65)	7.0 (80)	*P* < 0.01
Other clinical syndrome	7.9 (31)	5.2 (39)	6.1 (70)	ns
Skin and skin structure infection	3.1 (12)	3.8 (29)	3.6 (41)	ns
Osteomyelitis/septic arthritis	2.0 (8)	2.1 (16)	2.1 (24)	ns
Endocarditis right-sided	1.3 (5)	1.1 (8)	1.1 (13)	ns
Device-related infection with metastatic focus	0.8 (3)	0.8 (6)	0.8 (9)	ns
Total	392	754	1,146	

ns = not significant

* Fisher's exact test for difference in principal clinical manifestation and sex

Table 7: Principal clinical manifestation for *Enterococcus faecalis* and *E. faecium* bacteraemia, 2020

Principal clinical manifestation	*E. faecalis* % (*n*)	*E. faecium* % (*n*)	Total % (*n*)	Significance*
Urinary tract infection	25.3 (157)	6.1 (28)	17.2 (185)	*P* < 0.01
No focus	18.5 (115)	14.4 (66)	16.8 (181)	ns
Biliary tract infection (including cholangitis)	7.7 (48)	21.7 (99)	13.6 (147)	*P* < 0.01
Intra-abdominal infection other than biliary tract	9.2 (57)	17.1 (78)	12.5 (135)	*P* < 0.01

Device-related infection without metastatic focus	9.5 (59)	11.6 (53)	10.4 (112)	ns
Febrile neutropenia (where known)	1.9 (12)	16.4 (75)	8.1 (87)	*P* < 0.01
Endocarditis left-sided	11.3 (70)	1.8 (8)	7.2 (78)	*P* < 0.01
Other clinical syndrome	6.9 (43)	5.5 (25)	6.3 (68)	ns
Skin and skin structure infection	3.9 (24)	3.3 (15)	3.6 (39)	ns
Osteomyelitis/septic arthritis	3.1 (19)	0.9 (4)	2.1 (23)	0.01 < P < 0.05
Endocarditis right-sided	1.9 (12)	0.2 (1)	1.2 (13)	0.01 < P < 0.05
Device-related infection with metastatic focus	0.6 (4)	1.1 (5)	0.8 (9)	ns
Total	620	457	1,077	

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 2,487 (91.0%) episodes of SAB (Table 8). Overall, the most frequent principal clinical manifestation was osteomyelitis/septic arthritis (22.8%) followed by skin and skin structure infection (19.2%). A little under one-half (124/287, 43.2%) of the clinical manifestations in children were due to osteomyelitis/septic arthritis.

Of the hospital-onset SABs where data were available, the most common principal clinical manifestation was device-related infection without metastatic focus (149/513, 29.0%). Of the community-onset SABs where data were available, the most common principal clinical manifestation was osteomyelitis/septic arthritis (522/1,974, 26.4%).

Table 8: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient sex, 2020

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	20.1 (168)	24.2 (399)	22.8 (567)
Skin and skin structure infection	19.0 (159)	19.3 (318)	19.2 (477)
No focus	14.1 (118)	14.6 (241)	14.4 (359)
Device-related infection without metastatic focus	15.4 (129)	12.8 (211)	13.7 (340)
Other clinical syndrome	6.8 (57)	8.7 (143)	8.0 (200)
Endocarditis left-sided	6.3 (53)	5.5 (91)	5.8 (144)
Deep abscess(es) excluding those in the CNS	3.7 (31)	3.4 (56)	3.5 (87)
Pneumonia/empyema	3.3 (28)	2.8 (46)	3.0 (74)
Endocarditis right-sided	3.2 (27)	2.6 (43)	2.8 (70)
Device-related infection with metastatic focus	2.8 (23)	2.5 (41)	2.6 (64)
CNS infection (meningitis, abscess(es)	2.8 (23)	2.3 (38)	2.5 (61)
Febrile neutropenia (where known)	2.4 (20)	1.5 (24)	1.8 (44)
Total	836	1,651	2,487

CNS = central nervous system

The most common principal clinical manifestation for methicillin-susceptible *S. aureus* was osteomyelitis/septic arthritis (23.5%, 488/2,081), whereas for methicillin-resistant *S. aureus* it was skin and skin structure infection (20.9%, 85/406) (Table 9).

Table 9: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, 2020

Principal clinical manifestation	Methicillin-resistant % (*n*)	Methicillin-susceptible % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	19.5 (79)	23.5 (488)	22.8 (567)
Skin and skin structure infection	20.9 (85)	18.8 (392)	19.2 (477)
No focus	15.5 (63)	14.2 (296)	14.4 (359)
Device-related infection without metastatic focus	14.0 (57)	13.6 (283)	13.7 (340)
Other clinical syndrome	8.1 (33)	8.0 (167)	8.0 (200)
Endocarditis left-sided	3.4 (14)	6.2 (130)	5.8 (144)
Deep abscess(es) excluding those in the CNS	5.9 (24)	3.0 (63)	3.5 (87)
Pneumonia/empyema	5.2 (21)	2.5 (53)	3.0 (74)
Endocarditis right-sided	2.0 (8)	3.0 (62)	2.8 (70)
Device-related infection with metastatic focus	2.2 (9)	2.6 (55)	2.6 (64)
CNS infection (meningitis, abscess(es)	2.2 (9)	2.5 (52)	2.5 (61)
Febrile neutropenia (where known)	1.0 (4)	1.9 (40)	1.8 (44)
Total	406	2,081	2,487

CNS = central nervous system

3.6. Length of hospital stay following bacteraemic episode

Information on length of hospital stay following bacteraemia was available for 7,904 (90.3%) episodes involving gram-negative species, 1,143 (92.9%) episodes involving *Enterococcus* species, and 2,511 (91.8%) episodes involving *S. aureus*.

Over half (51.1%) of patients with a community-onset gram-negative bacteraemia had a length of hospital stay less than seven days. Almost 1 in 3 patients with hospital-onset bacteraemia caused by *Acinetobacter* spp. (41.0%) or *P. aeruginosa* (30.9%) remained in hospital for more than 30 days (Table 10). Overall, 22.8% of patients remained in hospital for more than 30 days after enterococcal bacteraemia (Table 11) and 24.7% after staphylococcal bacteraemia (Table 12).

Table 10: Length of hospital stay following gram-negative bacteraemia, by species and place of onset, 2020

	Length of hospital stay (days)				
Species	**<7, % (*n*)**	**7–14, % (*n*)**	**15–30, % (*n*)**	**>30, % (*n*)**	**Total**
Gram-negative species*	43.9 (3,473)	31.1 (2,461)	15.4 (1,217)	9.5 (753)	7,904
Community onset	51.1 (3,117)	31.7 (1,934)	12.1 (740)	5.1 (311)	6,102
Hospital onset	19.8 (356)	29.2 (527)	26.5 (477)	24.5 (442)	1,802
Acinetobacter species	40.6 (41)	26.7 (27)	15.8 (16)	16.8 (17)	101
Community onset	56.5 (35)	25.8 (16)	16.1 (10)	1.6 (1)	62
Hospital onset	15.4 (6)	28.2 (11)	15.4 (6)	41.0 (16)	39
Enterobacterales	45.3 (3,211)	30.9 (2,193)	15.1 (1,070)	8.7 (620)	7,094
Community onset	51.9 (2,911)	31.2 (1,749)	11.9 (667)	5.0 (279)	5,606
Hospital onset	20.2 (300)	29.8 (444)	27.1 (403)	22.9 (341)	1,488
Escherichia coli	50.5 (2,218)	30.0 (1,319)	13.3 (584)	6.2 (273)	4,394
Community onset	55.5 (2,064)	29.8 (1,109)	10.6 (395)	4.1 (152)	3,720
Hospital onset	22.8 (154)	31.2 (210)	28.0 (189)	18.0 (121)	674
Klebsiella pneumoniae complex	35.8 (364)	33.6 (342)	17.9 (182)	12.8 (130)	1,018
Community onset	44.0 (326)	34.3 (254)	15.2 (113)	6.5 (48)	741
Hospital onset	13.7 (38)	31.8 (88)	24.9 (69)	29.6 (82)	277
Enterobacter cloacae complex	30.0 (127)	30.3 (128)	21.5 (91)	18.2 (77)	423
Community onset	42.4 (98)	33.8 (78)	16.5 (38)	7.4 (17)	231
Hospital onset	15.1 (29)	26.0 (50)	27.6 (53)	31.3 (60)	192
Other *Enterobacterales* (*n* = 37)	39.9 (502)	32.1 (404)	16.9 (213)	11.1 (140)	1,259
Pseudomonas aeruginosa	31.2 (221)	34.0 (241)	18.5 (131)	16.4 (116)	709
Community onset	39.4 (171)	38.9 (169)	14.5 (63)	7.1 (31)	434
Hospital onset	18.2 (50)	26.2 (72)	24.7 (68)	30.9 (85)	275

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

Table 11: Length of hospital stay following *Enterococcus* species bacteraemia, by vancomycin resistance and place of onset, 2020

Species	Length of hospital stay following bacteraemia				Total
	<7 days % (*n*)	7–14 % days (*n*)	15–30 % days (*n*)	>30 days % (*n*)	
All species	22.8 (261)	31.1 (355)	23.3 (266)	22.8 (261)	1,143
E. faecalis	26.0 (161)	34.1 (211)	18.4 (114)	21.5 (133)	619
Vancomycin resistant	–* (1)	–* (0)	–* (0)	–* (0)	1
Vancomycin susceptible	25.8 (159)	34.2 (211)	18.5 (114)	21.6 (133)	617
E. faecium	17.6 (80)	27.5 (125)	29.3 (133)	25.6 (116)	454
Vancomycin resistant	17.8 (26)	24.0 (35)	30.8 (45)	27.4 (40)	146
Vancomycin susceptible	17.7 (54)	29.5 (90)	28.2 (86)	24.6 (75)	305
Other *Enterococcus* species (*n* = 8)	28.6 (20)	27.1 (19)	27.1 (19)	17.1 (12)	70
Community onset					
E. faecalis	29.1 (128)	35.9 (158)	18.4 (81)	16.6 (73)	440
Vancomycin resistant	–* (1)	–* (0)	–* (0)	–* (0)	1
Vancomycin susceptible	28.8 (126)	36.1 (158)	18.5 (81)	16.7 (73)	438
E. faecium	24.3 (37)	37.5 (57)	25.0 (38)	13.2 (20)	152
Vancomycin resistant	25.8 (8)	32.3 (10)	29.0 (9)	12.9 (4)	31
Vancomycin susceptible	24.4 (29)	39.5 (47)	22.7 (27)	13.4 (16)	119
Hospital onset					
E. faecalis	18.4 (33)	29.6 (53)	18.4 (33)	33.5 (60)	179
Vancomycin resistant	–* (0)	–* (0)	–* (0)	–* (0)	0
Vancomycin susceptible	18.4 (33)	29.6 (53)	18.4 (33)	33.5 (60)	179
E. faecium	14.2 (43)	22.5 (68)	31.5 (95)	31.8 (96)	302
Vancomycin resistant*	15.7 (18)	21.7 (25)	31.3 (36)	31.3 (36)	115
Vancomycin susceptible*	13.4 (25)	23.1 (43)	31.7 (59)	31.7 (59)	186

* Insufficient numbers (<10) to calculate percentage

Note: vancomycin susceptibility not available for three *E. faecium* (community, 2; hospital onset, 1) and one *E. faecalis* (community onset).

Table 12: Length of hospital stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, 2020

Species	Length of hospital stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Staphylococcus aureus	18.7 (469)	28.8 (722)	27.9 (700)	24.7 (620)	2,511
Methicillin resistant	19.8 (88)	24.1 (107)	27.9 (124)	28.2 (125)	444
Community onset	22.0 (75)	23.8 (81)	27.6 (94)	26.7 (91)	341
Hospital onset	12.6 (13)	25.2 (26)	29.1 (30)	33.0 (34)	103
Methicillin susceptible	18.4 (381)	29.8 (615)	27.9 (576)	23.9 (495)	2,067
Community onset	19.4 (321)	31.0 (511)	27.1 (448)	22.5 (371)	1,651
Hospital onset	14.4 (60)	25.0 (104)	30.8 (128)	29.8 (124)	416

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[33] using both CLSI breakpoints and EUCAST breakpoints, are shown in Table 13. Resistance (as defined by EUCAST) by state and territory to key antimicrobial groups (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) for *E. coli* and *K. pneumoniae* complex are shown in Figures 4 and 5; key antipseudomonal agents in Figure 6; methicillin resistance in *S. aureus* (Figure 7); glycopeptide resistance in *E. faecium*, and high-level gentamicin resistance in *E. faecalis* in Figure 8. Detailed resistance by state and territory can be found in Appendix C.

Supplementary data on percentages susceptible, susceptible – increased exposure (EUCAST), intermediate (CLSI), and resistant for each antimicrobial and all species, and the antimicrobial profiles by state and territory can be found in the 2020 reports for each program on the AGAR website. These reports provide summary susceptibility data (number and percentage for species if more than 10 isolates were tested) using both CLSI and EUCAST interpretive guidelines for all species isolated.

Table 13: Antimicrobial resistances (CLSI and EUCAST), 2020

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Acinetobacter baumannii complex					
Piperacillin–tazobactam	55	5.5 (3)	16.4 (9)	–*	–*
Ceftazidime	53	20.8 (11)	3.8 (2)	–*	–*
Cefepime	51	7.8 (4)	3.9 (2)	–*	–*
Gentamicin	60	1.7 (1)	3.3 (2)	–†	5.0 (3)
Tobramycin	60	1.7 (1)	1.7 (1)	–†	3.3 (2)
Amikacin	47	0.0 (0)	2.1 (1)	–†	2.1 (1)
Ciprofloxacin	54	0.0 (0)	3.7 (2)	96.3 (52)	3.7 (2)
Meropenem	60	0.0 (0)	1.7 (1)	0.0 (0)	1.7 (1)
Enterobacter cloacae complex					
Piperacillin–tazobactam	449	6.7 (30)	16.9 (76)	–†	26.3 (118)
Ceftriaxone	450	0.9 (4)	27.8 (125)	0.9 (4)	27.8 (125)
Ceftazidime	449	0.9 (4)	22.9 (103)	3.6 (16)	23.8 (107)
Cefepime	450	2.7 (12)§	3.6 (16)	7.1 (32)	4.4 (20)
Gentamicin	450	0.2 (1)	7.6 (34)	–†	8.4 (38)
Tobramycin	449	2.7 (12)	6.0 (27)	–†	9.1 (41)
Amikacin	450	0.0 (0)	0.4 (2)	–†	1.8 (8)
Ciprofloxacin	449	1.8 (8)	5.8 (26)	1.8 (8)	5.8 (26)
Meropenem	449	0.2 (1)	4.0 (18)	0.4 (2)	3.6 (16)
Enterococcus faecalis					
Ampicillin	666	–†	0.0 (0)	0.0 (0)	0.0 (0)
Benzylpenicillin	608	–†	1.3 (8)	–*	–*
Ciprofloxacin	406	4.9 (20)	6.9 (28)	–†	4.8 (19)#
Daptomycin	650	42.9 (279)	0.2 (1)	–*	–*

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Linezolid	663	1.1 (7)	0.0 (0)	–[†]	0.0 (0)
Teicoplanin	666	0.0 (0)	0.2 (1)	–[†]	0.2 (1)
Vancomycin	666	0.0 (0)	0.2 (1)	–[†]	0.2 (1)
Enterococcus faecium					
Ampicillin	485	–[†]	88.2 (428)	0.0 (0)	88.2 (428)
Benzylpenicillin	441	–[†]	88.9 (392)	–*	–*
Ciprofloxacin	319	2.8 (9)	88.1 (281)	–[†]	–**
Linezolid	487	0.4 (2)	0.0 (0)	–[†]	0.0 (0)
Teicoplanin	485	0.6 (3)	11.1 (54)	–[†]	13.0 (63)
Vancomycin	485	0.6 (3)	32.0 (155)	–[†]	32.6 (158)
Escherichia coli					
Ampicillin	4,863	1.7 (84)	51.4 (2,498)	–[†]	53.1 (2,582)
Amoxicillin–clavulanic acid (2:1 ratio)	4,227	11.8 (498)	7.7 (326)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio)	639	–*	–*	–[†]	31.6 (202)
Piperacillin–tazobactam	4,845	2.9 (141)	2.5 (123)	–[†]	6.6 (322)
Ceftriaxone	4,867	0.2 (9)	13.4 (650)	0.2 (9)	13.4 (650)
Ceftazidime	4,867	0.5 (25)	5.9 (289)	6.8 (331)	6.5 (314)
Cefepime	4,867	2.4 (118)[§]	2.6 (127)	7.0 (343)	3.6 (174)
Gentamicin	4,867	0.2 (8)	8.2 (401)	–[†]	8.8 (430)
Tobramycin	4,865	6.4 (309)	2.7 (131)	–[†]	9.5 (461)
Amikacin	4,866	0.1 (5)	0.1 (4)	–[†]	1.1 (54)
Ciprofloxacin	4,866	3.3 (163)	16.1 (783)	3.3 (163)	16.1 (783)
Meropenem	4,865	0.1 (4)	0.1 (3)	0.0 (1)	0.0 (2)
Klebsiella aerogenes					
Piperacillin–tazobactam	122	8.2 (10)	26.2 (32)	–[†]	36.9 (45)
Ceftriaxone	122	0.0 (0)	34.4 (42)	0.0 (0)	34.4 (42)
Ceftazidime	122	2.5 (3)	32.0 (39)	0.8 (1)	34.4 (42)
Cefepime	122	0.8 (1)[§]	0.8 (1)	3.3 (4)	0.8 (1)
Gentamicin	122	0.0 (0)	1.6 (2)	–[†]	1.6 (2)
Tobramycin	122	0.8 (1)	0.8 (1)	–[†]	1.6 (2)
Amikacin	122	0.0 (0)	0.0 (0)	–[†]	0.0 (0)
Ciprofloxacin	122	0.8 (1)	1.6 (2)	0.8 (1)	1.6 (2)
Meropenem	122	0.0 (0)	0.8 (1)	0.0 (0)	0.8 (1)
Klebsiella oxytoca					
Amoxicillin–clavulanic acid (2:1 ratio)	219	1.8 (4)	7.3 (16)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio)	35	–*	–*	–[†]	14.3 (5)
Piperacillin–tazobactam	254	1.2 (3)	8.7 (22)	–[†]	10.6 (27)
Ceftriaxone	254	2.0 (5)	5.9 (15)	2.0 (5)	5.9 (15)
Ceftazidime	254	0.4 (1)	0.8 (2)	0.8 (2)	1.2 (3)
Cefepime	254	0.4 (1)[§]	0.4 (1)	0.4 (1)	0.4 (1)
Gentamicin	254	0.0 (0)	0.8 (2)	–[†]	0.8 (2)
Tobramycin	254	0.0 (0)	0.8 (2)	–[†]	0.8 (2)
Amikacin	254	0.0 (0)	0.0 (0)	–[†]	0.0 (0)
Ciprofloxacin	254	0.4 (1)	0.8 (2)	0.4 (1)	0.8 (2)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Meropenem	254	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Klebsiella pneumoniae complex					
Amoxicillin–clavulanic acid (2:1 ratio)	1,002	4.3 (43)	5.0 (50)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio)	139	–*	–*	–†	18.7 (26)
Piperacillin–tazobactam	1,135	3.0 (34)	3.9 (44)	–†	12.5 (142)
Ceftriaxone	1,141	0.1 (1)	8.6 (98)	0.1 (1)	8.6 (98)
Ceftazidime	1,141	1.4 (16)	6.0 (68)	1.8 (21)	7.4 (84)
Cefepime	1,141	0.9 (10)§	2.6 (30)	3.9 (45)	3.1 (35)
Gentamicin	1,141	0.3 (3)	4.9 (56)	–†	5.4 (62)
Tobramycin	1,141	2.8 (32)	3.5 (40)	–†	6.5 (74)
Amikacin	1,141	0.1 (1)	0.1 (1)	–†	0.6 (7)
Ciprofloxacin	1,140	2.4 (27)	9.9 (113)	2.4 (27)	9.9 (113)
Meropenem	1,140	0.2 (2)	0.4 (5)	0.3 (3)	0.2 (2)
Proteus mirabilis					
Ampicillin	281	0.4 (1)	19.9 (56)	–†	20.3 (57)
Amoxicillin–clavulanic acid (2:1 ratio)	251	6.4 (16)	3.6 (9)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio)	30	–*	–*	–†	3.3 (1)
Piperacillin–tazobactam	280	0.4 (1)	0.0 (0)	–†	0.4 (1)
Ceftriaxone	281	1.1 (3)	2.5 (7)	1.1 (3)	2.5 (7)
Ceftazidime	281	0.4 (1)	0.4 (1)	1.4 (4)	0.7 (2)
Cefepime	281	1.1 (3)§	0.7 (2)	1.1 (3)	0.7 (2)
Gentamicin	281	0.4 (1)	3.2 (9)	–†	7.1 (20)
Tobramycin	281	2.8 (8)	0.7 (2)	–†	4.3 (12)
Amikacin	281	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	281	0.7 (2)	3.6 (10)	0.7 (2)	3.6 (10)
Meropenem	281	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin–tazobactam	763	8.9 (68)	5.5 (42)	85.6 (653)	14.4 (110)
Ceftazidime	763	3.0 (23)	4.7 (36)	92.3 (704)	7.7 (59)
Cefepime	765	3.8 (29)	2.1 (16)	94.1 (720)	5.9 (45)
Gentamicin	759	1.4 (11)	1.1 (8)	–*	–*
Tobramycin	766	0.3 (2)	0.7 (5)	–†	1.2 (9)
Amikacin	765	0.3 (2)	0.4 (3)	–†	0.7 (5)
Ciprofloxacin	762	3.7 (28)	4.5 (34)	91.9 (700)	8.1 (62)
Meropenem	760	4.7 (36)	4.3 (33)	5.5 (42)	3.6 (27)
Salmonella species (non-typhoidal)					
Ampicillin	91	1.1 (1)	4.4 (4)	–†	5.5 (5)
Amoxicillin–clavulanic acid (2:1 ratio)	89	2.2 (2)	0.0 (0)	–*	–*
Amoxicillin–clavulanic acid (fixed ratio)	3	–*	–*	–†	n/a (0)
Piperacillin–tazobactam	91	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ceftriaxone	92	0.0 (0)	1.1 (1)	0.0 (0)	1.1 (1)
Ceftazidime	92	0.0 (0)	1.1 (1)	0.0 (0)	1.1 (1)
Cefepime	92	0.0 (0)§	1.1 (1)	0.0 (0)	1.1 (1)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Ciprofloxacin§§	93	4.3 (4)	1.1 (1)	–†	5.4 (5)
Meropenem	92	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	163	0.6 (1)	0.0 (0)	–†	2.5 (4)
Ceftriaxone	195	0.0 (0)	2.6 (5)	0.0 (0)	2.6 (5)
Ceftazidime	195	0.0 (0)	1.0 (2)	0.0 (0)	1.0 (2)
Cefepime	195	0.0 (0)§	0.5 (1)	0.5 (1)	0.5 (1)
Gentamicin	195	0.5 (1)	1.0 (2)	–†	2.1 (4)
Tobramycin	195	11.3 (22)	2.1 (4)	–†	34.9 (68)
Amikacin	195	0.0 (0)	0.0 (0)	–†	1.0 (2)
Ciprofloxacin	195	1.5 (3)	2.1 (4)	1.5 (3)	2.1 (4)
Meropenem	195	0.0 (0)	1.0 (2)	0.5 (1)	0.5 (1)
Staphylococcus aureus					
Benzylpenicillin##	2,721	–†	82.7 (2,251)	–†	82.7 (2,251)
Cefoxitin (methicillin)***	2,734	–†	17.6 (481)	–†	17.6 (481)
Ciprofloxacin	2,731	0.5 (14)	7.5 (204)	92.0 (2,513)	8.0 (218)
Clindamycin (constitutive)	2,729	0.1 (2)	3.3 (91)	0.5 (15)	3.4 (93)
Clindamycin (constitutive + inducible resistance)	2,729	0.1 (2)	13.3 (362)	0.5 (13)	13.8 (377)
Daptomycin	2,730	0.3 (7)††	–†	–†	0.3 (7)
Erythromycin	2,731	28.2 (771)	15.9 (434)	0.7 (20)	16.4 (449)
Fusidic acid	2,730	–*	–*	–†	3.3 (89)
Gentamicin	2,731	1.2 (33)	1.8 (49)	–†	4.1 (113)
Linezolid	2,732	–†	0.0 (0)	–†	0.0 (0)
Mupirocin (high-level)§§§	2,071	–†	1.1 (22)	–†	1.1 (22)
Rifampicin	2,729	0.0 (0)	0.2 (6)	–###	0.3 (7)
Teicoplanin	2,731	0.0 (0)	0.0 (0)	–†	0.1 (4)
Tetracycline/doxycycline****	2,730	0.3 (7)****	4.0 (110)	0.6 (17)	4.4 (121)
Trimethoprim/sulfamethoxazole‡‡	2,724	0.1 (4)	0.8 (22)	0.1 (4)	0.8 (22)
Vancomycin	2,732	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
§ Includes sensitive dose dependent category for CLSI
# The ciprofloxacin ECOFF (4 mg/L, *E. faecalis*) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only
** The ciprofloxacin concentration range available on Vitek and Phoenix cards restricts the ability to determine non-wild type (ECOFF 8 mg/L) *E. faecium*
‡ 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 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
Benzylpenicillin resistance including beta-lactamase producers
*** Resistance as determined by cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix)
‡‡ Resistance not defined
§§§ Mupirocin high-level resistance screen
The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant
**** The doxycycline concentration range available on the Phoenix card used restricts the ability to accurately identify intermediate and resistant (CLSI) categories for enterococci
‡‡ Trimethoprim-sulfamethoxazole resistance, as determined by Vitek or Phoenix, confirmed by disc diffusion

Figure 4. 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, 2020

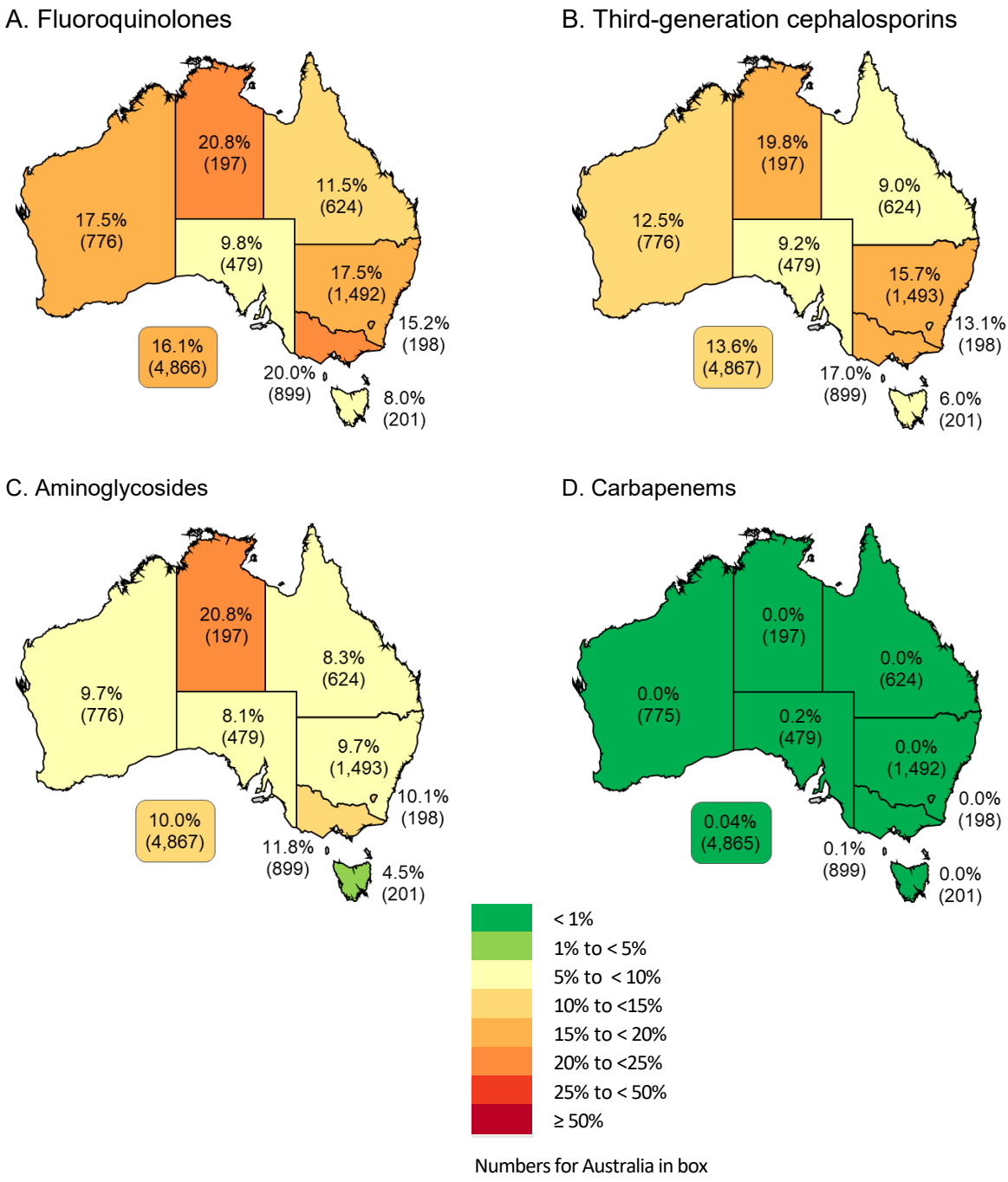


Figure 5. Percentage of *Klebsiella pneumoniae* complex from patients with bacteraemia with resistance as defined by EUCAST to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, 2020

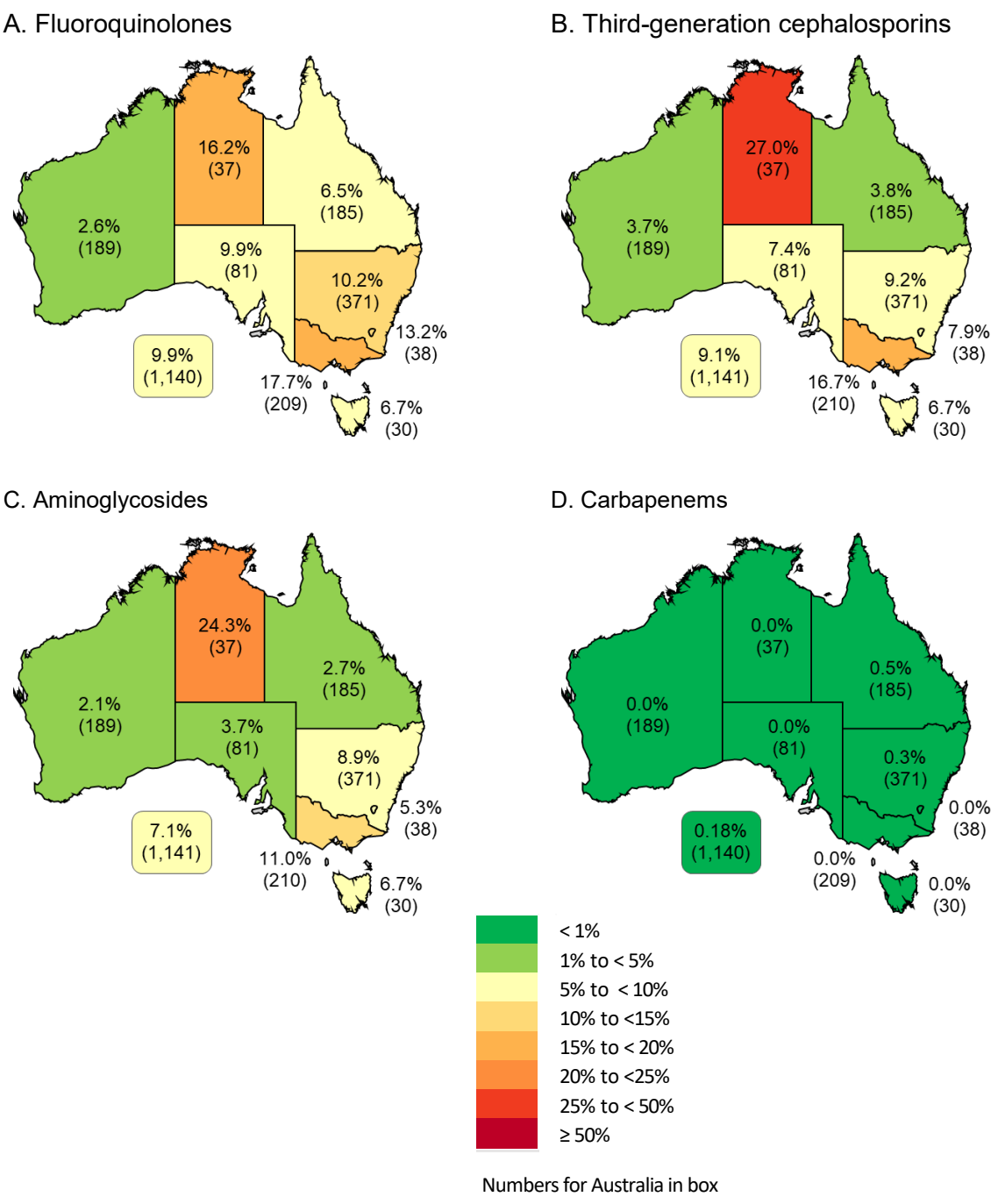


Figure 6. Percentage of *Pseudomonas aeruginosa* from patients with bacteraemia with resistance as defined by EUCAST to piperacillin–tazobactam (A), fluoroquinolones (B), ceftazidime (C) and carbapenems (D), Australia, 2020

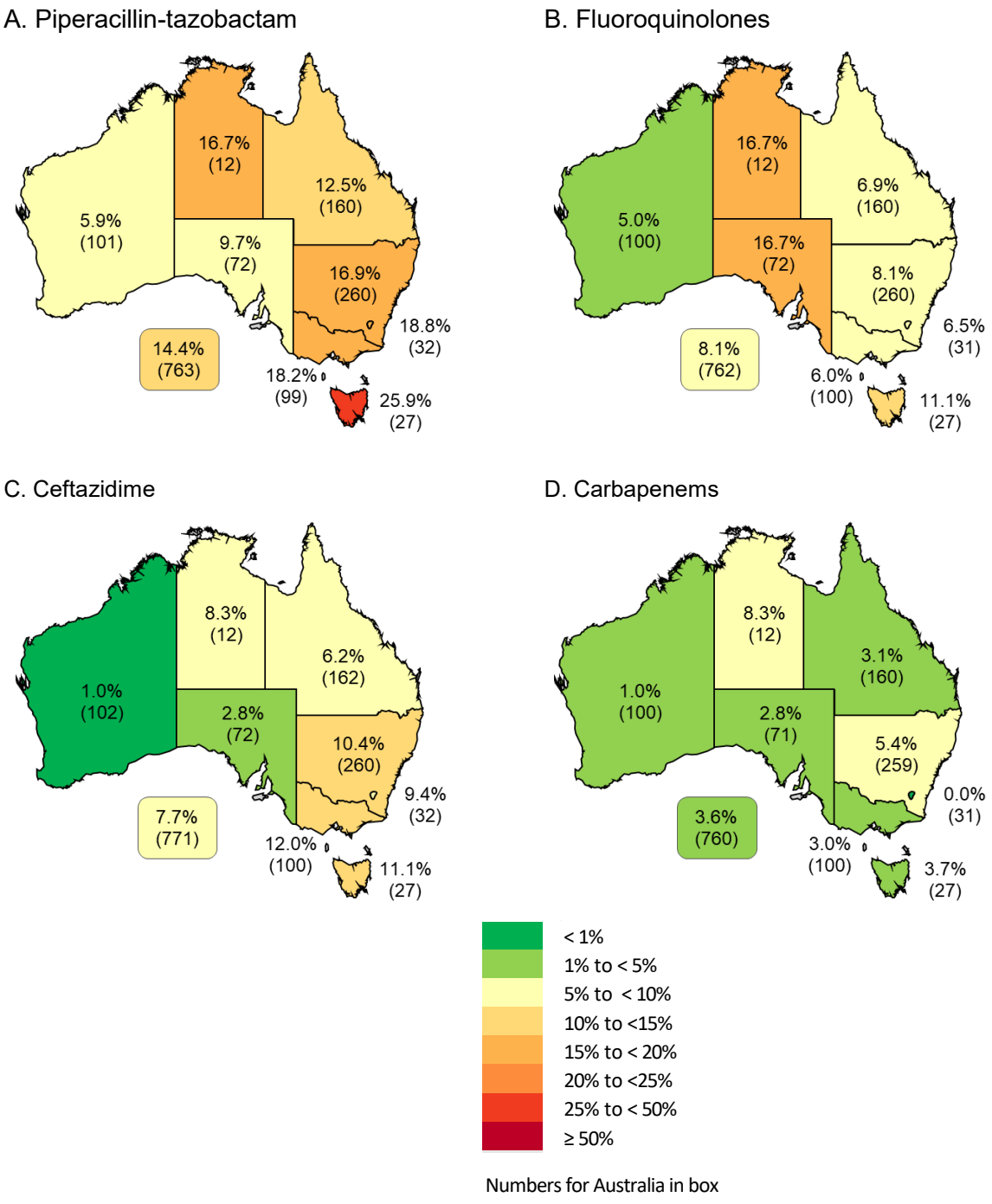


Figure 7. Percentage of *Staphylococcus aureus* from patients with bacteraemia with resistance as defined by EUCAST to methicillin, Australia, 2020

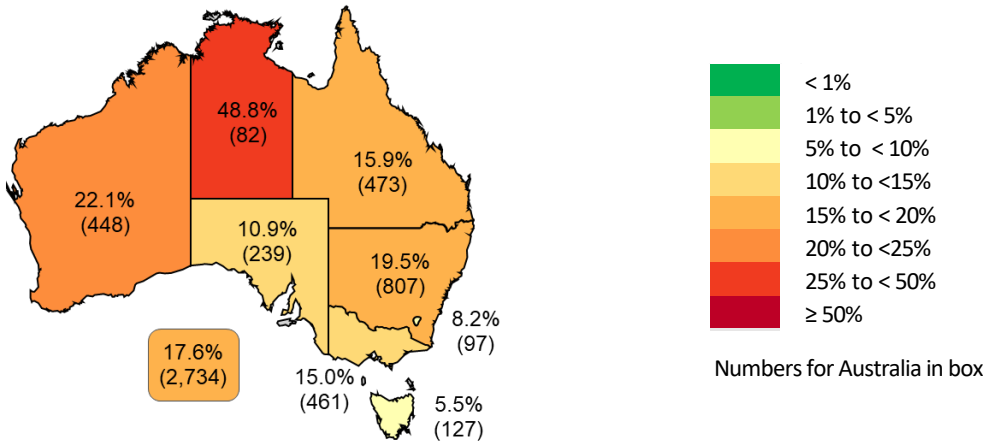
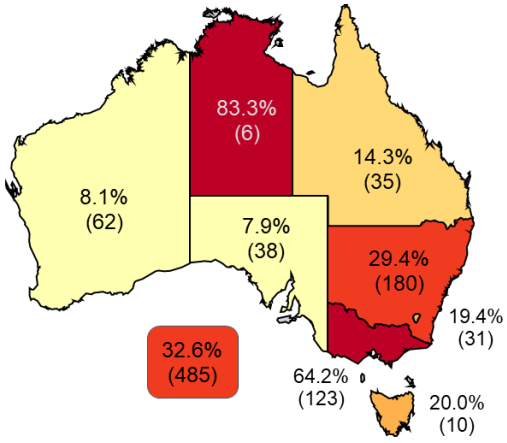
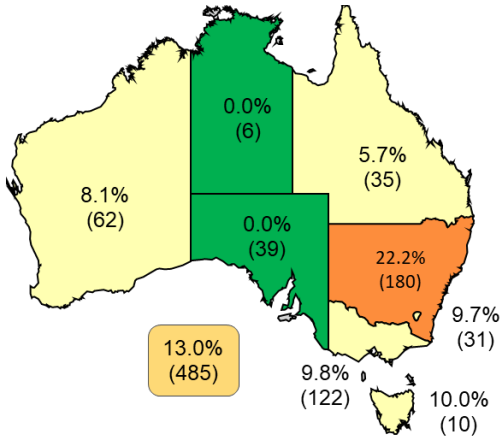


Figure 8. Percentage of *Enterococcus faecium* from patients with bacteraemia with resistance as defined by EUCAST to vancomycin (A) and teicoplanin (B), and *Enterococcus faecalis* with resistance to high-level gentamicin (C), Australia, 2020

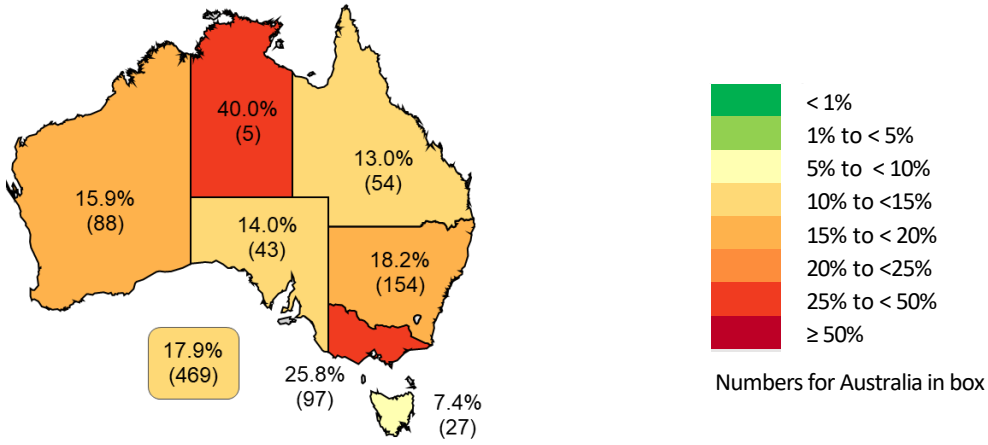
A. Vancomycin



B. Teicoplanin



C. High-level gentamicin



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: Antimicrobial resistances (CLSI, EUCAST), by place of onset, 2020

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Acinetobacter baumannii complex					
Piperacillin–tazobactam	55	3.4, –*	17.2, –*	7.7, –*	15.4, –*
Ceftriaxone	57	73.5, –*	2.9, –*	73.9, –*	8.7, –*
Ceftazidime	53	13.8, –*	3.4, –*	29.2, –*	4.2, –*
Cefepime	51	0.0, –*	3.8, –*	16.0, –*	4.0, –*
Gentamicin	60	0.0, –†	2.9, 2.9	3.8, –†	3.8, 7.7
Tobramycin	60	2.9, –†	0.0, 2.9	0.0, –†	3.8, 3.8
Amikacin	47	0.0, –†	0.0, 0.0	0.0, –†	5.3, 5.3
Ciprofloxacin	54	0.0, 97.0	3.0, 3.0	0.0, 95.2	4.8, 4.8
Meropenem	60	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.8, 3.8
Enterobacter cloacae complex					
Piperacillin–tazobactam	449	6.2, –†	12.3, 20.2	7.3, –†	22.3, 33.5
Ceftriaxone	450	1.2, 1.2	20.1, 20.1	0.5, 0.5	36.9, 36.9
Ceftazidime	449	0.4, 2.9	16.9, 17.3	1.5, 4.4	30.1, 31.6
Cefepime	450	1.6§, 6.1	3.3, 3.3	3.9§, 8.3	3.9, 5.8
Gentamicin	450	0.4, –†	3.3, 4.1	0.0, –†	12.6, 13.6
Tobramycin	449	2.1, –†	2.9, 4.9	3.4, –†	9.7, 14.1
Amikacin	450	0.0, –†	0.0, 0.0	0.0, –†	1.0, 3.9
Ciprofloxacin	449	1.6, 1.6	3.7, 3.7	1.9, 1.9	8.3, 8.3
Meropenem	449	0.0, 0.8	3.3, 2.5	0.5, 0.0	4.9, 4.9
Enterococcus faecalis					
Ampicillin	666	–†, 0.0	0.0, 0.0	–†, 0.0	0.0, 0.0
Benzylpenicillin	608	–†, –*	1.8, –*	–†, –*	0.0, –*
Ciprofloxacin	406	5.1, –†	6.5, 4.9#	4.4, –†	8.0, 4.6#
Daptomycin	650	43.1, –*	0.2, –*	42.6, –*	0.0, –*
Linezolid	663	1.3, –†	0.0, 0.0	0.5, –†	0.0, 0.0
Teicoplanin	666	0.0, –†	0.2, 0.2	0.0, –†	0.0, 0.0
Vancomycin	666	0.0, –†	0.2, 0.2	0.0, –†	0.0, 0.0
Enterococcus faecium					
Ampicillin	485	–†, 0.0	73.9, 73.9	–†, 0.0	95.4, 95.4
Benzylpenicillin	441	–†, –*	74.1, –*	–†, –*	95.7, –*
Ciprofloxacin	319	5.8, –†	72.8, –**	1.4, –†	95.4, –**
Linezolid	487	0.0, –†	0.0, 0.0	0.6, –†	0.0, 0.0
Teicoplanin	485	1.2, –†	6.2, 8.1	0.3, –†	13.6, 15.4
Vancomycin	485	0.6, –†	21.3, 21.9	0.6, –†	37.2, 37.8
Escherichia coli					
Ampicillin	4,863	1.8, –†	50.0, 51.8	1.2, –†	59.0, 60.2
Amoxicillin-clavulanic acid (2:1 ratio)#	4,227	11.6, –*	6.8, –*	13.1, –*	13.1, –*
Amoxicillin-clavulanic acid (fixed ratio)#	639	–*, –†	–*, 29.5	–*, –†	–*, 43.6
Piperacillin–tazobactam	4,845	2.6, –†	1.8, 5.6	4.4, –†	6.7, 12.8

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Ceftriaxone	4,867	0.2, 0.2	12.4, 12.4	0.1, 0.1	18.8, 18.8
Ceftazidime	4,867	0.5, 6.5	5.1, 5.7	0.4, 8.2	10.6, 11.0
Cefepime	4,867	2.3§, 6.9	2.2, 3.1	3.2§, 8.0	4.8, 6.4
Gentamicin	4,867	0.1, –†	8.1, 8.7	0.4, –†	8.8, 9.3
Tobramycin	4,865	6.3, –†	2.4, 9.2	6.7, –†	4.1, 11.2
Amikacin	4,866	0.1, –†	0.1, 1.1	0.0, –†	0.0, 1.2
Ciprofloxacin	4,866	3.4, 3.4	15.1, 15.1	3.2, 3.2	21.8, 21.8
Meropenem	4,865	0.0, 0.0	0.0, 0.0	0.3, 0.1	0.1, 0.0
Klebsiella aerogenes					
Piperacillin–tazobactam	122	8.8, –†	20.6, 30.9	7.4, –†	33.3, 44.4
Ceftriaxone	122	0.0, 0.0	26.5, 26.5	0.0, 0.0	44.4, 44.4
Ceftazidime	122	4.4, 0.0	23.5, 27.9	0.0, 1.9	42.6, 42.6
Cefepime	122	1.5§, 2.9	0.0, 0.0	0.0§, 3.7	1.9, 1.9
Gentamicin	122	0.0, –†	0.0, 0.0	0.0, –†	3.7, 3.7
Tobramycin	122	0.0, –†	0.0, 0.0	1.9, –†	1.9, 3.7
Amikacin	122	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Ciprofloxacin	122	0.0, 0.0	2.9, 2.9	1.9, 1.9	0.0, 0.0
Meropenem	122	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.9, 1.9
Klebsiella oxytoca					
Amoxicillin–clavulanic acid (2:1 ratio)	219	1.8, –*	3.6, –*	1.9, –*	18.9, –*
Amoxicillin–clavulanic acid (fixed ratio)	35	–*, –†	–*, 15.0	–*, –†	–*, 13.3
Piperacillin–tazobactam	254	1.1, –†	5.4, 7.0	1.5, –†	17.6, 20.6
Ceftriaxone	254	0.5, 0.5	3.8, 3.8	5.9, 5.9	11.8, 11.8
Ceftazidime	254	0.0, 1.1	0.5, 0.5	1.5, 0.0	1.5, 2.9
Cefepime	254	0.0§, 0.0	0.5, 0.5	1.5§, 1.5	0.0, 0.0
Gentamicin	254	0.0, –†	0.5, 0.5	0.0, –†	1.5, 1.5
Tobramycin	254	0.0, –†	0.5, 0.5	0.0, –†	1.5, 1.5
Amikacin	254	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Ciprofloxacin	254	0.0, 0.0	0.5, 0.5	1.5, 1.5	1.5, 1.5
Meropenem	254	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex					
Amoxicillin–clavulanic acid (2:1 ratio)	1,002	3.8, –*	4.0, –*	5.7, –*	7.7, –*
Amoxicillin–clavulanic acid (fixed ratio)	139	–*, –†	–*, 16.3	–*, –†	–*, 25.7
Piperacillin–tazobactam	1,135	2.4, –†	1.9, 10.1	4.7, –†	9.5, 19.3
Ceftriaxone	1,141	0.1, 0.1	7.8, 7.8	0.0, 0.0	10.8, 10.8
Ceftazidime	1,141	1.3, 1.8	5.3, 6.6	1.7, 2.0	7.8, 9.5
Cefepime	1,141	0.8§, 3.6	2.0, 2.4	1.0§, 5.1	4.4, 5.1
Gentamicin	1,141	0.2, –†	4.4, 4.7	0.3, –†	6.4, 7.4
Tobramycin	1,141	2.8, –†	2.8, 5.8	2.7, –†	5.4, 8.4
Amikacin	1,141	0.0, –†	0.0, 0.2	0.3, –†	0.3, 1.7
Ciprofloxacin	1,140	1.9, 1.9	8.3, 8.3	3.7, 3.7	14.5, 14.5
Meropenem	1,140	0.1, 0.1	0.2, 0.1	0.3, 0.7	1.0, 0.3
Proteus mirabilis					
Ampicillin	281	0.4, –†	19.7, 20.1	0.0, –†	21.4, 21.4

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Amoxicillin–clavulanic acid (2:1 ratio)	251	7.0, –*	3.3, –*	2.7, –*	5.4, –*
Amoxicillin–clavulanic acid (fixed ratio)	30	–*, –†	–*, 0.0	–*, –†	–*, n/a
Piperacillin–tazobactam	280	0.4, –†	0.0, 0.4	0.0, –†	0.0, 0.0
Ceftriaxone	281	1.3, 1.3	2.5, 2.5	0.0, 0.0	2.4, 2.4
Ceftazidime	281	0.4, 1.7	0.0, 0.4	0.0, 0.0	2.4, 2.4
Cefepime	281	1.3§, 1.3	0.8, 0.8	0.0§, 0.0	0.0, 0.0
Gentamicin	281	0.4, –†	3.3, 7.1	0.0, –†	2.4, 7.1
Tobramycin	281	2.9, –†	0.4, 4.2	2.4, –†	2.4, 4.8
Amikacin	281	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Ciprofloxacin	281	0.8, 0.8	3.8, 3.8	0.0, 0.0	2.4, 2.4
Meropenem	281	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Pseudomonas aeruginosa					
Piperacillin–tazobactam	763	8.6, 88.4	3.0, 11.6	9.5, 81.1	9.5, 18.9
Ceftazidime	763	2.1, 95.3	2.6, 4.7	4.4, 87.5	8.1, 12.5
Cefepime	765	2.8, 96.1	1.1, 3.9	5.4, 90.9	3.7, 9.1
Gentamicin	759	0.9, –*	0.6, –*	2.4, –*	1.7, –*
Tobramycin	766	0.0, –†	0.4, 0.9	0.7, –†	1.0, 1.7
Amikacin	765	0.2, –†	0.2, 0.4	0.3, –†	0.7, 1.0
Ciprofloxacin	762	3.4, 92.5	4.1, 7.5	4.0, 90.9	5.1, 9.1
Meropenem	760	3.7, 4.3	2.8, 2.2	6.4, 7.4	6.8, 5.7
Salmonella species (non-typhoidal)					
Ampicillin	91	0.0, –†	3.7, 3.7	11.1, –†	11.1, n/a
Amoxicillin–clavulanic acid (2:1 ratio)	89	1.3, –*	0.0, –*	11.1, –*	0.0, –*
Amoxicillin–clavulanic acid (fixed ratio)	3	–*, –†	–*, n/a	–*, –†	–*, n/a
Piperacillin–tazobactam	91	0.0, –†	0.0, 0.0	0.0, –†	0.0, n/a
Ceftriaxone	92	0.0, 0.0	1.2, 1.2	0.0, n/a	0.0, n/a
Ceftazidime	92	0.0, 0.0	1.2, 1.2	0.0, n/a	0.0, n/a
Cefepime	92	0.0§, 0.0	1.2, 1.2	0.0§, n/a	0.0, n/a
Ciprofloxacin§§	93	3.6, –†	1.2, 4.8	0.0, –†	0.0, n/a
Meropenem	92	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, n/a
Serratia marcescens					
Piperacillin–tazobactam	163	1.1, –†	0.0, 3.3	0.0, –†	0.0, 1.4
Ceftriaxone	195	0.0, 0.0	1.8, 1.8	0.0, 0.0	3.6, 3.6
Ceftazidime	195	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.4, 2.4
Cefepime	195	0.0§, 0.0	0.0, 0.0	0.0§, 1.2	1.2, 1.2
Gentamicin	195	0.0, –†	1.8, 2.7	1.2, –†	0.0, 1.2
Tobramycin	195	13.5, –†	1.8, 35.1	8.3, –†	2.4, 34.5
Amikacin	195	0.0, –†	0.0, 1.8	0.0, –†	0.0, 0.0
Ciprofloxacin	195	2.7, 2.7	1.8, 1.8	0.0, 0.0	2.4, 2.4
Meropenem	195	0.0, 0.0	0.0, 0.0	0.0, 1.2	2.4, 1.2
Staphylococcus aureus					
Benzylpenicillin##	2,721	–† ,–†	81.8, 81.8	–† ,–†	86.2, 86.2
Cefoxitin (methicillin)***	2,734	–† ,–†	17.0, 17.0	–† ,–†	20.0, 20.0
Ciprofloxacin	2,731	0.5, 92.6	6.9, 7.4	0.5, 89.9	9.6, 10.1

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Clindamycin (constitutive)	2,729	0.1, 0.5	3.2, 3.3	0.0, 0.9	3.8, 3.8
Clindamycin (constitutive + inducible resistance)	2,729	0.1, 0.4	12.7, 13.3	0.0, 0.9	15.4, 15.9
Daptomycin	2,730	0.2††, –†	–†, 0.2	0.4††, –†	–†, 0.4
Erythromycin	2,731	27.7, 0.8	15.4, 15.9	30.5, 0.5	17.9, 18.4
Fusidic acid	2,730	–*, –†	–*, 3.4	–*, –†	–*, 2.9
Gentamicin	2,731	1.1, –†	1.6, 3.8	1.6, –†	2.7, 5.6
Linezolid	2,732	–† ,–†	0.0, 0.0	–† ,–†	0.0, 0.0
Mupirocin (high-level) §§§	2,071	–† ,–†	1.2, 1.2	–† ,–†	0.7, 0.7
Rifampicin	2,729	0.0, –###	0.2, 0.2	0.0, –###	0.4, 0.4
Teicoplanin	2,731	0.0, –†	0.0, 0.1	0.0, –†	0.0, 0.4
Tetracycline/doxycycline****	2,730	0.3****, 0.5	3.8, 4.2	0.2****, 1.1	5.1, 5.4
Trimethoprim/sulfamethoxazole‡‡	2,724	0.1, 0.1	0.7, 0.7	0.2, 0.2	1.3, 1.3
Vancomycin	2,732	0.0, –†	0.0, 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
§ Includes sensitive dose dependent category for CLSI
# The ciprofloxacin ECOFF (4 mg/L, *E. faecalis*) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only
** The ciprofloxacin concentration range available on Vitek and Phoenix cards restricts the ability to determine non-wild type (ECOFF 8 mg/L) *E. faecium*
‡ 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 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
Benzylpenicillin resistance including beta-lactamase producers
*** Resistance as determined by cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix)
‡‡ Resistance not defined
§§§ Mupirocin high-level resistance screen
The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant
**** The doxycycline concentration range available on the Phoenix card used restricts the ability to accurately identify intermediate and resistant (CLSI) categories for enterococci
‡‡ 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 defined by Magiorakos et al.[34] were applied in this survey; where multi-drug resistance was defined as resistance to one or more agent in three or more antimicrobial categories. For each species, antimicrobials were excluded from the count if they were affected by natural resistance mechanisms.

Only isolates for which the full range of antimicrobial categories was tested were included for determination of multi-drug resistance. EUCAST breakpoints were primarily used in the analysis. For amoxicillin–clavulanic acid, CLSI breakpoints were used, as 27/30 laboratories used the Vitek AST-N246 card which has the CLSI formulation for this agent.

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 intrinsic resistance 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[35] and have been identified as a major AMR threat in Australian healthcare facilities.[36]

Table 15: Multiple acquired resistance in *Enterobacter cloacae* complex, by state and territory, 2020

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)				
		0	1	2	%	3	4	5	6	%
NSW	164	90	26	26	86.6	11	4	4	3	13.4
Vic	87	51	9	10	80.5	4	4	6	3	19.5
Qld	82	51	9	12	87.8	2	1	6	1	12.2
SA	22	12	4	4	n/a	2	0	0	0	n/a
WA	57	41	4	11	98.2	1	0	0	0	1.8
Tas	18	14	1	3	n/a	0	0	0	0	n/a
NT	6	4	0	1	n/a	0	1	0	0	n/a
ACT	10	6	1	3	n/a	0	0	0	0	n/a
Total	**446**	**269**	**54**	**70**	**88.1**	**20**	**10**	**16**	**7**	**11.9**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable, insufficient numbers (<30) to calculate percentage

Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Enterobacter cloacae* complex includes *E. asburiae* (*n* = 7), *E. bugandensis* (*n* = 6), *E. hormaechei* (*n* = 2), *E. kobei* (*n* = 1), and *E xiangfangensis* (*n* = 1).

Table 16: Multiple acquired resistance in *Escherichia coli*, by state and territory, 2020

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)								
		0	1	2	%	3	4	5	6	7	8	9	10	%
NSW	1,132	476	167	173	72.1	79	88	79	35	19	14	2	0	27.9
Vic	894	386	139	119	72.0	69	45	68	37	19	9	3	0	28.0
Qld	620	255	104	128	78.5	37	33	41	14	5	2	1	0	21.5
SA	188	91	39	30	85.1	11	4	8	2	0	1	2	0	14.9
WA	769	330	129	112	74.3	61	42	49	27	10	8	1	0	25.7
Tas	201	96	42	28	82.6	10	14	7	3	1	0	0	0	17.4
NT	197	60	17	43	60.9	18	22	19	13	4	1	0	0	39.1
ACT	197	91	30	28	75.6	17	15	10	3	2	1	0	0	24.4
Total	**4,198**	**1785**	**667**	**661**	**74.2**	**302**	**263**	**281**	**134**	**60**	**36**	**9**	**0**	**25.8**

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

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

Table 17: Multiple acquired resistance in *Klebsiella pneumoniae* complex, by state and territory, 2020

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)							
		0	1	2	%	3	4	5	6	7	8	9	%
NSW	285	218	17	14	87.4	7	13	5	9	2	0	0	12.6
Vic	208	138	20	7	79.3	9	8	7	9	7	3	0	20.7
Qld	183	140	18	14	94.0	4	2	4	0	0	1	0	6.0
SA	26	18	2	3	n/a	1	1	0	1	0	0	0	n/a
WA	188	160	11	6	94.1	5	1	3	2	0	0	0	5.9
Tas	30	28	0	0	93.3	0	0	2	0	0	0	0	6.7
NT	37	22	3	2	73.0	0	5	1	3	1	0	0	27.0
ACT	38	26	5	3	89.5	1	0	1	2	0	0	0	10.5
Total	**995**	**750**	**76**	**49**	**87.9**	**27**	**30**	**23**	**26**	**10**	**4**	**0**	**12.1**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable, insufficient numbers (<30) to calculate percentage

Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), non-extended cephalosporins (cefazolin), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins + β-lactamase inhibitor (amoxicillin-clavulanic acid, CLSI).
2. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 59).

Table 18: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, 2020

State or territory	Total	Number of categories (non multi-drug resistant)				Number of categories (multi-drug resistant)			
		0	1	2	%	3	4	5	%
NSW	258	208	16	18	93.8	7	6	3	6.2
Vic	99	73	13	11	98.0	2	0	0	2.0
Qld	160	134	10	12	97.5	3	1	0	2.5
SA	71	55	8	5	95.8	2	1	0	4.2
WA	100	90	6	3	99.0	1	0	0	1.0
Tas	27	19	2	5	n/a	1	0	0	n/a
NT	12	8	2	1	n/a	1	0	0	n/a
ACT	31	23	5	2	96.8	1	0	0	3.2
Total	**758**	**610**	**62**	**57**	**96.2**	**18**	**8**	**3**	**3.8**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable, insufficient numbers (<30) to calculate percentage

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

Table 19: Multiple acquired resistance in *Staphylococcus aureus* (methicillin resistant), by state and territory, 2020

State or territory	Number of categories (non-MDR)					Number of categories (MDR)									
	Total	0	1	2	%	3	4	5	6	7	8	9	10	11	%
NSW	155	53	31	21	67.7	17	11	18	4	0	0	0	0	0	32.3
Vic	69	27	13	12	75.4	5	6	6	0	0	0	0	0	0	24.6
Qld	74	39	14	8	82.4	3	5	1	3	1	0	0	0	0	17.6
SA	25	17	5	3	n/a	0	0	0	0	0	0	0	0	0	n/a
WA	99	64	12	14	90.9	7	2	0	0	0	0	0	0	0	9.1
Tas	7	2	3	1	n/a	1	0	0	0	0	0	0	0	0	n/a
NT	39	21	3	8	82.1	3	2	2	0	0	0	0	0	0	17.9
ACT	8	0	2	1	n/a	2	3	0	0	0	0	0	0	0	n/a
Total	476	**223**	**83**	**68**	**78.6**	**38**	**29**	**27**	**7**	1	**0**	**0**	**0**	**0**	**21.4**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable, insufficient numbers (<30) to calculate percentage

Note: Antimicrobials were aminoglycosides (gentamicin), ansamycins (rifampicin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), fucidanes (fusidic acid), glycopeptides (vancomycin or teicoplanin), lincosamides (clindamycin), lipopeptides (daptomycin), macrolides (erythromycin), oxazolidinones (linezolid), and tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™).

Table 20: Multiple acquired resistance in *Staphylococcus aureus* (methicillin susceptible), by state and territory, 2020

State or territory	Number of categories (non-MDR)					Number of categories (MDR)									
	Total	0	1	2	%	3	4	5	6	7	8	9	10	11	%
NSW	644	517	53	63	98.3	7	2	2	0	0	0	0	0	0	1.7
Vic	390	321	26	32	97.2	11	0	0	0	0	0	0	0	0	2.8
Qld	398	306	33	42	95.7	15	2	0	0	0	0	0	0	0	4.3
SA	212	177	21	10	98.1	4	0	0	0	0	0	0	0	0	1.9
WA	347	280	25	29	96.3	11	1	1	0	0	0	0	0	0	3.7
Tas	119	107	6	5	99.2	1	0	0	0	0	0	0	0	0	0.8
NT	42	32	1	6	92.9	1	2	0	0	0	0	0	0	0	7.1
ACT	88	73	3	7	94.3	3	2	0	0	0	0	0	0	0	5.7
Total	**2,240**	**1,813**	**168**	**194**	**97.1**	**53**	**9**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**2.9**

MDR = multi-drug 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, 55.0% 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, 13.4% were resistant to at least one antimicrobial group (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 22). For *P. aeruginosa,* 19.3% 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, Australia, 2020

Resistance pattern	Number	% of total*
Fully susceptible	2,188	45.0
Single resistance	1,615	33.2
Aminopenicillins	1,527	31.4
Fluoroquinolones	78	1.6
Aminoglycosides	10	0.2
Resistance to two antimicrobial groups	464	9.5
Aminopenicillins + third-generation cephalosporins	177	3.6
Aminopenicillins + fluoroquinolones	170	3.5
Aminopenicillins + aminoglycosides	113	2.3
Fluoroquinolones + aminoglycosides	4	0.1
Resistance to three antimicrobial groups	406	8.4
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	231	4.8
Aminopenicillins + fluoroquinolones + aminoglycosides	111	2.3
Aminopenicillins + third-generation cephalosporins + aminoglycosides	64	1.3
Resistance to four antimicrobial groups	188	3.9
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	186	3.8
Aminopenicillins + third-generation cephalosporins + aminoglycosides + carbapenems	2	0.0

Note: Only data from isolates tested against all five antimicrobial groups were included (*n* = 4,861).

Table 22: Resistance combinations among *Klebsiella pneumoniae* tested against fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems, Australia, 2020

Resistance pattern	Number	% of total
Fully susceptible	987	86.6
Single resistance	57	5.0
Fluoroquinolones	29	2.5
Third-generation cephalosporins	16	1.4
Aminoglycosides	12	1.1
Resistance to two antimicrobial groups	46	4.0
Third-generation cephalosporins + fluoroquinolones	27	2.4
Third-generation cephalosporins + aminoglycosides	11	1.0
Fluoroquinolones + aminoglycosides	8	0.7
Resistance to three antimicrobial groups	49	4.3
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	48	4.2
Third-generation cephalosporins + aminoglycosides + carbapenems	1	0.1
Resistance to four antimicrobial groups	1	0.1
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	1	0.1

Notes:
1. Only data from isolates tested against all four antimicrobial groups were included (*n* = 1,140).
2. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 75).

Table 23: Resistance combinations among *Pseudomonas aeruginosa* tested against piperacillin–tazobactam, ceftazidime, fluoroquinolones, aminoglycosides and carbapenems, Australia, 2020

Resistance pattern	Number	% of total
Fully susceptible	611	80.7
Single resistance	67	8.9
Piperacillin–tazobactam	32	4.2
Fluoroquinolones	28	3.7
Carbapenems	6	0.8
Aminoglycosides	1	0.1
Resistance to two antimicrobial groups	53	7.0
Piperacillin–tazobactam + ceftazidime	34	4.5
Piperacillin–tazobactam + fluoroquinolones	13	1.7
Piperacillin–tazobactam + carbapenems	4	0.5
Fluoroquinolones + ceftazidime	1	0.1
Fluoroquinolones + carbapenems	1	0.1
Resistance to three antimicrobial groups	16	2.1
Piperacillin–tazobactam + ceftazidime + carbapenems	6	0.8
Piperacillin–tazobactam + ceftazidime + fluoroquinolones	5	0.7
Piperacillin–tazobactam + fluoroquinolones + aminoglycosides	2	0.3
Piperacillin–tazobactam + fluoroquinolones + carbapenems	2	0.3
Fluoroquinolones + ceftazidime + aminoglycosides	1	0.1
Resistance to four antimicrobial groups	7	0.9
Piperacillin–tazobactam + ceftazidime + fluoroquinolones + carbapenems	4	0.5
Piperacillin–tazobactam + ceftazidime + fluoroquinolones + aminoglycosides	2	0.3
Piperacillin–tazobactam + ceftazidime + aminoglycosides + carbapenems	1	0.1
Resistance to five antimicrobial groups	3	0.4
Piperacillin–tazobactam + ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	3	0.4

Note: Only data from isolates tested against all five antimicrobial groups were included (n = 757).

Table 24: Resistance combinations among *Staphylococcus aureus* tested against methicillin, fluoroquinolones and rifampicin, 2020

Resistance pattern	N	% of total
Fully susceptible	2,176	80.1
Single resistance	382	14.1
Methicillin	318	11.7
Fluoroquinolones	58	2.1
Rifampicin	6	0.2
Resistance to two antimicrobial groups	157	5.8
Methicillin + fluoroquinolones	157	5.8
Resistance to three antimicrobial groups	1	0.0
Methicillin + fluoroquinolones + rifampicin	1	0.0

Note: Only data from isolates tested against all five antimicrobial groups were included (n = 2,716).

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.

Table 25: Multi-drug resistance, by onset setting and 30-day all-cause mortality, 2020

Species	Category	Total		Community onset		Hospital onset	
		Number	Deaths, % (n)	Number	Deaths,% (n)	Number	Deaths, % (n)
Escherichia coli	Total	2,783	9.5 (264)	2,316	8.3 (193)	467	15.2 (71)
	Non-MDR (≤2)	2,052	8.9 (182)	1,749	7.8 (136)	303	15.2 (46)
	MDR (>2)	731	11.2 (82)	567	10.1 (57)	164	15.2 (25)
Enterobacter cloacae complex	Total	358	13.1 (47)	194	11.9 (23)	164	14.6 (24)
	Non-MDR (≤2)	315	13.0 (41)	179	11.7 (21)	136	14.7 (20)
	MDR (>2)	43	14.0 (6)	15	13.3 (2)	28	14.3 (4)
Klebsiella pneumoniae complex	Total	697	12.5 (87)	503	11.7 (59)	194	14.4 (28)
	Non-MDR (≤2)	607	12.5 (76)	446	11.7 (52)	161	14.9 (24)
	MDR (>2)	90	12.2 (11)	57	12.3 (7)	33	12.1 (4)
Staphylococcus aureus	Total	2,200	13.5 (296)	1,740	12.8 (223)	460	17.6 (73)
	Non-MDR (≤2)	1,752	13.2 (231)	1,399	12.4 (173)	353	16.8 (58)
	MDR (>2)	448	14.5 (65)	341	14.7 (50)	107	20.5 (15)
Pseudomonas aeruginosa	Total	555	14.8 (82)	324	15.4 (50)	231	13.9 (32)
	Non-MDR (≤2)	532	13.9 (74)	314	14.6 (46)	218	12.8 (28)
	MDR (>2)	23	34.8 (8)	10	40.0 (4)	13	30.8 (4)

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

categories Notes:

1. Antimicrobial categories (agents) for each species are listed under Tables 15 to 20. For *Staphylococcus aureus,* anti-staphylococcal β-lactams (cefoxitin) is also included.
2. *Enterobacter cloacae* complex includes *E. asburiae* (*n* = 6), *E. bugandensis* (*n* = 5), *E. hormaechei* (*n* = 2), *E. kobei* (*n* = 1), and *E. xiangfangensis* (*n* = 1).
3. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 53).

3.9. PCR and whole genome sequencing

This section describes the results of molecular studies on the resistance mechanisms of gram-negative organisms, and the molecular epidemiology of *E. faecium* and MRSA. The benefits of molecular methods include increased accuracy in detecting the genetic mechanisms for AMR and clarifying the underlining epidemiology.

3.9.1. Gram-negative organisms

All referred *Enterobacterales* with meropenem MIC >0.125 mg/L (>0.25 mg/L if tested using Vitek®); and all referred *P. aeruginosa*, *Acinetobacter* species, *Salmonella* species and *Shigella* species were sequenced. A subset of *E. coli* and *K. pneumoniae* complex with meropenem ≤0.25 mg/L were selected for WGS based on their phenotype (ceftriaxone, ceftazidime and ciprofloxacin), and analysed for antimicrobial resistance determinants. The remaining isolates were screened for dominant ESBL and plasmid-borne AmpC as outlined in Appendix B.

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*. Recently, two new trends have appeared: ESBLs in *Enterobacter* species, and the emergence of specific types of ESBLs (CTX-M enzymes) in *E. coli* from the community. The latter is part of a global epidemic.[3-5] 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.[37]

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.

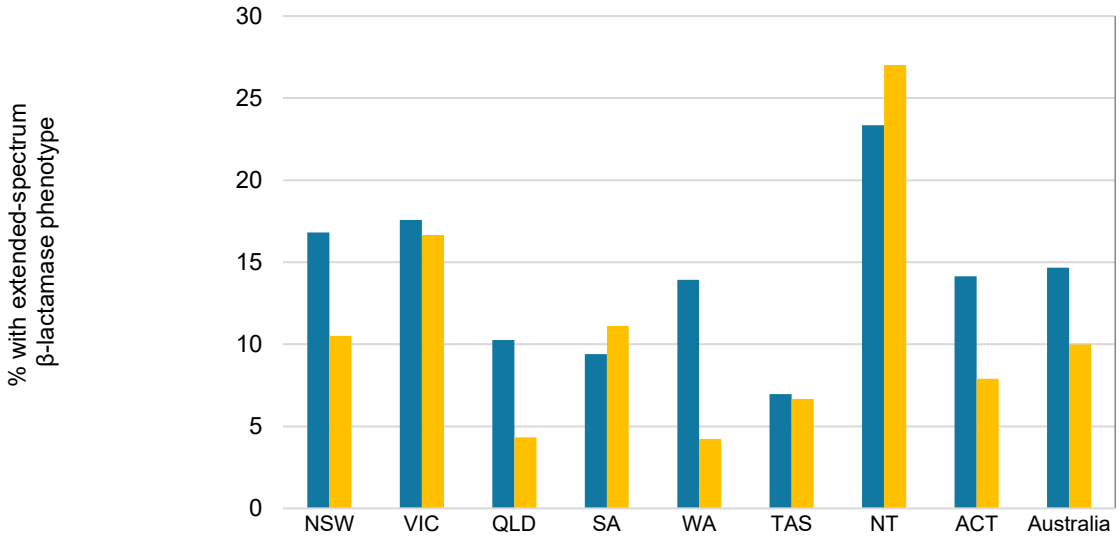
Most ESBL-producing isolates will be detected using the CLSI/EUCAST ceftriaxone ‘susceptible’ breakpoint of 1 mg/L. The CLSI ‘susceptible’ breakpoint of 4 mg/L for ceftazidime is less reliable for ESBL detection. Isolates with either ceftriaxone or ceftazidime minimum inhibitory concentrations (MICs) above 1 mg/L were selected for molecular testing.

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.[38] However, due to the cefepime concentration range available on the susceptibility cards, isolates with a cefepime MIC of greater than 1 mg/L were selected for molecular testing.

PCR testing included screening for bla_{SHV} with G→A substitution at position 700 and/or 703, encoding ESBL variants, $bla_{CTX\text{-}M}$ groups 1 and 9, and plasmid-borne *ampC* ($bla_{CMY\text{-}2\text{-}like}$, bla_{DHA}, $bla_{ACT/MIR}$) 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 9.

Figure 9. Percentage of *Escherichia coli* and *Klebsiella pneumoniae* with extended-spectrum β-lactamase phenotype, by state and territory, and nationally, 2020



	NSW	VIC	QLD	SA	WA	TAS	NT	ACT	Australia
E. coli, %	16.8	17.6	10.3	9.4	13.9	7.0	23.4	14.1	14.7
K. pneumoniae, %	10.5	16.7	4.3	11.1	4.2	6.7	27.0	7.9	10.0
E. coli (n = 4,867)	251	158	64	45	108	14	46	28	714
K. pneumoniae complex (n = 1,141)	39	35	8	9	8	2	10	3	114

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

Based on the tests performed in this study, ESBLs were more common among *E. coli* (579/4,867, 11.9% confirmed) and *K. pneumoniae* complex (88/1,141, 7.7% confirmed) than among other species (Table 26). For 50 *E. cloacae* complex with cefepime MIC greater than 1 mg/L, 28 (56.0%; 6.2% overall) contained an ESBL (CTX-M group 1 only [12], SHV ESBL only [10], CTX-M group 9 only [4], CTX-M group 9 and SHV ESBL [1], or CTX-M group 1 + CTX-M group 9 [1]).

Almost all (95%, 18/19) of *K. oxytoca* isolates with a ceftriaxone-resistant phenotype were presumably hyperproducers of *bla*$_{OXY}$, the natural chromosomal enzyme in this species, with characteristic resistance to piperacillin–tazobactam and borderline resistance to cefepime, but susceptibility to ceftazidime.[39, 40] 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 26: β-lactamase genes detected in *Enterobacterales* with extended-spectrum β-lactamase phenotype, 2020

β-lactamase mechanism	*Escherichia coli*	*Klebsiella pneumoniae* complex	*Enterobacter cloacae* complex	*Klebsiella oxytoca*	*Proteus mirabilis*	*Salmonella* spp.†
Total	4,867	1,141	453	254	281	129
ESBL phenotype*, % (n)	14.7 (714)	10.0 (114)	11.5 (52)	8.3 (21)	3.9 (11)	2.3 (3)
β-lactamase genes confirmed/number tested (%)	653/685 (95.3)	100/108 (92.6)	33/50 (66.0)	1/19 (5.3)	6/11 (54.5)	3/3 (100)
ESBL	551	86	18	1	5	3
ESBL, AmpC	26	1	0	0	0	0
ESBL, AmpC, Carb	1	1	0	0	0	0
ESBL, Carb	1	0	10	0	0	0
AmpC	69	11	0	0	1	0
AmpC, Carb	4	0	0	0	0	0
Carb	1	1	5	0	0	0
Not detected	32	8	17	18	5	0
n/a	29	6	2	2	0	0

AmpC = plasmid-borne *ampC* (CMY-2-like, DHA, ACT/MIR); Carb = carbapenemase (WGS); ESBL = extended-spectrum β-lactamase (SHV-ESBL, CTX-M groups 1 and 9, VEB); n/a = isolate not available for follow-up

* ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L; for *E. cloacae* complex, cefepime MIC > 1 mg/L
† Non-typhoidal (n = 92), typhoidal (n = 37)

Note: Not all isolates with ESBL phenotype were screened for carbapenemase genes (see to Appendix B)

bla$_{CTX-M}$-types continue to be the prominent ESBL gene in *E. coli* (Table 27). Of 579 with confirmed ESBLs, 574 (99.1%) had one or more *bla*$_{CTX-M}$ genes detected by PCR or WGS, either *bla*$_{CTX-M}$ group 9 (*n* = 304), *bla*$_{CTX-M}$ group 1 (*n* = 259), or both *bla*$_{CTX-M}$ group 1 + group 9 (*n* = 11). CTX-M group 9 types were more prevalent in all states and territories except for Victoria where CTX-M group 1 types dominated. Among *K. pneumoniae* complex with confirmed ESBLs, 76 of 88 (86.4%) contained a *bla*$_{CTX-M}$ gene: *bla*$_{CTX-M}$ group 1 (*n* = 67), *bla*$_{CTX-M}$ group 9 (*n* = 9).

An ESBL phenotype was significantly more likely to be found among hospital-onset than community-onset episodes of *E. coli* bacteraemia (155/729 [21.3%] vs 559/4,138 [13.5%], P < 0.01). Paediatric patients were significantly more likely to have an ESBL-producing *K. pneumoniae* bacteraemia than adults (15/61 [24.6%] vs 99/1,080 [9.2%], P < 0.01).

Table 27: β-lactamase genes among *Enterobacterales* with extended-spectrum β-lactamase phenotype, by state and territory, 2020

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,493	899	624	479	776	201	197	198	4,867
ESBL phenotype*, % (*n*)	16.8 (251)	17.6 (158)	10.3 (64)	9.4 (45)	13.9 (108)	7.0 (14)	23.4 (46)	14.1 (28)	14.7 (714)
ESBL types	194	141	47	39	85	10	36	27	579
CTX-M types	190	141	47	39	84	10	36	27	574
Group 1	89	78	16	15	33	4	12	12	259
Group 9	101	63	31	24	51	6	24	15	304
Group 1 + group 9	5	0	1	1	2	1	1	0	11
SHV (ESBL-types)	3	0	0	0	1	0	0	0	4
VEB types	2	1	0	0	0	0	0	0	3
Plasmid-borne AmpC	40	12	14	6	16	2	8	2	100
CMY-2-like	19	7	9	6	6	2	1	0	50
DHA	21	5	5	0	10	0	7	2	50
Carbapenemase	1	3	0	0	1	0	0	0	4
NDM-5	1	1	0	0	0	0	0	0	2
OXA-181	0	2	0	0	0	0	0	0	2
Klebsiella pneumoniae complex	371	210	185	81	189	30	37	38	1,141
ESBL phenotype*, % (*n*)	10.5 (39)	16.7 (35)	4.3 (8)	11.1 (9)	4.2 (8)	6.7 (2)	27.0 (10)	7.9 (3)	10.0 (114)
ESBL types	29	30	6	5	4	2	10	2	88
CTX-M types	28	22	5	4	4	2	9	2	76
Group 1	24	18	4	4	4	2	9	2	67
Group 9	4	4	1	0	0	0	0	0	9
SHV (ESBL-types)	3	9	1	1	0	0	1	0	15
Plasmid-borne AmpC	3	3	2	1	3	0	0	1	13
CMY-2-like	0	1	1	0	0	0	0	0	2
DHA	3	2	1	1	3	0	0	1	11
Carbapenemase	1	0	1	0	0	0	0	0	2
IMP-4	1	0	0	0	0	0	0	0	1
NDM-1	0	0	1	0	0	0	0	0	1
Enterobacter cloacae complex	165	88	83	23	59	19	6	10	453
ESBL phenotype*, % (*n*)	9.7 (16)	15.9 (14)	15.7 (13)	13.0 (3)	3.4 (2)	10.5 (2)	–† (2)	0.0 (0)	11.5 (52)
ESBL types									
CTX-M types	4	4	7	1	1	0	1	0	18
Group 1	3	1	7	1	0	0	0	0	12
Group 9	1	2	0	0	1	0	1	0	5
Group 1 + group 9	0	1	0	0	0	0	0	0	1
SHV (ESBL-types)	2	8	0	0	0	0	1	0	11
VEB types	1	0	0	0	0	0	0	0	1
Carbapenemase	4	9	2	0	0	0	0	0	15
IMP-4	4	8	2	0	0	0	0	0	14
NDM-1	0	1	0	0	0	0	0	0	1

ESBL = extended-spectrum β-lactamase (SHV-ESBL, CTX-M groups 1 and 9, VEB)

* ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L; for *E. cloacae* complex, cefepime MIC > 1 mg/L
† Insufficient numbers (<10) to calculate percentage

Notes:
1. Isolates may possess more than one type of β-lactamase gene
2. Not all isolates were screened for carbapenemase genes (see Appendix B)

WGS analysis was performed on a subset of 259 *E. coli.* This subset included 230 with an ESBL phenotype and 29 non-ESBL phenotype (Table 28). *bla*$_{CTX-M}$ genes were detected in 75.7% (174/230) of the *E. coli* subset with an ESBL phenotype. In the *bla*$_{CTX-M-1}$ group, *bla*$_{CTX-M-15}$ accounted for 91.0% (71/78). In the *bla*$_{CTX-M-9}$ group, *bla*$_{CTX-M-27}$ and *bla*$_{CTX-M-14}$ were the major genotypes, accounting for 69.8% (67/96) and 29.2% (28/96), respectively.

In the *bla*$_{CTX-M}$-positive isolates, SHV-type ESBLs were not detected. Among 56 *bla*$_{CTX-M}$-negative isolates with an ESBL phenotype, 39 harboured pAmpC, either alone (*bla*$_{DHA-1}$ [18], *bla*$_{CMY-2-like}$ [17], *bla*$_{CMY-42}$ [3]), or with a carbapenemase gene (*bla*$_{CMY-2-like}$ + *bla*$_{NDM-5}$ [1]). One harboured a carbapenemase gene alone (*bla*$_{OXA-181}$) and one harboured an ESBL (*bla*$_{SHV-2}$). β-lactam resistance mechanisms were not detected in the remaining 15 isolates.

Table 28: *Escherichia coli* subset, CTX-M variants, ESBL phenotype, sequence type, 2020

		Phenotype		Sequence type							
CTX-M variant	Number	ESBL	Non-ESBL	131	69	648	–*	38	1193	73	Other types (*n* = 44)
Not detected	86	57	29	5	11	8	7	2	3	6	43
CTX-M-1 group	78	78	0	43	5	3	2	1	4	3	17
CTX-M-15	71	71	0	43	4	3	2	0	3	2	14
CTX-M-3	3	3	0	0	1	0	0	0	1	1	0
CTX-M-55	3	3	0	0	0	0	0	0	0	0	3
CTX-M-143	1	1	0	0	0	0	0	1	0	0	0
CTX-M-9 group	96	96	0	59	4	3	4	9	4	1	12
CTX-M-27	67	67	0	51	2	0	3	3	4	0	4
CTX-M-14a	24	24	0	8	2	3	1	2	0	1	7
CTX-M-14b	4	4	0	0	0	0	0	4	0	0	0
CTX-M-65	1	1	0	0	0	0	0	0	0	0	1
	259	**230**	**29**	**107**	**20**	**14**	**13**	**12**	**11**	**10**	**72**

ESBL = extended-spectrum β-lactamase (SHV-ESBL, CTX-M groups 1 and 9, VEB)

* Not available

A little over one-half (58.6%, 102/174) of the ESBL-producing *E. coli* subset with confirmed ESBL types belong to sequence type 131 (ST131) (Table 29). The fluoroquinolone-resistant subclade, H30R, was the most prevalent subclade of ST131 (59.8%, 61/102). H30Rx (subclade C2) encompasses almost all (34/35) ST131 carrying *bla*$_{CTX-M-15}$, a finding reported globally.[41-43] Just over three-quarters (76.1%, 51/67) of isolates with *bla*$_{CTX-M-27}$ were ST131; 29/51 belonged to H41 subclade A, and 20/51 belonged to H30R subclade C1-M27.

ST1193 has recently been identified as an emerging multidrug-resistant type.[5, 44, 45] All ST1193 isolates were ciprofloxacin resistant, and half (4/8) harboured *bla*$_{CTX-M-27}$.

Table 29: ESBL-producing *Escherichia coli* subset, ST131, *fimH* allele, H30Rx, 2020

		ST131					
			H30				
ESBL type	Number	All	H30Rx	H30R	H41*	Others†	Non-ST131
CTX-M-15	71	43	34	1	6	2	28
CTX-M-27	67	51	0	20	29	2	16
CTX-M-14a	24	8	1	5	0	2	16
CTX-M-14b	4	0	0	0	0	0	4
CTX-M-55	3	0	0	0	0	0	3
CTX-M-3	3	0	0	0	0	0	3
CTX-M-143	1	0	0	0	0	0	1
CTX-M-65	1	0	0	0	0	0	1
	174	**102**	**35**	**26**	**35**	**6**	**72**

* Includes H41-like (*n* = 1)
† H99 (*n* = 2), H1196 (*n* = 1), H89 (*n* = 1), H54 (*n* = 1), H-new (*n* = 1)

Plasmid-borne AmpC β-lactamases

Plasmid-borne *ampC* β-lactamase genes have recently emerged internationally as a growing 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 chromosomally encoded AmpC enzymes.

Testing included screening referred isolates that were not selected for WGS for plasmid-borne *ampC* (CMY-2-like, DHA, ACT/MIR) genes using methods outlined in Appendix B.

The proportions of *E. coli* and *K. pneumoniae* complex with a cefoxitin MIC > 8 mg/L (non-wild type) remain low. A little over one-third (94/249, 37.8%) of *E. coli* and 18.6% (13/70) of *K. pneumoniae* complex with cefoxitin MIC > 8 mg/L that were available for confirmation contained one or more plasmid-borne *ampC* genes (Table 30).

A bla_{DHA} gene was found in 52.1% (49/94) of *E. coli* and 84.6% (11/13) of *K. pneumoniae* complex with plasmid-borne *ampC* genes.

Carbapenemase genes were detected in three of 155 *E. coli* (bla_{NDM-5} [1], $bla_{OXA-181}$ [1], bla_{OXA-48} [1]), and one of 57 cefoxitin non-wild type (MIC > 8 mg/L) *K. pneumoniae* complex (bla_{IMP-4}) that did not have plasmid-encoded *ampC* genes. Seven *E. coli* with a cefoxitin wild type (MIC ≤ 8 mg/L) also contained bla_{CMY-2}-like gene (*n* = 5) or bla_{DHA} (*n* = 2). No plasmid-encoded ampC genes were found in *K. pneumoniae* complex with cefoxitin MIC ≤ 8 mg/L.

Table 30: Numbers of isolates with presumptive plasmid-borne AmpC β-lactamase production, by state and territory, 2020

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,492	899	624	479	776	201	197	198	4,866
Cefoxitin MIC > 8 mg/L (%)	98 (6.6)	4 (5.5)	29 (4.6)	16 (3.3)	38 (4.9)	12 (6.0)	13 (6.6)	8 (4.0)	263 (5.4)
Confirmed/number tested	38/92	13/48	14/29	4/15	14/34	2/12	7/11	2/8	94/249
bla_{DHA}	20	6	5	0	9	0	7	2	49
$bla_{CMY\text{-}2\text{-}like}$	17	7	9	3	4	2	0	0	42
$bla_{CMY\text{-}2\text{-}like+DHA}$	1	0	0	1	1	0	0	0	3
Klebsiella pneumoniae complex	371	209	185	81	189	30	37	38	1,140
Cefoxitin MIC > 8 mg/L (%)	21 (5.7)	16 (7.7)	11 (5.9)	8 (9.9)	8 (4.2)	0 (0.0)	2 (5.4)	5 (13.2)	71 (6.2)
Confirmed/number tested	3/20	3/16	2/11	1/8	3/8	0/0	0/2	1/5	13/70
bla_{DHA}	3	2	1	1	3	0	0	1	11
$bla_{CMY\text{-}2\text{-}like}$	0	1	1	0	0	0	0	0	2

MIC = minimum inhibitory concentration

Note: Isolates with cefoxitin MIC = 8 mg/L (non-wild type) were screened for plasmid-borne AmpC.

Carbapenem resistance

All referred *Enterobacterales* with meropenem MIC >0.125 mg/L (>0.25 mg/L it tested using Vitek) (*n* = 79); and *Acinetobacter* species (*n* = 1) or *P. aeruginosa* (*n* = 30) with meropenem MIC ≥8 mg/L were sequenced for the presence of carbapenemase genes. Among meropenem-resistant (MIC >8 mg/L) isolates that were available, carbapenemase genes were found in 91.7% (22/24) of *Enterobacterales*, 12.5% (3/24) *P. aeruginosa*, and all *Acinetobacter* species (1/1) (Table 31). All four *Enterobacterales* with class D enzymes ($bla_{OXA\text{-}181}$, $bla_{OXA\text{-}48}$) had meropenem MIC of 1 or 2 mg/L.

Table 31: Numbers of isolates with carbapenemase genes, organism group, meropenem MIC, 2020

	Acinetobacter (*n* = 98)			*Enterobacterales* (*n* = 7,826)				*Pseudomonas* (*n* = 760)		
	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	97	0	1	7,770	24	7	25	691	42	27
Confirmed/number tested	0/2	–*	1/1	0/477	4/22	2/7	22/24	0/0	0/5	3/24
Carbapenemase type†										
Class A	–*	–*	0	0	0	0	1	–*	–*	3
Class B	–*	–*	0	0	0	2	21	–*	–*	0
Class D	–*	–*	1	0	4	0	0	–*	–*	0

* not applicable

† Carbapenemase molecular class: class A (IMI, GES); class B (metallo-β-lactamases - IMP, NDM); class D (oxacillinases – OXA-23, OXA-48, OXA-181)

Thirty-two (0.37% overall) isolates from 32 patients were found to harbour a carbapenemase gene (Table 32). Overall prevalence of carbapenemase genes among *Enterobacterales* was 0.36% (28/7,871); although for *E. cloacae* complex, it was 3.8% (17/453). $bla_{IMP\text{-}4}$ accounted for 67.9% (19/28) of all CPE in 2020. It was mostly detected in *E. cloacae* complex (15/17, 88%), 8/15 of which were detected from one institution. Other types detected in *Enterobacterales* were NDM-types (4), OXA-48-like types (4) and IMI (1).

bla$_{GES-5}$ was detected in three *P. aeruginosa* from the same institution. One *A. baumannii* complex harboured both *bla*$_{OXA-23}$ and *bla*$_{NDM-1}$.

For *P. aeruginosa*, the prevalence was 0.39% (3/771), and for *Acinetobacter* species it was 0.9% (1/110).

Table 32: Carbapenemase-producing organisms, carbapenemase genes, 2020

Species	Total	Carbapenemase type, number								
		IMP-4	NDM-1	NDM-5	OXA-48	OXA-181	GES-5	IMI-1	OXA-23 NDM-1	% (n)
Enterobacterales	7,871	19*	2	2	2	2	0	1	0	0.4 (28)
Enterobacter cloacae complex	453	15	1	0	0	0	0	1	0	3.8 (17)
Escherichia coli	4,882	0	0	2	1	2	0	0	0	0.1 (5)
Klebsiella pneumoniae	1,147	1	1	0	1	0	0	0	0	0.3 (3)
Citrobacter freundii complex	82	1	0	0	0	0	0	0	0	1.2 (1)
Klebsiella aerogenes	124	1	0	0	0	0	0	0	0	0.8 (1)
Serratia marcescens	195	1	0	0	0	0	0	0	0	0.5 (1)
Pseudomonas aeruginosa	771	0	0	0	0	0	3†	0	0	0.4 (3)
Acinetobacter species	110	0	0	0	0	0	0	0	1	0.9 (1)
Acinetobacter baumannii	60	0	0	0	0	0	0	0	1	1.7 (1)
All species	8,752	19*	2	2	2	2	3	1	1	0.4 (32)

* Eight isolates from one institution; † three isolates from one institution

Note: Carbapenemase class A: GES-5, IMI-1; class B: IMP-4, NDM-1, NDM-5; class D: OXA-48, OXA-181, OXA-23.

Isolates carrying carbapenemase genes were detected in 17 institutions from five states and territories. CPE infections are particularly notable in Victoria (13/1,460, 0.9%) and New South Wales (9/2,473, 0.4%), compared to other states and territories (Table 33). Eight of 13 (61.5%) CPE from Victoria were from one institution, all were *bla*$_{IMP-4}$. Over 40.6% (13/32) of carbapenemases were from two institutions (one in Victoria [8]; one in New South Wales [5]). Almost 2 in 3 (11/17, 64.7%) of the institutions had one carbapenemase-producing strain only.

Table 33: Carbapenemase genes, organism group, state and territory, 2020

Organism group and carbapenemase	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Total species, *n*	2,769	1,583	1,271	792	1,368	358	290	321	8,752
Acinetobacter species	32	23	15	12	14	5	7	2	110
Carbapenemase, % (*n*)	3.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.9 (1)
OXA-23, NDM-1	1	0	0	0	0	0	0	0	1
Enterobacterales	2,473	1,460	1,094	708	1,252	326	271	287	7,871
Carbapenemase, % (*n*)	0.4 (9)	0.9 (13)	0.3 (3)	0.0 (0)	0.2 (2)	0.0 (0)	0.0 (0)	0.3 (1)	0.4 (28)
IMP-4	7	9*	2	0	0	0	0	1	19
OXA-48	0	0	0	0	2	0	0	0	2
OXA-181	0	2	0	0	0	0	0	0	2
NDM-5	1	1	0	0	0	0	0	0	2
NDM-1	0	1	1	0	0	0	0	0	2
IMI-1	1	0	0	0	0	0	0	0	1
Pseudomonas aeruginosa	264	100	162	72	102	27	12	32	771
Carbapenemase, % (*n*)	1.1 (3)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.4 (3)
GES-5	3†	0	0	0	0	0	0	0	3
Prevalence, % (n)	0.5 (13)	0.8 (13)	0.2 (3)	0.0 (0)	0.1 (2)	0.0 (0)	0.0 (0)	0.3 (1)	0.4 (32)

Fluoroquinolone resistance

Multiple resistance mechanisms against quinolones have been described. Resistance is most commonly due to mutations in DNA gyrase (*gyrA*, *gyrB*) and topoisomerase IV (*parC*, *parE*). 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*).[46, 47] *oqxAB* genes are intrinsic in *Klebsiella* and *Enterobacter*.

Salmonella species

Ciprofloxacin resistance (MIC > 0.06 mg/L) in non-typhoidal species was 5.4% (5/93). However, for typhoidal *Salmonella* species, it was 77.5% (31/40) (serovar Paratyphi: 11/11, 100%; serovar Typhi: 20/29, 69%) (Table 34).

Table 34: *Salmonella* species, ciprofloxacin minimum inhibitory concentrations, 2020

	Ciprofloxacin minimum inhibitory concentration (mg/L)							
Organism	**≤0.06**	**0.125**	**0.25**	**0.5**	**1**	**2**	**≥4**	**Total**
Salmonella species (non-typhoidal)	88	1	3	0	0	0	1	93
Salmonella species (typhoidal)	9	0	4	10	12	1	4	40
S. Typhi	9	0	4	6	5	1	4	29
S. Paratyphi A	0	0	0	4	7	0	0	11
Total	**97**	**1**	**7**	**10**	**12**	**1**	**5**	**133**

Note: MICs determined using MIC strips on all *Salmonella* or on those where Vitek® MIC ≤0.25 mg/L.

All *S*. Typhi that were resistant to ciprofloxacin harboured a mutation in the quinolone resistance-determining region (QRDR), in codon 83 of *gyrA*, a common mutation conferring quinolone resistance.[48] Fifteen percent (3/20) of this group also had a second mutation in *gyrA* (codon 87) and one mutation in *parC* (Table 35).

Two *S*. Typhi were resistant to third-generation cephalosporins ($bla_{\text{CTX-M-15}}$) and ciprofloxacin (*gyrA* (S83F), *qnrS1*).

All serovar paratyphi A were ciprofloxacin resistant and have known mutations in both *gyrA* (S83F) and *parC* (T57S) (Table 35).[48]

One non-typhoidal isolate had an ESBL gene ($bla_{\text{CTX-M-15}}$) (ceftriaxone MIC >4 mg/L, ciprofloxacin MIC ≤0.06 mg/L.

Table 35: Fluroquinolone resistance determinants in ciprofloxacin-resistant *Salmonella* species, 2020

Species	Mutations in QRDR		PMQR genes	Total
	gyrA	*parC*		
Salmonella (non-typhoidal)				5
Salmonella (non-typhoidal) (*n* = 5)	S83F	–*	–*	1
	D83Y	–*	–*	1
	D87G	–*	–*	1
	D87Y	–*	–*	1
	S83F, D87N	S801	–*	1
Salmonella (typhoidal)				30
S. Paratyphi A (*n* = 10)	S83F	T57S	–*	10
S. Typhi (*n* = 20)	S83F	–*	–*	13
	S83F, D87N	S80I	–*	3
	S83F	E84G	–*	2
	S83F	–*	*qnrS1*	2

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

* Not detected

Notes:

1. Fluoroquinolone resistant determinants include mutations in either the quinolone resistance-determining region of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[49], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*).
2. Mutations in *gyrB* or *parE* were not detected.

Escherichia coli

Nationally, 19.4% (946/4,866) of *E. coli* had a ciprofloxacin MIC >0.25 mg/L, ranging from 10.9% (22/201) in Tasmania to 28.4% in the Northern Territory (56/197). A subset of 259 *E. coli* (5.3% of total, 33.9% of referred) were selected for WGS. This included 230 with an ESBL phenotype and 165 with ciprofloxacin MIC >0.25 mg/L (Table 36).

Table 36: *Escherichia coli*, ciprofloxacin susceptibility, ESBL phenotype, 2020

Subset	Phenotype	Ciprofloxacin MIC (mg/L)			Total	% of total	% of referred
		≤0.25	0.5	>0.5			
Total	ESBL	28.0 (200)	11.8 (84)	60.2 (430)	714	14.7	
	non-ESBL	89.6 (3,720)	1.9 (79)	8.5 (353)	4,152	85.3	
	Total	80.6 (3,920)	3.3 (163)	16.1 (783)	4,866		
Referred*	ESBL	191	81	413	685	95.9	
	non-ESBL	55	2	23	80	1.9	
	Total	246	83	436	765	15.7	
WGS	ESBL	76	28	126	230	32.2	33.6
	non-ESBL	18	1	10	29	0.7	36.3
	Total	94	29	136	259	5.3	33.9

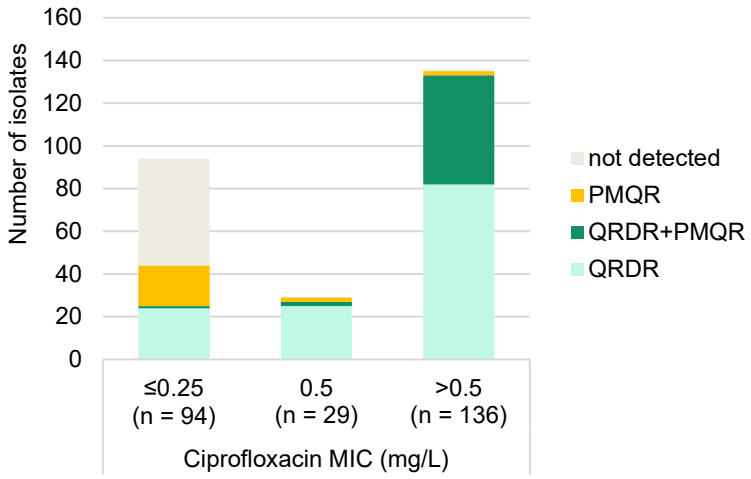
ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L; WGS = whole genome sequencing

* ESBL phenotype or ciprofloxacin MIC > 0.25 mg/L

Almost all (164/165, 99.4%) of the *E. coli* subset that had ciprofloxacin MIC > 0.25 mg/L harboured fluoroquinolone resistance determinants (Figure 10). Almost all (95.8%, 158/165) of this group harboured a QRDR mutation in codon 83 of *gyrA*. A substantial majority (90.1%, 118/131) of isolates resistant to ciprofloxacin (MIC > 0.5 mg/L) also had a second mutation in *gyrA* (codon 87),

and 91.6% (120/131) showed at least one mutation in *parC* (Table 37). PMQR genes (*qnr* variants) alone were more common in ciprofloxacin susceptible isolates.

Figure 10: *Escherichia coli*, fluoroquinolone resistance mechanisms*, ciprofloxacin MIC, 2020



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

* Mutations in either the quinolone resistance-determining region of the DNA gyrase and topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*), and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*, *oqxAB*) detected by whole genome sequence analysis

Almost two-thirds (64.7%, 88/136) of the ciprofloxacin resistant *E. coli* in the subset belonged to either ST131 (*n* = 77) or ST1193 (*n* = 11), both with reported distinguishing *parE* mutations.[50] Just over one-quarter (27.2%, 37/136) harboured *aac(6')-Ib-cr*, almost all (91.9%, 34/37) of which harboured $bla_{\text{CTX-M-15}}$.

Over 60% (34/56, 60.7%) of the isolates with $bla_{\text{CTX-M-15}}$ belonged to ST131-H30Rx clone.

Table 37: Fluoroquinolone resistance determinants* in *Escherichia coli* subset, 2020

QRDR mutations				Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*	*PMQR*	≤0.25	0.5	>0.5	Total
–†	–†	–†	–†	50	0	1	51
–†	–†	–†	*oqxAB*	1	0	0	1
–†	–†	–†	*qnrB4*	14	0	1	15
–†	–†	–†	*qnrS1*	2	2	1	5
–†	–†	–†	*aac(6')-Ib-crC*	2	0	0	2
–†	–†	**I529L**	–†	2	0	0	2
–†	–†	S458A	–†	0	0	1	1
–†	S80I	–†	–†	2	0	0	2
–†	S80I	–†	*qnrS1*	0	0	1	1
D87V	–†	–†	–†	1	0	0	1
S83A	–†	–†	*qnrB4*	1	0	0	1
S83L	–†	–†	–†	11	4	2	17
S83L	–†	–†	*qnrB4*	0	1	4	5
S83L	–†	–†	*qnrS1*	0	0	1	1
S83L	–†	**I529L**	–†	8	19	2	29
S83L	–†	**I529L**	*aac(6')-Ib-crC; qnrB*	0	1	0	1
S83L	–†	**L416F**	–†	0	1	0	1
S83L	–†	S458A	–†	0	0	1	1

QRDR mutations				Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*	*PMQR*	≤0.25	0.5	>0.5	Total
S83L	–[†]	S458A	*aac(6')-Ib-crC*	0	0	1	1
S83L	S80I	–[†]	–[†]	0	0	2	2
S83L, D87N	S57T, S80I	–[†]	–[†]	0	0	2	2
S83L, D87N	S80I	–[†]	–[†]	0	0	5	5
S83L, D87N	S80I	–[†]	*qnrS1*	0	0	1	1
S83L, D87N	S80I	E460D	–[†]	0	0	4	4
S83L, D87N	S80I	**L416F**	–[†]	0	0	5	5
S83L, D87N	S80I	**L416F**	*qnrB4*	0	0	3	3
S83L, D87N	S80I	**L416F**	*aac(6')-Ib-crC*	0	0	3	3
S83L, D87N	S80I	S458A	–[†]	0	0	8	8
S83L, D87N	S80I	S458A	*qepA*	0	0	2	2
S83L, D87N	S80I	S458A	*qnrS1*	0	0	2	2
S83L, D87N	S80I	S458A	*aac(6')-Ib-crC*	0	0	4	4
S83L, D87N	S80I	S458A	*aac(6')-Ib-crC; qnrB4*	0	0	1	1
S83L, D87N	S80I	S458T	–[†]	0	0	1	1
S83L, D87N	S80I, E84G	–[†]	–[†]	0	0	3	3
S83L, D87N	S80I, E84V	**I529L**	–[†]	0	1	44	45
S83L, D87N	S80I, E84V	**I529L**	*aac(6')-Ib-crC*	0	0	28	28
S83L, D87Y	S80I	S458A	–[†]	0	0	1	1
S83L, D87Y	S80I, E84V	**I529L**	–[†]	0	0	1	1
Total				**94**	**29**	**136**	**259**

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

[*] Not detected

Notes:

1. Fluoroquinolone resistant determinants include mutations in either the quinolone resistance-determining region of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[49], 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. Mutations in gyrB were not detected.

Klebsiella pneumoniae complex

Nationally, 12.3% (140/1,140) of *K. pneumoniae* complex had a ciprofloxacin MIC >0.25 mg/L, ranging from 5.3% in Western Australia (10/189) to 20.1% in Victoria (42/209). A subset of 77 *K. pneumoniae* complex (6.8% of total, 49.7% of referred) were selected for WGS. This included 60 with an ESBL phenotype and 52 with ciprofloxacin MIC >0.25 mg/L (Table 38).

Table 38: *Klebsiella pneumoniae* complex, ciprofloxacin susceptibility, ESBL phenotype, 2020

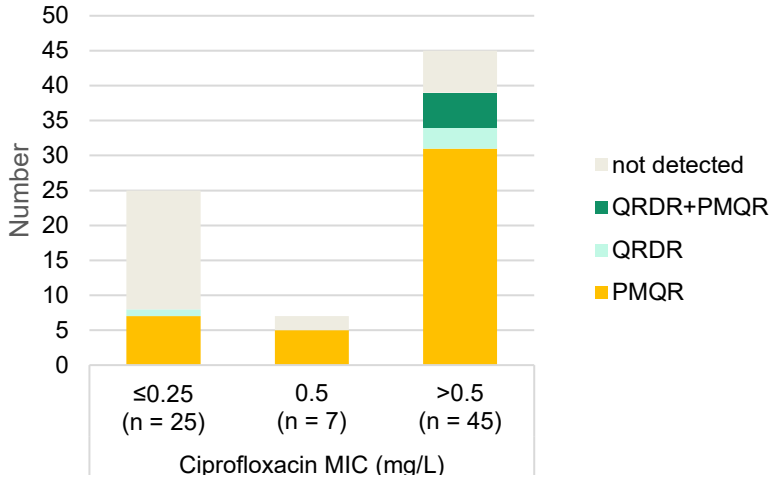
Subset	Phenotype	Ciprofloxacin MIC (mg/L)			Total	% of total	% of referred
		≤0.25	0.5	>0.5			
Total	ESBL	24.8 (28)	5.3 (6)	69.9 (79)	113	9.9	
	non-ESBL	94.6 (972)	2.0 (21)	3.3 (34)	1,027	90.1	
	Total	87.7 (1,000)	2.4 (27)	9.9 (113)	1,140		
Referred*	ESBL	27	6	74	107	94.7	
	non-ESBL	36	3	9	48	4.7	
	Total	63	9	83	155	13.6	
WGS	ESBL	17	5	38	60	53.1	56.1
	non-ESBL	8	2	7	17	1.7	35.4
	Total	25	7	45	77	6.8	49.7

ESBL = ceftriaxone or ceftazidime MIC > 1 mg/L; WGS = whole genome sequencing

* ESBL phenotype or ciprofloxacin MIC > 0.25 mg/L

Over 84% (44/52) of the *K. pneumoniae* complex subset that had ciprofloxacin MIC >0.25 mg/L harboured fluoroquinolone resistance determinants (Figure 11). PMQR genes either alone (82%, 36/44) or in combination with QRDR mutations in codon 83 of *gyrA* (11%, 5/44) were prevalent; only 3/44 had *gyrA* mutations alone. No mutations in *parC* were detected (Table 39).

Figure 11: *Klebsiella pneumoniae* complex (*n* = 77), fluoroquinolone resistance mechanisms*, ciprofloxacin MIC, 2020



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

* Mutations in either the quinolone resistance-determining region of the DNA gyrase or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*), and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*)

Table 39: Fluroquinolone resistance determinants in *Klebsiella pneumoniae* complex subset, 2020

QRDR mutations			Ciprofloxacin MIC (mg/L)			
gyrA	parC	PMQR	≤0.25	0.5	>0.5	Total
–*	–*	–*	17	2	6	25
–*	–*	*qnrB1*	1	0	2	3
–*	–*	*qnrB4*	0	4	4	8
–*	–*	*qnrS1*	0	1	12	13
–*	–*	*aac(6')-Ib-crA*	1	0	0	1
–*	–*	*aac(6')-Ib-crC*	4	0	0	4
–*	–*	*aac(6')-Ib-crC; qnrB1*	0	0	8	8
–*	–*	*aac(6')-Ib-crC; qnrB6*	0	0	2	2
–*	–*	*aac(6')-Ib-crC; qnrS1*	1	0	3	4
D87N	–*	–*	0	0	1	1
D87Y	–*	*aac(6')-Ib-crC*	0	0	1	1
S83F	–*	–*	0	0	2	2
S83F, D87A	–*	*aac(6')-Ib-crC*	0	0	1	1
S83I	–*	*qnrB1*	0	0	1	1
S83I	–*	*aac(6')-Ib-crC; qnrB1*	0	0	1	1
S83T	–*	–*	1	0	0	1
S83Y	–*	*aac(6')-Ib-crC*	0	0	1	1
Total			**25**	**7**	**45**	**77**

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

* Not detected

Notes:

1. Fluoroquinolone resistant determinants include mutations in either the quinolone resistance-determining region of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[49], 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*arE* were not detected.

Pseudomonas aeruginosa

Thirty-nine *P. aeruginosa* with meropenem MIC ≥ 8 mg/L (*n* = 30), or where MICs were not determined (*n* = 9) were referred for WGS. Of the meropenem-resistant isolates, three were also resistant to amikacin (MIC ≥ 64 mg/L).

Only 3/24 (12.5%) meropenem-resistant *P. aeruginosa* harboured a carbapenemase (bla_{GES-5}). One *P. aeruginosa* with meropenem MIC = 8 mg/L harboured $bla_{CTX-M-15}$ and *qnrS1*.

No 16S rRNA methyltransferase or *mcr* genes were found.

Plasmid-mediated colistin determinants

Of 1,230 referred isolates (excluding species intrinsically resistant to colistin), 568 were sequenced. *mcr-1.1* was detected in 1/259 *E. coli*. The isolate was from an 87-year-old female who was hospitalised in South Australia. The isolate was susceptible to meropenem (MIC ≤ 0.125 mg/L), ceftriaxone (MIC ≤ 0.5 mg/L), ciprofloxacin (MIC = 0.5 mg/L), and gentamicin (MIC ≤ 1 mg/L); and had a colistin MIC = 4 mg/L.

Thirteen isolates with the bla_{IMP-4} carbapenemase gene (*E. cloacae* complex [*n* = 11], *K. pneumoniae* [*n* = 1], *C. freundii* complex [*n* = 1]) and one *E. cloacae* complex with bla_{NDM-1} also harboured *mcr-9.1*. An additional *E. cloacae* complex with bla_{IMP-4} harboured *mcr-10*.

Two additional isolates (*E. cloacae* complex and *K. pneumoniae*) that did not produce a carbapenemase gene had *mcr-9.1*. *mcr-9* has recently been found among several species of *Enterobacterales*[51], often on an IncHI2 plasmid, but the two downstream genes reported to be involved in induction of *mcr-9* expression by subinhibitory concentrations of colistin[52] are not present here.

3.9.2. Molecular epidemiology of *Enterococcus faecium*

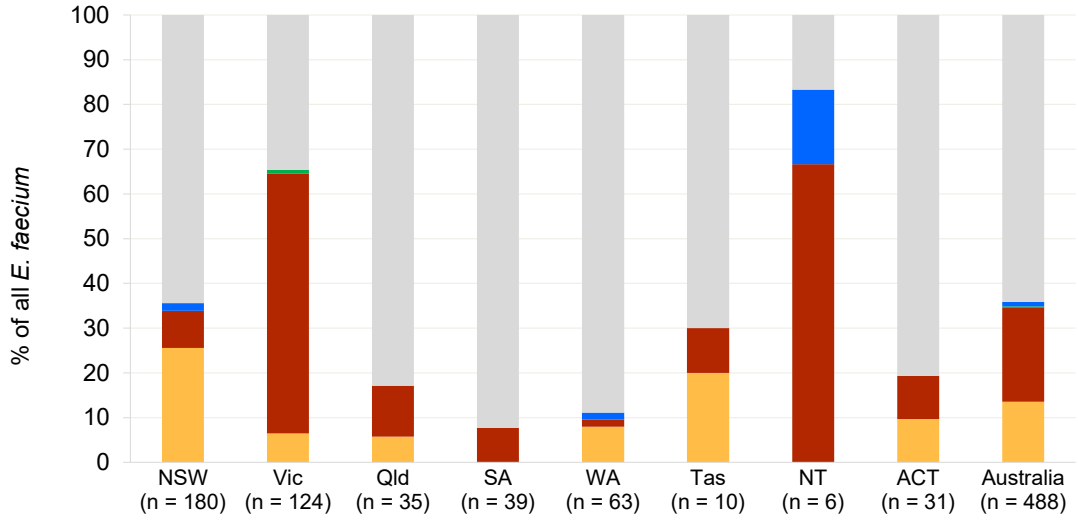
van genes

Results of polymerase chain reaction testing for *vanA* and *vanB* genes were available for 483 (99.0%) of the 488 *E. faecium* isolates. *van* genes were detected in 170/483 (35.2%) of *E. faecium*; *vanA* in 66 (13.7%), *vanB* in 103 (21.3%), and *vanA* and *vanB* in one (0.2%) isolate (Figure 12).

For vancomycin-resistant *E. faecium* (MIC > 4 mg/L), *vanA* was detected in 57/157 (36.3%), *vanB* in 99 (63.1%), and *vanA* and *vanB* in one (0.6%).

In 12 of 323 (3.7%) vancomycin-susceptible *E. faecium*, *van* genes were detected: 9 with *vanA* and three with *vanB*. All 12 isolates had vancomycin MIC ≤ 4 mg/L.

Figure 12: Vancomycin genotype of *Enterococcus faecium* isolates, by state and territory, and nationally, 2020



	NSW (n = 180)	Vic (n = 124)	Qld (n = 35)	SA (n = 39)	WA (n = 63)	Tas (n = 10)	NT (n = 6)	ACT (n = 31)	Australia (n = 488)
not vanA or vanB (n = 313)	64.4	34.7	82.9	92.3	88.9	70.0	16.7	80.6	64.1
Not determined (n = 5)	1.7	0.0	0.0	0.0	1.6	0.0	16.7	0.0	1.0
vanA and vanB (n = 1)	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	0.2
vanB (n = 103)	8.3	58.1	11.4	7.7	1.6	10.0	66.7	9.7	21.1
vanA (n = 66)	25.6	6.5	5.7	0.0	7.9	20.0	0.0	9.7	13.5

Multi-locus sequence type

Of the 488 *E. faecium* isolates reported, 469 (96.1%) were available for typing by whole genome sequencing (Table 40). Based on the MLST, 70 sequence types (STs) were identified. Overall, 81.9% of *E. faecium* could be characterised into eight STs: ST17 (*n* = 116); ST1424, formerly known as M-type 3 (*n* = 94); ST80 (*n* = 52); ST796 (*n* = 47); ST78 (*n* = 34); ST1421, formerly known as M-type 1 (*n* = 20); ST555 (*n* = 11) and ST117 (*n* = 10). The *pstS* housekeeping gene is absent in the M-type isolates. M-type 1 was initially identified in the 2015 AESOP survey.[53] In 2020, there were four M-type single locus variants. There were 49 STs with a single isolate.

ST17 was the predominant ST in Queensland, South Australia, and Western Australia. ST1424 was the dominant ST in New South Wales, ST80 in the Australian Capital Territory, ST796 in Victoria.

The distribution of vancomycin-resistant *E. faecium* sequence types throughout Australian states and territories is shown in Figure 13.

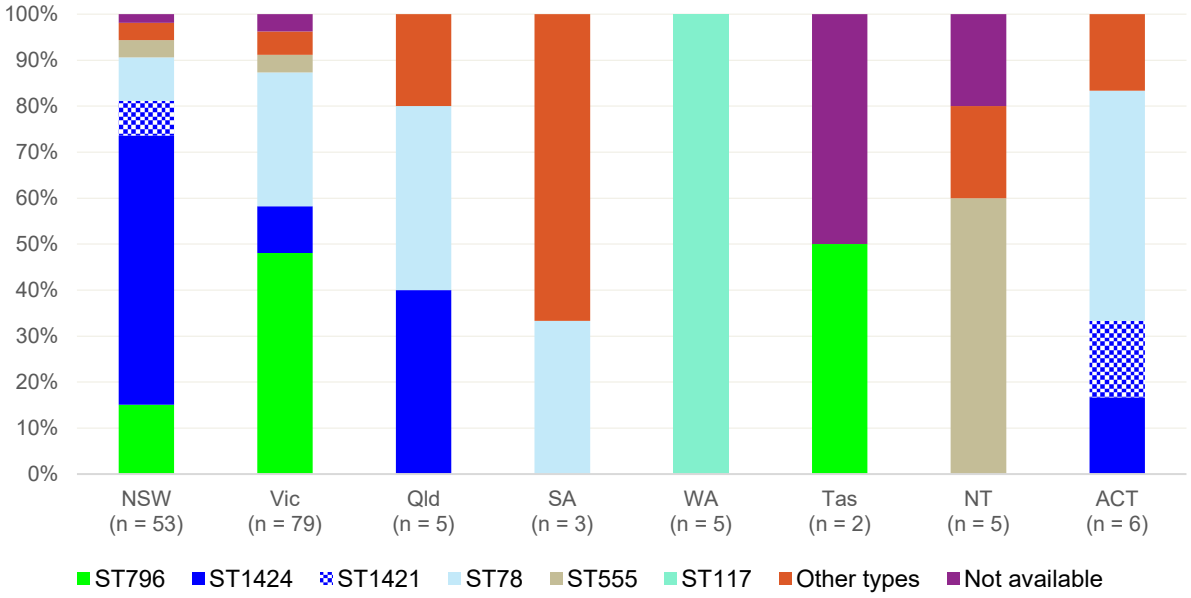
Table 40: *Enterococcus faecium* MLST, by state and territory, 2020

	Percentage, % (*n*)								
MLST	**NSW**	**Vic**	**QLD**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST17	13.8 (24)	12.6 (15)	55.9 (19)	45.9 (17)	62.3 (38)	–* (2)	–* (0)	3.2 (1)	24.7 (116)
ST1424†	36.2 (63)	12.6 (15)	8.8 (3)	0.0 (0)	1.6 (1)	–* (4)	–* (0)	25.8 (8)	20.0 (94)
ST80	12.6 (22)	5.9 (7)	5.9 (2)	8.1 (3)	8.2 (5)	–* (0)	–* (0)	41.9 (13)	11.1 (52)
ST796	4.6 (8)	31.9 (38)	0.0 (0)	0.0 (0)	0.0 (0)	–* (1)	–* (0)	0.0 (0)	10.0 (47)
ST78	2.9 (5)	19.3 (23)	5.9 (2)	2.7 (1)	0.0 (0)	–* (0)	–* (0)	9.7 (3)	7.2 (34)
ST1421†	10.9 (19)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	–* (0)	3.2 (1)	4.3 (20)
ST555	1.1 (2)	2.5 (3)	2.9 (1)	5.4 (2)	0.0 (0)	–* (0)	–* (3)	0.0 (0)	2.3 (11)
ST117	1.7 (3)	0.0 (0)	0.0 (0)	0.0 (0)	11.5 (7)	–* (0)	–* (0)	0.0 (0)	2.1 (10)
Other types (*n* = 63)	16.1 (28)	15.1 (18)	20.6 (7)	37.8 (14)	16.4 (10)	–* (2)	–* (0)	16.1 (5)	18.3 (86)
Total	**174**	**119**	**34**	**37**	**61**	**8**	**5**	**31**	**469**

MLST = multi-locus sequence type

* Insufficient numbers (<10) to calculate percentage
† *pstS*-null

Figure 13: Distribution of vancomycin-resistant *Enterococcus faecium* sequence types, by state and territory, 2020



MLST and *van* genes

The *vanA* gene alone was detected in seven STs; 87.5% (56/64) were found in three *pstS*-null STs (ST1424 (*n* = 46), ST1421 (*n* = 9), and ST1965 (*n* = 1). The four other STs were ST117 (*n* = 5), ST80 (*n* = 1), ST262 (*n* = 1), and ST780 (*n* = 1).

The *vanB* gene alone was detected in 10 STs: ST796 (*n* = 46), ST78 (*n* = 34), ST555 (*n* = 8), ST17 (*n* = 3), ST1424 (n = 2), ST80 (*n* = 2), and one each of ST203, ST1743, ST1929, and ST1977 (Table 41). One ST796 isolate harboured both *vanA* and *vanB* genes.

Table 41: *Enterococcus faecium* MLST harbouring *vanA* and/or *vanB* genes, 2020

	Percentage, %* (*n*)				
MLST	***vanA***	***vanB***	***vanA* and *vanB***	***vanA* or *vanB* not detected**	**Total, *n***
ST17	0.0 (0)	2.6 (3)	0.0 (0)	97.4 (113)	116
ST1424 (M-type 3)†	48.9 (46)	2.1 (2)	0.0 (0)	48.9 (46)	94
ST80	1.9 (1)	3.8 (2)	0.0 (0)	94.2 (49)	52
ST796	0.0 (0)	97.9 (46)	2.1 (1)	0.0 (0)	47
ST78	0.0 (0)	100.0 (34)	0.0 (0)	0.0 (0)	34
ST1421 (M-type 1)†	45.0 (9)	0.0 (0)	0.0 (0)	55.0 (11)	20
Other types (n = 64)	7.5 (8)	11.3 (12)	0.0 (0)	81.1 (86)	106
Total	**13.6 (64)**	**21.1 (99)**	**0.2 (1)**	**65.0 (305)**	**469**

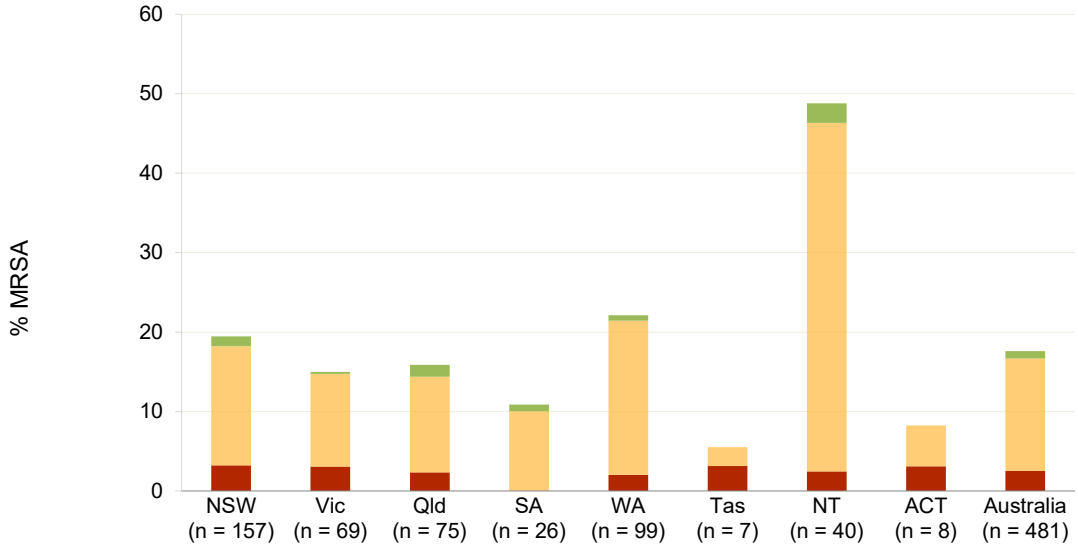
MLST = multi-locus sequence type

* Percentage of total with *van* genes
† *pstS*-null

3.9.3. Molecular epidemiology of methicillin-resistant *Staphylococcus aureus*

Of the 481 MRSA reported, 456 (94.8%) were available for typing by whole genome sequencing. There were marked differences among the states and territories in the percentage and types of MRSA clones. Prevalence of MRSA ranged from 5.5% (7/127) in Tasmania to 48.8% (40/82) in the Northern Territory (Figure 14).

Figure 14: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, 2020



	NSW (n = 157)	Vic (n = 69)	Qld (n = 75)	SA (n = 26)	WA (n = 99)	Tas (n = 7)	NT (n = 40)	ACT (n = 8)	Australia (n = 481)
Not available (n = 25)	1.2	0.2	1.5	0.8	0.7	0.0	2.4	0.0	0.9
Community associated (n = 387)	15.0	11.7	12.1	10.0	19.4	2.4	43.9	5.2	14.2
Healthcare associated (n = 69)	3.2	3.0	2.3	0.0	2.0	3.1	2.4	3.1	2.5

MRSA = methicillin-resistant *Staphylococcus aureus*

Notes:
1. *S. aureus* were categorised as MRSA based on cefoxitin screen ((Vitek) or cefoxitin MIC (Phoenix).
2. Twenty-five MRSA were not available for whole genome sequencing

Healthcare-associated MRSA

Based on the MLST and SCC*mec* type, five HA-MRSA clones were identified: ST22-IV (EMRSA-15), ST239-III (Aus 2/3 EMRSA), ST5-II (NY/Japan), ST8-II, and ST36-II (Tables 42, 43).

PVL-associated genes were not identified in HA-MRSA (Table 42). Five PVL positive ST22-IV isolates were identified: two in New South Wales, and one each in Victoria, Queensland, and the Australian Capital Territory. PVL positive ST22-IV are frequently isolated in the South Asian subcontinent; they are not related to EMRSA-15, and are not considered to be a HA-MRSA clone.[54]

The most frequently isolated HA-MRSA clone, ST22-IV, was identified in all states and territories except South Australia (Table 44). ST239-III was identified in three states (New South Wales, Victoria and Queensland), ST5-II was only identified in New South Wales, and ST8-II and ST36-II were only identified in Victoria.

Community-associated MRSA

Based on the MLST and SCC*mec* type, 48 CA-MRSA clones were identified. PVL was detected in 11 CA-MRSA clones. Overall, 43.9% (170/387) of CA MRSA were PVL positive (Table 45). The most frequently isolated CA-MRSA clone, ST93-IV (Qld CA-MRSA), was isolated in all states except Tasmania and the Australian Capital Territory.

Of the hospital-onset MRSA, 81.5% (88/108) were caused by CA-MRSA.

Table 42: MRSA clones, association, place of onset and PVL carriage, 2020

Clone	Clonal complex	Total, *n*	Community onset, % (*n*)*	Hospital onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)	22	59	72.9 (43)	27.1 (16)	0.0 (0)
ST239-III (Aus2/3 EMRSA)	8	7	–† (5)	–† (2)	–† (0)
ST5-II (NY/Japan)	5	1	–† (0)	–† (1)	–† (0)
ST8-II (Irish EMRSA-1)	8	1	–† (0)	–† (1)	–† (0)
ST36-II	30	1	–† (1)	–† (0)	–† (0)
Total HA-MRSA		69	71.0 (49)	29.0 (20)	0.0 (0)
Community-associated					
ST93-IV (Qld CA-MRSA)	93	100	88.0 (88)	12.0 (12)	99.0 (99)
ST5-IV	5	59	72.9 (43)	27.1 (16)	49.2 (29)
ST45-V	45	50	74.0 (37)	26.0 (13)	0.0 (0)
ST1-IV (WA1 MRSA)	1	29	75.9 (22)	24.1 (7)	0.0 (0)
ST30-IV (SWP MRSA)	30	21	90.5 (19)	9.5 (2)	81.0 (17)
ST8-IV	8	16	87.5 (14)	12.5 (2)	75.0 (12)
ST97-IV	97	14	71.4 (10)	28.6 (4)	0.0 (0)
ST78-IV (WA2 MRSA)	78	10	60.0 (6)	40.0 (4)	0.0 (0)
ST953-IV	97	8	–† (7)	–† (1)	–† (0)
ST6-IV	5	7	–† (3)	–† (4)	–† (0)
ST22-IV (PVL positive)	22	5	–† (4)	–† (1)	–† (5)
ST872-IV	1	5	–† (3)	–† (2)	–† (0)
ST188-IV	1	5	–† (3)	–† (2)	–† (0)
ST59-IV	Not assigned	5	–† (4)	–† (1)	–† (1)
ST59-V	Not assigned	5	–† (4)	–† (1)	–† (2)
Other (*n* = 33)		48	66.7 (32)	33.3 (16)	10.4 (5)
Total CA-MRSA		387	77.3 (299)	22.7 (88)	43.9 (170)
MRSA		**456**	**348**	**108**	

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

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

Table 43: MRSA clones, association, place of onset, 2020

Clone	Clonal complex	Community onset, % (*n*)*	Hospital onset, % (*n*)*	Total, % (*n*)
Healthcare-associated				
ST22-IV (EMRSA-15)	22	12.4 (43)	14.8 (16)	12.9 (59)
ST239-III (Aus2/3 EMRSA)	8	–† (5)	–† (2)	–† (7)
ST5-II (NY/Japan)	5	–† (0)	–† (1)	–† (1)
ST8-II (Irish EMRSA-1)	8	–† (0)	–† (1)	–† (1)
ST36-II	30	–† (1)	–† (0)	–† (1)
Total HA-MRSA		14.1 (49)	18.5 (20)	15.1 (69)
Community-associated				
ST93-IV (Qld CA-MRSA)	93	25.3 (88)	11.1 (12)	21.9 (100)
ST5-IV	5	12.4 (43)	14.8 (16)	12.9 (59)
ST45-V	45	10.6 (37)	12.0 (13)	11.0 (50)
ST1-IV (WA1 MRSA)	1	6.3 (22)	6.5 (7)	6.4 (29)
ST30-IV (SWP MRSA)	30	5.5 (19)	1.9 (2)	4.6 (21)
ST8-IV	8	4.0 (14)	1.9 (2)	3.5 (16)
ST97-IV	97	2.9 (10)	3.7 (4)	3.1 (14)
ST78-IV (WA2 MRSA)	78	1.7 (6)	3.7 (4)	2.2 (10)
ST953-IV	97	–† (7)	–† (1)	–† (8)
ST6-IV	5	–† (3)	–† (4)	–† (7)
ST22-IV (PVL positive)	22	–† (4)	–† (1)	–† (5)
ST872-IV	1	–† (3)	–† (2)	–† (5)
ST188-IV	1	–† (3)	–† (2)	–† (5)
ST59-IV	Not assigned	–† (4)	–† (1)	–† (5)
ST59-V	Not assigned	–† (4)	–† (1)	–† (5)
Other (*n* = 33)		9.2 (32)	14.8 (16)	10.5 (48)
Total CA-MRSA		85.9 (299)	81.5 (88)	84.9 (387)
MRSA		**76.3 (348)**	**23.7 (108)**	**456**

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

* Percentage of all MRSA

Table 44: Healthcare-associated MRSA clones, by state and territory, 2020

Clone	Percentage, % (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15)	84.6 (22)	78.6 (11)	72.7 (8)	n/a	–* (9)	–* (4)	–* (2)	–* (3)	85.5 (59)
ST239-III (Aus2/3 EMRSA)	11.5 (3)	7.1 (1)	27.3 (3)	n/a	–* (0)	–* (0)	–* (0)	–* (0)	10.1 (7)
ST5-II (NY/Japan)	3.8 (1)	0.0 (0)	0.0 (0)	n/a	–* (0)	–* (0)	–* (0)	–* (0)	1.4 (1)
ST8-II (Irish EMRSA-1)	0.0 (0)	7.1 (1)	0.0 (0)	n/a	–* (0)	–* (0)	–* (0)	–* (0)	1.4 (1)
ST36-II	0.0 (0)	7.1 (1)	0.0 (0)	n/a	–* (0)	–* (0)	–* (0)	–* (0)	1.4 (1)
Total	**26**	**14**	**11**	**0**	**9**	**4**	**2**	**3**	**69**

MRSA = methicillin-resistant *Staphylococcus aureus*; n/a = not applicable (no isolates)
* Insufficient numbers (<10) to calculate percentage

Table 45: Major community-associated MRSA clones (> 10 isolates) by state and territory and PVL carriage, 2020

Clone	Percentage, % (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST93-IV (Qld CA-MRSA)	9.1 (11)	31.5 (17)	22.8 (13)	33.3 (8)	36.8 (32)	–* (0)	52.8 (19)	–* (0)	25.8 (100)
Number PVL positive	10	17	13	8	32	0	19	0	99
Number PVL negative	1	0	0	0	0	0	0	0	1
ST5-IV	13.2 (16)	11.1 (6)	10.5 (6)	12.5 (3)	19.5 (17)	–* (1)	27.8 (10)	–* (0)	15.2 (59)
Number PVL positive	2	1	2	2	13	0	9	0	29
Number PVL negative	14	5	4	1	4	1	1	0	30
ST45-V	29.8 (36)	20.4 (11)	0.0 (0)	4.2 (1)	0.0 (0)	–* (0)	0.0 (0)	–* (2)	12.9 (50)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	36	11	0	1	0	0	0	2	50
ST1-IV	8.3 (10)	1.9 (1)	12.3 (7)	12.5 (3)	6.9 (6)	–* (1)	2.8 (1)	–* (0)	7.5 (29)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	10	1	7	3	6	1	1	0	29
ST30-IV	6.6 (8)	5.6 (3)	7.0 (4)	4.2 (1)	3.4 (3)	–* (0)	2.8 (1)	–* (1)	5.4 (21)
Number PVL positive	6	3	3	1	3	0	0	1	17
Number PVL negative	2	0	1	0	0	0	1	0	4
ST8-IV	6.6 (8)	1.9 (1)	5.3 (3)	0.0 (0)	4.6 (4)	–* (0)	0.0 (0)	–* (0)	4.1 (16)
Number PVL positive	8	1	2	0	1	0	0	0	12
Number PVL negative	0	0	1	0	3	0	0	0	4
ST97-IV	5.0 (6)	3.7 (2)	3.5 (2)	0.0 (0)	2.3 (2)	–* (1)	2.8 (1)	–* (0)	3.6 (14)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	6	2	2	0	2	1	1	0	14
ST78-IV	0.8 (1)	3.7 (2)	0.0 (0)	0.0 (0)	8.0 (7)	–* (0)	0.0 (0)	–* (0)	2.6 (10)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	1	2	0	0	7	0	0	0	10
Other clones (n = 40)	20.7 (25)	20.4 (11)	38.6 (22)	33.3 (8)	18.4 (16)	–* (0)	11.1 (4)	–* (2)	22.7 (88)
Number PVL positive	5	2	4	0	1	0	0	1	13
Number PVL negative	20	9	18	8	15	0	4	1	75
Total	**121**	**54**	**57**	**24**	**87**	**3**	**36**	**5**	**387**
PVL positive	31	24	24	11	50	0	28	2	170
PVL negative	90	30	33	13	37	3	8	3	217

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

* Insufficient numbers (<10) to calculate percentage

3.10. Trend analysis (2013–2020)

Trend data were available for *Enterobacterales, Enterococcus* species and *S. aureus* for the period 2013 to 2020. *Acinetobacter* species and *P. aeruginosa* were introduced to the program in 2015.

3.10.1. Gram-negative species

EUCAST interpretive criteria have been used throughout, with the notable exception of amoxicillin–clavulanic acid. CLSI interpretative criteria was used for this agent, as ninety percent of the pathology laboratories used Vitek® cards which have the CLSI formulation (2:1 ratio) for this agent.

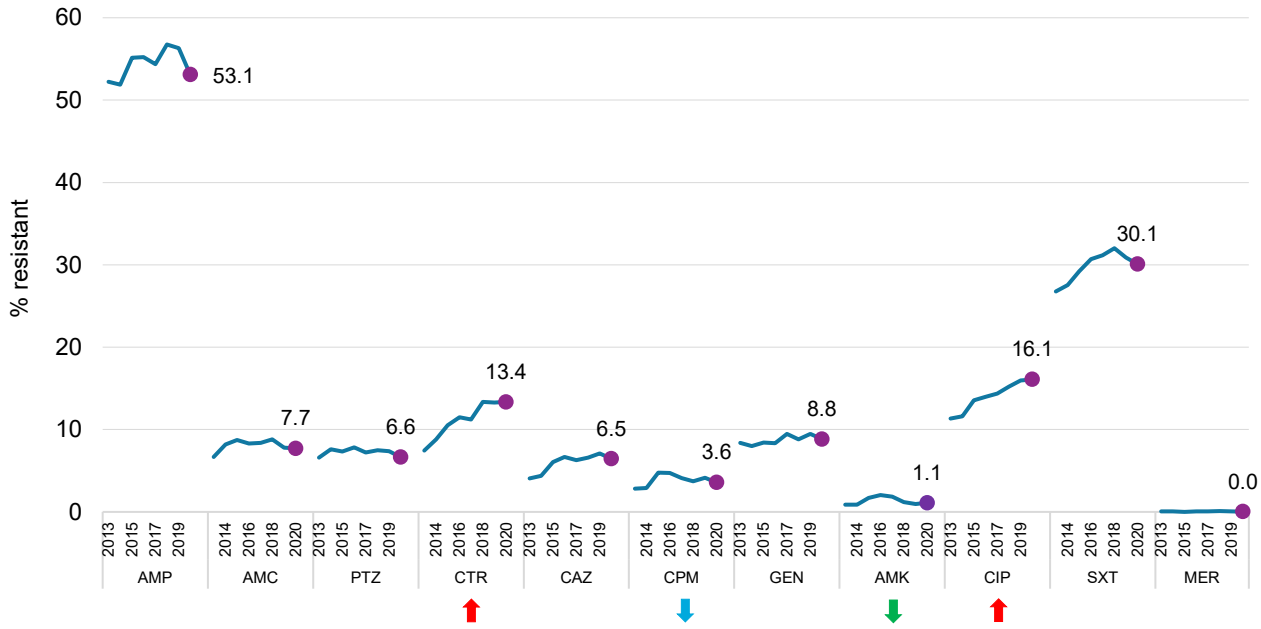
Escherichia coli

National

The percentage resistance for *E. coli* in 2020 was similar to 2019 for all antimicrobial agents tested, except for ampicillin, where a 5.7% decrease in resistance was seen relative to 2019 (2,749/4,881, 56.3% in 2019, 2,582/4,863, 53.1% in 2020; $P < 0.01$) (Figure 15).

Rates of resistance to key antimicrobial agents over the past five years (2016–2020) increased for ceftriaxone (X^2 for linear trend = 13.47, $P < 0.01$) and ciprofloxacin (X^2 for linear trend = 11.54, $P < 0.01$). There was a decrease in the rate of resistance to amikacin (X^2 for linear trend = 24.39, $P < 0.01$) and cefepime (X^2 for linear trend = 5.486, $P = 0.0192$) (Figure 15).

Figure 15. *Escherichia coli* resistance to key antimicrobials (EUCAST), Australia, 2013–2020



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

Notes:
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years. Filled circles indicate values for 2020.
2. Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the past five years (2016 to 2020).
3. Green arrows indicate antimicrobial agents with significant decrease ($P < 0.01$) over the past five years (2016 to 2020).
4. Blue arrows indicate antimicrobial agents with significant decrease ($0.01 < P < 0.05$) over the past five years (2016 to 2020).

State and territory

There were significantly increasing trends in fluoroquinolone- (Table 46) and third-generation cephalosporin resistance (Table 47) in *E. coli* over the past five years (2016-2020) in both Victoria and the Northern Territory, although both rates have stabilised since 2019. Aminoglycoside resistance increased in the Northern Territory, and decreased in Western Australia, (Table 48).

Table 46: *Escherichia coli*, percentage resistant to fluoroquinolones (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Tasmania	6.3 (79)	7.6 (79)	7.6 (79)	10.7 (168)	5.7 (174)	7.6 (184)	12.9 (201)	8.0 (201)	↔
South Australia	10.6 (379)	10.9 (386)	9.0 (454)	13.3 (429)	8.3 (288)	11.6 (405)	13.9 (440)	9.8 (479)	↔
Queensland	8.1 (652)	7.1 (742)	8.7 (691)	9.0 (811)	12.9 (858)	10.3 (868)	10.4 (817)	11.5 (624)	↔
Australian Capital Territory	13.6 (118)	12.5 (168)	10.7 (149)	13.6 (154)	12.0 (158)	17.8 (157)	20.5 (185)	15.2 (198)	↔
New South Wales	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)	↔
Western Australia	13.9 (524)	12.7 (510)	16.2 (650)	15.7 (677)	16.2 (770)	20.5 (801)	17.3 (736)	17.5 (776)	↔
Victoria	11.7 (530)	16.2 (722)	14.4 (727)	**15.7** (709)	**15.6** (794)	**18.1** (770)	**18.3** (919)	**20.0** (899)	▲
Northern Territory	10.3 (78)	8.2 (97)	9.5 (137)	**9.8** (153)	**15.6** (141)	**12.5** (160)	**20.0** (205)	**20.8** (197)	▲
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** (4,866)	▲

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

Notes:
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Fluoroquinolones refer to ciprofloxacin.

Table 47: *Escherichia coli*, percentage resistant to third-generation cephalosporins (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Tasmania	1.3 (80)	10.1 (79)	0.0 (79)	6.5 (168)	5.2 (174)	7.6 (184)	7.0 (201)	6.0 (201)	↔
Queensland	5.4 (652)	7.1 (742)	6.1 (691)	8.1 (811)	9.4 (858)	11.5 (868)	8.4 (817)	9.0 (624)	↔
South Australia	5.3 (379)	6.2 (386)	7.5 (454)	12.3 (431)	4.5 (289)	9.1 (405)	12.5 (440)	9.2 (479)	↔
Western Australia	6.3 (524)	6.3 (510)	9.7 (650)	11.7 (677)	11.5 (771)	15.6 (801)	12.2 (736)	12.5 (776)	↔
Australian Capital Territory	5.1 (118)	8.9 (168)	10.7 (149)	9.7 (154)	12.0 (158)	12.7 (157)	16.7 (186)	13.1 (198)	↔
New South Wales	11.0 (555)	9.9 (781)	15.4 (1,107)	15.1 (993)	14.2 (1,170)	13.5 (1,224)	15.4 (1,379)	15.7 (1,493)	↔
Victoria	11.1 (530)	13.0 (722)	12.4 (727)	**13.7** (709)	**14.2** (794)	**17.1** (770)	**16.9** (922)	**17.0** (899)	▲†
Northern Territory	9.0 (78)	9.3 (97)	8.8 (137)	**9.2** (153)	**9.2** (141)	**17.5** (160)	**16.1** (205)	**19.8** (197)	▲
Australia	7.6 (2,916)	9.0 (3,485)	10.7 (3,994)	**11.8** (4,096)	**11.5** (4,355)	**13.6** (4,569)	**13.5** (4,886)	**13.6** (4,867)	▲

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

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

Notes:

3. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
4. Third-generation cephalosporins refer to ceftriaxone or ceftazidime.

Table 48: *Escherichia coli*, percentage resistant to aminoglycosides (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Tasmania	2.5 (80)	8.9 (79)	2.5 (79)	6.0 (168)	3.4 (174)	3.8 (184)	7.0 (201)	4.5 (201)	↔
South Australia	6.9 (378)	6.5 (386)	9.0 (454)	10.7 (431)	6.6 (289)	9.6 (405)	9.3 (440)	8.1 (479)	↔
Queensland	7.2 (652)	8.1 (742)	7.7 (691)	8.1 (811)	9.7 (858)	7.7 (868)	8.4 (817)	8.3 (624)	↔
Western Australia	9.2 (524)	7.8 (511)	11.8 (650)	**14.8** (677)	**12.2** (771)	**13.0** (801)	**9.6** (736)	**9.7** (776)	▼
New South Wales	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)	↔
Australian Capital Territory	14.4 (118)	10.7 (168)	5.4 (149)	7.1 (154)	13.3 (158)	8.9 (157)	11.3 (186)	10.1 (198)	↔
Victoria	11.9 (530)	10.9 (722)	10.2 (727)	9.3 (709)	12.8 (794)	10.5 (770)	12.9 (922)	11.8 (899)	↔
Northern Territory	14.1 (78)	15.5 (97)	11.7 (137)	**12.4** (153)	**12.8** (141)	**16.9** (160)	**18.5** (205)	**20.8** (197)	▲
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 (4,867)	↔

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

Notes:

1. Percentage resistance determined using EUCAST 2021 breakpoints for all years
2. Aminoglycosides refer to gentamicin or tobramycin.

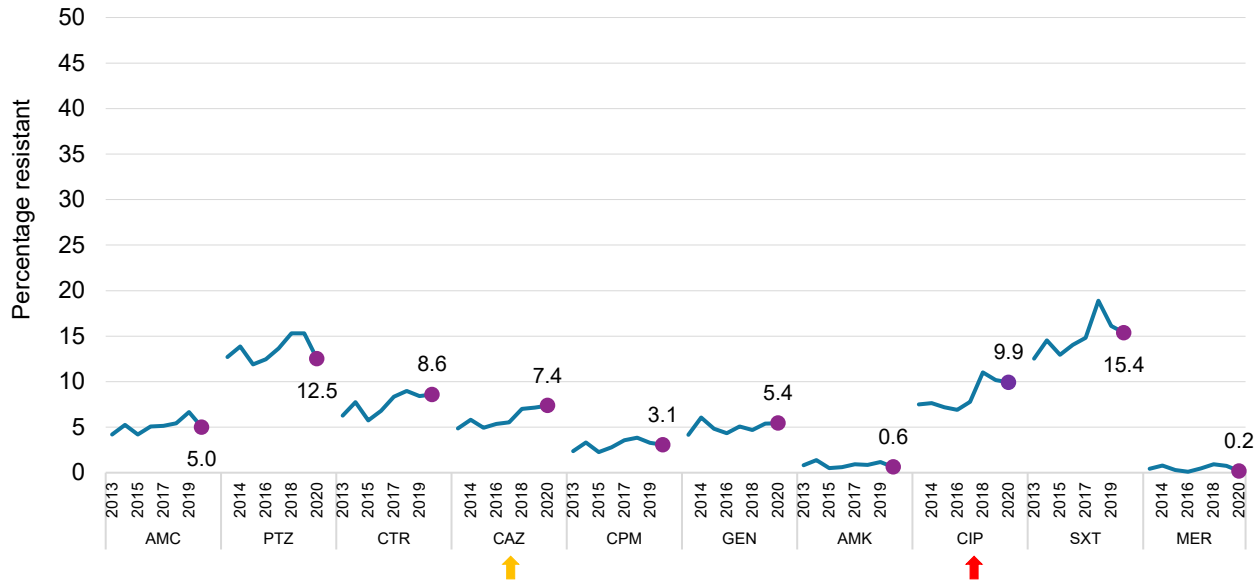
Klebsiella pneumoniae complex

National

Relative to 2019, the percentage resistance for *K. pneumoniae* complex in 2020 declined by more than 10% for four of the 10 antimicrobial agents tested; amoxicillin–clavulanic acid (71/1,066, 6.7% in 2019; 50/1,1002, 5.0% in 2020), piperacillin–tazobactam (182/1,189, 15.3% in 2019; 142/1,135, 12.5% in 2020), amikacin (14/1,190, 1.2% in 2019; 7/1,141, 0.6% in 2020), and meropenem (9/1,190, 0.8% in 2019; 2/1,140, 0.2% in 2020) (Figure 16).

There was a significant increasing trend in resistance to ciprofloxacin (X^2 for linear trend = 8.445, P < 0.01) and ceftazidime (X^2 for linear trend = 5.444, P = 0.0196) over the past five years (2016–2020) (Figure 16).

Figure 16. *Klebsiella pneumoniae* complex resistance to key antimicrobials (EUCAST), Australia, 2013–2020



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 2021 breakpoints for all years. Filled circles indicate values for 2020.
2. Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the past five years (2016 to 2020).
3. Orange arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the past five years (2016 to 2020).

State and territory

There was a significantly increasing trend in fluoroquinolone resistance (Table 49) in *K. pneumoniae* complex over the past five years (2016-2020) in the Northern Territory, although the rate has stabilised over the past three years. Third-generation cephalosporin resistance in *K. pneumoniae* complex from the Northern Territory increased from 2.6% (1/38) in 2016 to 27.0% (10/37) in 2020 (Table 50). Although an increasing aminoglycoside resistance trend was noted in all data from New South Wales, this was not observed when only data from institutions consistently reporting for all five years were included (Table 51).

Table 49: *Klebsiella pneumoniae* complex, percentage resistant to fluoroquinolones (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Western Australia	4.8 (124)	4.7 (149)	5.9 (187)	2.8 (181)	6.3 (159)	7.5 (186)	5.0 (160)	2.6 (189)	↔
Queensland	5.8 (207)	5.3 (208)	6.3 (189)	4.2 (189)	6.1 (246)	5.6 (270)	5.2 (249)	6.5 (185)	↔
Tasmania	7.1 (14)	11.1 (9)	5.6 (18)	5.6 (36)	0.0 (30)	11.8 (34)	7.8 (51)	6.7 (30)	↔
South Australia	13.3 (75)	5.4 (74)	4.7 (85)	7.4 (81)	2.8 (71)	8.8 (91)	15.7 (89)	9.9 (81)	↔
New South Wales	3.5 (113)	9.3 (205)	7.2 (236)	8.4 (226)	5.5 (293)	9.3 (301)	10.4 (347)	10.2 (371)	↔
Australian Capital Territory	4.5 (22)	7.7 (26)	5.7 (35)	5.3 (38)	7.7 (39)	8.3 (36)	8.3 (36)	13.2 (38)	↔
Northern Territory	10.5 (19)	16.1 (31)	4.3 (47)	**2.6** (38)	**6.7** (30)	**13.5** (37)	**15.6** (45)	**16.2** (37)	▲
Victoria	12.4 (145)	10.3 (174)	11.9 (177)	13.3 (180)	17.6 (199)	24.3 (214)	17.0 (212)	17.7 (209)	↔
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)	▲

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

Notes:
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Fluoroquinolone refer to ciprofloxacin.

Table 50: *Klebsiella pneumoniae* complex, percentage resistant to third-generation cephalosporins (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Western Australia	4.0 (124)	4.0 (149)	3.7 (187)	5.5 (181)	5.7 (159)	4.3 (186)	4.4 (160)	3.7 (189)	↔
Queensland	6.3 (207)	4.3 (208)	3.7 (189)	3.7 (189)	3.3 (246)	5.9 (270)	4.4 (249)	3.8 (185)	↔
Tasmania	7.1 (14)	11.1 (9)	5.6 (18)	5.6 (36)	3.3 (30)	11.8 (34)	7.8 (51)	6.7 (30)	↔
South Australia	2.7 (75)	4.1 (74)	3.5 (85)	7.4 (81)	5.6 (72)	9.9 (91)	9.0 (89)	7.4 (81)	↔
Australian Capital Territory	0.0 (22)	11.5 (26)	2.9 (35)	2.6 (38)	10.3 (39)	5.6 (36)	11.1 (36)	7.9 (38)	↔
New South Wales	2.7 (113)	12.1 (206)	7.6 (236)	9.7 (226)	7.5 (293)	8.9 (302)	9.8 (348)	9.2 (371)	↔
Victoria	13.1 (145)	10.9 (174)	10.7 (177)	13.9 (180)	19.6 (199)	19.2 (214)	16.0 (212)	16.7 (210)	↔
Northern Territory	15.8 (19)	6.5 (31)	6.4 (47)	**2.6** (38)	**6.7** (30)	**13.5** (37)	**15.6** (45)	**27.0** (37)	▲
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)	↔

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

Notes:
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Third-generation cephalosporins refer to ceftriaxone or ceftazidime.

Table 51: *Klebsiella pneumoniae* complex, percentage resistant to aminoglycosides (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Western Australia	3.2 (124)	2.7 (149)	3.2 (187)	5.0 (181)	3.8 (159)	3.8 (186)	3.1 (160)	2.1 (189)	↔
Queensland	3.9 (207)	4.3 (208)	4.2 (189)	3.7 (189)	3.3 (246)	3.0 (270)	2.4 (249)	2.7 (185)	↔
South Australia	5.3 (75)	1.4 (74)	5.9 (85)	3.7 (81)	4.2 (72)	7.7 (91)	7.9 (89)	3.7 (81)	↔
Australian Capital Territory	0.0 (22)	7.7 (26)	2.9 (35)	2.6 (38)	7.7 (39)	8.3 (36)	11.1 (36)	5.3 (38)	↔
Tasmania	7.1 (14)	11.1 (9)	11.1 (18)	2.8 (36)	3.3 (30)	8.8 (34)	5.9 (51)	6.7 (30)	↔
New South Wales	2.7 (113)	11.2 (206)	8.1 (236)	**6.2** (226)	**5.5** (293)	**5.0** (302)	**9.5** (348)	**8.9** (371)	▲†
Victoria	11.0 (145)	9.8 (174)	7.9 (177)	10.0 (180)	15.6 (199)	18.7 (214)	14.2 (212)	11.0 (210)	↔
Northern Territory	15.8 (19)	16.1 (31)	10.6 (47)	**2.6** (38)	**6.7** (30)	**16.2** (37)	**13.3** (45)	**24.3** (37)	▲
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)	↔

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

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

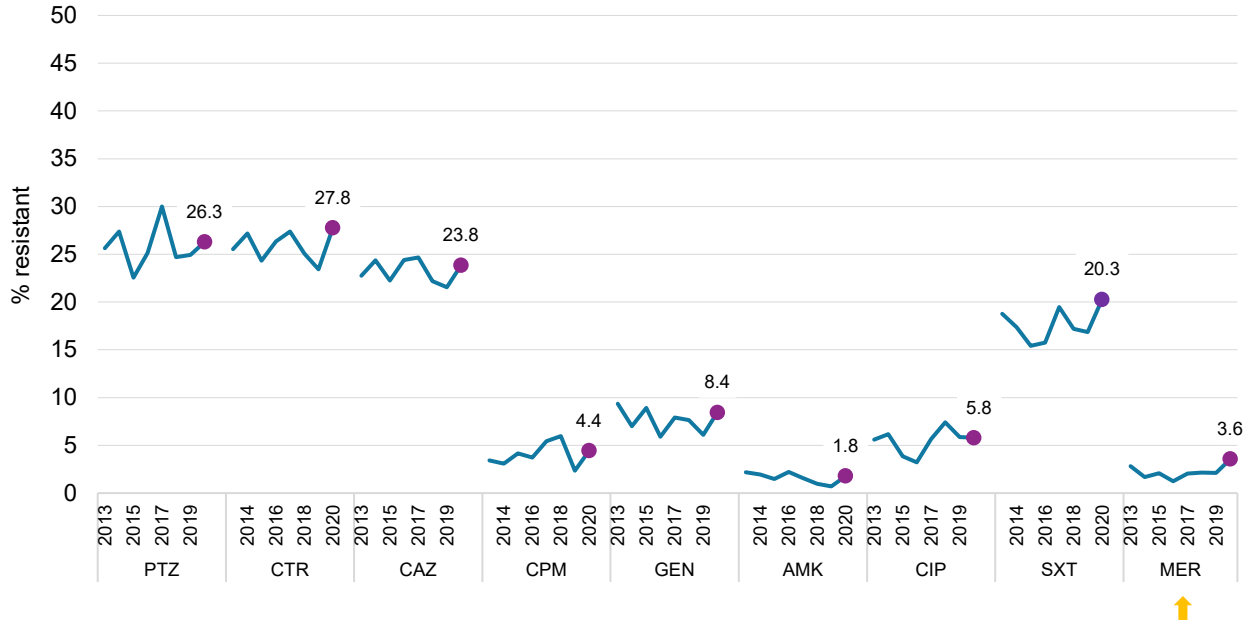
Notes:
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years
2. Aminoglycosides refer to gentamicin or tobramycin

Enterobacter cloacae complex

National

For *E. cloacae* complex, the percentage resistance to all key antimicrobials, except ciprofloxacin, increased in 2020 relative to 2019. There was a significant increasing trend in resistance to meropenem (X^2 for linear trend = 4.414, P = 0.0357) for *E. cloacae* complex over the past five-year period (2016–2020) (Figure 17).

Figure 17. *Enterobacter cloacae* complex resistance to key antimicrobials (EUCAST), Australia, 2013–2020



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

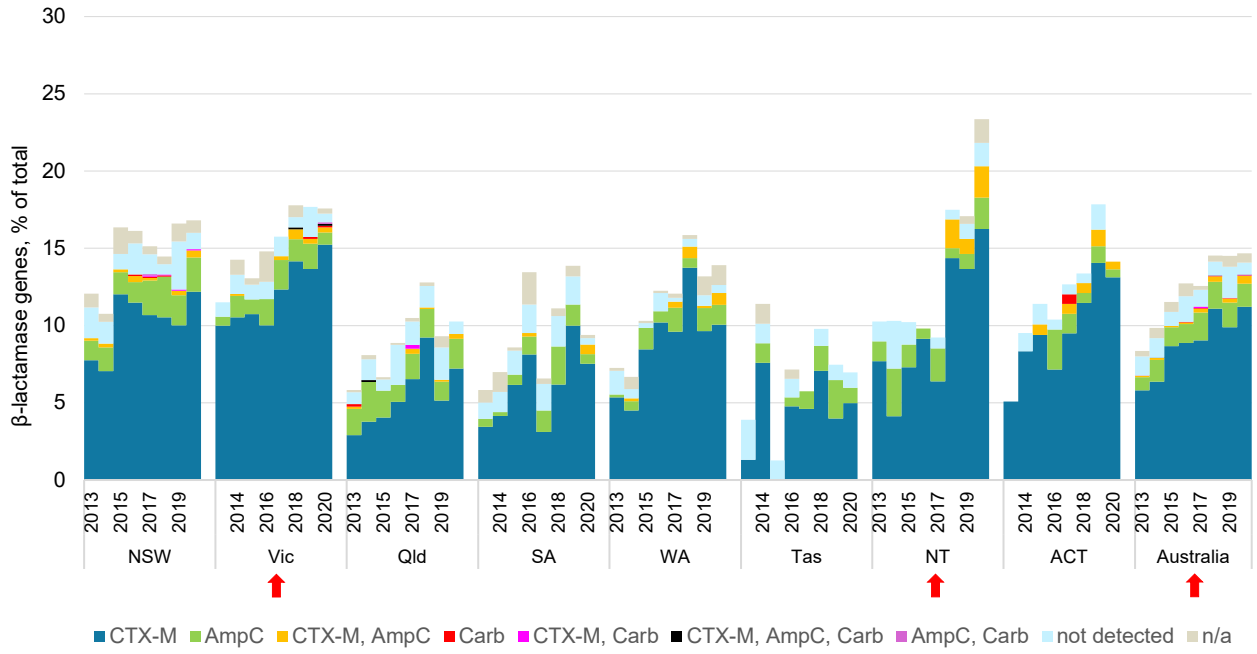
Notes:
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years. Filled circles indicate values for 2020.
2. Orange arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the past five years (2016 to 2020).

Extended-spectrum β-lactamases

CTX-M-type β-lactamase genes (alone or with other genes) continue to be the dominate β-lactam resistance mechanism among *E. coli* and *K. pneumoniae* complex isolates with an ESBL phenotype, with considerable regional variation noted. Overall, in the 2020 survey, there was a slight increase in the proportion of *E. coli* with CTX-M-types relative to 2019 (11.9% in 2020 versus 10.2% in 2019, $P = 0.0115$). In *K. pneumoniae* complex, the proportion of CTX-M types was the same for both years (7.8%).

Over the past 5 years (2016-2020), a significantly increasing trend in the proportion of *E. coli* with confirmed CTX-M-types was seen in Victoria (X^2 for linear trend = 6.736, $P < 0.01$), and the Northern Territory (X^2 for linear trend = 10.95, $P < 0.01$) (Figure 18); for *K. pneumoniae* complex isolates, only the Northern Territory had a significantly increasing trend (X^2 for linear trend = 8.391, $P < 0.01$ (Figure 19).

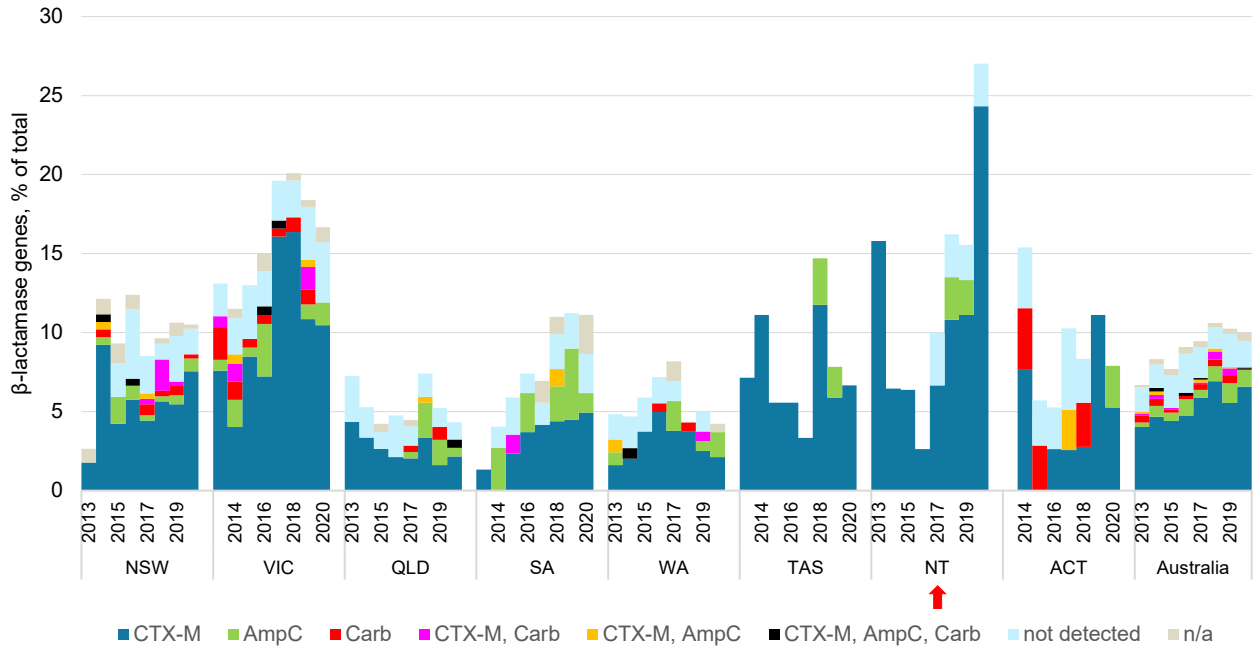
Figure 18. Proportion of β-lactamase genes in *Escherichia coli* by state and territory, and nationally, 2013–2020



AmpC = plasmid-borne AmpC; Carb = carbapenemase; n/a = isolate not available for molecular confirmation

Notes:
1. β-lactamase genes (CTX-M-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Red arrows indicate states and territories with significant increase ($P < 0.01$) over the past five years (2016 to 2020).

Figure 19. Proportion of β-lactamase genes in *Klebsiella pneumoniae* complex by state and territory, and nationally, 2013–2020



AmpC = plasmid-borne AmpC; Carb = carbapenemase; n/a = isolate not available for molecular confirmation

Notes:
1. β-lactamase genes (CTX-M-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Red arrows indicate states and territories with significant increase ($P < 0.01$) over the past five years (2016 to 2020).

3.10.2. *Enterococcus* species

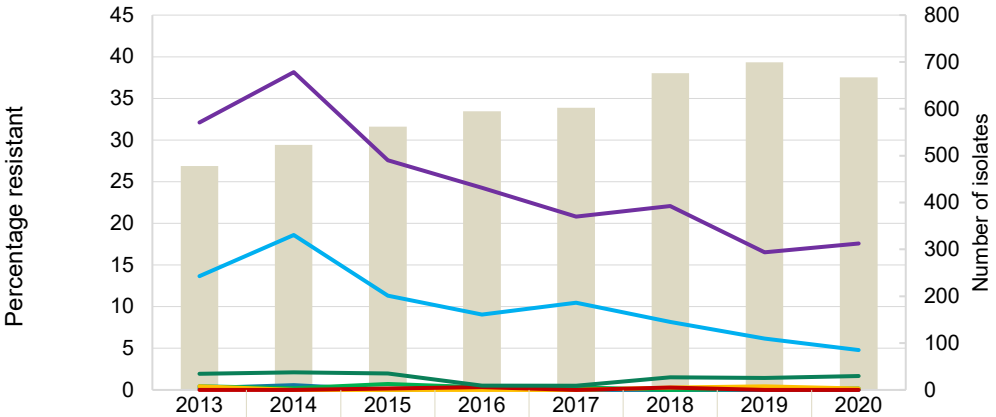
The 2020 program focused on the proportions of *E. faecium* and *E. faecalis* bacteraemia isolates demonstrating resistance to ampicillin, glycopeptides and other anti-enterococcal agents. Important trends for the period 2013–2020 are described below.

Enterococcus faecalis

National

Resistance (EUCAST) to key antimicrobial agents for *E. faecalis* over the eight-year period 2013 to 2020 is shown in Figure 20. There was a slight increase in the proportion of *E. faecalis* with gentamicin (high-level) (HLG) resistance in 2020 compared with 2019 (114/690, 16.5% in 2019; 116/660, 17.6% in 2020). Resistance to ampicillin, vancomycin, teicoplanin and linezolid remains rare. In 2020, one vancomycin-resistant (MIC ≥ 32 mg/L, *vanA*) *E. faecalis* was confirmed from Western Australia.

Figure 20. *Enterococcus faecalis*, resistance (EUCAST), Australia, 2013–2020



	2013	2014	2015	2016	2017	2018	2019	2020
Total, n	478	523	562	595	602	676	699	667
Ampicillin, %	0.2	0.6	0.0	0.2	0.0	0.0	0.0	0.0
Vancomycin, %	0.4	0.2	0.7	0.3	0.3	0.0	0.1	0.2
Teicoplanin, %	0.4	0.0	0.0	0.0	0.0	0.3	0.4	0.2
Linezolid, %	0.0	0.0	0.2	0.3	0.0	0.3	0.0	0.0
Gentamicin (high-level), %	32.1	38.2	27.6	24.3	20.8	22.1	16.5	17.6
Ciprofloxacin (ECOFF), %	13.7	18.6	11.3	9.0	10.5	8.2	6.1	4.8
Nitrofurantoin (ECOFF), %	1.9	2.1	2.0	0.5	0.5	1.5	1.4	1.7

ECOFF = epidemiological cut-off value; EUCAST = European Committee on Antimicrobial Susceptibility Testing

Notes
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Number of contributors per year - 2013-14, *n* = 27; 2015, *n* = 31; 2016, *n* = 32; 2017-18, *n* = 36; 2019-20, *n* = 39.
3. Ciprofloxacin susceptibility data only available for 26/39 (2020) institutions due to change in Vitek card used.
4. The ciprofloxacin ECOFF (4 mg/L) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only.
5. The nitrofurantoin ECOFF (32 mg/L) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only.

State and territory

The only significant change in antimicrobial resistance among *E. faecalis* in 2020, compared to 2019, was a decrease in HLG resistance in the Australian Capital Territory (16/36, 44.4% in 2019; 6/31, 19.4% in 2020, $P = 0.0383$) (Table 52).

Over the past 5 years (2016-2020), there was a significant decreasing trend in HLG resistance in both Queensland (X^2 for linear trend = 15.24, $P < 0.01$) and South Australia (X^2 for linear trend = 9.631, $P < 0.01$).

Table 52: *Enterococcus faecalis*, percentage resistant to gentamicin (high-level) (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
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)	↔
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)	▼
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)	▼
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)	↔
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)	↔
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)	↔
Victoria	34.0 (106)	38.7 (119)	27.4 (106)	22.3 (130)	19.7 (117)	23.1 (117)	22.2 (126)	24.8 (133)	↔
Northern Territory	–† (6)	–† (6)	40.0 (10)	–† (7)	10.0 (10)	18.2 (11)	–† (7)	–† (5)	–†
Australia	32.1 (408)	38.2 (519)	27.6 (544)	**24.3** (589)	**20.8** (591)	**22.1** (666)	**16.5** (690)	**17.6** (660)	▼

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

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

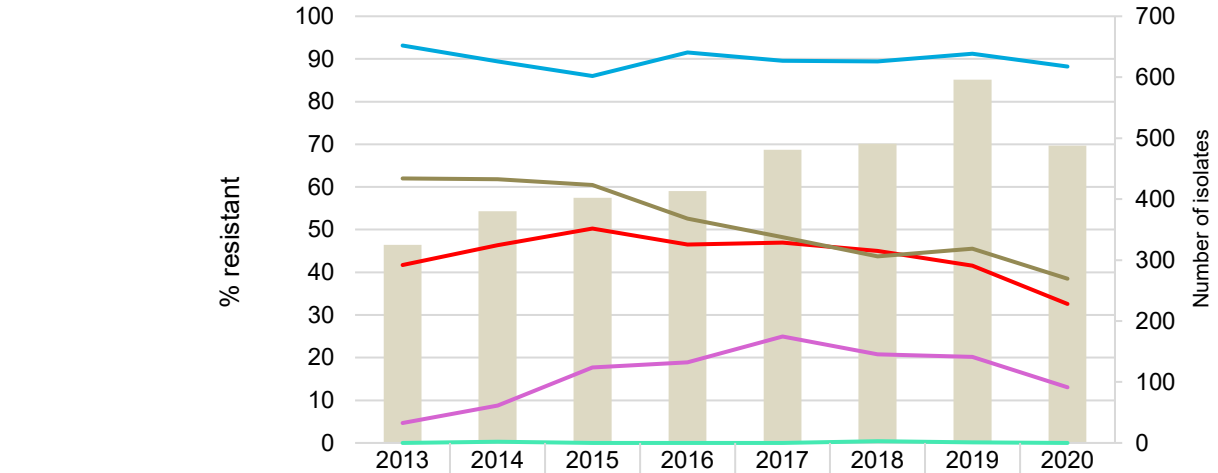
Note: Percentage resistance determined using EUCAST 2021 breakpoints for all years.

Enterococcus faecium

National

The total number of *E. faecium* isolated from patients with bacteraemia decreased 18.1% in 2020 compared to 2019 (*n* = 596 in 2019; *n* = 488 in 2020) (Figure 21). There was a significant decrease in the proportion of *E. faecium* isolates resistant to vancomycin (247/594, 41.6% in 2019, 158/485, 32.6% in 2020, $P < 0.01$) and teicoplanin (120/594, 20.2% in 2019, 63/485, 13.0% in 2020, $P < 0.01$). Resistance to gentamicin (high-level) is generally higher among vancomycin-resistant than vancomycin-susceptible *E. faecium*, there was a slight decrease in resistance among vancomycin-susceptible isolates in 2020 (Figure 22). No linezolid-resistant *E. faecium* were confirmed in 2020.

Figure 21. *Enterococcus faecium*, resistance (EUCAST), Australia, 2013–2020

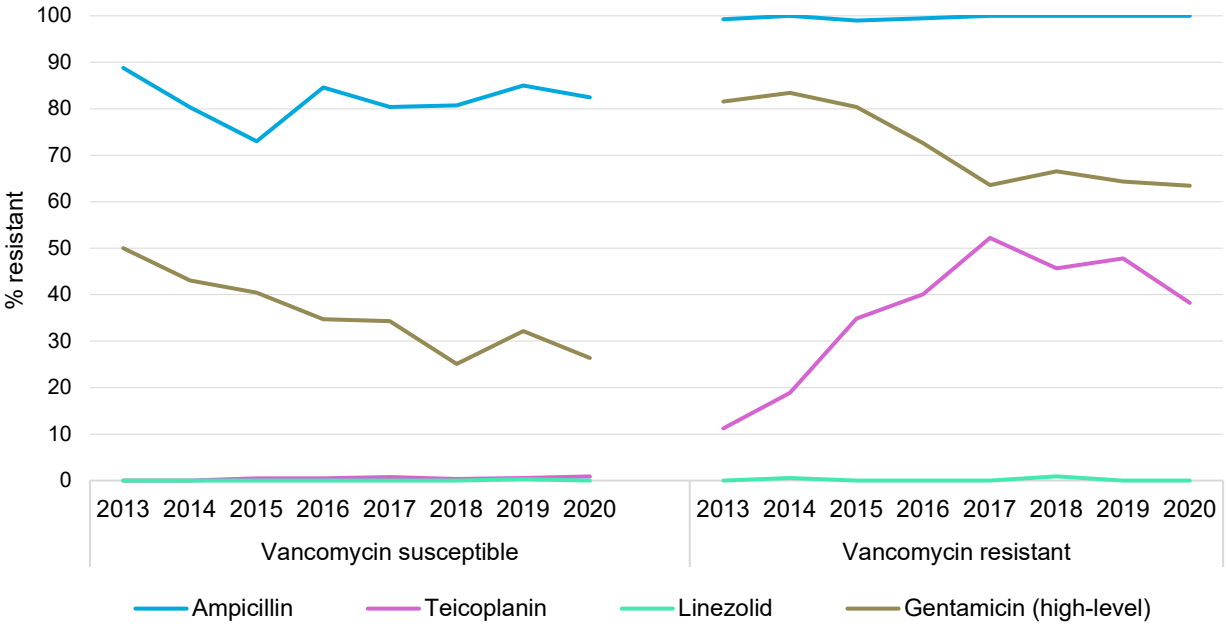


	2013	2014	2015	2016	2017	2018	2019	2020
Total, n	325	380	402	413	481	491	596	488
Ampicillin, %	93.1	89.4	86.0	91.5	89.6	89.4	91.2	88.2
Teicoplanin, %	4.7	8.8	17.7	18.9	24.9	20.8	20.2	13.0
Vancomycin, %	41.7	46.3	50.2	46.5	47.0	45.0	41.6	32.6
Linezolid, %	0.0	0.3	0.0	0.0	0.0	0.4	0.2	0.0
Gentamicin (high-level), %	62.0	61.8	60.5	52.6	48.2	43.7	45.5	38.5

ECOFF = epidemiological cut-off value; EUCAST = European Committee on Antimicrobial Susceptibility Testing

Notes
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Number of contributors per year - 2013-14, *n* = 27; 2015, *n* = 31; 2016, *n* = 32; 2017-18, *n* = 36; 2019-20, *n* = 39.

Figure 22: *Enterococcus faecium,* resistance (EUCAST), by vancomycin susceptibility, Australia, 2013–2020



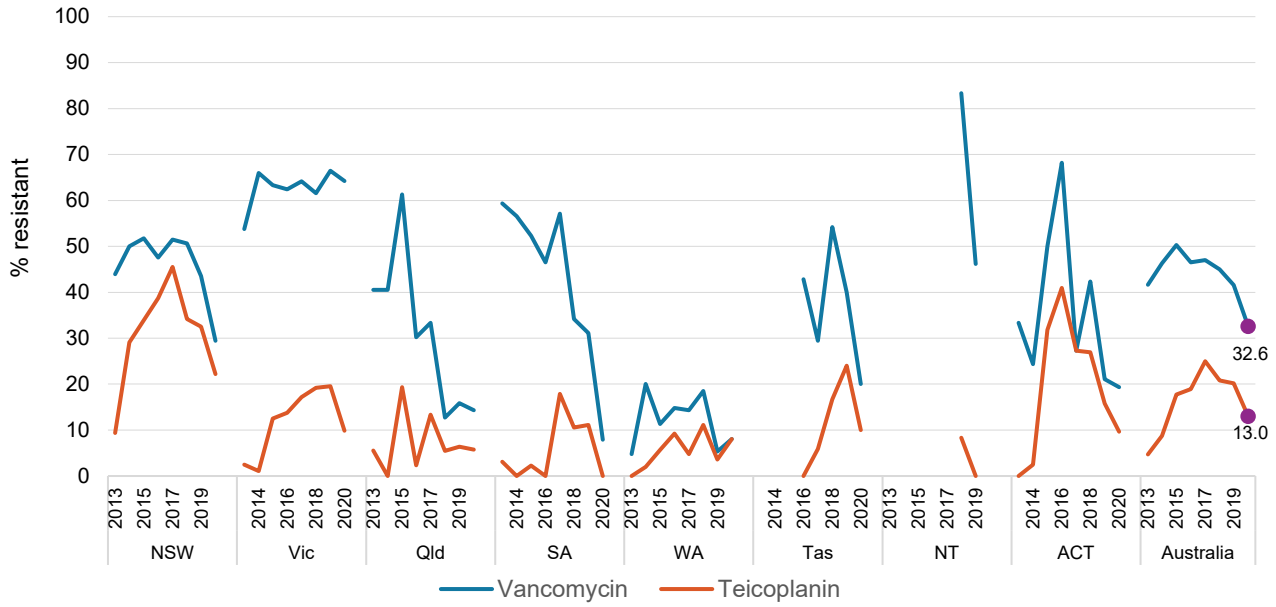
EUCAST = European Committee on Antimicrobial Susceptibility Testing

Notes
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Number of contributors per year - 2013-14, *n* = 27; 2015, *n* = 31; 2016, *n* = 32; 2017-18, *n* = 36; 2019-20, *n* = 39.

State and territory

The proportion of glycoside-resistant *E. faecium* by state and territory is shown in Figure 23. Nationally, the proportion of vancomycin-resistant *E. faecium* decreased by 21.7% in 2020 compared with 2019 (247/594, 41.6% in 2019; 158/485, 32.6% in 2020). Teicoplanin resistance in *E. faecium* decreased 35.7% (120/594, 20.2% in 2019; 63/485, 13.0% in 2020). The greatest decrease in glycoside resistance was in New South Wales.

Figure 23. *Enterococcus faecium*, glycopeptide resistance (EUCAST), by state and territory, and nationally, 2013–2020



Notes

1. Percentage resistance determined using EUCAST 2021 breakpoints for all years. Filled circles indicate values for 2020.
2. Number of contributors per year – 2013-14, *n* = 27; 2015, *n* = 31; 2016, *n* = 32; 2017-18, *n* = 36; 2019-2020, *n* = 39.
3. Insufficient numbers (< 10) to calculate percentage for Tasmania (2013–2015) and the Northern Territory (2013-2017, 2020).

There were significantly decreasing trends in vancomycin resistance in *E. faecium* over the past five years (2016-2020) in South Australia (X^2 for linear trend = 16.48, $P < 0.01$), New South Wales (X^2 for linear trend = 14.50, $P < 0.01$), the Australian Capital Territory (X^2 for linear trend = 11.16, $P < 0.01$), and Queensland (X^2 for linear trend = 6.641, $P = 0.01$) (Table 53). Over the same period, teicoplanin resistance in *E. faecium* decreased significantly in New South Wales (X^2 for linear trend = 16.68, $P < 0.01$) and the Australian Capital Territory only (X^2 for linear trend = 7.619, $P < 0.01$), (Table 54).

Table 53: *Enterococcus faecium*, percentage resistant to vancomycin (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
South Australia	59.4 (32)	56.5 (46)	52.3 (44)	46.5 (43)	57.1 (28)	34.2 (38)	31.1 (45)	7.9 (38)	▼
Western Australia	4.8 (42)	20.0 (50)	11.3 (53)	14.8 (54)	14.3 (63)	18.5 (54)	5.4 (56)	8.1 (62)	↔
Queensland	40.5 (37)	40.5 (37)	61.3 (31)	30.2 (43)	33.3 (45)	12.7 (55)	15.9 (63)	14.3 (35)	▼
Australian Capital Territory	33.3 (18)	24.4 (41)	50.0 (22)	68.2 (22)	27.3 (22)	42.3 (26)	21.1 (19)	19.4 (31)	▼
Tasmania	–† (5)	–† (7)	–† (8)	42.9 (14)	29.4 (17)	54.2 (24)	40.0 (25)	20.0 (10)	↔
New South Wales	43.9 (107)	50.0 (104)	51.7 (116)	47.6 (124)	51.5 (167)	50.7 (152)	43.5 (209)	29.4 (180)	▼
Victoria	53.8 (80)	66.0 (94)	63.3 (120)	62.4 (109)	64.2 (134)	61.5 (130)	66.5 (164)	64.2 (123)	↔
Northern Territory	–† (3)	–† (1)	–† (8)	–† (4)	–† (5)	83.3 (12)	46.2 (13)	–† (6)	–†
Australia	41.7 (324)	46.3 (380)	50.2 (402)	46.5 (413)	47.0 (481)	45.0 (491)	41.6 (594)	32.6 (485)	▼

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

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

Note: Percentage resistance determined using EUCAST 2021 breakpoints for all years.

Table 54: *Enterococcus faecium*, percentage resistant to teicoplanin (EUCAST) and number tested, state and territory, 2013–2020

State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Northern Territory	–† (3)	–† (1)	–† (8)	–† (4)	–† (5)	8.3 (12)	0.0 (13)	–† (6)	–†
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)	↔
Queensland	5.6 (36)	0.0 (36)	19.4 (31)	2.3 (43)	13.3 (45)	5.5 (55)	6.3 (63)	5.7 (35)	↔
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)	↔
Australian Capital Territory	0.0 (16)	2.4 (41)	31.8 (22)	40.9 (22)	27.3 (22)	26.9 (26)	15.8 (19)	9.7 (31)	▼
Victoria	2.5 (80)	1.1 (94)	12.5 (120)	13.8 (109)	17.2 (134)	19.2 (130)	19.5 (164)	9.8 (122)	↔
Tasmania	–† (5)	–† (7)	–† (8)	0.0 (14)	5.9 (17)	16.7 (24)	24.0 (25)	10.0 (10)	↔
New South Wales	9.3 (107)	29.1 (103)	33.9 (115)	38.7 (124)	45.5 (167)	34.2 (152)	32.5 (209)	22.2 (180)	▼
Australia	4.7 (321)	8.8 (377)	17.7 (401)	18.9 (413)	24.9 (481)	20.8 (491)	20.2 (594)	13.0 (485)	▼

* Chi-square test for trend for past five years (2016–2020), p-value <0.05, bold text significant increase ▲ or decrease ▼; ↔ no significant difference

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

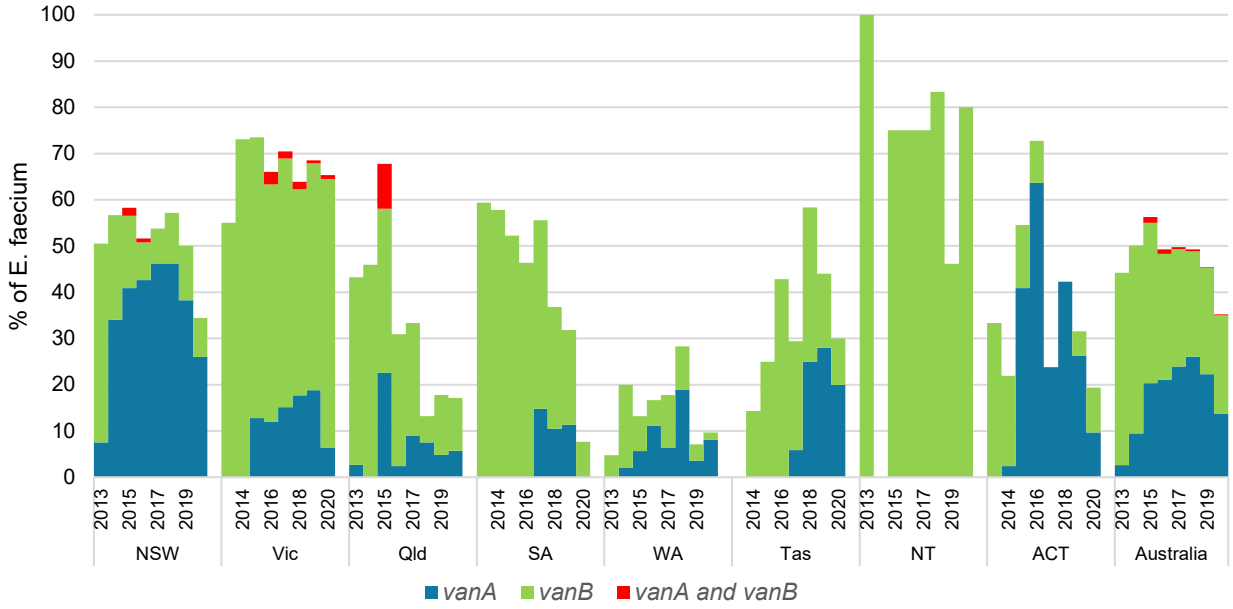
Note: Percentage resistance determined using EUCAST 2021 breakpoints for all years.

Glycopeptide-resistance in *Enterococcus faecium*

In 2020, glycopeptide resistance was predominantly due to *vanB* genes. Although the proportion of *vanB E. faecium* in 2020 remained stable compared to 2019, there was a significant decrease in the proportion of *vanA E. faecium* (131/588, 22.3% in 2019; 66/483, 13.7% in 2020). The decrease in *vanA* genes was predominantly among isolates from Victoria (31/165, 18.8% in 2019, 8/124, 6.5% in 2020, $P < 0.01$), and New South Wales (78/204, 38.2% in 2019; 46/177, 26.0% in 2020, $P = 0.0118$).

There is considerable variation in the proportion of *E. faecium* with *van* genes by state and territory, and the *van* type (Figure 24). From 2013–2019, almost one-half of *E. faecium* harboured *van* genes; in 2020, this fell to just over one-third. Over the past 5-year period (2016-2020), there was a significantly decreasing trend in the proportion of *E. faecium* with *van* genes; in New South Wales and the Australian Capital Territory *vanA* types decreased, while in South Australia and Queensland the decrease was in *vanB* types

Figure 24. Proportion of *van* genes in *Enterococcus faecium* by state and territory, and nationally, 2013–2020



3.10.3. *Staphylococcus aureus*

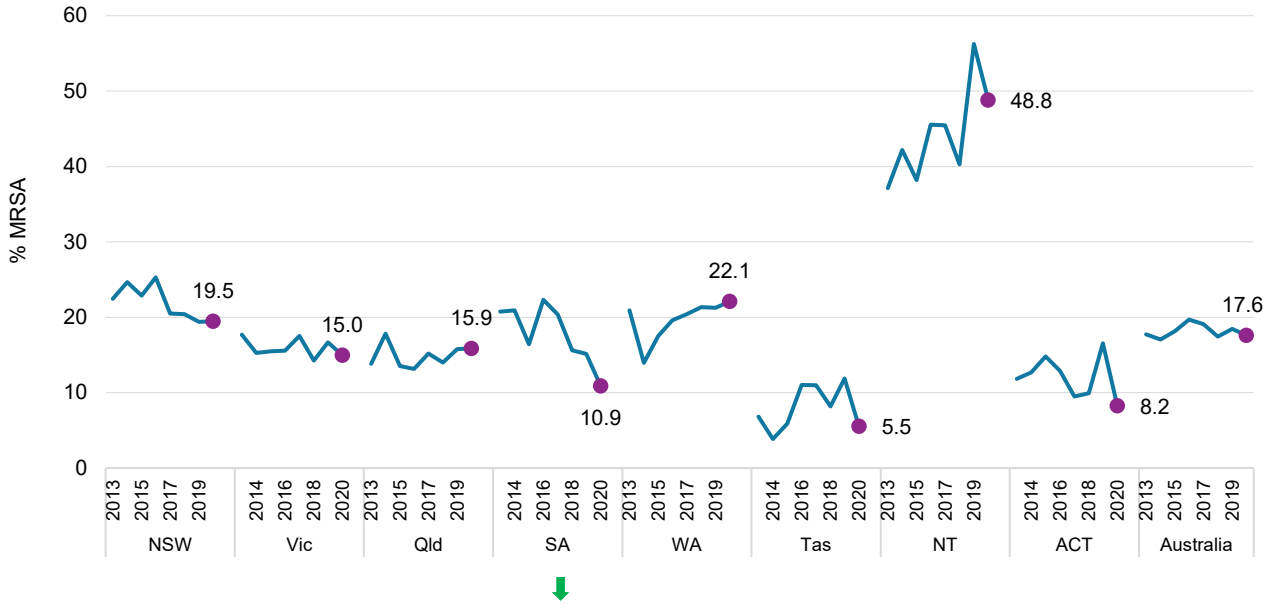
A primary objective of the ASSOP 2020 survey was to determine the proportion of *S. aureus* bacteraemia isolates demonstrating resistance to methicillin and other important anti-staphylococcal agents. The following sections describe the major trends observed for the period 2013–2020.

Methicillin-resistant *Staphylococcus aureus*

The proportion of *S. aureus* that was methicillin resistant throughout Australia remained stable over the years 2013–2020, although there were notable variations at state and territory level (Figure 25). Relative to 2019, there were no significant differences in the proportion of MRSA in the states and territories, however there was a decrease in the proportion of MRSA in South Australia (15.1% in 2019, 10.9% in 2020, down 28%), Tasmania (11.9% in 2019, 5.5% in 2020, down 53%), and the Australian Capital Territory (16.5% in 2019, 8.2% in 2020, down 50%).

Over the past five years (2016-2020) there was a significantly decreasing trend in MRSA in South Australia (χ^2 for linear trend = 13.70, $P < 0.01$) (Table 55).

Figure 25: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, 2013–2020



MRSA = methicillin-resistant *Staphylococcus aureus*

Notes:

1. Percentage resistance determined using EUCAST 2021 breakpoints for all years. Filled circles indicate values for 2020.
2. Number of contributors per year – 2013-14, *n* = 27; 2015, *n* = 31; 2016, *n* = 32; 2017-18, *n* = 36; 2019-2020, *n* = 39.
3. Green arrows indicate antimicrobial agents with significant decrease (P < 0.01) over the past five years (2016 to 2020).

Table 55: *Staphylococcus aureus*, percentage resistant to methicillin (EUCAST) and number tested, state and territory, 2013–2020

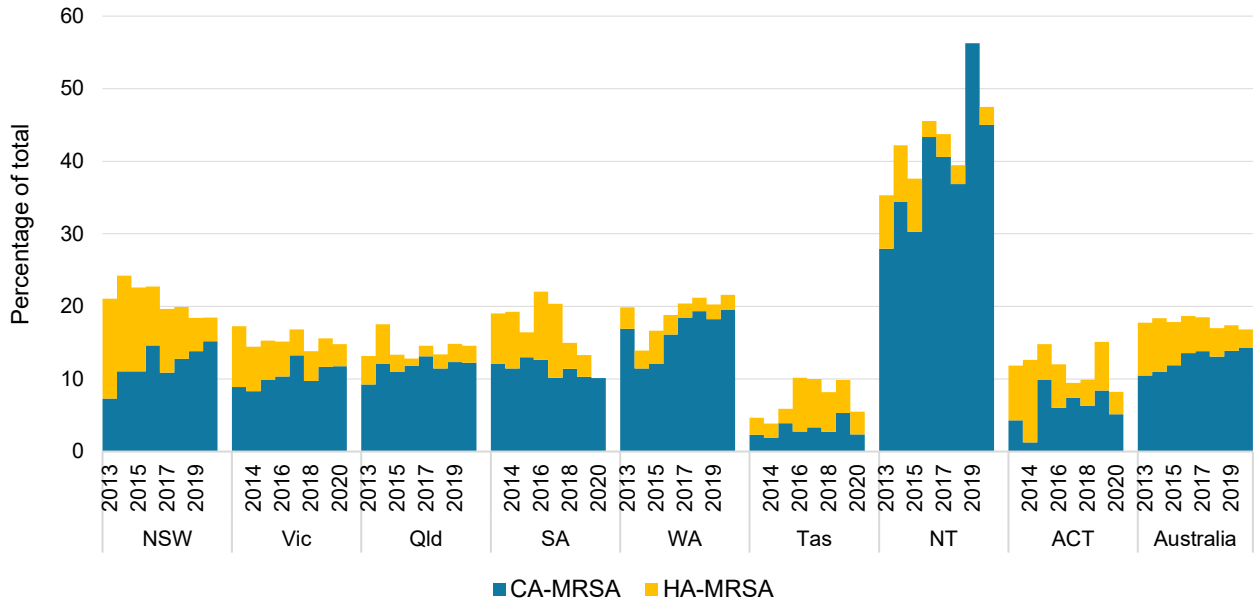
State and territory	Percentage resistant, (*n*) by year								Trend 2016–2020*
	2013	2014	2015	2016	2017	2018	2019	2020	
Tasmania	6.8 (44)	3.8 (52)	5.9 (51)	11.0 (109)	11.0 (91)	8.2 (110)	11.9 (135)	5.5 (127)	↔
Australian Capital Territory	11.8 (93)	12.7 (79)	14.8 (81)	12.9 (101)	9.5 (95)	9.9 (111)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

* Chi-square test for trend for past five years (2016–2020), p-value <0.01, bold text significant decrease ▼; ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2021 breakpoints for all years.

Since 2013, there were significant increases in the proportion of CA-MRSA clones nationally (X^2 for linear trend = 25.10, P < 0.01); notably in New South Wales, Western Australia and the Northern Territory (Figure 26). The proportion of HA-MRSA clones declined nationally (X^2 for linear trend = 109.0, P < 0.01), notably in New South Wales, Victoria, Queensland, South Australia, and the Northern Territory.

Figure 26: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory and association, 2013–2020



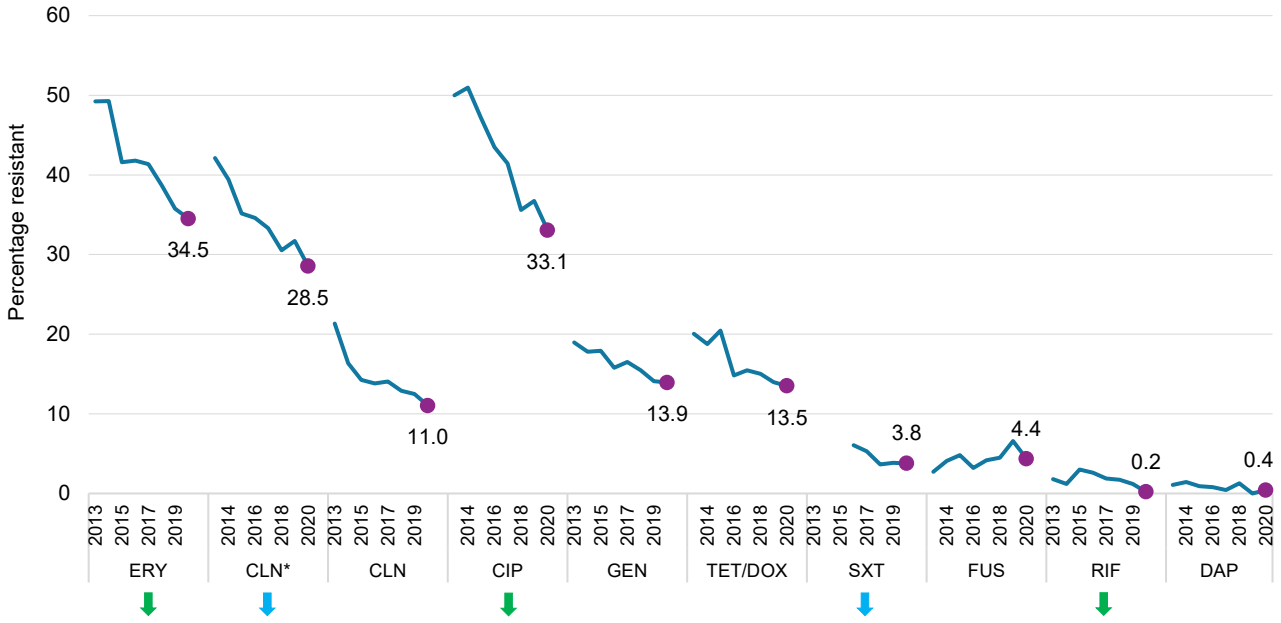
MRSA = methicillin-resistant *Staphylococcus aureus*; CA-MRSA = community-associated MRSA; HA-MRSA = healthcare-associated MRSA

Note: Note all MRSA isolates were available for whole genome sequencing.

Relative to 2019, the percentage resistance to antimicrobial agents tested against MRSA in 2020 remained stable, except for rifampicin (1.2% in 2019, 0.2% in 2020, down 82.8%), fusidic acid (6.6% in 2019, 4.4% in 2020, down 33.6%).

Rates of resistance in MRSA over the past five years (2016–2020) decreased for ciprofloxacin (χ^2 for linear trend = 13.56, $P < 0.01$), rifampicin (χ^2 for linear trend = 9.780, $P < 0.01$), erythromycin (χ^2 for linear trend = 8.624, $P = <0.01$), clindamycin (inducible + constitutive resistance [χ^2 for linear trend = 4.172, $P = 0.0411$], and trimethoprim-sulfamethoxazole [χ^2 for linear trend = 4.202, $P = 0.0404$]) (Figure 27).

Figure 27: Methicillin-resistant *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, 2013–2020



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; NIT = nitrofurantoin [CLSI]; RIF = rifampicin; SXT = trimethoprim–sulfamethoxazole, TET/DOX = tetracyclines (tetracycline, Vitek®; doxycycline, and Phoenix™)

Notes:

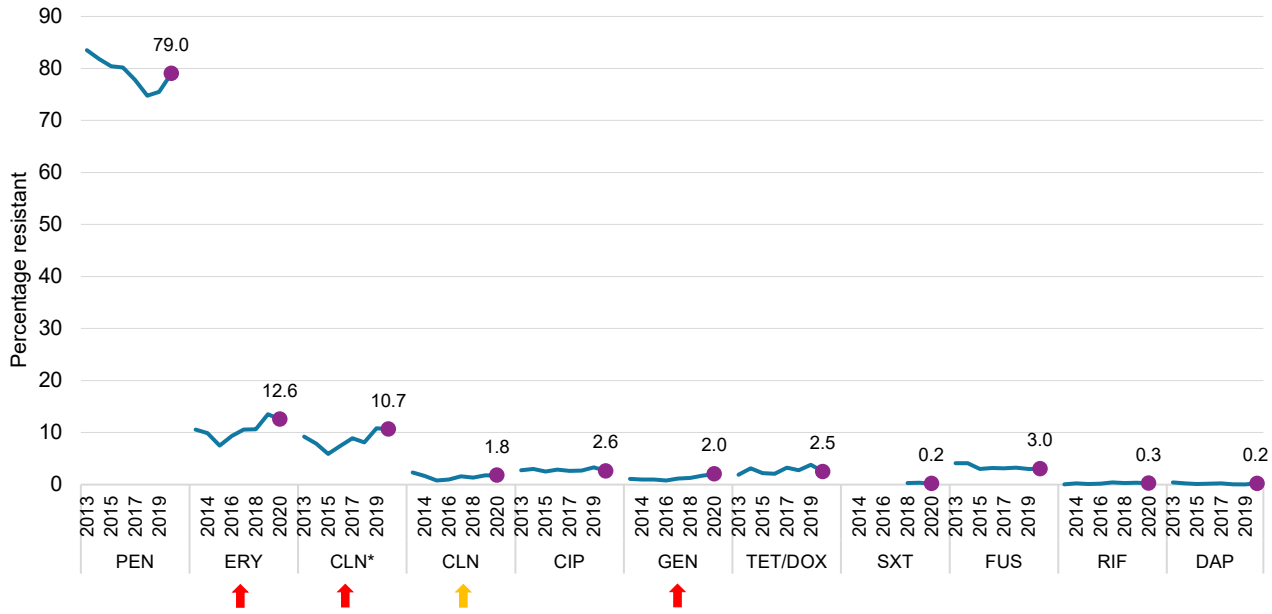
1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Green arrows indicate antimicrobial agents with significant decrease ($P < 0.01$) over the past five years (2016 to 2020).
3. Blue arrows indicate antimicrobial agents with significant decrease ($0.01 < P < 0.05$) over the past five years (2016 to 2020).
4. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek or Phoenix) was not confirmed by an alternative method in 2013–2015.

Methicillin-susceptible *Staphylococcus aureus*

Relative to 2019, the percentage resistance for MSSA in 2020 was similar to 2019 for the antimicrobial agents tested, except for tetracyclines (3.8% in 2019, 2.5% in 2020, down 34.1%, $P = 0.0133$) (Figure 28).

Rates of resistance in MSSA over the past five years (2016–2020) increased for erythromycin (χ^2 for linear trend = 19.74, $P < 0.01$), clindamycin (inducible + constitutive) (χ^2 for linear trend = 18.36, $P < 0.01$), and gentamicin (χ^2 for linear trend = 15.10, $P < 0.01$) (Figure 28).

Figure 28: Methicillin-susceptible *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, 2013–2020



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

Notes:

1. Percentage resistance determined using EUCAST 2021 breakpoints for all years.
2. Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the past five years (2016 to 2020).
3. Orange arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the past five years (2016 to 2020).
4. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek or Phoenix) was not confirmed by an alternative method in 2013–2017.

4. International comparisons

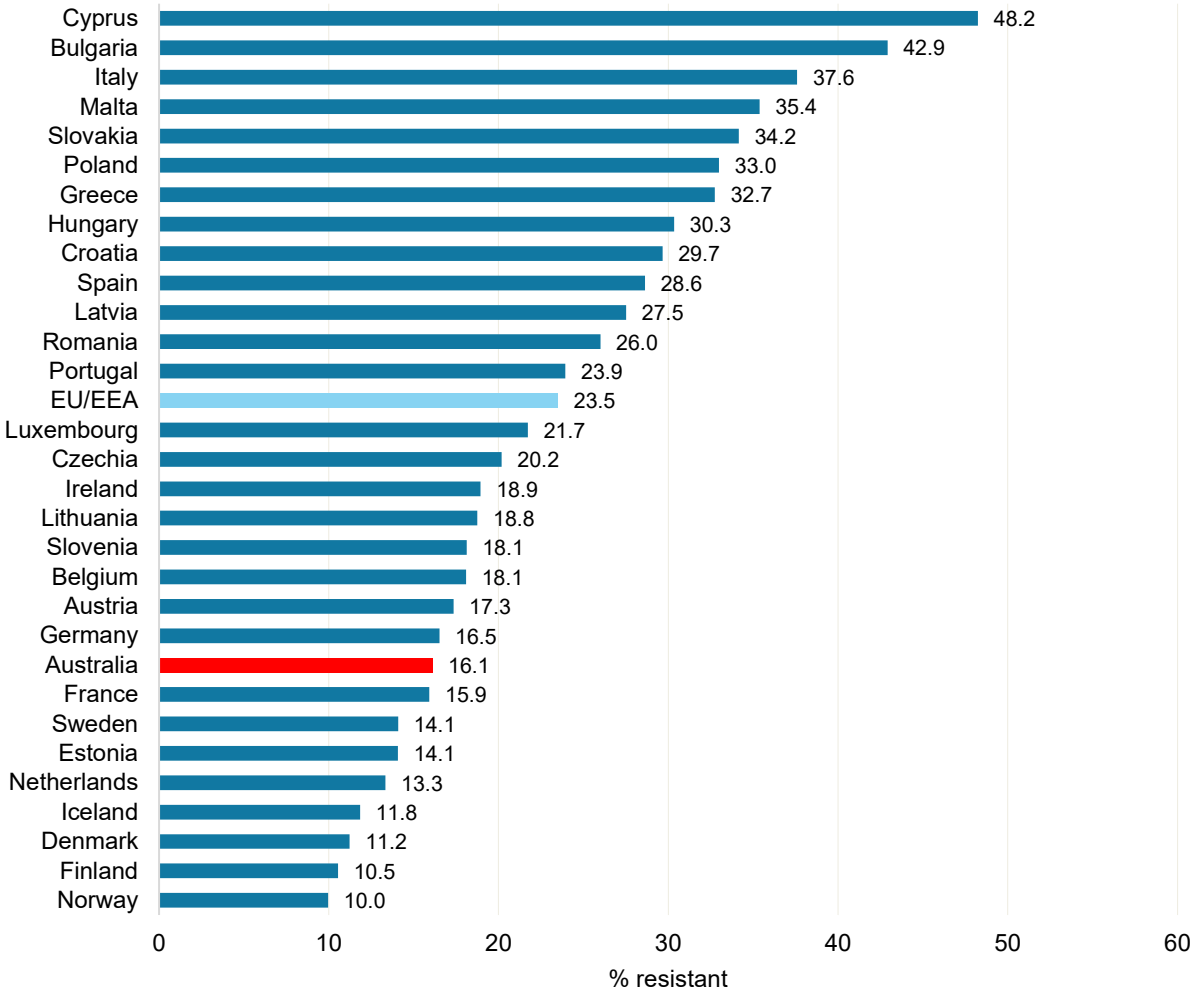
Data from AGAR can be compared with data from the European Antimicrobial Resistance Surveillance Network (EARs-Net) program[55], as both programs examine resistance in bacterial pathogens found in blood cultures.

Rates of resistance to fluoroquinolone in *E. coli* and *K. pneumoniae* (represented by resistance to ciprofloxacin) remain low in Australia compared with most European countries (Figures 29 and 30). Australia ranked third lowest in rates of resistance to fluoroquinolones in *E. coli* compared with European countries in 2015, but rose to ninth lowest in 2020, despite increases in resistance rates in most European countries.

Australia now ranks towards the middle in rates of resistance to third-generation cephalosporins in *E. coli* but remains lower than the European Union and European Economic Area average. Third-generation cephalosporin resistance in *K. pneumoniae* is low by comparison (Figures 31 and 32).

Australia ranks in the top third in rates of resistance to methicillin in *S. aureus* compared to all European countries (Figure 33). Australia also ranks in the top third in rates of resistance to vancomycin in *E. faecium* compared to all European countries (Figure 34), ranking 10th. In 2019, it was ranked fourth.

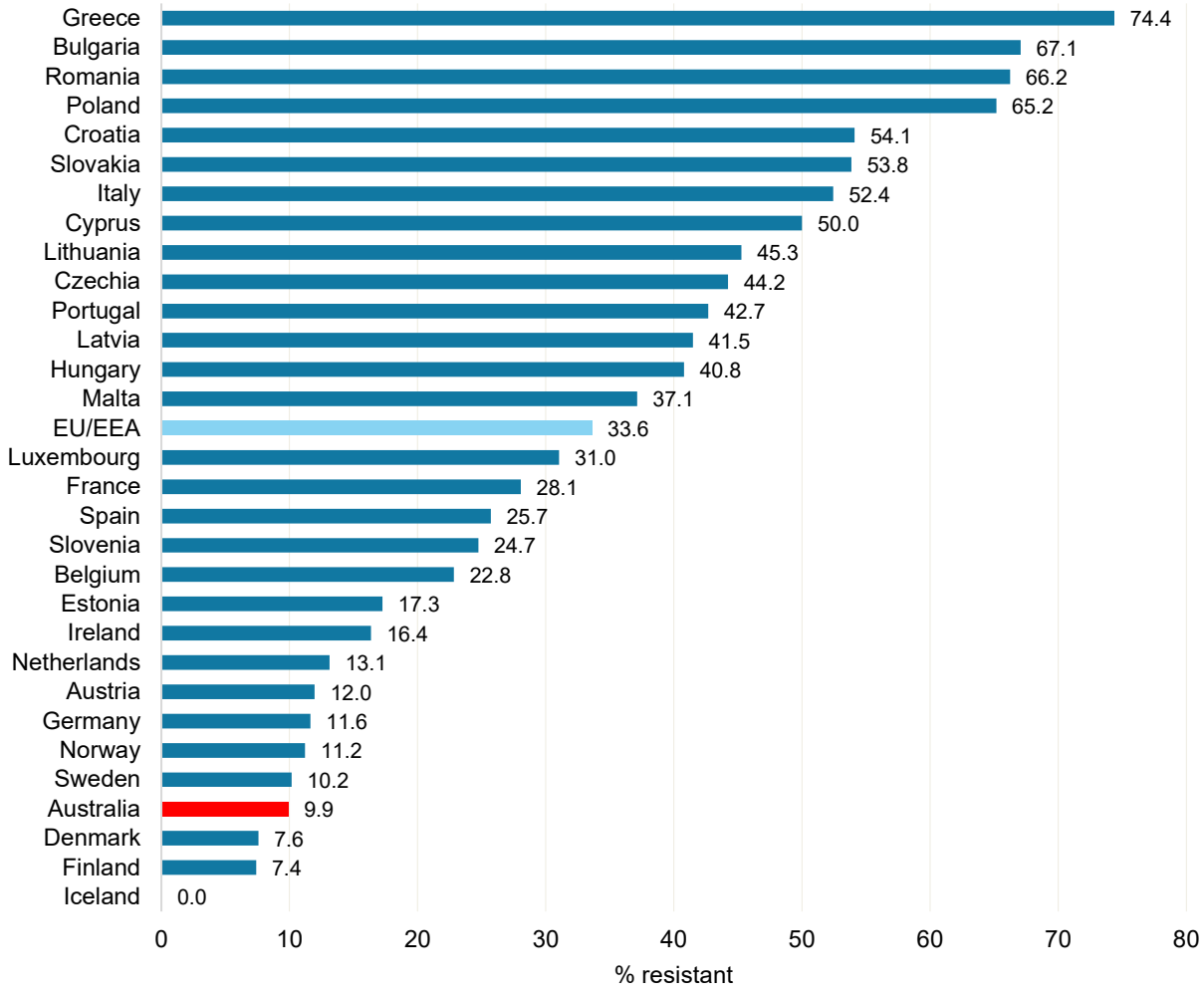
Figure 29: Comparison of *Escherichia coli* rates of resistance to ciprofloxacin in Australia and European countries, blood culture isolates, 2020



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

Source: EARS-Net (Europe)[56]

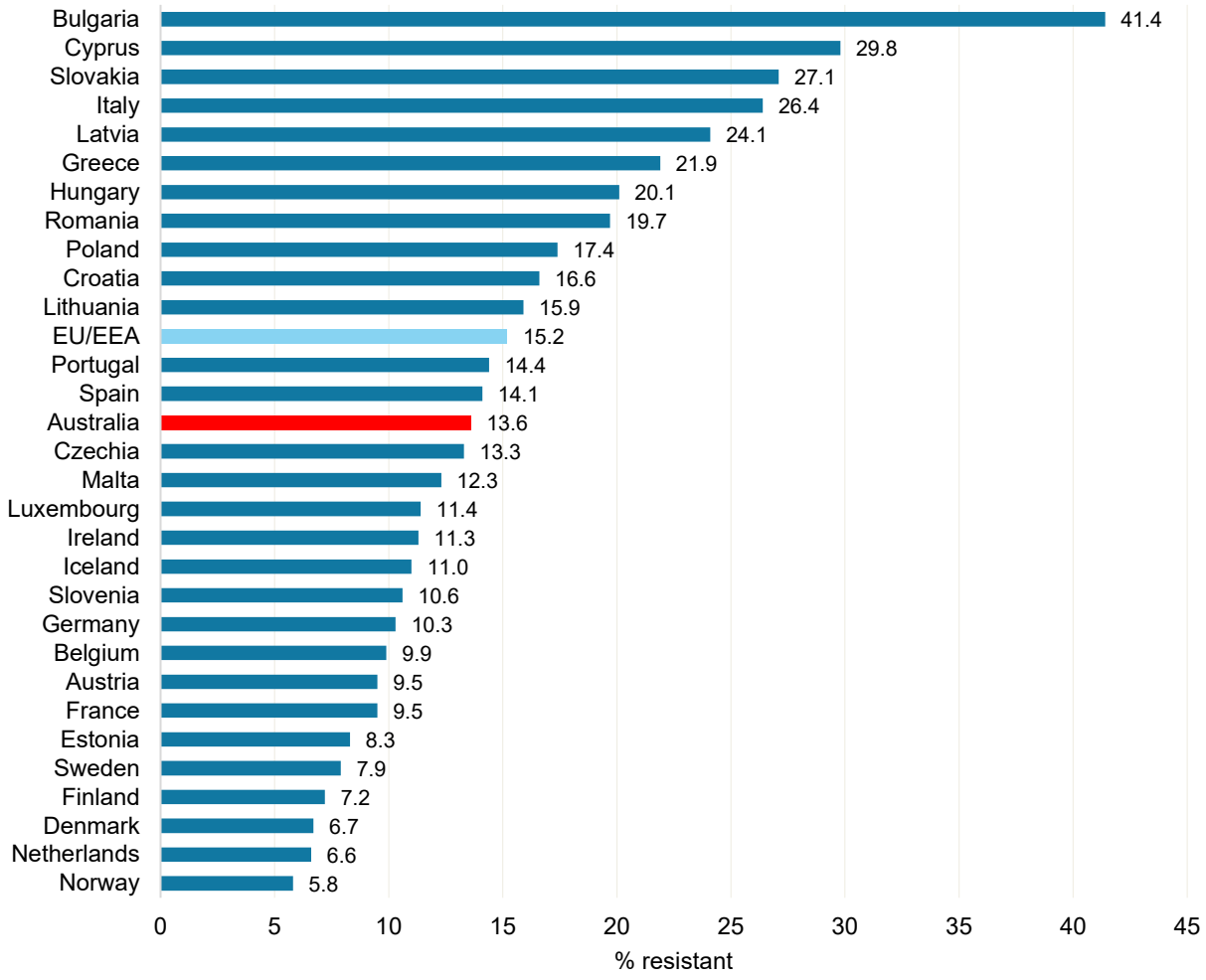
Figure 30: Comparison of *Klebsiella pneumoniae* rates of resistance to ciprofloxacin in Australia and European countries, blood culture isolates, 2020



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

Source: EARS-Net (Europe)[56]

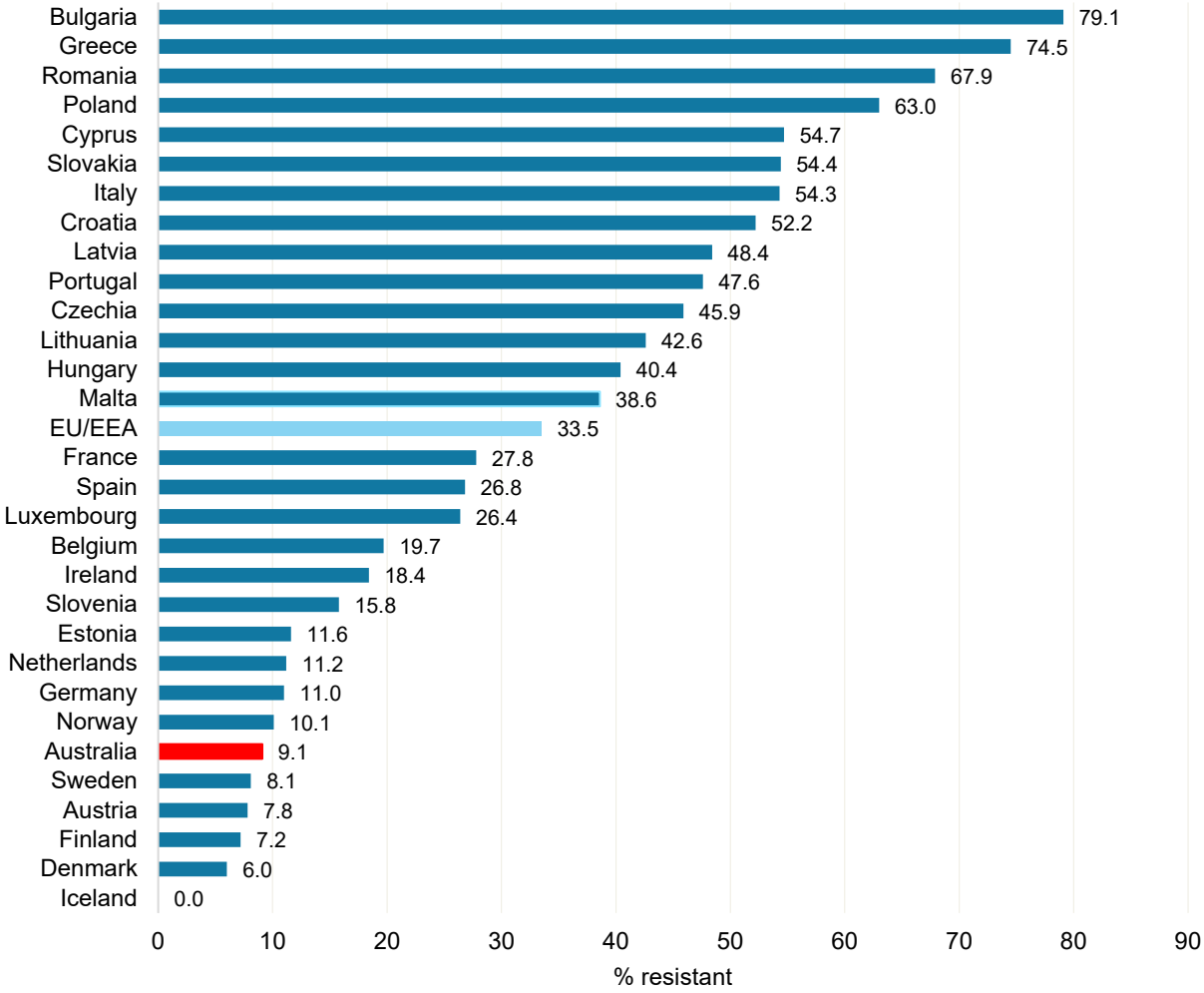
Figure 31: Comparison of *Escherichia coli* rates of resistance to third-generation cephalosporins in Australia and European countries, blood culture isolates, 2020



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

Source: EARS-Net (Europe)[56]

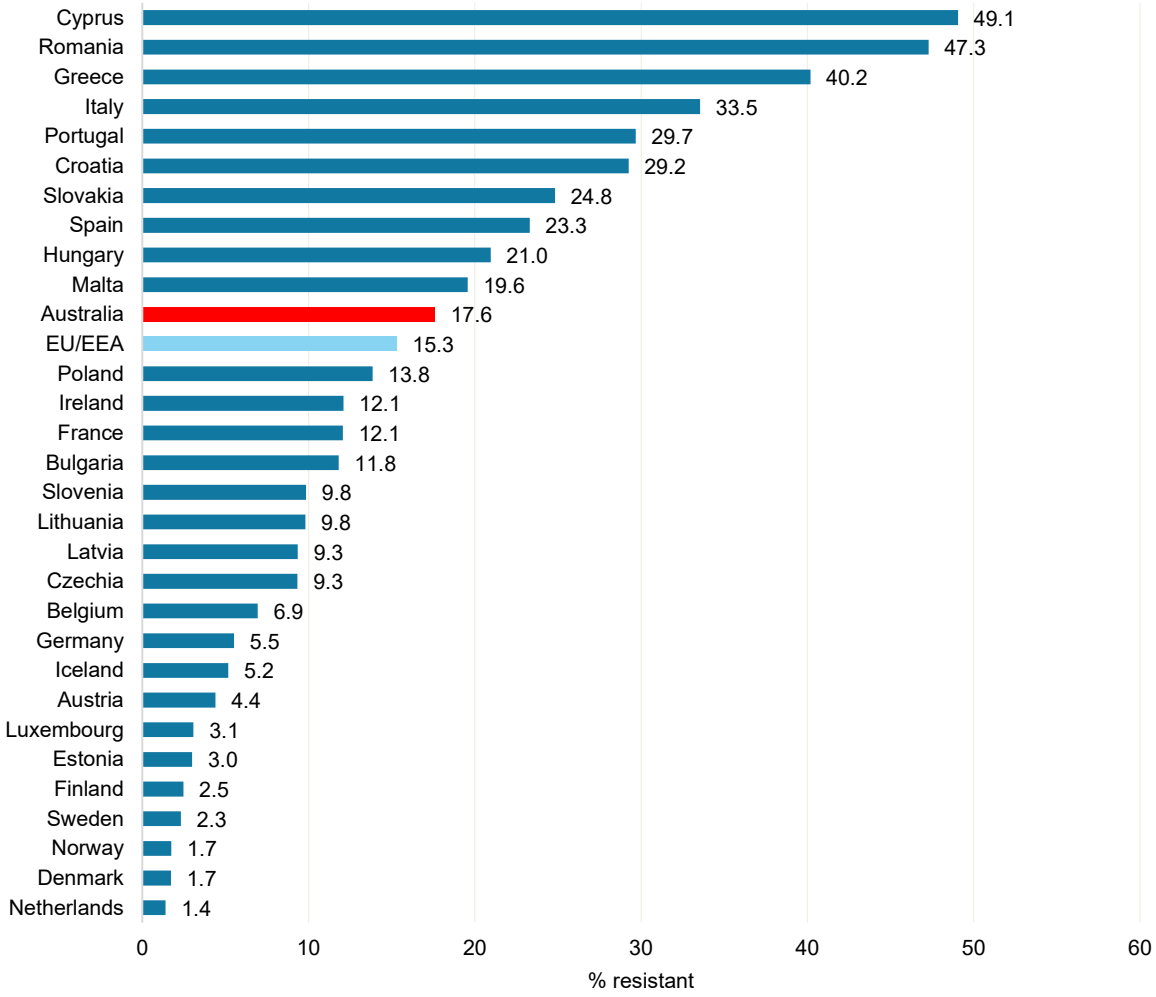
Figure 32: Comparison of *Klebsiella pneumoniae* rates of resistance to third-generation cephalosporins in Australia and European countries, blood culture isolates, 2020



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

Source: EARS-Net (Europe)[56]

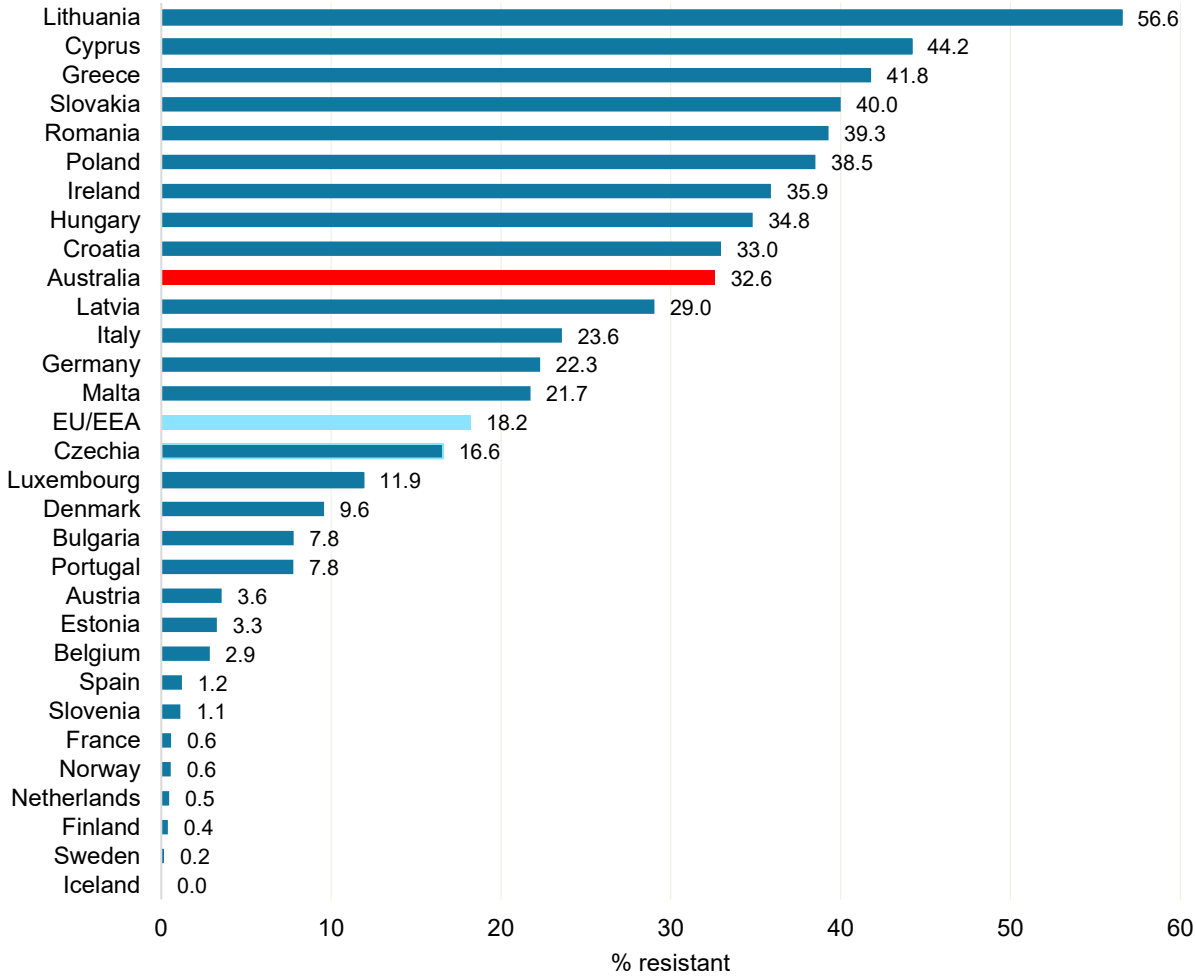
Figure 33: Comparison of *Staphylococcus aureus* rates of resistance to methicillin in Australia and European countries, blood culture isolates, 2020



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

Source: EARS-Net (Europe)[56]

Figure 34: Comparison of *Enterococcus faecium* rates of resistance to vancomycin in Australia and European countries, blood culture isolates, 2020



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

Source: EARS-Net (Europe)[56]

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 antibiotic use patterns all influence the types of resistance that are likely to be observed
- Although data have been collected from 38 large Australian hospitals and 11 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
- Because of the formulation of amoxicillin–clavulanic acid in the Vitek® cards used, interpretation using EUCAST guidelines for this agent was limited to data available from Phoenix™ cards
- Concentration ranges of some antimicrobial agents in both the Vitek® and Phoenix™ cards limit the ability to accurately identify 'susceptible' for some combinations of antimicrobial agents and species
- Data are classified into hospital- and community-onset infections; healthcare-associated community-onset infections may be included in the community-onset group
- Association with relevant mobile genetic element/s (for example, plasmid/s) is not included in this report.

In 2020, methods used to screen referred GNSOP isolates for mechanisms of resistance changed as follows:

- Selected isolates underwent whole genome sequencing
- In unsequenced strains: gene targets for ESBL and pAmpC genes were limited to the most prevalent variants
- *E. coli* were not screened for ST131-O25b by PCR.
- Not all referred isolates were screened for carbapenemases, ribosomal methyltransferases or *mcr* genes.

6. Discussion and conclusions

AGAR data show that in 2020 episodes of bacteraemia in Australia had their onset overwhelmingly in the community. For the GNSOP and the AESOP bacteraemia programs, the most frequent predisposing clinical manifestations were urinary tract infection and biliary tract infection. 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 the ASSOP, the most frequent principal clinical manifestations were osteomyelitis/septic arthritis and skin and skin structure infections. Strategies to reduce blood stream infections should take this information on clinical manifestation (sources of bacteraemia) into account.

AGAR data show a longitudinal trend of increasing *E. coli* resistance to key anti-gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin. The rate of resistance to in *E. coli* to ciprofloxacin was 16.1%). 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, it was 21.8% in 2020. In *K. pneumoniae* complex, rates of resistance to ciprofloxacin were lower than for *E. coli,* 9.9% in 2020.

Increasing fluoroquinolone resistance in Australia is a concern. A little over a decade ago, ciprofloxacin-resistance rates were consistently between 1% and 4%.[28, 57] This was attributed to regulatory controls in human and veterinary prescribing, and national therapeutic guidelines, which sought to restrict unnecessary fluoroquinolone use. This report shows that fluoroquinolones, which have been relied on historically as 'rear-guard' oral antimicrobials, can no longer be considered as a broadly reliable antimicrobial choice in empiric management of gram-negative infection. Despite this concerning increase, the percentage of fluoroquinolone-resistant *E. coli* in Australia remains low in comparison to most European countries.[55, 56, 58] 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.

Compared to 2019, there was little change in 2020 in the proportion of *E. coli* (14.7%) and *K. pneumoniae* complex (10.0%) with an ESBL phenotype. Over 78% of ESBL-producing *E. coli* bacteraemias were community onset. This indicates that a substantial reservoir of resistance exists in the community, particularly in the elderly population and in long-term residential care settings.[59] If the rate continues to rise, it will potentially affect the application of therapeutic guidelines for empirical treatment of severe infections. Current Australian guidelines recommend third-generation cephalosporins for empirical treatment for many conditions, partly to minimise prescribing of broader-spectrum antimicrobials, especially carbapenems. The AGAR data suggest that customised patient risk assessment may be required in empirical treatment decisions. Rates of *E. coli* resistance to ceftriaxone in hospital-onset bacteraemia rose from 13.0% in 2016 to 20.2% in 2019; it was 18.8% in 2020. Community-onset ceftriaxone resistance has remained steady (11.1% in 2016, 11.9% in 2019, and 12.4% in 2020).

To date, carbapenemase-producing *Enterobacterales* (CPE) remain uncommon (0.1% in *E. coli* and 0.3% in *K. pneumoniae* complex). The overall low rates of CPE bacteraemia are encouraging; however, some organisms harbour them more commonly; 3.5% of *E. cloacae* complex infections harboured a carbapenemase (4.3% hospital-onset; 2.9% community-onset) in 2020. Examining previous and current AGAR surveys, most CPEs are endemic in origin.[33, 60] Nineteen of the 28 CPEs had $bla_{\text{IMP-4}}$, reported, predominately from Victoria (9/19, 47.4%) and New South Wales (7/15, 46.7%); two isolates with $bla_{\text{IMP-4}}$ were isolated in Queensland and one in the Australian Capital Territory. Eight of the nine $bla_{\text{IMP-4}}$ from Victoria were from the one institution. This reinforces the importance of infection control programs and adherence to carbapenemase management guidelines to limit transmission of CPE.[6] No KPC-types have been reported since the 2018 survey.

One *E. coli* harbouring mobile colistin resistance genes (*mcr-1.1*) was detected from all isolates referred for PCR testing (*n* = 1,230). Thirteen *Enterobacterales* with the $bla_{\text{IMP-4}}$ carbapenemase

gene (*E. cloacae* complex [*n* = 11], *K. pneumoniae* [*n* = 1], *C. freundii* [*n* = 1]) and one *E. cloacae* with bla_{NDM-1} also harboured *mcr-9.1*. One *E. cloacae* isolate with bla_{IMP-4} harboured *mcr-10.1*. Two additional isolates (*E. cloacae* and *K. pneumoniae*) that did not produce a carbapenemase gene had *mcr-9.1*. *mcr-9* has recently been found among several species of *Enterobacterales*[51] often on an IncHI2 plasmid, but the two downstream genes reported to be involved in induction of *mcr-9* expression by sub-inhibitory concentrations of colistin[52] are not present here.

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 hospital stay in all Australian public hospitals in 2018–19 was 5.4 days.[61] Thirty-day all-cause mortality due to *E. faecium* in 2020 was 19.6% (CO, 13.8%; HO, 22.5%); there were no significant differences in 30-day all-cause mortality between vancomycin-susceptible and resistant episodes. The 30-day all-cause mortality associated with *E. coli*, *K. pneumoniae* complex and *E. faecium* hospital-onset infections exceeds community-onset infections.

In the 2020 survey, 35.2% of *E. faecium* harboured *vanA* or *vanB* genes, or both; in 2019 it was 45.4%. Vancomycin, which until recently was the mainstay of therapy for *E. faecium*, can no longer be recommended empirically; agents with less certain efficacy 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, 48.8% of vancomycin-resistant *E. faecium* bacteraemias were due to *vanA*; increasing from 6.1% in 2013. Since 2017, *vanA* genotype has remained around 50% (2018, 52.7%, 2019, 48.2%), in 2020 it fell to 36.3%. This type of vancomycin resistance has emerged rapidly in the past seven years, particularly in New South Wales and the Australian Capital Territory, where it is now the dominant genotype. This in turn has reduced the overall teicoplanin susceptibility of *E. faecium* in Australia.

The percentage of *E. faecium* bacteraemia isolates that are resistant to vancomycin in Australia is significantly higher than that seen in almost all European countries. In 2020, the European Union/European Economic Area (EU/EEA) population-weighted mean percentage was 18.2%. Australia ranks in the top third in rates of resistance to vancomycin in *E. faecium* (32.6%) compared to all European countries, and ranking tenth. In 2019, it was ranked fourth.[55, 56, 58]

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 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 slightly from 18.5% in 2019[62] to 17.6% in the 2020 study. This compares with the 2020 EU/EEA population-weighted mean MRSA percentage of 15.3%, ranging from 1.4% in the Netherlands to 49.1% in Cyprus.[55, 56, 58]

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, ST5-IV ST45-V, and HA-MRSA strains, for example, ST22-IV, were more frequently found in hospital-onset bacteraemia. The molecular characterisation of MRSA contained within this report aids in identifying opportunities for control of MRSA bacteraemia in the Australian setting.

The rapidly changing picture of MRSA in Australia, drawing from 15 years of AGAR surveillance, is further explored in *Methicillin-resistant* Staphylococcus aureus *in Australia. MRSA bacteraemia – 2013 to 2018*.[54] 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 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 multidrug-resistant organisms occur in hospitals and other institutional care settings, and substantial transmission occurs before invasive blood stream infections develop. AGAR data may therefore underestimate local or regional spread of multidrug-

resistant organisms and may not assist with early detection of sentinel resistances, such as certain CPEs. AGAR bacteraemia data need to be assessed with other sources of information to provide broader insights into antimicrobial resistance in Australia. The AURA Surveillance System enables these assessments via Australian Passive AMR Surveillance (APAS) and National Alert System for Critical Antimicrobial Resistances (CARAlert) data, which complement AGAR data.

It is clear that AGAR surveillance remains core to Australia's response to the problem of increasing AMR. AGAR data contribute to understanding AMR in Australian human health settings, and to informing the national response to AMR.

Abbreviations

Abbreviation	Term
AGAR	Australian Group on Antimicrobial Resistance
ANCU	*AURA National Coordinating Unit*
APAS	Australian Passive AMR Surveillance
AURA	Antimicrobial Use and Resistance in Australia
CI	Confidence interval
CLSI	Clinical and Laboratory Standards Institute
GLASS	Global Antimicrobial Resistance and Use Surveillance System
GNSOP	Gram-negative Sepsis Outcome Program
QRDR	Quinolone resistant determining region
ESBL	Extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
MDR	Multi-drug resistant
MIC	Minimum inhibitory concentration
PCR	Polymerase chain reaction
PMQR	Plasmid mediated quinolone resistance
RMT	Ribosomal methyltransferase
WGS	Whole genome sequencing
WHO	World Health Organization

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Reference laboratories

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- All *Enterobacterales* with meropenem MIC >0.125 mg/L (>0.25 mg/L if tested using Vitek)
- all referred isolates of *P. aeruginosa*
- all referred isolates of *Acinetobacter* species
- all referred *Salmonella* and *Shigella* species
- a subset of *E. coli* and *K. pneumoniae* complex isolates based on phenotype (ceftriaxone, ceftazidime and ciprofloxacin) and region.

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Appendix A. Study design

Forty-nine institutions participated in the 2020 survey, 42 adult and seven children's hospitals. All states and territories were represented. The hospital peer group/type[63] represented were:

Principal referral hospitals (*n* = 25)
Public acute group A hospitals (*n* = 4)
Children's hospitals (*n* = 6)
Combined Women's and children's hospitals (*n* = 1)
Private acute group A hospitals (*n* = 2)
Regional and district hospitals from north-west regional Western Australia (*n* = 11)

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

The laboratories that serviced the institutions that participated in AGAR collected all isolates from different patient episodes of bacteraemia for either all isolates or up to 200 isolates for the Gram-negative Sepsis Outcome Program. In patients with more than one isolate, a new episode was defined as a new positive blood culture more than two weeks after the initial positive culture.

An episode was defined as community onset if the first positive blood culture was collected ≤48 hours after admission, and as hospital onset if collected >48 hours after admission.

All laboratories obtained basic laboratory information for each patient episode plus varying demographic information, depending on the level at which they are enrolled in the program. There are two levels of enrolment: Bronze and Silver (Tables A1–A3). At Bronze level, participating laboratories provided date of collection, date of birth, sex, postcode and admission date. At Silver level, participating laboratories provided discharge date, device-related infection, principal clinical manifestation, intensive care unit admission, outcome at seven and 30 days, and date of death.

Table A1: Level of participation of institutions that contributed data on gram-negative* bacteraemia, by state and territory, 2020

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	11	2	9
Victoria	7	0	7
Queensland	6	0	6
South Australia	3	0	3
Western Australia	17†	13	4
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	49	16	33

* *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
† Includes 11 regional and district hospitals from north-west regional Western Australia

Table A2: Level of participation of institutions that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2020

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	10	1	10
Victoria	7	0	7
Queensland	7	0	6
South Australia	3	0	3
Western Australia	17*	13	4
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	49	15	34

* Includes 11 regional and district hospitals from north-west regional Western Australia

Table A3: Level of participation of institutions that contributed data on enterococcal bacteraemia, by state and territory, 2020

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	11	1	10
Victoria	7	0	7
Queensland	6	0	6
South Australia	3	0	3
Western Australia	17*	13	4
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	49	15	34

* Includes 11 regional and district hospitals from north-west regional Western Australia

Appendix B. Methods

Species identification

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

Susceptibility testing

Testing was performed using two commercial semi-automated methods: Vitek 2 (bioMérieux) (*n* = 27) and Phoenix (BD) (*n* = 3), which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution. Commercially available Vitek 2 (AST-N246, 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[30] and the EUCAST v11.0[31] breakpoints from January 2021 were used in the analysis.

S. aureus were classified as MRSA if cefoxitin screen positive (Vitek) or cefoxitin MIC > 4 mg/L (Phoenix). Cefoxitin screen negative isolates that were oxacillin resistant underwent mecA/nuc PCR. If mecA was detected, the isolate was reported as MRSA. All *S. aureus* with penicillin MIC ≤ 0.12 mg/L and no β-lactamase results provided were tested for penicillinase by disc diffusion. A sharp zone edge around a penicillin 1 unit disc was recorded as a penicillinase producer.[31]

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[64-66]

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

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 > 8 mg/L (*E. faecalis*) or ampicillin ≤ 4 mg/L (*E. faecium*), or if MIC not provided
- *van* gene PCR on *E. faecalis*, if not provided:
    - Vancomycin MIC > 4 mg/L or teicoplanin > 2 mg/L, or vancomycin or teicoplanin MIC not provided.

Antimicrobials tested

The antimicrobials tested is shown in Table B1.

Table B1: Antimicrobials available on susceptibility testing cards and interpretive guidelines for CLSI and EUCAST

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v10.0†		
	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							
Enterobacterales	≤8/4		16/8	≥32/16	≤8**	–§	>8**
Enterococcus spp.	–#		–#	–#	≤4**	8**	>8**
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	≤8	–§	>8

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v10.0†		
	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
Enterococcus spp.§§	≤1		2	≥4	≤4##	–##	>4##
E. faecalis (ECOFF)##					≤4	–§	>4
E. faecium (ECOFF)##					≤8	–§	>8
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	0.5	>0.5
Colistin (Phoenix card)							
Acinetobacter spp.	–#		≤2	≥4	≤2	–§	>2
Enterobacterales	–#		≤2	≥4	≤2	–§	>2
Pseudomonas spp.	–#		≤2	≥4	≤2	–§	>2
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	2	>2
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	2	>2
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	≤1	–§	>1
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

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v10.0†		
	S	SDD	I	R	S, SD	S, IE	R
Enterobacterales	≤1		2	≥4	≤2	4–8	>8
Pseudomonas spp.	≤2		4	≥8	≤2	4–8	>8
Nitrofurantoin							
Enterobacterales	≤32		64	≥128	≤64†‡	–§	>64†‡
Enterococcus spp.	≤32		64	≥128	–#	–#	–#
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
Rifampicin							
Enterococcus spp.	≤1		2	≥4	–#	–#	–#
Staphylococcus aureus	≤1		2	≥4	≤0.06§§§	0.12–0.5	>0.5
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	2	>2
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 2020

* The breakpoints selected to identify resistance are described in the *Performance Standards for Antimicrobial Susceptibility Testing. 31st ed. CLSI supplement* M100, 2021

† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 11.0, 2021 (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 concentration range available on the current Vitek® card restricts the ability to identify the susceptible category. For analysis, breakpoints of ≤4 mg/L for susceptible and ≥8 mg/L for resistant were applied

§§ The 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 susceptibility on all *Salmonella* or on those where Vitek® MIC ≤0.25 mg/L

The ciprofloxacin concentration range on the Phoenix™ card restricts the ability to categorise *Enterococcus* spp.

†† Breakpoints apply to *E. coli* only

‡‡ Breakpoints apply to *E. faecalis* only

*** The rifampicin concentration on the cards restricts category interpretation to non-resistant or resistant

§§§ The trimethoprim–sulfamethoxazole concentration on the cards restricts category interpretation to non-resistant or resistant.

Molecular confirmation of resistance

E. coli, *Klebsiella* spp., and *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone MIC >1 mg/L, or cefoxitin MIC >8 mg/L; any other *Enterobacterales* with cefepime MIC >1 mg/L; all *Enterobacterales* with meropenem MIC >0.125 mg/L (>0.25 if tested using Vitek); all *Acinetobacter* species or *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 PCR screening or WGS.

All *P. aeruginosa*, *Acinetobacter* spp., *Salmonella* spp., and *Enterobacterales* with meropenem MIC >0.125 mg/L (>0.25 mg/L if tested using Vitek) underwent WGS. A subset of *E. coli* and *K. pneumoniae* complex isolates based on phenotypic data (ceftriaxone, ceftazidime and ciprofloxacin) were also analysed by WGS. The remaining isolates were screened using real-time multiplex polymerase chain reaction (PCR) using published primers to detect ESBLs ($bla_{\text{SHV-ESBL}}$ with G→A substitution at position 700 and/or 703, $bla_{\text{CTX-M}}$ groups 1 and 9, bla_{VEB}), plasmid-borne AmpC ($bla_{\text{CMY-2-like}}$, bla_{DHA}).[67]

Other extended spectrum β-lactamases targets ($bla_{\text{ACT/MIR}}$) were detected using in-house, NATA accredited primers and probes in routine use by the Centre for Infectious Diseases & Microbiology Laboratory Services, ICPMR, at Westmead Hospital.

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[32], incorporating searching contigs against the NCBI AMRFinder database (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA313047) using ABRicate[68] and AMRFinder[69], followed by a custom AMR-specific pipeline which includes a read-based search using ARIBA[70] against the CARD[71] and NCBI databases. Ambiguities and potential multiple gene copies/variants were checked manually by mapping reads to reference genes from https://www.ncbi.nlm.nih.gov/pathogens/isolates#/refgene/ using Geneious. Reported chromosomal mutations were derived from ARIBA result tables (quinolone mutations) or its mapping-based reassemblies (all other mutations). Additional mutations in *gyr* and *par* genes identified by PointFinder[49] potentially contributing to resistance were also examined manually. *FimH* typing was predicted by FimTyper.[72] Detection of *H30-Rx* specific SNPs were carried out by in silico PCR.[73]

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[32] 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 or <0 years
- 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 most common gram-negative species, *E. faecium, E. faecalis* and *S. aureus* are shown in Table C1. For some antimicrobials, the concentration range tested did not distinguish between intermediate susceptibility (I) and resistant (R), and the term non- susceptible (NS) was used to describe these isolates.

Table C1: Susceptibility (CLSI and EUCAST) to antimicrobial agents in indicator species of national priority, by state and territory, 2020

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	10	10	9	4	6	0	7	1	47
	%R	10.0, 10.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	2.1, 2.1
Enterobacter cloacae complex	n	164	88	83	23	57	19	6	10	450
	%R	0.6, 1.8	1.1, 5.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 1.8
Escherichia coli	n	1,493	899	623	479	776	201	197	198	4,866
	%R	0.0, 0.9	0.2, 1.8	0.2, 1.1	0.0, 0.2	0.1, 1.4	0.0, 0.0	0.0, 2.0	0.0, 0.5	0.1, 1.1
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%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	371	210	185	81	189	30	37	38	1,141
	%R	0.0, 0.5	0.0, 1.4	0.5, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.6
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%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	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	260	100	161	72	101	27	12	32	765
	%R	1.2, 1.2	0.0, 1.0	0.0, 0.0	0.0, 0.0	0.0, 1.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.4, 0.7
Salmonella species (non-typhoidal)	n	27	7	19	2	18	5	11	3	92
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%R	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%R	0.0, 0.0	0.0, 3.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 1.0
Amoxicillin–clavulanic acid (2:1 ratio)†										
Escherichia coli	n	1,144	899	624	188	776	201	197	198	4,227
	%I	12.5, –§	13.1, –§	12.0, –§	10.6, –§	9.4, –§	13.4, –§	12.7, –§	8.6, –§	11.8, –§
	%R	9.4, –§	7.2, –§	7.7, –§	4.8, –§	7.5, –§	6.5, –§	9.6, –§	3.5, –§	7.7, –§
Klebsiella oxytoca	n	51	54	34	9	39	20	2	10	219

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%I	0.0, –[§]	5.6, –[§]	0.0, –[§]	n/a	0.0, –[§]	0.0, –[§]	n/a	0.0, –[§]	1.8, –[§]
	%R	3.9, –[§]	5.6, –[§]	8.8, –[§]	n/a	7.7, –[§]	5.0, –[§]	n/a	20.0, –[§]	7.3, –[§]
Klebsiella pneumoniae complex	n	287	210	185	26	189	30	37	38	1,002
	%I	5.2, –[§]	5.2, –[§]	2.2, –[§]	0.0, –[§]	1.6, –[§]	3.3, –[§]	18.9, –[§]	5.3, –[§]	4.3, –[§]
	%R	4.5, –[§]	8.1, –[§]	4.3, –[§]	11.5, –[§]	3.7, –[§]	0.0, –[§]	2.7, –[§]	2.6, –[§]	5.0, –[§]
Proteus mirabilis	n	85	55	39	8	45	7	6	6	251
	%I	7.1, –[§]	9.1, –[§]	0.0, –[§]	n/a	6.7, –[§]	n/a	n/a	n/a	6.4, –[§]
	%R	3.5, –[§]	5.5, –[§]	0.0, –[§]	n/a	6.7, –[§]	n/a	n/a	n/a	3.6, –[§]
Salmonella species (non-typhoidal)	n	24	7	19	2	18	5	11	3	89
	%I	8.3, –[§]	n/a	0.0, –[§]	n/a	0.0, –[§]	n/a	0.0, –[§]	n/a	2.2, –[§]
	%R	0.0, –[§]	n/a	0.0, –[§]	n/a	0.0, –[§]	n/a	0.0, –[§]	n/a	0.0, –[§]
Salmonella species (typhoidal)	n	11	11	6	0	1	3	0	1	33
	%I	0.0, –[§]	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –[§]
	%R	0.0, –[§]	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –[§]
Amoxicillin–clavulanic acid (fixed ratio)[†]										
Escherichia coli	n	348	0	0	291	0	0	0	0	639
	%R	–[§], 34.2	n/a	n/a	–[§], 28.5	n/a	n/a	n/a	n/a	–[§], 31.6
Klebsiella oxytoca	n	21	0	0	14	0	0	0	0	35
	%R	–[§], 9.5	n/a	n/a	–[§], 21.4	n/a	n/a	n/a	n/a	–[§], 14.3
Klebsiella pneumoniae complex	n	84	0	0	55	0	0	0	0	139
	%R	–[§], 22.6	n/a	n/a	–[§], 12.7	n/a	n/a	n/a	n/a	–[§], 18.7
Proteus mirabilis	n	15	0	0	15	0	0	0	0	30
	%R	–[§], 0.0	n/a	n/a	–[§], 6.7	n/a	n/a	n/a	n/a	–[§], 3.3
Salmonella species (non-typhoidal)	n	3	0	0	0	0	0	0	0	3
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonella species (typhoidal)	n	4	0	0	0	0	0	0	0	4
	%R	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Ampicillin										
Enterococcus faecalis	n	224	134	97	59	89	27	5	31	666
	%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
Enterococcus faecium	n	179	123	34	39	63	10	6	31	485
	%R	88.3, 88.3	91.9, 91.9	82.4, 82.4	76.9, 76.9	87.3, 87.3	90.0, 90.0	n/a	96.8, 96.8	88.2, 88.2
Escherichia coli	n	1,490	899	623	479	776	201	197	198	4,863
	%I	1.5, –[#]	2.3, –[#]	1.0, –[#]	1.7, –[#]	1.5, –[#]	2.5, –[#]	2.0, –[#]	2.5, –[#]	1.7, –[#]
	%R	53.1, 54.6	49.9, 52.3	53.0, 53.9	46.8, 48.4	50.4, 51.9	46.3, 48.8	63.5, 65.5	48.0, 50.5	51.4, 53.1

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	100	55	39	23	45	7	6	6	281
	%I	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	n/a	n/a	n/a	0.4, –[#]
	%R	18.0, 18.0	29.1, 29.1	12.8, 12.8	17.4, 17.4	22.2, 22.2	n/a	n/a	n/a	19.9, 20.3
Salmonella species (non-typhoidal)	n	26	7	19	2	18	5	11	3	91
	%I	0.0, –[#]	n/a	0.0, –[#]	n/a	5.6, –[#]	n/a	0.0, –[#]	n/a	1.1, –[#]
	%R	11.5, 11.5	n/a	0.0, 0.0	n/a	5.6, 11.1	n/a	0.0, 0.0	n/a	4.4, 5.5
Salmonella species (typhoidal)	n	13	11	6	0	1	3	0	1	35
	%I	7.7, –[#]	0.0, –[#]	n/a	n/a	n/a	n/a	n/a	n/a	2.9, –[#]
	%R	15.4, 23.1	9.1, 9.1	n/a	n/a	n/a	n/a	n/a	n/a	20.0, 22.9
Benzylpenicillin										
Enterococcus faecalis	n	220	94	97	59	89	13	5	31	608
	%R	0.5, –[§]	1.1, –[§]	0.0, –[§]	1.7, –[§]	5.6, –[§]	0.0, –[§]	n/a	0.0, –[§]	1.3, –[§]
Enterococcus faecium	n	178	87	34	38	62	5	6	31	441
	%R	87.6, –[§]	93.1, –[§]	85.3, –[§]	78.9, –[§]	91.9, –[§]	n/a	n/a	93.5, –[§]	88.9, –[§]
Staphylococcus aureus	n	799	460	473	239	446	125	82	97	2,721
	%R**	82.6, 82.6	81.5, 81.5	83.3, 83.3	85.4, 85.4	83.6, 83.6	78.4, 78.4	90.2, 90.2	75.3, 75.3	82.7, 82.7
Cefazolin										
Escherichia coli	n	1,144	899	623	188	776	201	197	198	4,226
	%R	26.2, 26.2	25.8, 25.8	18.0, 18.0	13.3, 13.3	21.8, 21.8	17.9, 17.9	31.5, 31.5	19.7, 19.7	23.1, 23.1
Klebsiella oxytoca	n	51	54	34	9	39	20	2	10	219
	%R	49.0, 49.0	59.3, 59.3	41.2, 41.2	n/a	69.2, 69.2	50.0, 50.0	n/a	50.0, 50.0	54.3, 54.3
Klebsiella pneumoniae complex	n	287	209	185	26	189	30	37	38	1,001
	%R	11.5, 11.5	19.6, 19.6	6.5, 6.5	7.7, 7.7	5.8, 5.8	6.7, 6.7	29.7, 29.7	7.9, 7.9	11.5, 11.5
Proteus mirabilis	n	85	55	39	8	45	7	6	6	251
	%R	20.0, 20.0	23.6, 23.6	12.8, 12.8	n/a	13.3, 13.3	n/a	n/a	n/a	17.5, 17.5
Cefepime										
Acinetobacter baumannii	n	19	6	7	4	6	2	7	0	51
	%I	5.3, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	n/a	7.8, –[§]
	%R	5.3, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	n/a	3.9, –[§]
Enterobacter cloacae complex	n	164	88	83	23	57	19	6	10	450
	%SDD/I	2.4, 7.3	6.8, 8.0	2.4, 6.0	0.0, 13.0	0.0, 3.5	0.0, 5.3	n/a	0.0, 0.0	2.7, 7.1
	%R	2.4, 2.4	4.5, 8.0	8.4, 9.6	0.0, 0.0	0.0, 0.0	5.3, 5.3	n/a	0.0, 0.0	3.6, 4.4
Escherichia coli	n	1,493	899	624	479	776	201	197	198	4,867
	%SDD/I	3.1, 7.2	2.1, 9.3	0.8, 5.4	3.3, 3.1	2.8, 7.6	0.5, 2.5	3.0, 10.7	1.0, 8.6	2.4, 7.0
	%R	3.5,	3.8,	0.5,	4.0,	1.7,	1.0,	1.0,	1.0,	2.6, 3.6

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		4.8	4.7	0.8	5.0	2.6	1.0	3.6	1.5	
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%SDD/I	3.1, 6.3	0.0, 0.0	0.0, 4.2	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 3.3
	%R	3.1, 3.1	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%SDD/I	1.4, 1.4	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	4.3, 4.3	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
Klebsiella pneumoniae complex	n	371	210	185	81	189	30	37	38	1,141
	%SDD/I	1.1, 4.0	1.4, 4.8	0.5, 2.2	1.2, 3.7	0.0, 1.6	0.0, 3.3	2.7, 18.9	0.0, 5.3	0.9, 3.9
	%R	3.0, 3.5	4.3, 5.7	1.1, 1.1	4.9, 4.9	0.5, 0.5	3.3, 3.3	5.4, 5.4	0.0, 0.0	2.6, 3.1
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%SDD/I	3.0, 3.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.1, 1.1
	%R	1.0, 1.0	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.7, 0.7
Pseudomonas aeruginosa	n	260	100	161	72	101	27	12	32	765
	%I	4.6, 92.7	5.0, 92.0	1.9, 98.1	8.3, 91.7	1.0, 98.0	0.0, 92.6	8.3, 83.3	3.1, 90.6	3.8, 94.1
	%R	2.7, 7.3	3.0, 8.0	0.0, 1.9	0.0, 8.3	1.0, 2.0	7.4, 7.4	8.3, 16.7	6.3, 9.4	2.1, 5.9
Salmonella species (non-typhoidal)	n	27	7	19	2	18	5	11	3	92
	%SDD/I	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
	%R	3.7, 3.7	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.1, 1.1
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%SDD/I	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	6.7, 6.7	9.1, 9.1	n/a	n/a	n/a	n/a	n/a	n/a	5.4, 5.4
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%SDD/I	0.0, 0.0	0.0, 3.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.5
	%R	1.4, 1.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.5, 0.5
Cefoxitin										
Escherichia coli	n	1,492	899	624	479	776	201	197	198	4,866
	%R/ecoff	3.8, 6.6	3.3, 5.5	3.7, 4.6	2.1, 3.3	2.7, 4.9	4.0, 6.0	4.6, 6.6	2.0, 4.0	3.3, 5.4
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%R/ecoff	1.4, 1.4	1.9, 3.7	2.9, 2.9	4.3, 8.7	2.6, 2.6	0.0, 5.0	n/a	0.0, 0.0	2.0, 3.1
Klebsiella pneumoniae complex	n	371	209	185	81	189	30	37	38	1,140
	%R/ecoff	4.6, 5.7	5.3, 7.7	4.3, 5.9	8.6, 9.9	3.2, 4.2	0.0, 0.0	5.4, 5.4	10.5, 13.2	4.8, 6.2
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%R/ecoff	0.0, 2.0	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.4, 1.1

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Salmonella species (non-typhoidal)	n	27	7	19	2	18	5	11	3	92
	%R/ecoff	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%R/ecoff	6.7, 6.7	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	2.7, 2.7
Ceftazidime										
Acinetobacter baumannii complex	n	18	6	9	4	6	2	7	1	53
	%I	16.7, –§	n/a	n/a	n/a	n/a	n/a	n/a	n/a	20.8, –§
	%R	5.6, –§	n/a	n/a	n/a	n/a	n/a	n/a	n/a	3.8, –§
Enterobacter cloacae complex	n	164	87	83	23	57	19	6	10	449
	%I	1.8, 4.3	0.0, 3.4	0.0, 3.6	0.0, 8.7	1.8, 1.8	0.0, 0.0	n/a	0.0, 0.0	0.9, 3.6
	%R	22.6, 24.4	28.7, 28.7	24.1, 24.1	21.7, 21.7	15.8, 17.5	10.5, 10.5	n/a	30.0, 30.0	22.9, 23.8
Escherichia coli	n	1,493	899	624	479	776	201	197	198	4,867
	%I	0.9, 7.3	0.2, 7.6	0.0, 5.0	1.7, 3.1	0.1, 7.3	0.0, 3.0	0.5, 12.7	0.0, 10.1	0.5, 6.8
	%R	7.0, 7.8	8.1, 8.3	4.5, 4.5	4.0, 5.6	5.3, 5.4	3.0, 3.0	6.6, 7.1	2.5, 2.5	5.9, 6.5
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%I	0.0, 3.1	3.7, 0.0	0.0, 0.0	n/a	4.2, 0.0	n/a	n/a	n/a	2.5, 0.8
	%R	34.4, 34.4	33.3, 37.0	29.2, 29.2	n/a	33.3, 37.5	n/a	n/a	n/a	32.0, 34.4
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%I	1.4, 0.0	0.0, 1.9	0.0, 0.0	0.0, 4.3	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.8
	%R	1.4, 2.8	0.0, 0.0	0.0, 0.0	4.3, 4.3	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.8, 1.2
Klebsiella pneumoniae complex	n	371	210	185	81	189	30	37	38	1,141
	%I	1.3, 1.9	1.4, 2.4	0.0, 0.5	1.2, 3.7	1.1, 1.1	0.0, 3.3	13.5, 2.7	0.0, 2.6	1.4, 1.8
	%R	6.5, 7.8	10.5, 11.9	3.2, 3.2	6.2, 7.4	2.1, 3.2	3.3, 3.3	10.8, 24.3	5.3, 5.3	6.0, 7.4
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%I	1.0, 2.0	0.0, 3.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.4, 1.4
	%R	0.0, 1.0	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.4, 0.7
Pseudomonas aeruginosa	n	260	99	161	71	101	27	12	32	763
	%I	5.4, 89.6	4.0, 87.9	3.1, 93.8	0.0, 97.2	0.0, 99.0	0.0, 88.9	0.0, 91.7	0.0, 90.6	3.0, 92.3
	%R	5.0, 10.4	8.1, 12.1	3.1, 6.2	2.8, 2.8	1.0, 1.0	11.1, 11.1	8.3, 8.3	9.4, 9.4	4.7, 7.7
Salmonella species (non-typhoidal)	n	27	7	19	2	18	5	11	3	92
	%I	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
	%R	3.7, 3.7	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.1, 1.1
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%I	0.0,	0.0,	n/a	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
		0.0	0.0							
	%R	6.7, 6.7	9.1, 9.1	n/a	n/a	n/a	n/a	n/a	n/a	5.4, 5.4
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%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	1.4, 1.4	3.0, 3.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.0, 1.0
Ceftriaxone										
Acinetobacter baumannii complex	n	18	11	9	3	6	2	7	1	57
	%I	61.1, –§	90.9, –§	n/a	n/a	n/a	n/a	n/a	n/a	72.4, –§
	%R	5.6, –§	0.0, –§	n/a	n/a	n/a	n/a	n/a	n/a	5.2, –§
Enterobacter cloacae complex	n	164	88	83	23	57	19	6	10	450
	%I	0.6, 0.6	1.1, 1.1	2.4, 2.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.9, 0.9
	%R	29.9, 29.9	31.8, 31.8	28.9, 28.9	26.1, 26.1	17.5, 17.5	15.8, 15.8	n/a	30.0, 30.0	27.8, 27.8
Escherichia coli	n	1,493	899	624	479	776	201	197	198	4,867
	%I	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.2, 0.2	0.4, 0.4	0.0, 0.0	1.5, 1.5	0.5, 0.5	0.2, 0.2
	%R	15.3, 15.3	17.0, 17.0	9.0, 9.0	9.0, 9.0	12.4, 12.4	6.0, 6.0	18.3, 18.3	13.1, 13.1	13.4, 13.4
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	37.5, 37.5	37.0, 37.0	29.2, 29.2	n/a	33.3, 33.3	n/a	n/a	n/a	34.4, 34.4
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%I	0.0, 0.0	3.7, 3.7	2.9, 2.9	8.7, 8.7	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	2.0, 2.0
	%R	5.6, 5.6	1.9, 1.9	5.9, 5.9	13.0, 13.0	7.7, 7.7	5.0, 5.0	n/a	10.0, 10.0	5.9, 5.9
Klebsiella pneumoniae complex	n	371	210	185	81	189	30	37	38	1,141
	%I	0.3, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
	%R	8.6, 8.6	16.2, 16.2	3.8, 3.8	7.4, 7.4	2.6, 2.6	6.7, 6.7	27.0, 27.0	5.3, 5.3	8.6, 8.6
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%I	2.0, 2.0	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.1, 1.1
	%R	5.0, 5.0	3.6, 3.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	2.5, 2.5
Salmonella species (non-typhoidal)	n	27	7	19	2	18	5	11	3	92
	%I	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
	%R	3.7, 3.7	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.1, 1.1
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%I	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	6.7, 6.7	9.1, 9.1	n/a	n/a	n/a	n/a	n/a	n/a	5.4, 5.4

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%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	2.7, 2.7	3.0, 3.0	0.0, 0.0	0.0, 0.0	4.2, 4.2	n/a	n/a	n/a	2.6, 2.6
Ciprofloxacin										
Acinetobacter baumannii complex	n	20	11	3	4	6	2	7	1	54
	%I	0.0, 95.0	0.0, 100.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 96.3
	%R	5.0, 5.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	3.7, 3.7
Enterococcus faecalis	n	156	98	0	44	89	13	5	1	406
	%R/ecoff‡	6.4, 3.3	7.1, 7.1	n/a	9.1, 0.0	5.6, 5.6	7.7, 7.7	n/a	n/a	6.9, 4.8
Enterococcus faecium	n	133	86	1	26	62	5	6	0	319
	%R/ecoff§§	92.5, n/a	86.0, n/a	n/a	76.9, n/a	85.5, n/a	n/a	n/a	n/a	88.1, n/a
Staphylococcus aureus	n	805	461	473	239	447	127	82	97	2,731
	%R	11.6, 11.7	8.2, 8.9	5.5, 6.3	2.1, 2.5	5.4, 6.3	3.9, 3.9	6.1, 6.1	8.2, 9.3	7.5, 8.0
Methicillin-resistant *S. aureus*	n	157	69	75	26	99	7	40	8	481
	%R	45.9, 46.5	42.0, 42.0	28.0, 29.3	7.7, 7.7	17.2, 18.2	n/a, n/a	10.0, 10.0	n/a, n/a	32.4, 33.1
Methicillin-susceptible *S. aureus*	n	648	392	398	213	348	120	42	89	2,250
	%R	3.2, 3.2	2.3, 3.1	1.3, 2.0	1.4, 1.9	2.0, 2.9	0.8, 0.8	2.4, 2.4	1.1, 2.2	2.1, 2.6
Enterobacter cloacae complex	n	164	87	83	23	57	19	6	10	449
	%I	1.8, 1.8	3.4, 3.4	1.2, 1.2	0.0, 0.0	1.8, 1.8	0.0, 0.0	n/a	0.0, 0.0	1.8, 1.8
	%R	6.7, 6.7	6.9, 6.9	9.6, 9.6	4.3, 4.3	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	5.8, 5.8
Escherichia coli	n	1,492	899	624	479	776	201	197	198	4,866
	%I	3.2, 3.2	3.0, 3.0	2.9, 2.9	4.2, 4.2	3.0, 3.0	3.0, 3.0	7.6, 7.6	3.0, 3.0	3.3, 3.3
	%R	17.5, 17.5	20.0, 20.0	11.5, 11.5	9.8, 9.8	17.5, 17.5	8.0, 8.0	20.8, 20.8	15.2, 15.2	16.1, 16.1
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%I	0.0, 0.0	3.7, 3.7	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
	%R	3.1, 3.1	0.0, 0.0	0.0, 0.0	n/a	4.2, 4.2	n/a	n/a	n/a	1.6, 1.6
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%I	1.4, 1.4	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	2.9, 2.9	4.3, 4.3	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.8, 0.8
Klebsiella pneumoniae complex	n	371	209	185	81	189	30	37	38	1,140
	%I	2.4, 2.4	2.4, 2.4	2.2, 2.2	4.9, 4.9	2.6, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.4, 2.4
	%R	10.2, 10.2	17.7, 17.7	6.5, 6.5	9.9, 9.9	2.6, 2.6	6.7, 6.7	16.2, 16.2	13.2, 13.2	9.9, 9.9
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%I	1.0, 1.0	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.7, 0.7

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	5.0, 5.0	3.6, 3.6	0.0, 0.0	0.0, 0.0	2.2, 2.2	n/a	n/a	n/a	3.6, 3.6
Pseudomonas aeruginosa	n	260	100	160	72	100	27	12	31	762
	%I	4.6, 91.9	3.0, 94.0	2.5, 93.1	4.2, 83.3	2.0, 95.0	7.4, 88.9	8.3, 83.3	3.2, 93.5	3.7, 91.9
	%R	3.5, 8.1	3.0, 6.0	4.4, 6.9	12.5, 16.7	3.0, 5.0	3.7, 11.1	8.3, 16.7	3.2, 6.5	4.5, 8.1
Salmonella species (non-typhoidal)##	n	27	7	19	2	19	5	11	3	93
	%I	11.1, –#	n/a	0.0, –#	n/a	5.3, –#	n/a	0.0, –#	n/a	4.3, –#
	%R	3.7, 14.8	n/a	0.0, 0.0	n/a	0.0, 5.3	n/a	0.0, 0.0	n/a	1.1, 5.4
Salmonella species (typhoidal)##	n	16	12	6	0	2	3	0	1	40
	%I	37.5, –#	8.3, –#	n/a	n/a	n/a	n/a	n/a	n/a	35.0, –#
	%R	31.3, 68.8	75.0, 83.3	n/a	n/a	n/a	n/a	n/a	n/a	42.5, 77.5
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%I	4.1, 4.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.5, 1.5
	%R	2.7, 2.7	6.1, 6.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	2.1, 2.1
Clindamycin (inducible + constitutive resistance)										
Staphylococcus aureus	n	804	461	472	239	447	127	82	97	2,729
	%R	13.4, 13.9	13.7, 14.1	16.1, 16.1	5.9, 5.9	12.5, 14.1	5.5, 6.3	25.6, 26.8	17.5, 17.5	13.3, 13.8
Methicillin-resistant *S. aureus*	n	157	69	74	26	99	7	40	8	480
	%R	31.2, 31.2	34.8, 37.7	24.3, 24.3	7.7, 7.7	19.2, 21.2	n/a, n/a	35.0, 35.0	n/a, n/a	27.5, 28.5
Methicillin-susceptible *S. aureus*	n	647	392	398	213	348	120	42	89	2,249
	%R	9.1, 9.7	9.9, 9.9	14.6, 14.6	5.6, 5.6	10.6, 12.1	5.0, 5.0	16.7, 19.0	13.5, 13.5	10.2, 10.7
Daptomycin										
Enterococcus faecalis	n	222	134	97	59	89	13	5	31	650
	%R	0.0, –§	0.0, –§	0.0, –§	1.7, –§	0.0, –§	0.0, –§	n/a	0.0, –§	0.2, –§
Enterococcus faecium	n	34	0	0	26	2	0	0	0	62
	%R	0.0, –§	n/a	n/a	11.5, –§	n/a	n/a	n/a	n/a	4.8, –§
Staphylococcus aureus	n	907	546	647	237	498	135	64	121	3,155
	%NS***/R	0.1, 0.1	0.4, 0.4	0.4, 0.4	0.0, 0.0	0.4, 0.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.3
Methicillin-resistant *S. aureus*	n	157	69	75	26	99	7	40	8	481
	%NS***/R	0.6, 0.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.0, 1.0	n/a, n/a	0.0, 0.0	n/a, n/a	0.4, 0.4
Methicillin-susceptible *S. aureus*	n	648	391	398	213	349	119	42	89	2,249
	%NS***/R	0.0, 0.0	0.5, 0.5	0.5, 0.5	0.0, 0.0	0.3, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
Erythromycin										
Staphylococcus aureus	n	805	461	473	239	447	127	82	97	2,731
	%R	18.0, 18.3	14.8, 15.2	18.8, 19.2	10.9, 10.9	13.4, 15.0	5.5, 6.3	26.8, 28.0	17.5, 17.5	15.9, 16.4
Methicillin-resistant	n	157	69	75	26	99	7	40	8	481

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
S. aureus	%R	40.8, 40.8	36.2, 39.1	32.0, 33.3	19.2, 19.2	21.2, 23.2	n/a, n/a	37.5, 37.5	n/a, n/a	33.3, 34.5
Methicillin-susceptible *S. aureus*	n	648	392	398	213	348	120	42	89	2,250
	%R	12.5, 12.8	11.0, 11.0	16.3, 16.6	9.9, 9.9	11.2, 12.6	5.0, 5.0	16.7, 19.0	13.5, 13.5	12.2, 12.6
Fusidic acid										
Staphylococcus aureus	n	804	461	473	239	447	127	82	97	2,730
	%R	–§, 4.1	–§, 2.4	–§, 4.0	–§, 4.2	–§, 1.3	–§, 2.4	–§, 6.1	–§, 2.1	–§, 3.3
Methicillin-resistant *S. aureus*	n	157	69	75	26	99	7	40	8	481
	%R	–§, 6.4	–§, 4.3	–§, 4.0	–§, 7.7	–§, 0.0	–§, n/a	–§, 7.5	–§, n/a	–§, 4.4
Methicillin-susceptible *S. aureus*	n	647	392	398	213	348	120	42	89	2,249
	%R	–§, 3.6	–§, 2.0	–§, 4.0	–§, 3.8	–§, 1.7	–§, 2.5	–§, 4.8	–§, 2.2	–§, 3.0
Gentamicin										
Acinetobacter baumannii complex	n	20	11	9	4	6	2	7	1	60
	%R	5.0, 10.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	3.3, 5.0
Enterobacter cloacae complex	n	164	88	83	23	57	19	6	10	450
	%R	6.7, 7.9	18.2, 19.3	7.2, 7.2	0.0, 0.0	0.0, 0.0	5.3, 5.3	n/a	0.0, 0.0	7.6, 8.4
Escherichia coli	n	1,493	899	624	479	776	201	197	198	4,867
	%R	8.2, 8.8	9.5, 10.1	7.1, 7.9	6.7, 6.9	7.3, 7.9	4.5, 4.5	17.3, 17.8	8.6, 10.1	8.2, 8.8
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%R	0.0, 0.0	3.7, 3.7	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	1.6, 1.6
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%R	1.4, 1.4	0.0, 0.0	0.0, 0.0	4.3, 4.3	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.8, 0.8
Klebsiella pneumoniae complex	n	371	210	185	81	189	30	37	38	1,141
	%R	6.7, 7.3	7.1, 7.6	1.6, 2.2	2.5, 2.5	1.6, 1.6	0.0, 6.7	16.2, 16.2	5.3, 5.3	4.9, 5.4
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%R	2.0, 10.0	3.6, 3.6	2.6, 2.6	4.3, 17.4	2.2, 2.2	n/a	n/a	n/a	3.2, 7.1
Pseudomonas aeruginosa	n	261	100	160	72	101	22	12	31	759
	%R	1.9, –§	0.0, –§	0.6, –§	1.4, –§	0.0, –§	0.0, –§	0.0, –§	3.2, –§	1.1, –§
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%R	0.0, 1.4	3.0, 6.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.0, 2.1
Staphylococcus aureus	n	805	461	473	239	447	127	82	97	2,731
	%R	4.0, 7.5	0.9, 3.0	1.3, 3.2	0.8, 1.7	0.4, 1.3	0.0, 0.8	2.4, 8.5	1.0, 6.2	1.8, 4.1
Methicillin-resistant *S. aureus*	n	157	69	75	26	99	7	40	8	481
	%R	14.0, 28.7	4.3, 8.7	4.0, 9.3	0.0, 3.8	1.0, 1.0	n/a, n/a	2.5, 10.0	n/a, n/a	6.4, 13.9
Methicillin-susceptible *S. aureus*	n	648	392	398	213	348	120	42	89	2,250
	%R	1.5, 2.3	0.3, 2.0	0.8, 2.0	0.9, 1.4	0.3, 1.4	0.0, 0.8	2.4, 7.1	0.0, 3.4	0.8, 2.0
Linezolid										

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Enterococcus faecalis	n	224	133	97	59	88	26	5	31	663
	%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
Enterococcus faecium	n	180	123	35	39	63	10	6	31	487
	%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	805	461	473	239	448	127	82	97	2,732
	%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	157	69	75	26	99	7	40	8	481
	%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	648	392	398	213	349	120	42	89	2,251
	%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	20	11	9	4	6	2	7	1	60
	%I	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	5.0, 5.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	1.7, 1.7
Enterobacter cloacae complex	n	164	88	83	22	57	19	6	10	449
	%I	0.0, 0.6	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.2, 0.4
	%R	4.3, 3.7	10.2, 9.1	2.4, 2.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	4.0, 3.6
Escherichia coli	n	1,492	899	624	479	775	201	197	198	4,865
	%I	0.1, 0.1	0.2, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.0
	%R	0.1, 0.0	0.1, 0.1	0.0, 0.0	0.2, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.0
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	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	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%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	0.0, 0.0	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	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex	n	371	209	185	81	189	30	37	38	1,140
	%I	0.3, 0.3	0.0, 0.5	0.0, 0.0	0.0, 0.0	0.5, 0.0	0.0, 0.0	0.0, 0.0	0.0, 2.6	0.2, 0.3
	%R	0.5, 0.3	0.5, 0.0	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.6, 0.0	0.4, 0.2
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%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	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
Pseudomonas aeruginosa	n	259	100	160	71	100	27	12	31	760
	%I	6.6, 8.1	3.0, 4.0	4.4, 4.4	1.4, 1.4	3.0, 3.0	7.4, 7.4	8.3, 8.3	6.5, 9.7	4.7, 5.5

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	6.9, 5.4	4.0, 3.0	3.1, 3.1	2.8, 2.8	1.0, 1.0	3.7, 3.7	8.3, 8.3	3.2, 0.0	4.3, 3.6
Salmonella species (non-typhoidal)	n	27	7	19	2	18	5	11	3	92
	%I	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%I	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%I	0.0, 1.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.5
	%R	1.4, 0.0	3.0, 3.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.0, 0.5
Mupirocin (high-level)††										
Staphylococcus aureus	n	470	268	473	239	447	76	1	97	2,071
	%R	0.6, 0.6	0.4, 0.4	2.7, 2.7	0.4, 0.4	0.4, 0.4	1.3, 1.3	n/a, n/a	1.0, 1.0	1.1, 1.1
Methicillin-resistant *S. aureus*	n	78	36	75	26	99	4	1	8	327
	%R	1.3, 1.3	0.0, 0.0	4.0, 4.0	0.0, 0.0	0.0, 0.0	n/a, n/a	n/a, n/a	n/a, n/a	1.2, 1.2
Methicillin-susceptible *S. aureus*	n	392	232	398	213	348	72	0	89	1,744
	%R	0.5, 0.5	0.4, 0.4	2.5, 2.5	0.5, 0.5	0.6, 0.6	1.4, 1.4	n/a, n/a	1.1, 1.1	1.0, 1.0
Nitrofurantoin										
Enterococcus faecalis	n	223	134	97	59	88	27	5	31	664
	%R/ecoff§§§	0.4, 1.3	0.0, 1.5	0.0, 2.1	0.0, 0.0	0.0, 2.3	0.0, 7.4	n/a	0.0, 0.0	0.2, 1.7
Enterococcus faecium	n	156	86	31	37	61	5	6	31	413
	%R	62.8, –§	27.9, –§	61.3, –§	54.1, –§	68.9, –§	n/a	n/a	67.7, –§	55.2, –§
Enterobacter cloacae complex	n	143	75	83	23	57	19	6	10	416
	%R	21.0, –§	13.3, –§	21.7, –§	21.7, –§	15.8, –§	0.0, –§	n/a	10.0, –§	17.5, –§
Escherichia coli	n	1,492	899	624	479	776	201	197	198	4,866
	%R	1.2, 1.2	0.9, 0.9	0.8, 0.8	0.6, 0.6	1.0, 1.0	1.0, 1.0	1.0, 1.0	0.0, 0.0	0.9, 0.9
Klebsiella aerogenes	n	28	22	24	4	24	6	1	4	113
	%R	17.9, –§	59.1, –§	33.3, –§	n/a	58.3, –§	n/a	n/a	n/a	38.9, –§
Klebsiella oxytoca	n	60	42	34	23	39	20	2	10	230
	%R	1.7, –§	2.4, –§	0.0, –§	13.0, –§	2.6, –§	0.0, –§	n/a	0.0, –§	2.6, –§
Klebsiella pneumoniae complex	n	331	164	185	81	189	29	37	38	1,054
	%R	29.3, –§	43.9, –§	37.3, –§	22.2, –§	37.6, –§	10.3, –§	21.6, –§	47.4, –§	33.8, –§
Proteus mirabilis	n	91	55	39	23	45	7	6	0	266
	%R	94.5, –§	92.7, –§	100.0, –§	82.6, –§	97.8, –§	n/a	n/a	n/a	94.4, –§
Salmonella species (non-	n	26	2	19	2	18	5	11	0	83

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
typhoidal)	%R	30.8, –§	n/a	5.3, –§	n/a	11.1, –§	n/a	0.0, –§	n/a	13.3, –§
Salmonella species (typhoidal)	n	15	3	6	0	1	3	0	0	28
	%R	0.0, –§	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –§
Serratia marcescens	n	56	33	32	17	24	8	0	7	177
	%R	100.0, –§	93.9, –§	100.0, –§	100.0, –§	100.0, –§	n/a	n/a	n/a	98.9, –§
Oxacillin/methicillin										
Staphylococcus aureus	n	807	461	473	239	448	127	82	97	2,734
	%R	19.5, 19.5	15.0, 15.0	15.9, 15.9	10.9, 10.9	22.1, 22.1	5.5, 5.5	48.8, 48.8	8.2, 8.2	17.6, 17.6
Piperacillin–tazobactam										
Acinetobacter baumannii complex	n	20	6	9	4	6	2	7	1	55
	%R	20.0, –§	n/a	n/a	n/a	n/a	n/a	n/a	n/a	16.4, –§
Enterobacter cloacae complex	n	164	88	82	23	57	19	6	10	449
	%R	19.5, 28.7	17.0, 27.3	15.9, 25.6	21.7, 26.1	10.5, 22.8	10.5, 10.5	n/a	20.0, 30.0	16.9, 26.3
Escherichia coli	n	1,487	894	620	479	770	201	197	197	4,845
	%R	3.1, 7.7	3.1, 7.8	1.6, 6.6	1.7, 2.5	2.2, 7.0	2.5, 6.0	2.5, 5.6	2.0, 3.6	2.5, 6.6
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%R	21.9, 34.4	33.3, 48.1	29.2, 29.2	n/a	29.2, 37.5	n/a	n/a	n/a	26.2, 36.9
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%R	5.6, 6.9	7.4, 7.4	8.8, 11.8	21.7, 21.7	7.7, 12.8	5.0, 5.0	n/a	20.0, 20.0	8.7, 10.6
Klebsiella pneumoniae complex	n	369	208	184	81	188	30	37	38	1,135
	%R	4.9, 13.6	5.8, 16.8	2.7, 9.2	4.9, 16.0	2.1, 8.0	0.0, 0.0	2.7, 18.9	0.0, 13.2	3.9, 12.5
Proteus mirabilis	n	100	55	39	23	44	7	6	6	280
	%R	0.0, 1.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.4
Pseudomonas aeruginosa	n	260	99	160	72	101	27	12	32	763
	%R	6.5, 16.9	10.1, 18.2	4.4, 12.5	2.8, 9.7	2.0, 5.9	3.7, 25.9	8.3, 16.7	6.3, 18.8	5.5, 14.4
Salmonella species (non-typhoidal)	n	27	7	18	2	18	5	11	3	91
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	15	10	6	0	1	3	0	1	36
	%R	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Serratia marcescens	n	65	30	32	17	4	8	0	7	163
	%R	0.0, 1.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	0.0, 2.5
Rifampicin										
Staphylococcus aureus	n	804	461	472	239	447	127	82	97	2,729
	%R	0.1, 0.1	0.0, 0.2	0.4, 0.4	0.0, 0.0	0.7, 0.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.3
Methicillin-resistant *S. aureus*	n	157	69	74	26	99	7	40	8	480
	%R	0.0, 0.0	0.0, 0.0	1.4, 1.4	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0, 0.0	n/a, n/a	0.2, 0.2

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Methicillin-susceptible *S. aureus*	n	647	392	398	213	348	120	42	89	2,249
	%R	0.2, 0.2	0.0, 0.3	0.3, 0.3	0.0, 0.0	0.9, 0.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.3
Teicoplanin										
Enterococcus faecalis	n	224	134	97	59	89	27	5	31	666
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 1.1	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.2
Enterococcus faecium	n	122	35	39	62	10	6	31	485	122
	%R	7.4, 9.8	5.7, 5.7	0.0, 0.0	8.1, 8.1	n/a	n/a	9.7, 9.7	11.1, 13.0	7.4, 9.8
Staphylococcus aureus	n	804	461	473	239	448	127	82	97	2,731
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1
Tetracycline/doxycycline###										
Enterococcus faecalis	n	181	94	78	44	89	13	5	1	505
	%NS	70.7, –§	75.5, –§	70.5, –§	65.9, –§	66.3, –§	76.9, –§	n/a	n/a	70.7, –§
Enterococcus faecium	n	156	87	32	26	62	5	6	0	374
	%NS	60.3, –§	81.6, –§	71.9, –§	3.8, –§	69.4, –§	n/a	n/a	n/a	64.2, –§
Staphylococcus aureus	n	804	461	473	239	447	127	82	97	2,730
	%NS/R	5.1, 5.8	5.2, 5.2	3.2, 3.2	0.0, 2.1	4.7, 4.7	1.6, 1.6	2.4, 2.4	5.2, 5.2	4.0, 4.4
Methicillin-resistant *S. aureus*	n	157	69	75	26	99	7	40	8	481
	%NS/R	21.0, 22.3	20.3, 20.3	9.3, 9.3	0.0, 3.8	5.1, 5.1	n/a, n/a	2.5, 2.5	n/a, n/a	12.9, 13.5
Methicillin-susceptible *S. aureus*	n	647	392	398	213	348	120	42	89	2,249
	%NS/R	1.2, 1.9	2.6, 2.6	2.0, 2.0	0.0, 1.9	4.6, 4.6	1.7, 1.7	2.4, 2.4	3.4, 3.4	2.1, 2.5
Ticarcillin–clavulanic acid										
Acinetobacter baumannii complex	n	13	6	9	1	6	2	7	1	45
	%R	7.7, –§	n/a	n/a	n/a	n/a	n/a	n/a	n/a	4.4, –§
Enterobacter cloacae complex	n	117	88	82	15	57	19	6	10	394
	%R	31.6, 35.0	23.9, 31.8	23.2, 30.5	26.7, 40.0	17.5, 21.1	10.5, 15.8	n/a	30.0, 40.0	24.6, 30.7
Escherichia coli	n	988	899	623	188	776	201	197	198	4,070
	%R	8.6, 18.4	7.2, 17.0	5.9, 15.4	5.9, 12.8	6.8, 14.2	4.5, 13.9	7.1, 17.8	3.0, 11.1	6.9, 16.0
Klebsiella aerogenes	n	26	27	24	1	24	6	1	4	113
	%R	30.8, 42.3	29.6, 37.0	25.0, 29.2	n/a	29.2, 37.5	n/a	n/a	n/a	28.3, 37.2
Klebsiella oxytoca	n	48	54	34	9	39	20	2	10	216
	%R	4.2, 4.2	9.3, 9.3	8.8, 8.8	n/a	7.7, 7.7	5.0, 5.0	n/a	20.0, 20.0	8.8, 8.8
Klebsiella pneumoniae complex	n	250	209	185	26	189	30	37	38	964
	%R	6.4, 10.8	8.1, 12.4	4.3, 7.0	11.5, 11.5	2.6, 6.3	3.3, 3.3	5.4, 21.6	2.6, 7.9	5.5, 9.6
Proteus mirabilis	n	69	55	39	8	45	7	6	6	235
	%R	0.0, 1.4	0.0, 1.8	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.9
Pseudomonas aeruginosa	n	171	99	160	22	100	27	12	31	622
	%R	18.7,	20.2,	11.9,	9.1,	5.0,	18.5,	8.3,	16.1,	14.3,

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		58.5	56.6	51.9	59.1	43.0	51.9	33.3	51.6	52.9
Salmonella species (non-typhoidal)	n	21	7	18	2	18	5	11	3	85
	%R	4.8, 9.5	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.2, 2.4
Salmonella species (typhoidal)	n	11	11	6	0	1	3	0	1	33
	%R	0.0, 9.1	0.0, 9.1	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 18.2
Serratia marcescens	n	41	23	32	10	24	8	0	7	145
	%R	0.0, 0.0	4.3, 4.3	0.0, 0.0	0.0, 0.0	0.0, 4.2	n/a	n/a	n/a	1.4, 2.8
Tobramycin										
Acinetobacter baumannii complex	n	20	11	9	4	6	2	7	1	60
	%R	5.0, 5.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	1.7, 3.3
Enterobacter cloacae complex	n	164	88	82	23	57	19	6	10	449
	%R	6.1, 9.1	10.2, 19.3	8.5, 8.5	0.0, 0.0	0.0, 0.0	5.3, 5.3	n/a	0.0, 0.0	6.0, 9.1
Escherichia coli	n	1,492	899	623	479	776	201	197	198	4,865
	%R	2.5, 9.2	4.0, 11.5	1.4, 7.4	2.1, 8.1	3.5, 9.0	0.5, 4.5	4.6, 20.3	1.0, 8.6	2.7, 9.5
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%R	0.0, 0.0	0.0, 3.7	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 1.6
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%R	1.4, 1.4	0.0, 0.0	0.0, 0.0	4.3, 4.3	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.8, 0.8
Klebsiella pneumoniae complex	n	371	210	185	81	189	30	37	38	1,141
	%R	5.1, 8.1	4.3, 10.5	1.6, 2.2	2.5, 3.7	1.1, 2.1	0.0, 0.0	10.8, 24.3	2.6, 5.3	3.5, 6.5
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%R	1.0, 5.0	0.0, 3.6	0.0, 2.6	4.3, 8.7	0.0, 2.2	n/a	n/a	n/a	0.7, 4.3
Pseudomonas aeruginosa	n	261	100	161	72	101	27	12	32	766
	%R	1.5, 1.9	0.0, 0.0	0.0, 0.6	1.4, 1.4	0.0, 1.0	0.0, 0.0	0.0, 0.0	0.0, 3.1	0.7, 1.2
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%R	0.0, 32.4	6.1, 33.3	0.0, 28.1	5.9, 64.7	0.0, 37.5	n/a	n/a	n/a	2.1, 34.9
Trimethoprim										
Enterobacter cloacae complex	n	164	88	82	23	57	19	6	10	449
	%R	23.2, 23.2	28.4, 28.4	22.0, 22.0	21.7, 21.7	10.5, 12.3	5.3, 5.3	n/a	10.0, 10.0	21.2, 21.4
Escherichia coli	n	1,493	899	623	479	776	201	197	198	4,866
	%R	33.1, 33.3	30.0, 30.4	34.8, 35.3	29.9, 29.9	32.2, 32.6	21.4, 21.4	52.8, 53.3	28.3, 28.8	32.4, 32.7
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%R	3.1, 3.1	7.4, 7.4	4.2, 4.2	n/a	0.0, 0.0	n/a	n/a	n/a	3.3, 3.3
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%R	9.7, 9.7	1.9, 1.9	2.9, 2.9	8.7, 8.7	2.6, 2.6	5.0, 5.0	n/a	0.0, 0.0	5.5, 5.5
Klebsiella pneumoniae complex	n	371	210	185	81	189	30	37	38	1,141
	%R	17.5,	28.1,	13.5,	16.0,	6.9,	6.7,	40.5,	18.4,	17.4,

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		18.6	28.6	14.1	16.0	6.9	6.7	40.5	21.1	18.1
Proteus mirabilis	n	100	55	39	23	45	7	6	6	281
	%R	16.0, 16.0	29.1, 30.9	12.8, 12.8	13.0, 13.0	15.6, 15.6	n/a	n/a	n/a	18.9, 19.2
Salmonella species (non-typhoidal)	n	27	7	18	2	18	5	11	3	91
	%R	3.7, 3.7	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.1, 1.1
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%R	13.3, 13.3	9.1, 9.1	n/a	n/a	n/a	n/a	n/a	n/a	18.9, 18.9
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%R	1.4, 2.7	3.0, 3.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.0, 1.5
Trimethoprim–sulfamethoxazole										
Acinetobacter baumannii complex	n	20	11	9	4	6	2	7	1	60
	%R	10.0, 10.0	18.2, 18.2	n/a	n/a	n/a	n/a	n/a	n/a	13.3, 10.0
Enterobacter cloacae complex	n	164	88	83	23	57	18	6	10	449
	%R	22.6, 22.6	27.3, 27.3	20.5, 20.5	21.7, 21.7	8.8, 8.8	5.6, 5.6	n/a	10.0, 10.0	20.3, 20.3
Escherichia coli	n	1,488	899	624	479	774	201	197	198	4,860
	%R	31.1, 31.0	27.9, 27.4	33.0, 33.0	28.2, 27.8	29.5, 29.2	17.9, 17.9	50.3, 50.3	27.8, 27.8	30.3, 30.1
Klebsiella aerogenes	n	32	27	24	4	24	6	1	4	122
	%R	3.1, 3.1	0.0, 0.0	4.2, 4.2	n/a	0.0, 0.0	n/a	n/a	n/a	1.6, 1.6
Klebsiella oxytoca	n	72	54	34	23	39	20	2	10	254
	%R	9.7, 9.7	1.9, 1.9	2.9, 2.9	4.3, 4.3	2.6, 2.6	5.0, 5.0	n/a	0.0, 0.0	4.7, 4.7
Klebsiella pneumoniae complex	n	371	209	184	81	189	30	37	38	1,139
	%R	15.6, 15.4	25.4, 24.9	12.5, 12.0	14.8, 14.8	6.3, 6.3	6.7, 6.7	29.7, 29.7	18.4, 18.4	15.6, 15.4
Proteus mirabilis	n	100	54	39	23	45	7	6	6	280
	%R	15.0, 15.0	24.1, 24.1	12.8, 12.8	4.3, 4.3	8.9, 6.7	n/a	n/a	n/a	15.4, 15.0
Salmonella species (non-typhoidal)	n	27	7	18	2	18	5	11	3	91
	%R	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	15	11	6	0	1	3	0	1	37
	%R	13.3, 13.3	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	16.2, 16.2
Serratia marcescens	n	74	33	32	17	24	8	0	7	195
	%R	1.4, 0.0	3.0, 3.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.0, 0.5
Staphylococcus aureus	n	801	461	473	237	447	127	81	97	2,724
	%R	0.7, 0.7	0.2, 0.2	1.5, 1.5	0.4, 0.4	0.2, 0.2	0.0, 0.0	7.4, 7.4	0.0, 0.0	0.8, 0.8
Methicillin-resistant *S. aureus*	n	155	69	75	25	99	7	39	8	477
	%R	3.2, 3.2	1.4, 1.4	9.3, 9.3	0.0, 0.0	0.0, 0.0	n/a, n/a	12.8, 12.8	n/a, n/a	3.8, 3.8
Methicillin-susceptible *S. aureus*	n	646	392	398	212	348	120	42	89	2,247
	%R	0.2,	0.0,	0.0,	0.5,	0.3,	0.0,	2.4,	0.0,	0.2, 0.2

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.2	0.0	0.0	0.5	0.3	0.0	2.4	0.0	
Vancomycin										
Enterococcus faecalis	n	224	134	97	59	89	27	5	31	666
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.1, 1.1	0.0, 0.0	n/a	0.0, 0.0	0.2, 0.2
Enterococcus faecium	n	180	123	35	38	62	10	6	31	485
	%R	29.4, 29.4	62.6, 64.2	14.3, 14.3	7.9, 7.9	8.1, 8.1	n/a	n/a	19.4, 19.4	32.0, 32.6
Staphylococcus aureus	n	805	461	473	239	448	127	82	97	2,732
	%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 beta-lactamase producers

‡ The ciprofloxacin ECOFF (4 mg/L, *E. faecalis*) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only

§§ The ciprofloxacin concentration range available on Vitek and Phoenix cards restricts the ability to determine non-wild type (ECOFF 8 mg/L) *E. faecium*

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 nitrofurantoin ECOFF (32 mg/L, *E. faecalis*) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only

The doxycycline concentration range available on the Phoenix card used restricts the ability to accurately identify intermediate and resistant (CLSI) categories for enterococci

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

The most problematic pathogens are those with multiple acquired resistances. The definitions defined by Magiorakos et al.[34] were applied in this survey; where multi-drug resistance was defined as resistance to one or more agent in three or more antimicrobial categories. For each species, antimicrobials were excluded from the count if they were affected by natural resistance mechanisms, and/or neither CLSI nor EUCAST breakpoints were available. For this analysis, resistance included intermediate susceptibility, if applicable.

Tables D1–D10 show multiple acquired resistances for a number of 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. For amoxicillin–clavulanic acid, CLSI breakpoints were used, as 27/30 pathology laboratories used the Vitek® AST-N246 card which has the CLSI formulation for this agent.

Table D1: Multiple acquired resistance in *Acinetobacter baumannii* complex, by state and territory, 2020

State or territory		Number of categories (non multi-drug resistant)				Number of categories (multi-drug resistant)		
	Total	0	1	2	%	3	4	%
NSW	20	17	2	0	–*	0	1	–*
Vic	11	9	2	0	–*	0	0	–*
Qld	3	3	0	0	–*	0	0	–*
SA	4	4	0	0	–*	0	0	–*
WA	6	4	1	1	–*	0	0	–*
Tas	2	2	0	0	–*	0	0	–*
NT	7	7	0	0	–*	0	0	–*
ACT	1	1	0	0	–*	0	0	–*
Total	**54**	**47**	**5**	**1**	**98.1**	**0**	**1**	**1.9**

Multi-drug 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 or amikacin), carbapenems (meropenem), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim-sulfamethoxazole).
2. *Acinetobacter baumannii* complex includes *A. pittii* (*n* = 5), *A. nosocomialis* (*n* = 1), *A. calcoaceticus* (*n* = 1).

Table D2: Multiple acquired resistance in *Citrobacter koseri,* by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	17	16	0	1	–*	0	0	0	0	0	0	0	–*
Vic	5	5	0	0	–*	0	0	0	0	0	0	0	–*
Qld	10	8	0	2	–*	0	0	0	0	0	0	0	–*
SA	3	3	0	0	–*	0	0	0	0	0	0	0	–*
WA	16	13	3	0	–*	0	0	0	0	0	0	0	–*
Tas	6	5	0	1	–*	0	0	0	0	0	0	0	–*
NT	5	4	0	1	–*	0	0	0	0	0	0	0	–*
ACT	2	1	0	0	–*	0	1	0	0	0	0	0	–*
Total	**64**	**55**	**3**	**5**	**98.4**	**0**	**1**	**0**	**0**	**0**	**0**	**0**	**1.6**

Multi-drug 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 or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), non-extended cephalosporins (cefazolin), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins + β-lactamase inhibitor (amoxicillin–clavulanic acid, CLSI).

Table D3: Multiple acquired resistance in *Citrobacter freundii* complex, by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	27	22	1	2	–*	0	1	0	1	–*
Vic	11	8	2	1	–*	0	0	0	0	–*
Qld	12	6	3	2	–*	1	0	0	0	–*
SA	9	5	0	4	–*	0	0	0	0	–*
WA	12	7	3	2	–*	0	0	0	0	–*
Tas	8	6	1	1	–*	0	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	n/a
ACT	3	2	0	0	–*	0	1	0	0	–*
Total	**82**	**56**	**10**	**12**	**95.1**	**1**	**2**	**0**	**1**	**4.9**

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 (<30) to calculate

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

Table D4: Multiple acquired resistance in *Klebsiella aerogenes*, by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	32	20	0	11	96.9	1	0	0	0	3.1
Vic	27	14	3	9	–*	1	0	0	0	–*
Qld	24	16	1	7	–*	0	0	0	0	–*
SA	4	3	0	1	–*	0	0	0	0	–*
WA	24	14	1	9	–*	0	0	0	0	–*
Tas	6	4	0	2	–*	0	0	0	0	–*
NT	1	1	0	0	–*	0	0	0	0	–*
ACT	4	2	0	1	–*	0	1	0	0	–*
Total	**122**	**74**	**5**	**40**	**97.5**	**2**	**1**	**0**	**0**	**2.5**

Multi-drug 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 or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D5: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	51	24	24	1	96.1	0	1	1	0	0	0	0	3.9
Vic	54	21	28	2	94.4	1	2	0	0	0	0	0	5.6
Qld	34	20	10	0	88.2	1	2	1	0	0	0	0	11.8
SA	9	3	4	0	–*	0	0	1	0	1	0	0	–*
WA	39	12	21	2	89.7	1	3	0	0	0	0	0	10.3
Tas	20	10	8	1	–*	0	0	1	0	0	0	0	–*
NT	2	1	0	1	–*	0	0	0	0	0	0	0	–*
ACT	10	5	3	0	–*	1	1	0	0	0	0	0	–*
Total	**219**	**96**	**98**	**7**	**91.8**	**4**	**9**	**4**	**0**	**1**	**0**	**0**	**8.2**

Multi-drug 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 or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), non-extended cephalosporins (cefazolin), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins + β-lactamase inhibitor (amoxicillin–clavulanic acid, CLSI).

Table D6: Multiple acquired resistance in *Morganella morganii*, by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	31	16	12	0	90.3	3	0	0	0	0	9.7
Vic	13	5	8	0	–*	0	0	0	0	0	–*
Qld	8	3	5	0	–*	0	0	0	0	0	–*
SA	9	4	5	0	–*	0	0	0	0	0	–*
WA	14	8	5	1	–*	0	0	0	0	0	–*
Tas	2	0	2	0	–*	0	0	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	0	n/a
ACT	1	1	0	0	–*	0	0	0	0	0	–*
Total	**78**	**37**	**37**	**1**	**96.2**	**3**	**0**	**0**	**0**	**0**	**3.8**

Multi-drug 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 or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D7: Multiple acquired resistance in *Proteus mirabilis*, by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)								
	Total	0	1	2	%	3	4	5	6	7	8	9	10	%
NSW	85	61	5	7	85.9	5	4	1	2	0	0	0	0	14.1
Vic	54	32	7	9	88.9	2	2	0	2	0	0	0	0	11.1
Qld	39	31	4	1	92.3	2	1	0	0	0	0	0	0	7.7
SA	8	8	0	0	–*	0	0	0	0	0	0	0	0	–*
WA	44	35	0	7	95.5	1	1	0	0	0	0	0	0	4.5
Tas	7	5	1	1	–*	0	0	0	0	0	0	0	0	–*
NT	6	4	1	0	–*	0	1	0	0	0	0	0	0	–*
ACT	6	3	1	1	–*	0	0	1	0	0	0	0	0	–*
Total	**249**	**179**	**19**	**26**	**90.0**	**10**	**9**	**2**	**4**	**0**	**0**	**0**	**0**	**10.0**

Multi-drug 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 or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), non-extended cephalosporins (cefazolin), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), penicillins (ampicillin), and penicillins + β-lactamase inhibitor (amoxicillin–clavulanic acid, CLSI).

Table D9: Multiple acquired resistance in *Salmonella* species (non-typhoidal), by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	23	20	1	2	–*	0	0	0	0	0	0	0	–*
Vic	7	7	0	0	–*	0	0	0	0	0	0	0	–*
Qld	18	18	0	0	–*	0	0	0	0	0	0	0	–*
SA	2	2	0	0	–*	0	0	0	0	0	0	0	–*
WA	18	15	3	0	–*	0	0	0	0	0	0	0	–*
Tas	5	5	0	0	–*	0	0	0	0	0	0	0	–*
NT	11	11	0	0	–*	0	0	0	0	0	0	0	–*
ACT	3	3	0	0	–*	0	0	0	0	0	0	0	–*
Total	**87**	**81**	**4**	**2**	**100.0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0.0**

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

* Not applicable (insufficient numbers)

Note: Antimicrobial categories (agents) were antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), non-extended cephalosporins (cefazolin), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), penicillins (ampicillin), and penicillins + β-lactamase inhibitor (amoxicillin–clavulanic acid, CLSI).

Table D10: Multiple acquired resistance in *Salmonella* species (typhoidal), by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	9	4	3	0	–*	1	0	1	0	0	0	0	–*
Vic	10	2	7	0	–*	0	1	0	0	0	0	0	–*
Qld	6	1	4	0	–*	0	1	0	0	0	0	0	–*
SA	0	0	0	0	n/a	0	0	0	0	0	0	0	n/a
WA	1	0	0	1	–*	0	0	0	0	0	0	0	–*
Tas	3	0	1	0	–*	0	2	0	0	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	0	0	0	n/a
ACT	1	0	1	0	–*	0	0	0	0	0	0	0	–*
Total	**30**	**7**	**16**	**1**	**80.0**	**1**	**4**	**1**	**0**	**0**	**0**	**0**	**20.0**

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) were antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), non-extended cephalosporins (cefazolin), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), penicillins (ampicillin), and penicillins + β-lactamase inhibitor (amoxicillin–clavulanic acid, CLSI).

Table D10: Multiple acquired resistance in *Serratia marcescens*, by state and territory, 2020

State or territory	Number of categories (non multi-drug resistant)					Number of categories (multi-drug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	65	19	31	13	96.9	2	0	0	0	0	3.1
Vic	30	12	13	3	93.3	0	1	1	0	0	6.7
Qld	32	13	16	3	100.0	0	0	0	0	0	0.0
SA	17	4	10	3	–*	0	0	0	0	0	–*
WA	4	2	0	1	–*	0	1	0	0	0	–*
Tas	8	6	2	0	–*	0	0	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	0	n/a
ACT	7	1	4	1	–*	1	0	0	0	0	–*
Total	**163**	**57**	**76**	**24**	**96.3**	**3**	**2**	**1**	**0**	**0**	**3.7**

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) were aminoglycosides (gentamicin or tobramycin or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole).

References

1. Australian Government Department of Health, Department of Agriculture Water and the Environment. Australia's National Antimicrobial Resistance Strategy–2020 and Beyond. [Internet] Canberra: Australian Government; 2020 [cited 2021 Jun] Available from: https://www.amr.gov.au/resources/australias-national-antimicrobial-resistance-strategy-2020-and-beyond.
2. Australian Commission on Safety and Quality in Health Care. Preventing and Controlling Healthcare-Associated Infection Standard. [Internet] Sydney: ACSQHC; [cited August] Available from: https://www.safetyandquality.gov.au/standards/nsqhs-standards/preventing-and-controlling-healthcare-associated-infection-standard.
3. 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.
4. 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.
5. 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.
6. Australian Commission on Safety and Quality in Health Care. Recommendations for the control of carbapenemase-producing *Enterobacterales* (CPE) : a guide for acute care health facilities. Sydney: ACSQHC, 2021.
7. National Health and Medical Research Council. Australian Guidelines for the Prevention and Control of Infection in Healthcare (2019). Canberra: NHMRC; 2019.
8. Australian Commission on Safety and Quality in Health Care. Management of Peripheral Intravenous Catheters Clinical Care Standard. Sydney: ACSQHC, 2021 Contract No.: June.
9. Antibiotic Expert Groups. Therapeutic guidelines: antibiotic. Melbourne: Therapeutic Guidelines Limited; 2019.
10. Australian Commission on Safety and Quality in Health Care. Priority Antibacterial List for antimicrobial resistance containment: a stewardship resource for human health. Sydney: ACSQHC, 2020.
11. Deshpande LM, Fritsche TR, Moet GJ, Biedenbach DJ, Jones RN. Antimicrobial resistance and molecular epidemiology of vancomycin-resistant enterococci from North America and Europe: a report from the SENTRY antimicrobial surveillance program. Diagn Microbiol Infect Dis. 2007;58(2):163-170.
12. 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.
13. Murray BE. The life and times of the Enterococcus. Clin Microbiol Rev. 1990;3(1):46-65.
14. 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.
15. 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.
16. 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.
17. 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.

18. 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.
19. Laupland KB. Incidence of bloodstream infection: a review of population-based studies. Clin Microbiol Infect. 2013;19(6):492-500.
20. Johnson AP, Pearson A, Duckworth G. Surveillance and epidemiology of MRSA bacteraemia in the UK. J Antimicrob Chemother. 2005;56(3):455-462.
21. 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.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
28. Nimmo GR, Bell JM, Collignon PJ, Australian Group for Antimicrobial Resistance. Fifteen years of surveillance by the Australian Group for Antimicrobial Resistance (AGAR). Commun Dis Intell Q Rep. 2003;27 Suppl:S47-54.
29. 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.
30. CLSI. Performance standards for antimicrobial susceptibility testing. CLSI document M100. 31th ed. Wayne, PA: Clinical and Laboratory Standards Institute; 2021.
31. European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 11.0, valid from 2021-01-01. 2021.
32. 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.
33. Australian Commission on Safety and Quality in Health Care. AURA 2019: third Australian report on antimicrobial use and resistance in human health. Sydney: ACSQHC, 2019.
34. 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.
35. Centers for Disease Control and Prevention. Antibiotic resistance threats in the United States, 2019. Atlanta, GA: CDC, 2019.
36. 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.
37. 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.
38. Bell JM, Turnidge JD, Jones RN, Participants SA-P. 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.
39. Livermore DM. β-lactamases in laboratory and clinical resistance. Clin Microbiol Rev. 1995;8(4):557-584.

40. 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.
41. 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.
42. 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.
43. Pitout JD, DeVinney R. *Escherichia coli* ST131: a multidrug-resistant clone primed for global domination. F1000Res. 2017;6:195.
44. 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.
45. 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.
46. 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).
47. Hooper DC, Jacoby GA. Mechanisms of drug resistance: quinolone resistance. Ann N Y Acad Sci. 2015;1354:12-31.
48. 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.
49. 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.
50. 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.
51. 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.
52. 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.
53. Coombs GW, Daley DA, Lee YT, Pang S, Australian Group on Antimicrobial R. Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2016. Commun Dis Intell (2018). 2018;42.
54. Coombs G, Daley D, Nimmo G, Collignon P, Bell JM, Daveson K. *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.
55. European Centre for Disease Prevention and Control. Antimicrobial resistance in the EU/EEA (EARS-Net) - annual epidemiological report 2019. [Internet] Stockholm: ECDC; 2020 [updated 18 Nov 2020] Available from: https://www.ecdc.europa.eu/en/publications-data/surveillance-antimicrobial-resistance-europe-2019.
56. European Centre for Disease Prevention and Control. Additional tables - antimicrobial resistance in the EU/EEA 2019. [Internet] Stockholm: ECDC; 2020 [updated 18 Nov 2020] Available from: https://www.ecdc.europa.eu/sites/default/files/documents/Additional-tables-EUEEA-population-weighted-mean-2019.pdf.

57. Pearson J, Turnidge J, Franklin C, Bell J, and the 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.
58. European Centre for Disease Prevention and Control. Data from the ECDC Surveillance Atlas - Antimicrobial resistance. [Internet] Stockholm: ECDC; 2021 [updated 18 Nov 2021] Available from: https://www.ecdc.europa.eu/en/antimicrobial-resistance/surveillance-and-disease-data/data-ecdc.
59. Australian Commission on Safety and Quality in Health Care. Australian Passive Antimicrobial Resistance Surveillance. First report: multi-resistant organisms. Sydney: 2018.
60. Australian Group for Antimicrobial Resistance. The evolution of carbapenemases in major gram-negative bacteria in Australia. 2016.
61. Australian Institute of Health and Welfare. Australia's hospitals at a glance 2018–19. Cat. no. HSE 247. Canberra: AIHW, 2020.
62. Coombs G, Bell JM, Daley D, Collignon P, Cooley L, Gottlieb T, et al. Australian Group on Antimicrobial Resistance: Sepsis Outcome Programs: 2019 report. Sydney: Australian Commission on Safety and Quality in Health Care, 2021.
63. Australian Institute of Health and Welfare. Australian hospital peer groups. Health services series no. 66. Cat. no. HSE 170. Canberra: AIHW, 2015 16 Nov 2015. Report No.
64. 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.
65. 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.
66. 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.
67. Ellem J, Partridge SR, Iredell JR. Efficient direct extended-spectrum β-lactamase detection by multiplex real-time PCR: accurate assignment of phenotype by use of a limited set of genetic markers. J Clin Microbiol. 2011;49(8):3074-3077.
68. Seemann T. *Abricate*, Github. [Internet] 2020 Available from: https://github.com/tseemann/abricate.
69. National Center for Biotechnology Information. AMRFinder. [Internet]: NCBI; 2020 Available from: https://ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/AMRFinder/
70. 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.
71. 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.
72. 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.
73. 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.