AUSTRALIAN COMMISSION ON SAFETY AND QUALITY IN HEALTH CARE

AURA
Antimicrobial Use and Resistance in Australia

AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Sepsis Outcome Programs

2018 report

AGAR

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Overview

The Antimicrobial Use and Resistance in Australia (AURA) Surveillance System, is coordinated by the Australian Commission on Safety and Quality in Health Care (the Commission). AURA provides essential information to develop and implement strategies to prevent and contain antimicrobial resistance (AMR) in human health and improve antimicrobial use across hospital, aged care home and community healthcare settings. AURA also supports the National Safety and Quality Health Service (NSQHS) Standard Preventing and Controlling Healthcare-Associated Infection[1] and Australia's National Antimicrobial Resistance Strategy (2015–2019).[2] Funding for AURA is provided by the Australian Government Department of Health and state and territory health departments.

The Australian Group on Antimicrobial Resistance (AGAR), which is auspiced by the Australian Society for Antimicrobials (ASA), conducts targeted surveillance of selected pathogens; collects demographic, treatment and outcome data, and data on antimicrobial resistance rates; and analyses and reports on these data as part of AURA.

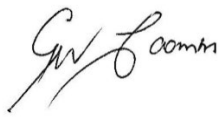
AGAR complements two AMR surveillance programs that also contribute to AURA: the National Alert System for Critical Antimicrobial Resistances (CARAlert) and Australian Passive AMR Surveillance (APAS).

AGAR is a longstanding collaboration of clinicians and scientists from major microbiology laboratories around Australia. AGAR tests and gathers information on the level of antimicrobial resistance in bacteria that cause important and life-threatening infections. The group commenced in 1985, when it involved 13 teaching hospitals. It has subsequently grown to involve 36 institutions across Australia, including four private laboratories (Table 1).

Antimicrobial-resistant bacteria and their resistance genes can spread readily between people. This occurs in the community, primary care services, hospitals and residential aged care facilities. It can happen rapidly, and can go unnoticed. The spread of these bacteria can significantly affect the community, patients, health services and the health system. Therefore, it is critical that resistant bacteria with the highest risk of causing harm to humans are identified and monitored through enhanced surveillance programs such as AGAR, and managed appropriately.

AMR is a risk to patient safety because it reduces the range of antimicrobials available to treat infections. It also increases morbidity and mortality associated with infections caused by multidrug-resistant organisms. AMR may limit future capacity to perform medical procedures such as organ transplantation, cancer chemotherapy, diabetes management and major surgery because of a lack of effective antimicrobials.

To protect the public from harm and improve the quality of health service provision, the Commission developed the National Safety and Quality Health Service (NSQHS) Standards in collaboration with the states and territories, clinical experts, patients and carers. The Preventing and Controlling Healthcare-Associated Infection Standard requires health service organisations to monitor patterns of AMR and antimicrobial use, and use this information to guide antimicrobial stewardship practices and meet infection control requirements. Data from AGAR directly support this Standard. The Commission will continue to support states and territories and the private health sector to act on the opportunities to refine infection prevention and control, antimicrobial stewardship and antibiotic treatment approaches, identified by analyses of the AGAR data, so that patients receive the best possible care.



AGAR Chairperson

Key findings and implications for health care; 2018

A. Key findings

Gram-negative species

- A total of 8,350 episodes of gram-negative bacteraemia were reported, including Enterobacterales (90.0%), *Pseudomonas aeruginosa* (8.9%) and *Acinetobacter* species (1.1%); three genera – *Escherichia* (61.0%), *Klebsiella* (20.4%) and *Enterobacter* (5.6%) – contributed 87.0% of all Enterobacterales bacteraemias
- The all-cause 30-day mortality for gram-negative bacteraemia was 11.4% (9.4% in *Escherichia coli*, 19.1% in *P. aeruginosa*)
- Urinary tract infection was the most frequent source of sepsis (41.4%)
- 85% of all *E. coli* bacteraemia cases were community onset. Over 12% of these isolates were ceftriaxone resistant
- There was a significant difference in 30-day all-cause mortality between community- and hospital onset (8.6% versus 13.4%) *E coli* bacteraemia episodes
- In 2018, extended-spectrum β-lactamase (ESBL) phenotypes were found in 14.5% of *E. coli* and 11.1% of *Klebsiella pneumoniae* and were more common in hospital onset episodes
- The CTX-M type gene was present in 86.3% of *E. coli* with an ESBL phenotype
- Increasing fluoroquinolone resistance in *E. coli* was most striking in hospital onset bacteraemia, increasing from 14.3% to 19.8% between 2013 and 2018; by comparison community onset bacteraemia resistance increased from 11.5% to 14.4% over the same period
- Fluoroquinolone resistance is commonly associated with CTX-M type ESBL genes; the O25b-ST131 clone accounted for 62.6% of *E. coli* ESBL phenotypes that were ciprofloxacin resistant
- Carbapenemase-producing Enterobacterales (CPE) bacteraemias were rare (0.1% in *E. coli* and 0.9% in *K. pneumoniae*), although the *Enterobacter cloacae* complex hospital onset CPE rates increased to 4.1% – mostly due to the presence of IMP-4 carbapenemases
- The rate of colistin resistance – when tested for and excluding species with intrinsic resistance – was 0.3% (3/1,006); two mobile colistin resistance genes were detected among all referred isolates.

Enterococcus species

- A total of 1,248 episodes of enterococcal bacteraemia were reported; the majority (93.5%) of enterococcal bacteraemia episodes were caused by *Enterococcus faecalis* or *E. faecium*
- The majority of *E. faecalis* bacteraemia were community onset (68.2%), while in *E. faecium* bacteraemia only 30.8% were community onset
- The most frequent source of sepsis or clinical manifestation for *E. faecalis* was urinary tract infection (25.1%); for *E. faecium*, febrile neutropenia was the most common association (21.1%)
- The combined 30-day all-cause mortality for *E. faecalis* and *E. faecium* was 20.0%; the 30-day all-cause mortality for *E. faecium* bacteraemia was higher, particularly in hospital onset vancomycin-susceptible (27.2%) and vancomycin-resistant (33.1%) isolates
- There was a significant difference in 30-day all-cause mortality between *E. faecalis* (14.7%) and *E. faecium* (27.2%)
- The length of stay following enterococcal bacteraemia was more than 30 days for 23.1% of patients
- Overall, 49.3% of *E. faecium* harboured *vanA* or *vanB* genes or both, with 52.7% of vancomycin-resistant *E. faecium* bacteraemias due to *vanA*. This type of vancomycin resistance has emerged rapidly in the past six years and is now the dominant genotype in the Australian Capital Territory, New South Wales, and Western Australia).

- Of bloodstream infections caused by *E. faecium*, 45.0% were phenotypically vancomycin resistant, and 49.3% of *E. faecium* harboured *vanA* and/or *vanB* genes (*vanA* 26.1%, *vanB* 22.8%, both 0.4%)
- There were 59 *E. faecium* multilocus sequence types (STs), of which ST17, ST1424, ST796, ST1421, ST80, and ST262 were the six most frequently identified
- *vanA* genes were detected in nine STs, and *vanB* genes were detected in 12 STs; two STs harboured *vanA* and *vanB* genes and the clonal diversity varies across Australia
- The percentage of *E. faecium* bacteraemia isolates resistant to vancomycin remains higher in Australia than all European countries except Cyprus.

Staphylococcus aureus

- A total of 2,673 *Staphylococcus aureus* bacteraemia episodes were reported, 78.9% of which were community onset. Almost one in five of all episodes were methicillin resistant (17.4%)
- The 30-day all-cause mortality was 14.2%. Mortality was higher for methicillin-resistant *S. aureus* (MRSA) (17.1%) than for methicillin-susceptible *S. aureus* (MSSA) (13.6%). Similarly, mortality was higher for hospital onset (16.1%) than for community onset (13.6%) bacteraemia
- Osteomyelitis/septic arthritis (20.5%) and skin and skin structure infections (20.0%) were the most common principal clinical manifestations
- The hospital length of stay was more than 30 days in 27.0% of patients (28.7% in MRSA, 26.6% in MSSA)
- In MRSA, resistance to erythromycin, clindamycin, and ciprofloxacin 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
- Four 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 arise in the community, which is consistent with the prevalence of this clone in aged care facilities in Australia
- Forty-five CA-MRSA clones were identified; the dominant CA-MRSA clone was ST93-IV (Queensland clone)
- Overall, 41.8% of CA-MRSA isolates harboured the PVL associated genes
- The Queensland clone of CA-MRSA (ST93-IV), which harbours the PVL associated genes, is now seen throughout Australia; it is now the most common CA-MRSA clone in Queensland, South Australia, Western Australia and the Northern Territory.
- The ST45-V MRSA clone remains prominent in New South Wales, and is associated with both community- and hospital onset 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 2018. AGAR has increased the number of laboratories from 25 in 2013 to 36 in 2018 and 2019. In addition, the relative distribution of sites has changed with the addition of three more paediatric and/or obstetric institutions from 2017, and one regional/remote site in 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.

Continued rises in gram-negative resistance

E. coli non-susceptibility to key antimicrobial agents has continued to rise. Ceftriaxone non-susceptibility in *E. coli* is now 13.5%, increasing from 11.3% in 2017. This represents a large increase in just one year to this commonly used agent. Rates of non-susceptibility to amoxicillin–clavulanic acid in *E. coli* (22.4%) are no longer substantially different from rates of non-

susceptibility to ciprofloxacin (19.2%). Aminoglycosides such as gentamicin have lower non-susceptibility rates (8.8%) as well as greater activity across a broader range of bacteraemia-associated pathogens such as *K. pneumoniae* and *E. cloacae* complex than ceftriaxone and piperacillin-tazobactam. These ongoing changes in resistance may mean increasing treatment failures and greater reliance on last-line antimicrobials such as carbapenems.

Prevalence of extended spectrum beta-lactamases (ESBLs)

ESBLs in gram-negative organisms have a considerable impact on resistance patterns and limit choices for therapy. Almost one in seven (14.5%) *E. coli* isolates displayed this phenotype in 2018. This phenotype is more common in hospital onset compared to community onset *E. coli* infection, with one in five (21.3%) demonstrating this pattern in hospital onset infection compared to 13.3% for community onset isolates. In hospital onset *K. pneumoniae* isolates this phenotype is more than double that of community onset isolates (19.2% versus 8.2%). The prevalence rates of ESBLs also vary by state and territory. These variations are small for *E. coli* but for *K. pneumoniae* proportions are noticeably higher in Victoria, Tasmania 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 Enterobacterales

Carbapenem resistance in organisms such as *K. pneumoniae* (1.0%) and *E. cloacae* complex (2.7%) is concerning, particularly as carbapenemase-producing *K. pneumoniae* remain uncommon (0.9%). Invasive CPE infections are particularly notable in New South Wales (19 isolates, 1.8%) compared to other states and territories. The Australian Capital Territory had the same number of CPE found in tested isolates as Victoria and Queensland (n = 2).

Guidelines about reducing acquisition and subsequent invasive infection due to carbapenem resistant organisms and CPE is available in the *Recommendations for the Control of Carbapenemase-Producing Enterobacterales*: *A guide for acute care health facilities.*[3]

Changing patterns in *Enterococcus* species

Total numbers of enterococcal bacteraemias identified by AGAR rose in 2018 even though the number of contributing institutions did not change from 2017. There was an increase in *E. faecalis* (676 versus 602 in 2017), and to a lesser extent *E. faecium* isolates (491 versus 481). The number of vancomycin-resistant *E. faecium* isolates remained fairly stable at 221 in 2018 compared to 226 in 2017 resulting in a slight reduction in overall vancomycin resistance rates in *E. faecium* from 47% to 45%. Overall, VRE fell as a proportion of all enterococcal isolates from 19.9% in 2017 to 17.7% in 2018, despite a 9.8% increase in all enterococcal bacteraemias. Queensland had a notable reduction in VRE in one year (33.3% to 12.7%) that likely contributed to reductions in enterococcal bacteraemias identified as harbouring *vanB*. The contribution of *vanA* genes to VRE continues to rise, particularly in New South Wales and the Australian Capital Territory, whilst *vanB* genes are in decline.

Antimicrobial substitutions, particularly reduced use of piperacillin-tazobactam as well as improved infection control practices have been proposed as a possible causative factors in reduced VRE in the hospital setting, although the reduction was modest at best.[4, 5] Optimising all VRE control mechanisms will be required to control Australia's resistance in *E. faecium*.

Reduced methicillin resistance in *Staphylococcus aureus*

Methicillin resistance in *S. aureus* has decreased by 1.6% overall. A five percent decrease in the rate of resistance occurred in hospital onset infections (24.5% to 19.5%) whilst community MRSA rates remained stable. The rate of methicillin resistance in the community onset infections was relatively stable at 16.9%. Reductions in hospital onset infections were attributed to both ongoing decreases in the healthcare-associated ST22-IV (37 to 30) and ST239-III (17 to 6), predominantly occurring in New South Wales, and to reductions in community-associated clones ST93-IV (17 to 11) and ST45-V (17 to 12) across Australia. Reductions in community-associated clones were also seen in community onset infections due to ST93-IV. ST93-IV decreased from 113 cases in 2017 to 99 cases in 2018, predominantly because of reductions in Queensland and the Northern Territory. There were notable increases in another community clone, with ST30-IV cases rising to 21 from 10 in 2017. Control of MRSA in the community will require greater focus if it is to mirror reductions in methicillin resistance seen in hospital-associated blood stream infections.

Epidemiology of clinical manifestations

Urinary tract infection remains the most common manifestation associated with blood stream infection in both gram-negative and enterococcal episodes. Febrile neutropenia has become the most common clinical manifestation associated with *E. faecium*, in contrast to 2017 where it was third to biliary and non-biliary intra-abdominal infections. The number of enterococcal bacteraemias associated with febrile neutropenia increased by 26% in one year. It is noteworthy that many Australian protocols for febrile neutropenia were changed in response to the piperacillin-tazobactam shortage in 2018 to include agents with less activity against enterococci such as cefepime.

Device related blood stream infections accounted for 9.9% (1,013/10,190) of bacteraemia across all the AGAR surveillance programs in 2018. The rate in 2017 was 8.7%, a relative increase of 14% in one year. The most notable increases were in those related to enterococcal bacteraemia without metastatic focus, with an increase of 60% in one year from 90 to 144 blood stream infections in 2018. Total numbers are dominated by gram-negative (n = 371) bacteria and *S. aureus* (n = 484) infections. Gram-negative infections commonly arise from urinary infections associated with the use of indwelling catheter, urinary stent or biliary stent infections. By contrast, *S. aureus* bacteraemia is commonly associated with intra-vascular catheters and/or devices and prosthetic joints. Continuing attention to Action 3.10 of the National Safety and Quality Health Service (NSQHS) Standards, on optimum medical device management[6] is required in all institutions.

Variation across states and territories

Non-susceptibility rates vary considerably across states and territories. The National Antimicrobial Usage Surveillance Program (NAUSP)[7] also demonstrates considerable variability in the usage of antimicrobials. Methicillin resistance in *S. aureus* ranges from 8.2% in Tasmania to 40.3% in the Northern Territory. *E. coli* resistance to third-generation cephalosporins ranges from 7.6% in Tasmania to 17.5% in the Northern Territory. Aminoglycoside resistance varies from 3.8% in Tasmania to 16.9% in the Northern Territory. Fluoroquinolone-resistance varies from 7.6% in Tasmania to 20.5% in Western Australia. *K. pneumoniae* third-generation cephalosporin resistance is lowest in Western Australia (4.8%) but accounts for almost one in five isolates in Victoria (19.8%) where aminoglycoside resistance is also highest (19.3%). Rates of vancomycin resistance in *E. faecium* ranges from 12.7% in Queensland to 83.3% in the Northern Territory. Teicoplanin resistance is more common in New South Wales (34.2%) and the Australian Capital Territory (26.9%) and the overall variations in teicoplanin resistance (5.5% to 34.2%) is generally consistent with the variations in v*anA*/*vanB* proportions by jurisdiction. Optimising local treatment guidelines is essential to minimise the overuse of broad-spectrum agents whilst balancing delivery of the right antimicrobial for severe infections.

Variations between hospital and community settings

Blood stream infections and associated resistance can vary between hospital and community settings. For example, organisms such as *E. cloacae* complex are evenly distributed between community and hospital onset infections, whilst others such as *E. coli* are more commonly community onset. *E. faecium* (69.2%) is more commonly hospital onset than *E. faecalis* (31.8%). Vancomycin resistance in *E. faecium* blood stream infections accounted for 6.7% (45/668) of all community onset enterococcal blood stream infections compared to 30.3% (176/580) in hospital onset disease. *E. coli* and *K. pneumoniae* resistance in the community can be half or less than what it is seen in hospital onset bacteraemias. These variations have implications for choice of empiric antimicrobial therapy and guidelines in community versus hospital onset settings and also need to take into account those with an onset in nursing homes (which are included in the community onset group in our data but not distinguished as such).

International comparisons

Rates of resistance to fluoroquinolone in *E. coli* and *K. pneumoniae* (represented by resistance to ciprofloxacin) remain very low in Australia, compared with most European countries. Australia now ranks towards the middle in rates of resistance to third-generation cephalosporins in *E. coli*, and is now above that of the European Union and European Economic Area average. Third-generation resistance in *K. pneumoniae* is low by comparison.

Australia ranks in the top half in rates of resistance to methicillin in *S. aureus*, and higher than all European countries except Cyprus in rates of resistance to vancomycin in *E. faecium*.

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[8] and other expert guideline development groups to ensure that data such as the rates of gram-negative resistance is taken into consideration
- Work with states and territories and the private laboratory sector to encourage the use of local antibiograms by stewardship services. These are tables of antimicrobial susceptibilities that are used to inform local empirical and therapeutic antimicrobial recommendations and formulary management. This work will capture geographic variation
- Promote prescribing practices that are tailored to local resistance patterns and regular review of prescribing guidance by local antimicrobial stewardship 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
- 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 antimicrobial resistance
- Maintain and enhance the AURA Surveillance System and ensure that antimicrobial resistance 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*: *A guide for acute care health facilities*[3], to limit the transmission of carbapenemase-producing Enterobacterales

- Support development of guidance for surveillance, prevention and control of specific organisms and resistances
- Promote effective implementation of systems that address the requirements of the NSQHS Standards relevant to the control of hospital onset blood stream infections, particularly Action 3.10 – invasive medical devices.

1. Background and objectives

This third 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 that were reported by 36 participating Australian public and private laboratories across Australia in 2018.

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 aligns 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 36 institutions across Australia that currently contribute to AGAR, including four private laboratories, are listed in Table 1.

Historically, the main focus of AGAR was antimicrobial resistance in *Staphylococcus aureus*. The scope has broadened over time to include studies on *Escherichia coli*, *Enterobacter* species, *Klebsiella* species, *Haemophilus influenzae, Streptococcus pneumoniae* and *Enterococcus* species.

AGAR publishes detailed annual reports on each program on its website (www.agargroup.org).

Table 1: Hospitals that contributed to AGAR, by state and territory, 2018

State or territory	Hospital
New South Wales	Concord Repatriation General Hospital
	John Hunter Hospital
	Nepean Hospital
	Royal North Shore Hospital
	Royal Prince Alfred Hospital
	St Vincent's Hospital, Sydney
	Westmead Hospital
	Wollongong Hospital
Victoria	Alfred Hospital
	Austin Hospital (Austin Health)
	Monash Children's Hospital
	Monash Medical Centre (Monash Health)
	Royal Children's Hospital
	St Vincent's Hospital
Queensland	Cairns Base Hospital
	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
	Kimberley regional hospitals (Broome, Kununurra, Derby)
	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 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, 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 resistances. *Enterobacter* species are less common in the community, but of high importance because of their intrinsic resistance to first-line antimicrobials. Taken together, the three groups of species surveyed are considered to be valuable sentinels for multidrug resistance and emerging resistance in enteric gram-negative bacilli. In 2013, AGAR began the Enterobacteriaceae (now 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 changed its name to the Gram-negative Sepsis Outcome Program (GNSOP).

Resistances of particular interest include resistance to β-lactams due to β-lactamases, especially 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 2018 surveillance program were to:

- Monitor resistance in Enterobacterales, *P. aeruginosa* and *Acinetobacter* species isolated from blood cultures taken from patients presenting to the hospital or already in hospital
- Study the extent of co-resistance and multidrug resistance in the major species
- Detect emerging resistance to newer last-line agents such as carbapenems and colistin
- Examine the molecular basis of resistance to third-generation cephalosporins, quinolones and carbapenems
- Monitor the epidemiology of *E. coli* sequence type (ST) 131.

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.[9, 10] In the 1970s healthcare-associated enterococcal infections were primarily due to *Enterococcus faecalis*. Subsequently there has been a steadily increasing prevalence of *E. faecium* nosocomial infections.[11-13] 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 antibiotics, *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, Pseudomonas aeruginosa,* and *Enterobacter* species) pathogens requiring new therapies.[14]

AGAR began surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[15] In 2011, AGAR commenced the Australian Enterococcal Sepsis Outcome Program (AESOP).[16]

In order to provide data to support improved antimicrobial prescribing and patient care, the objective of AESOP 2018 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
- 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.[17] 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.[18]

Despite standardised treatment protocols for SAB, including prolonged antimicrobial therapy and prompt source control[19], mortality ranged from as low as 2.5% to as high as 40%.[20-22] Mortality rates are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[23, 24] 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.[25]

AGAR began surveillance of antimicrobial resistance in *S. aureus* in 1986.[26] In 2013, AGAR commenced the Australian Staphylococcal Sepsis Outcome Program (ASSOP).[27]

The primary objective of ASSOP 2018 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

Thirty-six institutions, in each state and territory of Australia, were enrolled in the 2018 AGAR programs. The AGAR laboratories collected either all isolates or up to 200 isolates of Enterobacterales, *Acinetobacter* species and *P. aeruginosa* from unique patient episodes of bacteraemia from 1 January 2018 to 31 December 2018. 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, the outcome at seven and 30 days (including whether the patient died within 30 days), and if applicable, the date of death (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 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. calcoaceticus*, *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*; 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–A29[28] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v9.0.[29]

2.4. Molecular testing

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 isolates with ciprofloxacin MIC >0.25 mg/L; all isolates with meropenem MIC >0.25 mg/L; and all isolates with amikacin MIC >32 mg/L, were referred to a central laboratory molecular confirmation of resistance.

All referred isolates were screened using real-time polymerase chain reaction (PCR) (Roche LightCycler® 480 platform) and published primers for the presence of bla_{TEM} and bla_{SHV}, CTX-M-type genes (groups 1, 2, 9, 8/25), plasmid-borne AmpC (bla_{CIT}, bla_{DHA}, bla_{EBC}, bla_{ACC}, bla_{FOX}, bla_{MOX}), and carbapenemase genes (bla_{IMP}, bla_{NDM}, bla_{KPC}, $bla_{OXA-48-like}$, bla_{VIM}, bla_{GES}, bla_{SME}, bla_{IMI}).[30-32]

PCRs were also used to detect bla_{IMP} types, known plasmid-mediated quinolone resistance mechanisms (*qnr*, efflux [*qepA*, *oqxAB*] and *aac* (*6')-Ib-cr*), aminoglycoside ribosomal methyltransferases (armA, rmtB, rmtC, rmtF), and mobile colistin resistance genes (mcr-1, mcr-2, mcr-3)[33-38]. All referred *E. coli* were examined for membership of the O25b-ST131 clone.[39] All isolates with demonstrated carbapenemase activity and any amikacin resistant isolates were also screened for OXA-23-like, -24, and -58 carbapenemases.[40]

All gram-negative isolates with carbapenemase activity, *E. faecium* and MRSA were subjected to whole genome sequencing using the Illumina MiSeq platform. Data were analysed using the Nullarbor bioinformatic pipeline.[41] The pipeline was used to identify the multi-locus sequence type and the resistome.

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

3. Results

3.1. Isolates recovered

A total of 8,350 gram-negative isolates (49 species, 19 genera) were reported from 36 participating hospitals. Enterobacterales accounted for 90.0%, followed by *P. aeruginosa* (8.9%) and *Acinetobacter* species (1.1%). Of the Enterobacterales, three genera – *Escherichia* (61.0%), *Klebsiella* (20.4%) and *Enterobacter* (5.6%) – contributed 87.0% of all isolates. The top 10 species by rank were *E. coli* (54.8%), *K. pneumoniae* (13.3%), *P. aeruginosa* (8.9%), *E. cloacae* complex (5.0%), *Proteus mirabilis* (3.1%), *K. oxytoca* (2.8%), *Serratia marcescens* (2.4%), *K. aerogenes* (1.5%), *Salmonella* species (non-typhoidal) (1.3%), and *Citrobacter freundii* (1.1%). These 10 species comprised 94.1% of all isolates (Table 2).

There were 1,248 episodes of enterococcal bacteraemia. *E. faecalis* and *E. faecium* accounted for 93.5% of all enterococcal isolates (Table 2).

Of 2,673 SAB episodes, 466 (17.4%; 95% confidence interval [CI] 16.0-18.9) were methicillin resistant, ranging from 8.2% (95%CI 4.4-14.8) in Tasmania to 40.3% (95%CI: 30.0-51.4) in the Northern Territory (Table 2).

Table 2: Number of each species recovered, by state and territory, 2018

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Gram-negative species*	2,268	1,392	1,714	719	1,371	331	274	281	8,350
Escherichia coli	1,226	770	869	409	801	185	160	157	4,577
Klebsiella pneumoniae	287	207	269	79	166	31	37	31	1,107
Pseudomonas aeruginosa	228	78	179	72	104	30	20	32	743
Enterobacter cloacae complex	116	66	117	30	54	16	12	9	420
Proteus mirabilis	74	44	43	28	49	7	8	8	261
Klebsiella oxytoca	66	52	29	20	34	16	2	11	230
Serratia marcescens	65	35	42	14	27	8	3	5	199
Klebsiella aerogenes	38	27	18	11	20	4	3	4	125
Salmonella species (non-typhoidal)	26	16	29	4	15	4	12	1	107
Citrobacter freundii complex	31	15	19	4	12	3	1	6	91
Morganella morganii	25	16	16	10	8	5	1	0	81
Klebsiella variicola	16	7	1	13	20	3	0	5	65
Acinetobacter baumannii complex	10	4	23	1	8	5	11	1	63
Citrobacter koseri	19	12	11	4	15	2	0	0	63
Salmonella species (typhoidal)	7	14	8	1	10	1	1	4	46
Raoultella ornithinolytica	2	3	4	0	9	1	0	3	22
Providencia rettgeri	5	0	6	4	1	0	0	1	17
Acinetobacter species	3	0	2	4	4	0	0	0	13
Raoultella planticola	1	5	3	0	0	2	0	0	11
Hafnia alvei	6	1	1	0	1	1	0	0	10
Pantoea species	1	0	3	2	1	2	1	0	10
Proteus vulgaris	1	3	3	0	2	1	0	0	10
Other species (*n* = 27)	15	17	19	9	10	4	2	3	79
Enterococcus species	381	265	201	103	158	59	25	56	1,248
Enterococcus faecalis	211	118	131	57	91	31	11	26	676
vancomycin susceptible, percent	100	100	100	100	100	100	100	100	100
vancomycin resistant, percent	0.0	0.0	0.0	0.0	0.0	0.0	.0.	0.0	0.0

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Enterococcus faecium	152	130	55	38	54	24	12	26	491
vancomycin resistant, percent	50.7	61.5	12.7	34.2	18.5	54.2	83.3	42.3	45.0
vancomycin susceptible, percent	49.3	38.5	87.3	65.8	81.5	45.8	16.7	57.7	55.0
Other enterococcal species	18	17	15	8	13	4	2	4	81
Enterococcus gallinarum	5	7	7	4	5	0	0	1	29
Enterococcus casseliflavus	5	5	3	1	4	1	1	1	21
Enterococcus avium	3	3	2	3	4	0	1	2	18
Enterococcus hirae	3	1	2	0	0	0	0	0	6
Enterococcus raffinosus	0	1	1	0	0	1	0	0	3
Enterococcus durans	1	0	0	0	0	2	0	0	3
Enterococcus species	1	0	0	0	0	0	0	0	1
Staphylococcus aureus	647	414	571	256	487	110	77	111	2,673
methicillin resistant, percent	20.4	14.3	14.0	15.6	21.4	8.2	40.3	9.9	17.4
methicillin susceptible, percent	79.6	85.7	86.0	84.4	78.6	91.8	59.7	90.1	82.6

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

† Insufficient numbers (<10) to calculate percentage

3.2. Place of onset of bacteraemia

Almost all patients with bacteraemia were admitted to hospital (gram-negative species, 98.1%; *Enterococcus* species, 99.1%; *S. aureus*, 97.7%).

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

For gram-negative species, 76.9% of all episodes were community onset, although differences were observed with different species. Episodes involving *E. faecalis* and 'other' *Enterococcus* species were predominantly community onset (68.2%, 95%CI: 64.6-71.6 for *E. faecalis*). However, *E. faecium* episodes were predominantly hospital onset (69.2%; 95%CI: 65.0-73.2). Most SABs were community onset (78.9%; 95%CI 77.3-80.4).

Table 3: Species recovered, by place of onset, 2018

Organism	Community onset % (*n*)	Hospital onset % (*n*)	Total, 100%
Enterococcus species	53.5 (668)	46.5 (580)	1,248
Enterococcus faecalis	68.2 (461)	31.8 (215)	676
Vancomycin resistant	0 (0.0)	0 (0.0)	0
Vancomycin susceptible	68.1 (460)	31.9 (215)	675
Enterococcus faecium	30.8 (151)	69.2 (340)	491
Vancomycin resistant	20.4 (45)	79.6 (176)	221
Vancomycin susceptible	39.3 (106)	60.7 (164)	270
Other *Enterococcus* species (*n* = 7)	69.1 (56)	30.9 (25)	81
Gram-negative species*	76.9 (6,417)	23.1 (1,933)	8,350
Escherichia coli	84.7 (3,876)	15.3 (701)	4,577
Klebsiella pneumoniae	73.1 (809)	26.9 (298)	1,107
Pseudomonas aeruginosa	59.1 (439)	40.9 (304)	743
Enterobacter cloacae complex	52.6 (221)	47.4 (199)	420
Proteus mirabilis	85.1 (222)	14.9 (39)	261
Klebsiella oxytoca	71.3 (164)	28.7 (66)	230

Organism	Community onset % (*n*)	Hospital onset % (*n*)	Total, 100%
Serratia marcescens	51.3 (102)	48.7 (97)	199
Klebsiella aerogenes	55.2 (69)	44.8 (56)	125
Salmonella species (non-typhoidal)	91.6 (98)	8.4 (9)	107
Citrobacter freundii complex	64.8 (59)	35.2 (32)	91
Morganella morganii	71.6 (58)	28.4 (23)	81
Klebsiella variicola	64.6 (42)	35.4 (23)	65
Acinetobacter baumannii complex	52.4 (33)	47.6 (30)	63
Citrobacter koseri	77.8 (49)	22.2 (14)	63
Salmonella species (typhoidal)	100.0 (46)	0.0 (0)	46
Raoultella ornithinolytica	86.4 (19)	13.6 (3)	22
Providencia rettgeri	100.0 (17)	0.0 (0)	17
Acinetobacter species	76.9 (10)	23.1 (3)	13
Raoultella planticola	72.7 (8)	27.3 (3)	11
Hafnia alvei	100.0 (10)	0.0 (0)	10
Pantoea species	80.0 (8)	20.0 (2)	10
Proteus vulgaris	90.0 (9)	10.0 (1)	10
Other gram-negative species (*n* = 27)	62.0 (49)	38.0 (30)	79
Staphylococcus aureus	78.9 (2,108)	21.1 (565)	2,673
Methicillin resistant	76.4 (356)	23.6 (110)	466
Methicillin susceptible	79.4 (1,752)	20.6 (455)	2,207

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

Note: Vancomycin MIC not available for one *Enterococcus faecalis*

3.3. Onset versus 30-day all-cause mortality

Information on 30-day all-cause mortality was available for 5,640 (67.5%) episodes involving gram-negative species; 1,034 (82.8%) involving *Enterococcus* species and 2,122 (79.4%) involving *S. aureus*. 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* ($P < 0.01$), *K. pneumoniae* ($P = 0.0412$), and *E. faecium* ($P = 0.0275$) (Table 4).

There was a significant difference in the 30-day all-cause mortality between *E. faecium* (27.2%) and *E. faecalis* (14.7%) episodes ($P < 0.0001$). However, there was no significant difference in 30-day all-cause mortality between vancomycin-resistant and vancomycin-susceptible *E. faecium* episodes.

For *S. aureus*, there was no significant difference in 30-day all-cause mortality between methicillin-susceptible *S. aureus* (MSSA) (13.6%) and MRSA (17.1%) episodes, or between healthcare-associated MRSA (HA-MRSA) (19.3%) and community-associated MRSA (CA-MRSA) (16.4%) clones.

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), 2018

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Enterococcus species	535	15.5 (83)	499	24.2 (121)	1,034	19.7 (204)
Enterococcus faecalis	371	14.8 (55)	185	14.6 (27)	556	14.7 (82)
Enterococcus faecium	119	19.3 (23)	293	30.4 (89)	412	27.2 (112)
Vancomycin resistant	39	17.9 (7)	157	33.1 (52)	196	30.1 (59)
Vancomycin susceptible	80	20.0 (16)	136	27.2 (37)	216	24.5 (53)
Other enterococcal species (*n* = 6)	45	11.1 (5)	21	23.8 (5)	66	15.2 (10)
Gram-negative species*	4,177	10.3 (430)	1,463	14.6 (214)	5,640	11.4 (644)
Escherichia coli	2,425	8.6 (208)	523	13.4 (70)	2,948	9.4 (278)
Klebsiella pneumoniae	551	10.5 (58)	232	15.9 (37)	783	12.1 (95)
Pseudomonas aeruginosa	305	20.0 (61)	228	18.0 (41)	533	19.1 (102)
Enterobacter cloacae complex	163	11.7 (19)	152	11.8 (18)	315	11.7 (37)
Proteus mirabilis	149	12.8 (19)	33	15.2 (5)	182	13.2 (24)
Klebsiella oxytoca	119	16.0 (19)	52	9.6 (5)	171	14.0 (24)
Serratia marcescens	71	14.1 (10)	68	22.1 (15)	139	18.0 (25)
Klebsiella aerogenes	47	10.6 (5)	41	9.8 (4)	88	10.2 (9)
Citrobacter freundii complex	47	6.4 (3)	22	13.6 (3)	69	8.7 (6)
Salmonella species (non-typhoidal)	53	1.9 (1)	8	–† (0)	61	3.3 (2)
Morganella morganii	37	13.5 (5)	18	33.3 (6)	55	20.0 (11)
Acinetobacter baumannii complex	27	3.7 (1)	25	12.0 (3)	52	7.7 (4)
Klebsiella variicola	31	9.7 (3)	17	11.8 (2)	48	10.4 (5)
Citrobacter koseri	28	7.1 (2)	13	15.4 (2)	41	9.8 (4)
Salmonella species (typhoidal)	27	0.0 (0)	0	–† (0)	27	0.0 (0)
Raoultella ornithinolytica	14	7.1 (1)	2	–† (0))	16	6.3 (1)
Providencia rettgeri	11	36.4 (4)	0	–† (0)	11	36.4 (4)
Proteus vulgaris	9	–† (0)	1	–† (0))	10	30.0 (3)
Raoultella planticola	7	–† (0)	3	–† (0)	10	10.0 (1)
Other gram-negative species (*n* = 27)	56	12.5 (7)	25	8.0 (2)	81	11.1 (9)

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Staphylococcus aureus	1,646	13.6 (224)	477	16.1 (77)	2,123	14.2 (301)
Methicillin resistant	262	16.8 (44)	94	18.1 (17)	356	17.1 (61)
CA-MRSA	207	16.9 (35)	55	14.5 (8)	262	16.4 (43)
HA-MRSA	50	18.0 (9)	34	20.6 (7)	84	19.0 (16)
Methicillin susceptible	1,384	13.0 (180)	383	15.7 (60)	1,767	13.6 (240)

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

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

† Insufficient numbers (<10) to calculate percentage

Note: Five Methicillin-resistant *Staphylococcus aureus* not available for whole genome sequencing

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 54.6%. For *Enterococcus* species and SAB, 64.0% and 64.1%, respectively, were male.

Increasing age was a surrogate risk factor for bacteraemia (Figures 1-3); only 14.7% of gram-negative species episodes, 11.4% of *Enterococcus* species episodes and 21.7% of *S. aureus* episodes were in patients aged less than 40 years.

Figure 1: Number of episodes of bacteraemia due to gram-negative species, by patient decade of life and sex, 2018

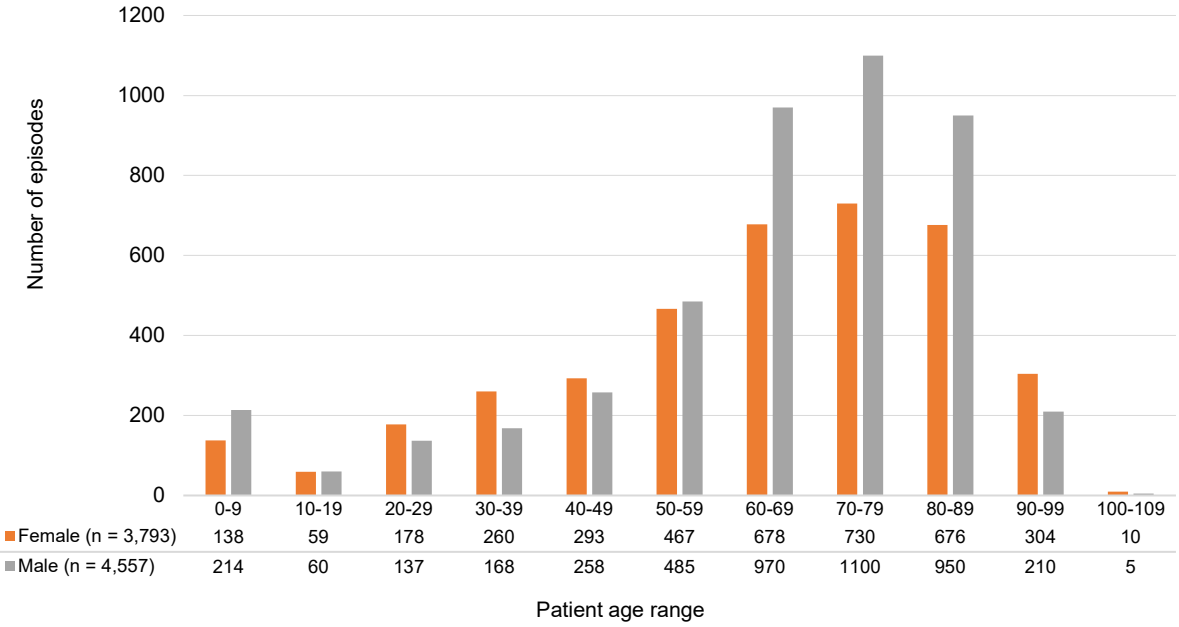


Figure 2: Number of episodes of bacteraemia due to *Enterococcus* species, by patient decade of life and sex, 2018

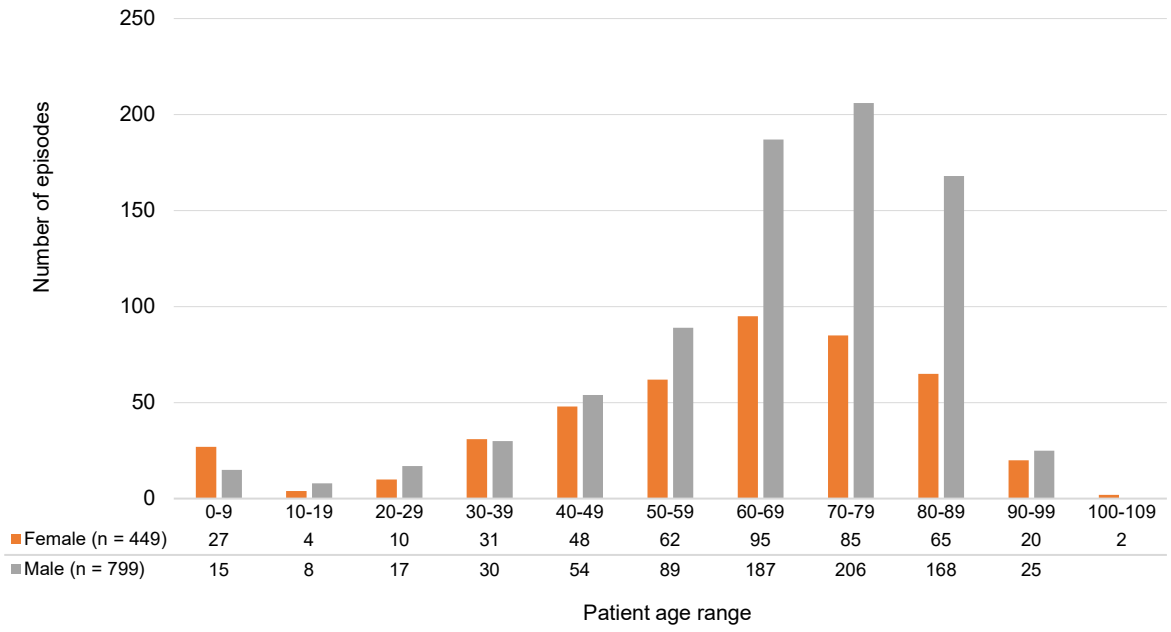
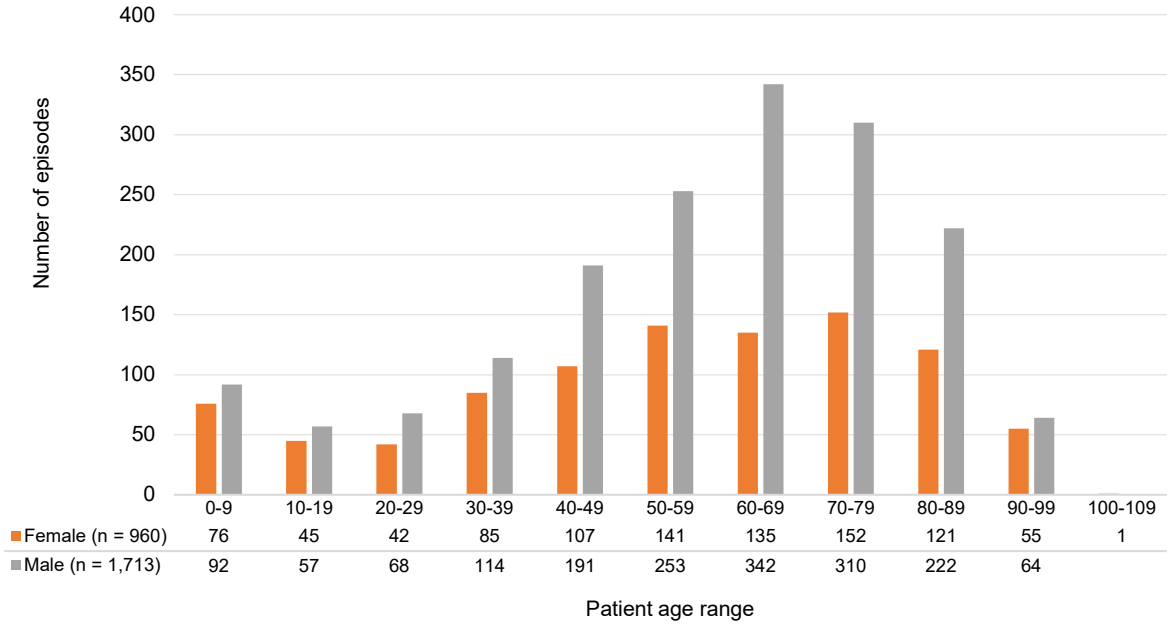


Figure 3: Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient decade of life and sex, 2018



3.5. Principal clinical manifestation

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

Gram-negative bacteria

The principal clinical manifestation was documented for 6,623 (79.3%) patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations were urinary tract infection (41.4%), biliary tract infection (15.4%) and other intra-abdominal infection (10.1%) (Table 5).

Urinary tract infection was the most frequent principal clinical manifestation for both community onset (49.3%) and hospital onset (22.7%) episodes caused by Enterobacterales. For *P. aeruginosa*, urinary tract infection was most common for community onset (28.5%) and febrile neutropenia was the most common association for hospital onset (23.2%) episodes.

Table 5: Principal clinical manifestation for gram-negative* bacteraemia, by patient sex, 2018

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance†
Urinary tract infection	50.3 (1,494)	34.2 (1,250)	41.4 (2,744)	$P < 0.01$
Biliary tract infection (including cholangitis)	12.5 (372)	17.8 (651)	15.4 (1,023)	$P < 0.01$
Intra-abdominal infection other than biliary tract	8.4 (250)	11.5 (420)	10.1 (670)	$P < 0.01$
Febrile neutropenia (where specified)	7.3 (218)	10.3 (378)	9.0 (596)	$P < 0.01$
Other clinical syndrome	6.9 (204)	8.1 (297)	7.6 (501)	ns
No focus (setting not known)	6.6 (197)	7.7 (282)	7.2 (479)	ns
Device-related infection without metastatic focus	4.7 (139)	5.7 (210)	5.3 (349)	ns
Skin and skin structure	2.5 (74)	3.1 (115)	2.9 (189)	ns
Osteomyelitis/septic arthritis	0.4 (12)	1.0 (38)	0.8 (50)	$0.01 < P < 0.05$
Device-related infection with metastatic focus	0.3 (10)	0.3 (12)	0.3 (22)	ns
Total	2,970	3,653	6,623	

ns = not significant; – = insufficient numbers
* Enterobacterales, *Acinetobacter* species and *Pseudomonas aeruginosa*
† Fisher's exact test for difference in principal clinical manifestation and sex

Enterococcus species

The principal clinical manifestation was known for 1,196 (95.8%) patient episodes of enterococcal bacteraemia. Overall, the most frequent principal clinical manifestations were urinary tract and biliary tract infections (both 16.0%) and no focus (setting not known) (14.0%) (Table 6). There were some significant gender differences in terms of principle clinical manifestation.

Of the hospital onset episodes where data were available, the most frequent principal clinical manifestation was febrile neutropenia (18.8%). Of the community onset episodes where data were available, the most frequent principal clinical manifestations were biliary tract infection (including cholangitis) (22.3%) and urinary tract infection (22.2%).

The principal manifestation was known for 1,117 of the 1,167 (95.7%) *E. faecalis* and *E. faecium* episodes (Table 7). The most common clinical manifestation for *E. faecalis* was urinary tract infection, whereas for *E. faecium* it was febrile neutropenia (when specified). 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, 2018

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance*
Urinary tract infection	11.2 (48)	18.8 (145)	16.1 (193)	$P < 0.01$
Biliary tract infection (including cholangitis)	17.1 (73)	15.5 (119)	16.0 (192)	ns
No focus (setting not known)	17.8 (76)	11.9 (92)	14.0 (168)	$P < 0.01$
Device-related infection without metastatic focus	14.5 (62)	10.6 (82)	12.0 (144)	ns
Intra-abdominal infection other than biliary tract	10.8 (46)	11.7 (90)	11.4 (136)	ns
Febrile neutropenia (when specified)	12.0 (51)	9.1 (70)	10.1 (121)	ns
Endocarditis, left-sided	4.4 (19)	8.8 (68)	7.3 (87)	$P < 0.01$
Skin and skin structure infections	5.6 (24)	4.4 (34)	4.8 (58)	ns
Other clinical syndrome	3.3 (14)	4.9 (38)	4.3 (52)	ns
Osteomyelitis/septic arthritis	0.9 (4)	2.1 (16)	1.7 (20)	ns
Device-related infection with metastatic focus	1.6 (7)	0.9 (7)	1.2 (14)	ns
Endocarditis, right-sided	0.5 (2)	1.2 (9)	0.9 (11)	ns
Total	426	770	1,196	

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

Table 7: Principal clinical manifestation for *Enterococcus faecalis* and *E. faecium* bacteraemia, 2018

Principal clinical manifestation	*E. faecalis* % (*n*)	*E. faecium* % (*n*)	Total % (*n*)	Significance*
Urinary tract infection	25.1 (163)	5.8 (27)	17.0 (190)	$P < 0.01$
No focus (setting not known)	14.3 (93)	14.9 (70)	14.6 (163)	ns
Biliary tract infection (including cholangitis)	10.6 (69)	17.9 (84)	13.7 (153)	$P < 0.01$
Device-related infection without metastatic focus	11.1 (72)	15.1 (71)	12.8 (143)	ns
Intra-abdominal infection other than biliary tract	7.9 (51)	14.5 (68)	10.6 (119)	$P < 0.01$
Febrile neutropenia (when specified)	2.5 (16)	21.1 (99)	10.3 (115)	$P < 0.01$
Endocarditis, left-sided	12.5 (81)	1.1 (5)	7.7 (86)	$P < 0.01$
Skin and skin structure infections	4.8 (31)	4.9 (23)	4.8 (54)	ns
Other clinical syndrome	5.4 (35)	3.2 (15)	4.5 (50)	ns
Osteomyelitis/septic arthritis	2.6 (17)	0.4 (2)	1.7 (19)	$P < 0.01$
Device-related infection with metastatic focus	1.5 (10)	0.9 (4)	1.3 (14)	ns
Endocarditis, right-sided	1.5 (10)	0.2 (1)	1.0 (11)	$0.01 < P < 0.05$
Total	648	469	1,117	

ns = not significant; – = insufficient numbers
* 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 2,371 (88.7%) episodes of SAB (Table 8). Overall, the most frequent principal clinical manifestation was osteomyelitis/septic arthritis (20.5%), followed by skin and skin structure infection (20.0%) and device-related infection without metastatic focus (18.4%).

Of the hospital onset SABs where data were available, the most common principal clinical manifestation was device-related infection without metastatic focus (34.2%). Of the community onset SABs where data were available, the most common principal clinical manifestation was osteomyelitis/septic arthritis (23.6%).

Table 8: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient sex, 2018

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	18.7 (160)	21.6 (327)	20.5 (487)
Skin and skin structure infections	19.6 (168)	20.3 (307)	20.0 (475)
Device-related infection without metastatic focus	21.1 (181)	16.8 (254)	18.4 (435)
No focus (setting not known)	11.8 (101)	12.0 (182)	11.9 (283)
Other clinical syndrome	5.6 (48)	8.0 (121)	7.1 (169)
Endocarditis, left-sided	5.3 (45)	6.1 (92)	5.8 (137)
Pneumonia/empyema	5.3 (45)	4.2 (64)	4.6 (109)
Deep abscess(es) excluding those in the CNS	3.3 (28)	3.0 (45)	3.1 (73)
Endocarditis, right-sided	3.3 (28)	2.2 (33)	2.6 (61)
CNS infection (meningitis, abscess(es)	2.2 (19)	2.6 (40)	2.5 (59)
Device-related infection with metastatic focus	2.3 (20)	1.9 (29)	2.1 (49)
Febrile neutropenia (when specified)	1.5 (13)	1.4 (21)	1.4 (34)
Total	856	1,515	2,371

CNS = central nervous system

The most common principal clinical manifestation for methicillin-susceptible *S. aureus* was osteomyelitis/septic arthritis (20.4%), whereas for methicillin-resistant *S. aureus* it was skin and skin structure infection (26.0%) (Table 9).

Table 9: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, 2018

Principal clinical manifestation	Methicillin-susceptible % (*n*)	Methicillin-resistant % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	20.4 (404)	21.4 (83)	487
Skin and skin structure infections	18.9 (374)	26.0 (101)	475
Device-related infection without metastatic focus	19.5 (387)	12.4 (48)	435
No focus (setting not known)	11.9 (235)	12.4 (48)	283
Other clinical syndrome	6.9 (136)	8.5 (33)	169
Endocarditis, left-sided	6.2 (123)	3.6 (14)	137
Pneumonia/empyema	4.2 (84)	6.4 (25)	109
Deep abscess(es) excluding those in the CNS	2.8 (55)	4.6 (18)	73
Endocarditis, right-sided	2.9 (57)	1.0 (4)	61
CNS infection (meningitis, abscess(es)	2.8 (55)	1.0 (4)	59
Device-related infection with metastatic focus	2.1 (42)	1.8 (7)	49
Febrile neutropenia (when specified)	1.6 (31)	0.8 (3)	34
Total	1,983	388	2,371

CNS = central nervous system

3.6. Length of hospital stay following bacteraemic episode

Information on length of stay following bacteraemia was available for 7,342 (87.9%) episodes involving gram-negative species, 1,199 (96.1%) episodes involving *Enterococcus* species and 2,467 (92.3%) episodes involving *S. aureus*.

The most common length of stay (45.6%) for patients with a gram-negative bacteraemia was less than seven days (Table 10). Overall, 23.1% of patients remained in hospital for more than 30 days after enterococcal bacteraemia (Table 11) and 27.0% after staphylococcal bacteraemia (Table 12).

Table 10: Length of stay following gram-negative bacteraemia, by species and place of onset, 2018

Species	Percentage length of stay following bacteraemia (*n*)				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Gram-negative species*	45.6 (3,345)	30.9 (2,269)	14.2 (1,042)	9.3 (686)	7,342
Acinetobacter species	36.6 (30)	25.6 (21)	12.2 (10)	25.6 (21)	82
Community onset	47.7 (21)	34.1 (15)	9.1 (4)	9.1 (4)	44
Hospital onset	23.7 (9)	15.8 (6)	15.8 (6)	44.7 (17)	38
Enterobacterales	46.9 (3,098)	30.7 (2,028)	13.6 (896)	8.8 (581)	6,603
Escherichia coli	52.8 (2,114)	29.5 (1,182)	11.0 (440)	6.7 (270)	4,006
Community onset	58.5 (1,970)	28.6 (964)	8.3 (280)	4.5 (152)	3,366
Hospital onset	22.5 (144)	34.1 (218)	25.0 (160)	18.4 (118)	640
Klebsiella pneumoniae	37.8 (373)	35.0 (345)	16.6 (164)	10.5 (104)	986
Community onset	43.2 (307)	37.2 (264)	13.5 (96)	6.1 (43)	710
Hospital onset	23.9 (66)	29.3 (81)	24.6 (68)	22.1 (61)	276
Enterobacter cloacae complex	26.1 (99)	32.7 (124)	24.8 (94)	16.4 (62)	379
Community onset	36.7 (72)	36.7 (72)	20.4 (40)	6.1 (12)	196
Hospital onset	14.8 (27)	28.4 (52)	29.5 (54)	27.3 (50)	183
Other Enterobacterales (*n* = 32)	41.6 (512)	30.6 (377)	16.1 (198)	11.8 (145)	1,232
Pseudomonas aeruginosa	33.0 (217)	33.5 (220)	20.7 (136)	12.8 (84)	657
Community onset	42.7 (162)	34.8 (132)	18.7 (71)	3.7 (14)	379
Hospital onset	19.8 (55)	31.7 (88)	23.4 (65)	25.2 (70)	278

* Enterobacterales, *Acinetobacter* species and *Pseudomonas aeruginosa*. The totals are greater than the sum of the figures for the species listed because some *Acinetobacter* and *Pseudomonas* species that contributed to the totals are not included in the table.

Table 11: Length of stay following *Enterococcus* species bacteraemia, by vancomycin resistance and place of onset, 2018

Species	Percentage length of stay following bacteraemia (*n*)				Total
	<7 days % (*n*)	7–14 % days (*n*)	15–30 % days (*n*)	>30 days % (*n*)	
All species	23.3 (279)	27.7 (332)	25.9 (311)	23.1 (277)	1,199
E. faecalis	24.2 (157)	29.7 (193)	25.8 (167)	20.2 (131)	648
E. faecium	20.1 (95)	23.9 (113)	27.9 (132)	28.1 (133)	473
Vancomycin resistant	17.9 (39)	22.5 (49)	28.9 (63)	30.7 (67)	218
Vancomycin susceptible	22.0 (56)	25.1 (64)	27.1 (69)	25.9 (66)	255
Other *Enterococcus* species (*n* = 7)	34.6 (27)	33.3 (26)	15.4 (12)	16.7 (13)	78
Community onset					
E. faecalis	28.4 (124)	32.8 (143)	24.5 (107)	14.2 (62)	436
E. faecium	25.4 (36)	31.7 (45)	26.8 (38)	16.2 (23)	142
Vancomycin resistant	15.9 (7)	29.5 (13)	29.5 (13)	25.0 (11)	44
Vancomycin susceptible	29.6 (29)	32.7 (32)	25.5 (25)	12.2 (12)	98
Hospital onset					
E. faecalis	15.6 (33)	23.6 (50)	28.3 (60)	32.5 (69)	212
E. faecium	17.8 (59)	20.5 (68)	28.4 (94)	33.2 (110)	331
Vancomycin resistant	18.4 (32)	20.7 (36)	28.7 (50)	32.2 (56)	174
Vancomycin susceptible	17.2 (27)	20.4 (32)	28.0 (44)	34.4 (54)	157

Table 12: Length of stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, 2018

Species	Percentage length of stay following bacteraemia (*n*)				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Staphylococcus aureus	17.5 (431)	26.4 (652)	29.1 (719)	27.0 (665)	2,467
Methicillin resistant	18.4 (78)	26.6 (113)	26.4 (112)	28.7 (122)	425
Community onset	17.6 (57)	30.7 (99)	27.6 (89)	24.1 (78)	323
Hospital onset	20.6 (21)	13.7 (14)	22.5 (23)	43.1 (44)	102
Methicillin susceptible	17.3 (353)	26.4 (539)	29.7 (607)	26.6 (543)	2,042
Community onset	19.0 (305)	27.0 (435)	28.2 (453)	25.9 (416)	1,609
Hospital onset	11.1 (48)	24.0 (104)	35.6 (154)	29.3 (127)	433

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 multidrug 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[42], using both CLSI breakpoints and EUCAST breakpoints, are shown in Table 13. Resistance by state and territory to key antimicrobial groups (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) for *E. coli* and *K. pneumoniae* 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.

For some antimicrobials, the concentration range tested did not distinguish between intermediate susceptibility and resistance; the term non-susceptible was used to describe these results. In *Salmonella*, non-resistant refers to isolates that were susceptible or intermediate.

Supplementary data on percentages susceptible, intermediate and resistant for each antimicrobial and all species, and the antimicrobial profiles by state and territory can be found in the 2018 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), 2018

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Acinetobacter baumannii complex					
Piperacillin–tazobactam	60	11.7 (7)	15.0 (9)	–*	–*
Ceftazidime	56	10.7 (6)	3.6 (2)	–*	–*
Cefepime	57	3.5 (2)	5.3 (3)	–*	–*
Gentamicin	63	0.0 (0)	3.2 (2)	–†	3.2 (2)
Tobramycin	63	0.0 (0)	3.2 (2)	–†	3.2 (2)
Amikacin	61	0.0 (0)	3.3 (2)	0.0 (0)	3.3 (2)
Ciprofloxacin	63	6.3 (4)	1.6 (1)	92.1 (58)§	7.9 (5)
Meropenem	63	0.0 (0)	3.2 (2)	0.0 (0)	3.2 (2)
Enterobacter cloacae complex					
Piperacillin–tazobactam	413	3.9 (16)	18.2 (75)	2.7 (11)	22.0 (91)
Ceftriaxone	419	0.5 (2)	25.1 (105)	0.5 (2)	25.1 (105)
Ceftazidime	419	0.5 (2)	21.7 (91)	2.4 (10)	22.2 (93)
Cefepime	419	5.3 (22)#	3.3 (14)	7.4 (31)	6.0 (25)
Gentamicin	419	1.0 (4)	6.0 (25)	0.7 (3)	6.9 (29)
Tobramycin	419	3.6 (15)	4.3 (18)	0.7 (3)	7.9 (33)
Amikacin	417	0.0 (0)	0.0 (0)	1.0 (4)	0.0 (0)
Ciprofloxacin	419	1.0 (4)	7.4 (31)	1.0 (4)	7.4 (31)
Meropenem	418	0.5 (2)	2.6 (11)	0.5 (2)	2.2 (9)
Enterococcus faecalis					
Ampicillin	675	–†	0.0 (0)	0.0 (0)	0.0 (0)
Benzylpenicillin	654	–†	0.8 (5)	–*	–*
Ciprofloxacin	548	2.6 (14)	10.4 (57)	–†	9.9 (54)§
Daptomycin	673	38.8 (261)#	0.3 (2)	–*	–*
Linezolid	675	0.4 (3)	0.3 (2)	–†	0.3 (2)
Teicoplanin	675	0.0 (0)	0.0 (0)	–†	0.3 (2)
Tetracycline/doxycycline	504	0.2 (1)	74.6 (376)	–*	–*
Vancomycin	675	0.0 (0)	0.0 (0)	–†	0.0 (0)
Enterococcus faecium					
Ampicillin	491	–†	89.4 (439)	0.2 (1)	89.4 (439)
Benzylpenicillin	478	–†	89.7 (429)	–*	–*
Ciprofloxacin	390	3.3 (13)	87.7 (342)	–†	86.9 (339)§
Linezolid	490	0.4 (2)	0.4 (2)	–†	0.4 (2)
Teicoplanin	491	1.8 (9)	17.5 (86)	–†	20.8 (102)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Tetracycline/doxycycline	408	0.5 (2)	62.3 (254)	–*	–*
Vancomycin	491	2.4 (12)	42.6 (209)	–†	45.0 (221)
Escherichia coli					
Ampicillin	4,567	2.1 (94)	54.7 (2,496)	–†	56.8 (2,592)
Amoxicillin–clavulanic acid	4,533	13.6 (615)	8.8 (399)	–**	–**
Piperacillin–tazobactam	4,546	3.0 (137)	3.0 (136)	1.5 (67)	6.0 (273)
Ceftriaxone	4,569	0.1 (4)	13.4 (611)	0.1 (4)	13.4 (611)
Ceftazidime	4,569	0.7 (31)	5.9 (271)	6.1 (278)	6.6 (302)
Cefepime	4,569	1.7 (77)#	2.9 (133)	6.9 (313)	3.7 (169)
Gentamicin	4,570	0.2 (11)	8.2 (375)	0.4 (17)	8.4 (386)
Tobramycin	4,569	6.0 (274)	3.3 (149)	0.7 (31)	9.3 (423)
Amikacin	4,567	0.2 (9)	0.0 (0)	1.0 (46)	0.2 (9)
Ciprofloxacin	4,569	4.0 (181)	15.2 (695)	4.0 (181)	15.2 (695)
Meropenem	4,568	<0.1 (2)	0.1 (6)	<0.1 (2)	0.1 (4)
Klebsiella (*Enterobacter*) *aerogenes*					
Piperacillin–tazobactam	125	6.4 (8)	24.8 (31)	6.4 (8)	31.2 (39)
Ceftriaxone	125	0.0 (0)	30.4 (38)	0.0 (0)	30.4 (38)
Ceftazidime	125	1.6 (2)	28.0 (35)	2.4 (3)	29.6 (37)
Cefepime	125	3.2 (4)#	3.2 (4)	2.4 (3)	4.8 (6)
Gentamicin	125	0.8 (1)	4.0 (5)	0.0 (0)	4.8 (6)
Tobramycin	125	0.0 (0)	4.8 (6)	0.0 (0)	4.8 (6)
Amikacin	125	0.8 (1)	0.8 (1)	0.0 (0)	1.6 (2)
Ciprofloxacin	125	0.0 (0)	4.8 (6)	0.0 (0)	4.8 (6)
Meropenem	125	0.0 (0)	2.4 (3)	0.8 (1)	1.6 (2)
Klebsiella oxytoca					
Amoxicillin–clavulanic acid	229	3.5 (8)	9.2 (21)	–**	–**
Piperacillin–tazobactam	229	0.9 (2)	9.6 (22)	3.5 (8)	10.5 (24)
Ceftriaxone	230	0.9 (2)	7.9 (18)	0.9 (2)	7.9 (18)
Ceftazidime	230	0.0 (0)	0.4 (1)	0.4 (1)	0.4 (1)
Cefepime	230	0.0 (0)#	0.0 (0)	0.4 (1)	0.0 (0)
Gentamicin	230	0.4 (1)	0.0 (0)	0.0 (0)	0.4 (1)
Tobramycin	230	0.4 (1)	0.0 (0)	0.0 (0)	0.4 (1)
Amikacin	230	0.0 (0)	0.0 (0)	0.4 (1)	0.0 (0)
Ciprofloxacin	230	0.4 (1)	0.4 (1)	0.4 (1)	0.4 (1)
Meropenem	230	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Klebsiella pneumoniae					
Amoxicillin–clavulanic acid	1,095	6.3 (69)	5.5 (60)	–**	–**
Piperacillin–tazobactam	1,099	3.6 (40)	4.3 (47)	7.5 (82)	7.9 (87)
Ceftriaxone	1,104	0.2 (2)	9.4 (104)	0.2 (2)	9.4 (104)
Ceftazidime	1,105	1.3 (14)	6.1 (67)	3.1 (34)	7.3 (81)
Cefepime	1,104	1.3 (14)#	3.2 (35)	4.0 (44)	4.0 (44)
Gentamicin	1,105	0.1 (1)	4.3 (48)	0.5 (5)	4.4 (49)
Tobramycin	1,105	3.8 (42)	3.6 (40)	0.1 (1)	7.4 (82)
Amikacin	1,105	0.1 (1)	0.3 (3)	0.5 (6)	0.4 (4)
Ciprofloxacin	1,104	1.4 (16)	11.3 (125)	1.4 (16)	11.3 (125)
Meropenem	1,104	0.0 (0)	1.0 (11)	0.2 (2)	0.8 (9)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Proteus mirabilis					
Ampicillin	258	1.2 (3)	17.1 (44)	–[†]	18.2 (47)
Amoxicillin–clavulanic acid	257	5.8 (15)	2.7 (7)	–[**]	–[**]
Piperacillin–tazobactam	258	0.8 (2)	0.0 (0)	0.0 (0)	0.8 (2)
Ceftriaxone	258	0.4 (1)	1.6 (4)	0.4 (1)	1.6 (4)
Ceftazidime	258	0.4 (1)	1.2 (3)	0.4 (1)	1.6 (4)
Cefepime	258	0.0 (0)[#]	0.8 (2)	0.8 (2)	0.8 (2)
Gentamicin	258	0.8 (2)	1.2 (3)	6.2 (16)	1.9 (5)
Tobramycin	258	0.8 (2)	0.8 (2)	0.8 (2)	1.6 (4)
Amikacin	258	0.0 (0)	0.0 (0)	0.4 (1)	0.0 (0)
Ciprofloxacin	258	0.0 (0)	2.7 (7)	0.0 (0)	2.7 (7)
Meropenem	258	0.4 (1)	0.0 (0)	0.0 (0)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin–tazobactam	727	6.1 (44)	5.1 (37)	–[†]	11.1 (81)
Ceftazidime	730	3.6 (26)	4.5 (33)	–[†]	8.1 (59)
Cefepime	730	3.0 (22)	2.6 (19)	–[†]	5.6 (41)
Gentamicin	730	1.5 (11)	0.7 (5)	–[†]	2.2 (16)
Tobramycin	730	0.0 (0)	0.5 (4)	–[†]	0.5 (4)
Amikacin	730	0.7 (5)	0.4 (3)	1.5 (11)	1.1 (8)
Ciprofloxacin	730	4.1 (30)	3.6 (26)	0.0 (0)	7.7 (56)
Meropenem	729	3.2 (23)	4.5 (33)	4.5 (33)	3.2 (23)
Salmonella species (non-typhoidal)					
Ampicillin	106	0.0 (0)	8.5 (9)	–[†]	8.5 (9)
Amoxicillin–clavulanic acid	101	2.0 (2)	1.0 (1)	–[**]	–[**]
Piperacillin–tazobactam	106	0.9 (1)	0.0 (0)	0.0 (0)	0.9 (1)
Ceftriaxone	106	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Ceftazidime	106	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Cefepime	106	0.0 (0)[§]	0.0 (0)	0.0 (0)	0.0 (0)
Ciprofloxacin	105	–[§]	0.0 (0)	–[§]	0.0 (0)
Meropenem	106	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	172	0.6 (1)	0.0 (0)	1.2 (2)	0.6 (1)
Ceftriaxone	198	0.0 (0)	4.0 (8)	0.0 (0)	4.0 (8)
Ceftazidime	198	0.0 (0)	0.0 (0)	1.0 (2)	0.0 (0)
Cefepime	198	0.0 (0)[#]	0.0 (0)	1.0 (2)	0.0 (0)
Gentamicin	198	0.0 (0)	0.5 (1)	1.0 (2)	0.5 (1)
Tobramycin	198	18.7 (37)	0.0 (0)	14.6 (29)	18.7 (37)
Amikacin	198	0.0 (0)	0.0 (0)	0.5 (1)	0.0 (0)
Ciprofloxacin	198	1.5 (3)	3.5 (7)	1.5 (3)	3.5 (7)
Meropenem	198	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Staphylococcus aureus					
Benzylpenicillin	2,667	–[†]	78.9 (2,105)	–[†]	78.9 (2,105)
Ciprofloxacin	2,668	0.7 (20)	7.7 (206)	–[†]	8.5 (226)
Clindamycin (constitutive)	2,666	0.1 (3)	3.3 (87)	0.3 (8)	3.4 (90)
Clindamycin (inducible + constitutive resistance)	2,666	0.1 (3)	13.7 (366)	0.3 (8)	13.8 (369)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Daptomycin	2,672	0.3 (7)††	–†	–†	0.3 (7)
Erythromycin	2,599	7.7 (199)	14.6 (379)	0.2 (4)	15.5 (402)
Gentamicin	2,668	1.1 (30)	1.9 (51)	–†	3.7 (100)
Linezolid	2,672	0.0 (0)	0.0 (0)	–†	0.0 (0)
Oxacillin (methicillin)	2,673	–†	17.4 (466)	–†	17.4 (466)
Rifampicin	2,666	0.0 (0)	0.6 (15)	–§§	0.6 (15)
Trimethoprim–sulfamethoxazole	2,666	–†	3.7 (98)	0.3 (9)	3.3 (89)
Teicoplanin	2,672	0.0 (0)	0.0 (0)	–†	0.1 (2)
Tetracycline/doxycycline	2,668	0.0 (0)	4.6 (124)##	0.3 (9)	4.9 (131)
Vancomycin	2,672	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

§ The ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible and intermediate categories (EUCAST) for Acinetobacter spp.; intermediate and resistant categories (EUCAST) for *Enterococcus* species; and susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species

Includes sensitive dose dependent category for CLSI

** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanic acid at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines. All cards used in this study have a 2:1 ratio; therefore, no EUCAST categories can be determined.

‡ Non-susceptible; resistance not defined

§§ The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant

Tetracycline/doxycycline concentration range restricts ability to accurately identify intermediate and resistant category

Figure 4. Percentage of *Escherichia coli* from patients with bacteraemia with resistance to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, 2018.

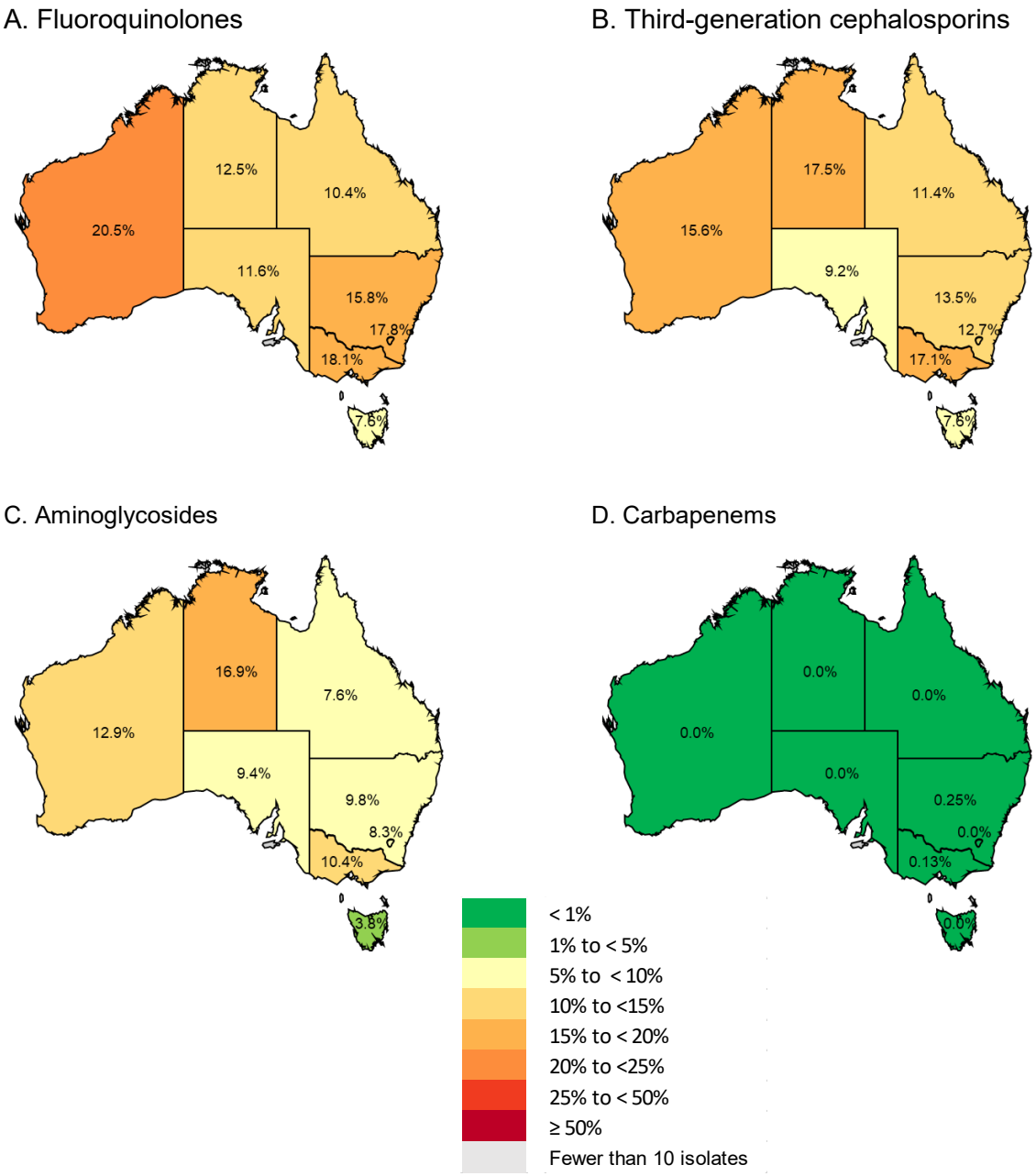
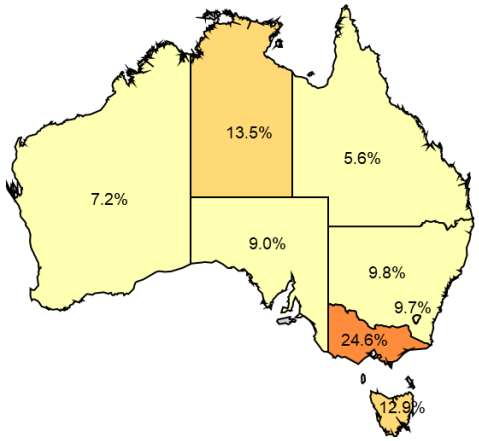
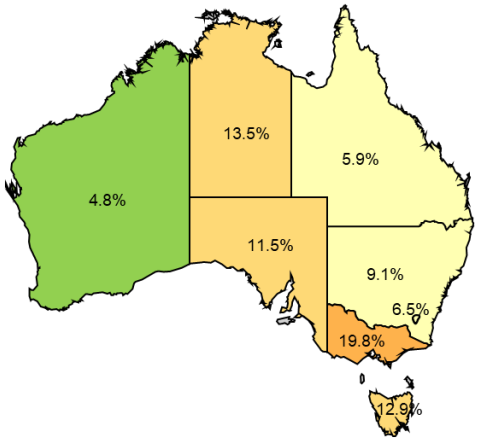


Figure 5. Percentage of *Klebsiella pneumoniae* from patients with bacteraemia with resistance to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, 2018.

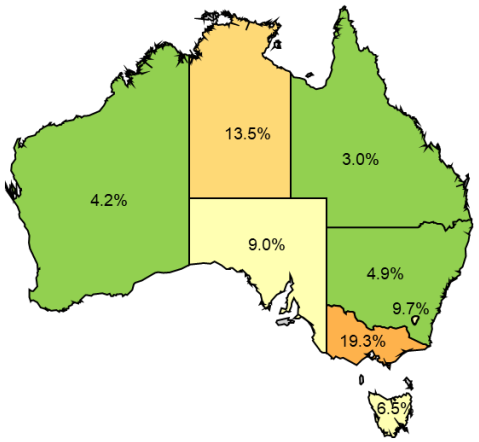
A. Fluoroquinolones



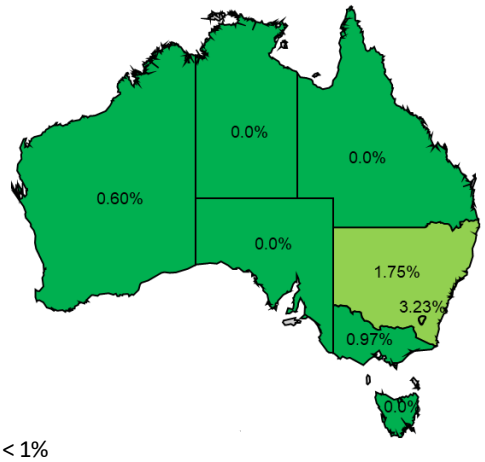
B. Third-generation cephalosporins



C. Aminoglycosides



D. Carbapenems



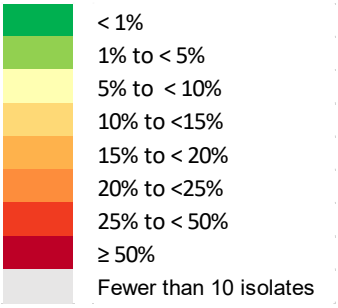


Figure 6. Percentage of *Pseudomonas aeruginosa* from patients with bacteraemia with resistance to piperacillin–tazobactam (A), fluoroquinolones (B), ceftazidime (C) and carbapenems (D), Australia, 2018.

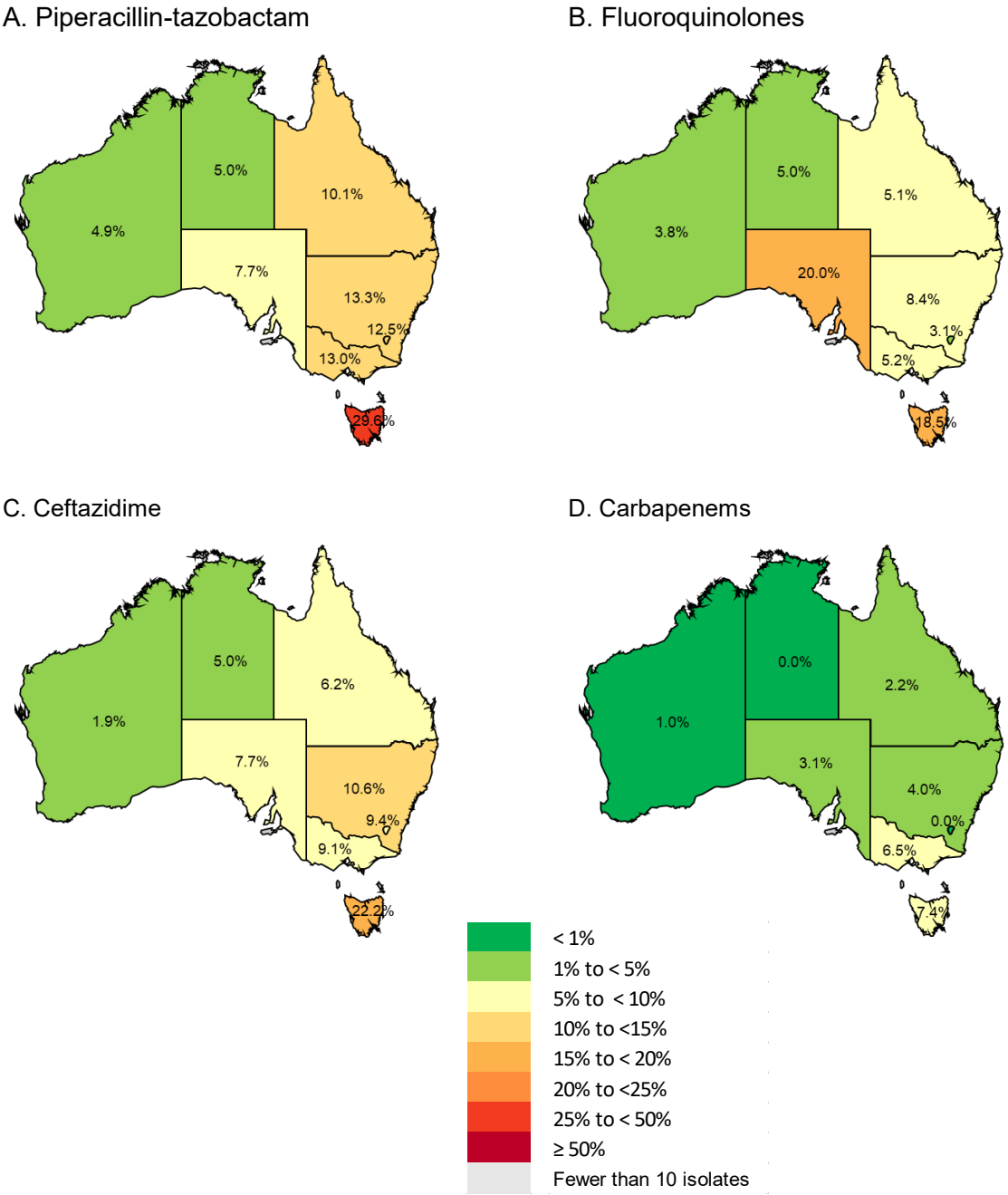


Figure 7. Percentage of *Staphylococcus aureus* from patients with bacteraemia with resistance to methicillin, Australia, 2018.

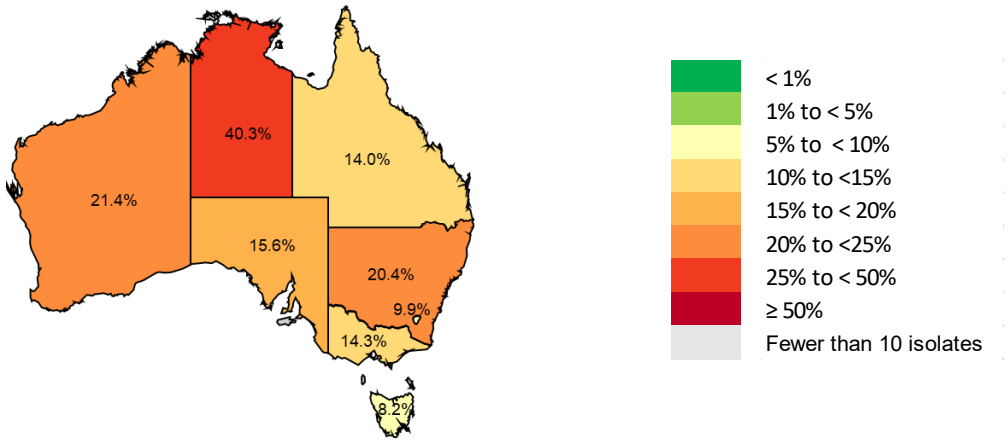
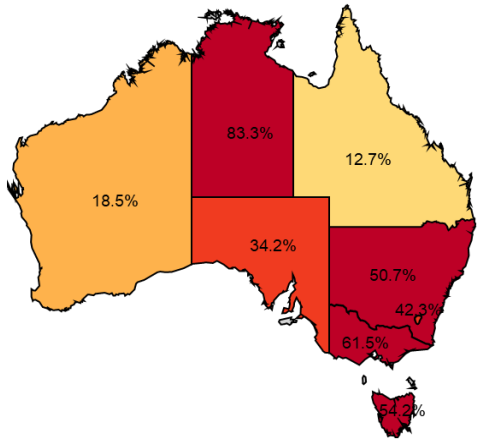
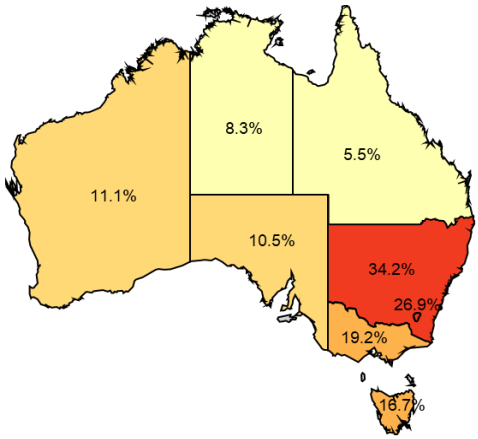


Figure 8. Percentage of *Enterococcus faecium* from patients with bacteraemia with resistance to vancomycin (A) and teicoplanin (B), and *Enterococcus faecalis* with resistance to high-level gentamicin (C), Australia, 2017.

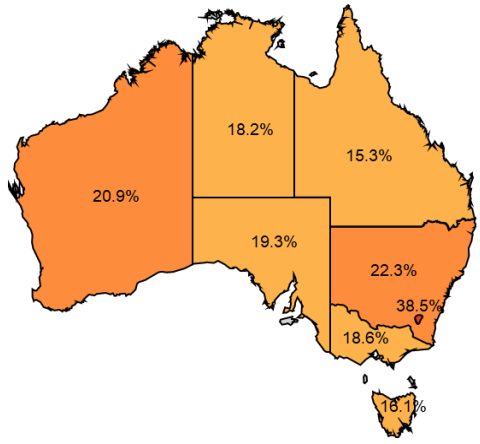
A. Vancomycin

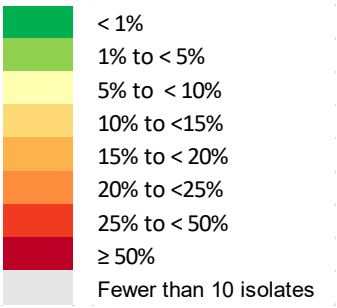


B. Teicoplanin



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, 2018

		Community onset		Hospital onset	
Species and antimicrobial	**Number**	**% intermediate**	**% resistant**	**% intermediate**	**% resistant**
Acinetobacter baumannii complex					
Piperacillin–tazobactam	60	16.7, –*	10.0, –*	6.7, –*	20.0, –*
Ceftriaxone	58	80.6, –*	6.5, –*	77.8, –*	7.4, –*
Ceftazidime	56	10.3, –*	0.0, –*	11.1, –*	7.4, –*
Cefepime	57	0.0, –*	0.0, –*	0.0, –*	11.1, –*
Gentamicin	63	0.0, –†	0.0, 0.0	0.0, –†	6.7, 6.7
Tobramycin	63	0.0, –†	0.0, 0.0	0.0, –†	6.7, 6.7
Amikacin	61	0.0, 0.0	0.0, 0.0	0.0, 0.0	6.9, 6.9
Ciprofloxacin	63	6.1, 93.9§	0.0, 6.1	6.7, 90.0§	3.3, 10.0
Meropenem	63	0.0, 0.0	0.0, 0.0	0.0, 0.0	6.7, 6.7
Enterobacter cloacae complex					
Piperacillin–tazobactam	413	3.2, 2.8	14.3, 17.5	4.6, 2.6	22.4, 27.0
Ceftriaxone	419	0.0, 0.0	19.5, 19.5	1.0, 1.0	31.3, 31.3
Ceftazidime	419	0.5, 3.2	15.8, 16.3	0.5, 1.5	28.3, 28.8
Cefepime	419	2.7#, 5.4	2.3, 3.6	8.1#, 9.6	4.5, 8.6
Gentamicin	419	1.8, 0.0	3.6, 5.4	0.0, 1.5	8.6, 8.6
Tobramycin	419	3.2, 0.0	2.7, 5.9	4.0, 1.5	6.1, 10.1
Amikacin	417	0.0, 0.9	0.0, 0.0	0.0, 1.0	0.0, 0.0
Ciprofloxacin	419	1.4, 1.4	5.9, 5.9	0.5, 0.5	9.1, 9.1
Meropenem	418	0.5, 0.5	1.4, 0.9	0.5, 0.5	4.1, 3.6
Enterococcus faecalis					
Ampicillin	675	–†, 0.0	0.0, 0.0	–†, 0.0	0.0, 0.0
Benzylpenicillin	654	–†, –*	0.9, –*	–†, –*	0.5, –*
Ciprofloxacin	548	2.9, –†	9.6, 9.1§	1.7, –†	12.1, 11.5§
Daptomycin	673	40.0#, –*	0.4, –*	36.3#, –*	0.0, –*
Linezolid	675	0.7, –†	0.4, 0.4	0.0, –†	0.0, 0.0
Teicoplanin	675	0.0, –†	0.0, 0.4	0.0, –†	0.0, 0.0
Tetracycline/doxycycline	504	0.0, –*	74.6, –*	0.6, –*	74.7, –*
Vancomycin	675	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Enterococcus faecium					
Ampicillin	491	–†, 0.0	74.2, 74.2	–†, 0.3	96.2, 96.2
Benzylpenicillin	478	–†, –*	74.3, –*	–†, –*	96.4, –*
Ciprofloxacin	390	7.8, –†	73.0, 71.3§	1.5, –†	93.8, 93.5§
Linezolid	490	0.7, –†	0.0, 0.0	0.3, –†	0.6, 0.6
Teicoplanin	491	0.7, –†	10.6, 11.9	2.4, –†	20.6, 24.7
Tetracycline/doxycycline	408	0.0, –*	55.5, –*	0.7, –*	64.8, –*
Vancomycin	491	1.3, –†	28.5, 29.8	2.9, –†	48.8, 51.8
Escherichia coli					
Ampicillin	4,567	2.1, –†	53.6, 55.8	2.0, –†	60.2, 62.2
Amoxicillin–clavulanic acid	4,533	13.6, –**	8.1, –**	13.6, –**	12.9, –**
Piperacillin–tazobactam	4,546	2.8, 1.4	2.4, 5.2	4.3, 1.9	6.4, 10.7

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% intermediate	% resistant
Ceftriaxone	4,569	0.1, 0.1	12.2, 12.2	0.0, 0.0	19.8, 19.8
Ceftazidime	4,569	0.7, 5.7	5.2, 5.9	0.7, 8.0	10.0, 10.7
Cefepime	4,569	1.7[#], 6.4	2.5, 3.3	1.9[#], 9.4	5.1, 6.0
Gentamicin	4,570	0.2, 0.4	7.8, 8.0	0.6, 0.3	10.6, 11.1
Tobramycin	4,569	5.7, 0.7	2.9, 8.7	7.3, 0.4	5.3, 12.6
Amikacin	4,567	0.2, 0.9	0.0, 0.2	0.4, 1.4	0.0, 0.4
Ciprofloxacin	4,569	4.0, 4.0	14.4, 14.4	4.0, 4.0	19.8, 19.8
Meropenem	4,568	0.1, 0.0	0.1, 0.1	0.0, 0.3	0.6, 0.3
Klebsiella (*Enterobacter*) *aerogenes*					
Piperacillin–tazobactam	125	8.7, 7.2	17.4, 26.1	3.6, 5.4	33.9, 37.5
Ceftriaxone	125	0.0, 0.0	23.2, 23.2	0.0, 0.0	39.3, 39.3
Ceftazidime	125	2.9, 0.0	20.3, 23.2	0.0, 5.4	37.5, 37.5
Cefepime	125	1.4[#], 2.9	2.9, 2.9	5.4[#], 1.8	3.6, 7.1
Gentamicin	125	0.0, 0.0	2.9, 2.9	1.8, 0.0	5.4, 7.1
Tobramycin	125	0.0, 0.0	2.9, 2.9	0.0, 0.0	7.1, 7.1
Amikacin	125	0.0, 0.0	0.0, 0.0	1.8, 0.0	1.8, 3.6
Ciprofloxacin	125	0.0, 0.0	5.8, 5.8	0.0, 0.0	3.6, 3.6
Meropenem	125	0.0, 1.4	2.9, 1.4	0.0, 0.0	1.8, 1.8
Klebsiella oxytoca					
Amoxicillin–clavulanic acid	229	3.7, –**	5.5, –**	3.1, –**	18.5, –**
Piperacillin–tazobactam	229	0.6, 3.1	5.5, 6.1	1.5, 4.5	19.7, 21.2
Ceftriaxone	230	0.0, 0.0	4.3, 4.3	3.0, 3.0	16.7, 16.7
Ceftazidime	230	0.0, 0.0	0.6, 0.6	0.0, 1.5	0.0, 0.0
Cefepime	230	0.0[#], 0.0	0.0, 0.0	0.0[#], 1.5	0.0, 0.0
Gentamicin	230	0.0, 0.0	0.0, 0.0	1.5, 0.0	0.0, 1.5
Tobramycin	230	0.0, 0.0	0.0, 0.0	1.5, 0.0	0.0, 1.5
Amikacin	230	0.0, 0.0	0.0, 0.0	0.0, 1.5	0.0, 0.0
Ciprofloxacin	230	0.6, 0.6	0.6, 0.6	0.0, 0.0	0.0, 0.0
Meropenem	230	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae					
Amoxicillin–clavulanic acid	1,095	5.4, –**	4.1, –**	8.8, –**	9.2, –**
Piperacillin–tazobactam	1,099	3.5, 6.9	2.4, 5.9	4.0, 9.1	9.4, 13.5
Ceftriaxone	1,104	0.2, 0.2	6.7, 6.7	0.0, 0.0	16.8, 16.8
Ceftazidime	1,105	1.2, 1.9	4.3, 5.6	1.3, 6.4	10.7, 12.1
Cefepime	1,104	0.7[#], 2.7	2.1, 2.6	2.7[#], 7.4	6.1, 7.7
Gentamicin	1,105	0.1, 0.4	3.7, 3.8	0.0, 0.7	6.0, 6.0
Tobramycin	1,105	2.9, 0.1	2.9, 5.7	6.4, 0.0	5.7, 12.1
Amikacin	1,105	0.0, 0.2	0.4, 0.4	0.3, 1.3	0.0, 0.3
Ciprofloxacin	1,104	1.6, 1.6	8.9, 8.9	1.0, 1.0	17.8, 17.8
Meropenem	1,104	0.0, 0.2	0.5, 0.2	0.0, 0.0	2.4, 2.4
Proteus mirabilis					
Ampicillin	258	0.9, –[†]	17.4, 18.3	2.6, –[†]	15.4, 17.9
Amoxicillin–clavulanic acid	257	6.4, –**	2.7, –**	2.6, –**	2.6, –**
Piperacillin–tazobactam	258	0.9, 0.0	0.0, 0.9	0.0, 0.0	0.0, 0.0
Ceftriaxone	258	0.5, 0.5	1.8, 1.8	0.0, 0.0	0.0, 0.0
Ceftazidime	258	0.5, 0.5	1.4, 1.8	0.0, 0.0	0.0, 0.0

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% intermediate	% resistant
Cefepime	258	0.0[#], 0.9	0.9, 0.9	0.0[#], 0.0	0.0, 0.0
Gentamicin	258	0.5, 5.9	1.4, 1.8	2.6, 7.7	0.0, 2.6
Tobramycin	258	0.9, 0.5	0.9, 1.8	0.0, 2.6	0.0, 0.0
Amikacin	258	0.0, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0
Ciprofloxacin	258	0.0, 0.0	2.7, 2.7	0.0, 0.0	2.6, 2.6
Meropenem	258	0.5, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Pseudomonas aeruginosa					
Piperacillin–tazobactam	727	5.1, –[†]	3.3, 8.4	7.4, –[†]	7.7, 15.2
Ceftazidime	730	1.9, –[†]	3.7, 5.6	6.0, –[†]	5.7, 11.7
Cefepime	730	0.0, –[†]	2.1, 4.4	0.0, –[†]	3.3, 7.4
Gentamicin	730	1.4, –[†]	0.7, 2.1	1.7, –[†]	0.7, 2.3
Tobramycin	730	0.0, –[†]	0.5, 0.5	0.0, –[†]	0.7, 0.7
Amikacin	730	0.7, 1.6	0.5, 1.2	0.7, 1.3	0.3, 1.0
Ciprofloxacin	730	3.9, 0.0	2.8, 6.7	4.3, 0.0	4.7, 9.0
Meropenem	729	2.8, 4.2	2.8, 1.4	3.7, 5.0	7.0, 5.7
Salmonella species (non-typhoidal)					
Ampicillin	106	0.0, –[†]	8.2, 8.2	0.0, –[†]	11.1, 11.1
Amoxicillin–clavulanic acid	101	2.2, –[**]	1.1, –[**]	0.0, –[**]	0.0, –[**]
Piperacillin–tazobactam	106	1.0, 0.0	0.0, 1.0	0.0, 0.0	0.0, 0.0
Ceftriaxone	106	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Ceftazidime	106	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Cefepime	106	0.0[#], 0.0	0.0, 0.0	0.0[#], 0.0	0.0, 0.0
Ciprofloxacin	105	–[§]	0.0, 0.0	–[§]	0.0, 0.0
Meropenem	106	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Serratia marcescens					
Piperacillin–tazobactam	172	0.0, 1.2	0.0, 0.0	1.1, 1.1	0.0, 1.1
Ceftriaxone	198	0.0, 0.0	3.9, 3.9	0.0, 0.0	4.2, 4.2
Ceftazidime	198	0.0, 1.0	0.0, 0.0	0.0, 1.0	0.0, 0.0
Cefepime	198	0.0[#], 0.0	0.0, 0.0	0.0[#], 2.1	0.0, 0.0
Gentamicin	198	0.0, 0.0	0.0, 0.0	0.0, 2.1	1.0, 1.0
Tobramycin	198	12.7, 15.7	0.0, 12.7	25.0, 13.5	0.0, 25.0
Amikacin	198	0.0, 0.0	0.0, 0.0	0.0, 1.0	0.0, 0.0
Ciprofloxacin	198	0.0, 0.0	4.9, 4.9	3.1, 3.1	2.1, 2.1
Meropenem	198	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Staphylococcus aureus					
Benzylpenicillin	2,667	–[†], –[†]	78.8 78.8	–[†], –[†]	79.3, 79.3
Ciprofloxacin	2,668	0.5, –[†]	6.8, 7.3	1.8, –[†]	11.0, 12.7
Clindamycin (constitutive)	2,666	0.1, 0.3	3.3, 3.4	0.2, 0.4	3.2, 3.4
Clindamycin (inducible + constitutive resistance)	2,666	0.1, 0.3	13.5, 13.6	0.2, 0.4	14.5, 14.7
Daptomycin	2,672	0.3[‡], –[†]	–[†], 0.3	0.2[‡], –[†]	–[†], 0.2
Erythromycin	2,599	7.5, 0.1	14.1, 15.1	8.4, 0.2	16.5, 16.8
Gentamicin	2,668	1.0, –[†]	1.6, 3.1	1.8, –[†]	3.2, 6.2
Linezolid	2,672	0.0, –[†]	0.0, 0.0	0.0, –[†]	0.0, 0.0
Oxacillin (methicillin)	2,673	–[†], –[†]	16.9, 16.9	–[†], –[†]	19.5, 19.5
Rifampicin	2,666	0.0, <0.0[§§]	0.6, 0.6	0.0, 0.0[§§]	0.5, 0.5

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% intermediate	% resistant
Trimethoprim–sulfamethoxazole	2,666	–†, 0.3	3.6, 3.3	–†, 0.4	3.9, 3.5
Teicoplanin	2,672	0.0, –†	0.0, <0.0	0.0, –†	0.0, 0.2
Tetracycline/doxycycline	2,668	0.0, 0.3	4.3##,4.4	0.0, 0.5	6.0##, 6.7
Vancomycin	2,672	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

§ The ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible and intermediate categories (EUCAST) for Acinetobacter spp.; intermediate and resistant categories (EUCAST) for *Enterococcus* species; and susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species

Includes sensitive dose dependent category for CLSI

** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanic acid at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines. All cards used in this study have a 2:1 ratio; therefore, no EUCAST categories can be determined.

‡ Non-susceptible; resistance not defined

§§ The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant

Tetracycline/doxycycline concentration range restricts ability to accurately identify intermediate and resistant category

3.8. Multidrug resistance

The most problematic pathogens are those with multiple acquired resistances. The definitions defined by Magiorakos et al.[43] were applied in this survey; where multidrug 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 multidrug resistance. EUCAST breakpoints were primarily used in the analysis. For cefazolin, the EUCAST-approved Australian National Antimicrobial Susceptibility Testing Committee guidelines were used. For amoxicillin–clavulanic acid, CLSI breakpoints were used, because the CLSI formulation for this agent was used in the Vitek® and Phoenix™ susceptibility cards.

Multiple acquired resistances for key species are shown in Tables 15 to 21. The agents included for each species are listed in the notes after each table. For other common species, refer to Appendix D.

Table 15: Multiple acquired resistance in *Enterobacter cloacae* complex, by state and territory, 2018

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)				
		0	1	2	%	3	4	5	6	%
NSW	112	67	10	20	86.6	2	5	4	4	13.4
Vic	63	35	9	14	92.1	3	0	2	0	7.9
Qld	114	77	14	13	91.2	1	3	5	1	8.8
SA	30	17	6	6	96.7	0	1	0	0	3.3
WA	52	36	7	9	100.0	0	0	0	0	0.0
Tas	10	8	0	2	–*	0	0	0	0	–*
NT	12	6	3	2	–*	1	0	0	0	–*
ACT	9	5	3	0	–*	1	0	0	0	–*
Total	**402**	**251**	**52**	**66**	**91.8**	**8**	**9**	**11**	**5**	**8.2**

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

* Not applicable (insufficient numbers)

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), and *E hormaechei* (n = 1)

Table 16: Multiple acquired resistance in *Enterococcus faecalis*, by state and territory, 2018

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)			
		0	1	2	%	3	4	5	%
NSW	169	122	31	16	100	0	0	0	0.0
Vic	93	69	14	10	100	0	0	0	0.0
Qld	118	97	14	7	100	0	0	0	0.0
SA	44	31	10	3	100	0	0	0	0.0
WA	90	67	21	2	100	0	0	0	0.0
Tas	16	13	2	1	–*	0	0	0	–*
NT	11	9	1	1	–*	0	0	0	–*
ACT	0†	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**541**	**408**	**93**	**40**	**100**	**0**	**0**	**0**	**0.0**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable

* Not applicable (insufficient numbers)
† Isolates not tested against all included agents

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin (high level)), fluoroquinolones (ciprofloxacin), glycopeptides (vancomycin or teicoplanin), oxazolidinones (linezolid), and penicillins (ampicillin)

Table 17: Multiple acquired resistance in *Enterococcus faecium*, by state and territory, 2018

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)			
		0	1	2	%	3	4	5	%
NSW	140	15	2	18	25.0	62	43	0	75.0
Vic	86	5	1	21	31.4	29	30	0	68.6
Qld	50	13	1	26	80.0	7	3	0	20.0
SA	30	3	1	13	56.7	3	10	0	43.3
WA	54	4	1	36	75.9	11	2	0	24.1
Tas	17	1	0	3	–*	1	12	0	–*
NT	12	1	0	0	–*	2	9	0	–*
ACT	0†	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**389**	**42**	**6**	**117**	**42.4**	**115**	**109**	**0**	**57.6**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable

* Not applicable (insufficient numbers)
† Isolates not tested against all included agents

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin (high level), fluoroquinolones (ciprofloxacin), glycopeptides (vancomycin or teicoplanin), oxazolidinones (linezolid), and penicillins (ampicillin)

Table 18: Multiple acquired resistance in *Escherichia coli*, by state and territory, 2018

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	1,185	466	176	215	72.3	83	84	97	40	15	6	1	2	27.7
Vic	765	239	139	149	68.9	55	67	53	39	12	8	3	1	31.1
Qld	863	355	142	164	76.6	69	50	51	15	10	4	3	0	23.4
SA	401	183	75	56	78.3	21	26	25	9	4	2	0	0	21.7
WA	797	308	134	119	70.4	66	50	55	35	22	5	3	0	29.6
Tas	181	92	33	28	84.5	5	10	6	4	3	0	0	0	15.5
NT	160	45	27	31	64.4	12	22	14	6	1	2	0	0	35.6
ACT	156	58	37	24	76.3	10	6	8	11	2	0	0	0	23.7
Total	**4,508**	**1,746**	**763**	**786**	**73.1**	**321**	**315**	**309**	**159**	**69**	**27**	**10**	**3**	**26.9**

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 19: Multiple acquired resistance in *Klebsiella pneumoniae*, by state and territory, 2018

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)							
		0	1	2	%	3	4	5	6	7	8	9	%
NSW	272	188	37	18	89.3	9	5	4	3	0	3	5	10.7
Vic	207	125	23	13	77.8	4	5	15	10	9	1	2	22.2
Qld	267	198	33	11	90.6	8	5	9	2	1	0	0	9.4
SA	78	52	14	2	87.2	2	1	2	2	2	1	0	12.8
WA	165	135	17	4	94.5	2	2	1	3	0	1	0	5.5
Tas	31	20	6	0	83.9	2	2	0	0	1	0	0	16.1
NT	37	28	3	1	86.5	0	1	3	0	1	0	0	13.5
ACT	31	22	4	1	87.1	0	0	2	0	2	0	0	12.9
Total	**1,088**	**768**	**137**	**50**	**87.8**	**27**	**21**	**36**	**20**	**16**	**6**	**7**	**12.2**

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), and penicillins + β-lactamase inhibitor (amoxicillin-clavulanic acid, CLSI).

Table 20: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, 2018

State or territory	Total	Number of categories (non- multidrug resistant)				Number of categories (multi-drug resistant)			
		0	1	2	%	3	4	5	%
NSW	224	184	10	16	93.8	8	5	1	6.3
Vic	76	66	3	3	94.7	2	2	0	5.3
Qld	178	149	18	6	97.2	3	2	0	2.8
SA	65	47	10	6	96.9	1	0	1	3.1
WA	103	96	4	1	98.1	1	1	0	1.9
Tas	27	16	4	3	–*	3	1	0	–*
NT	20	18	0	2	–*	0	0	0	–*
ACT	32	25	4	3	100	0	0	0	0.0
Total	**725**	**601**	**53**	**40**	**95.7**	**18**	**11**	**2**	**4.3**

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

* 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), fluoroquinolones (ciprofloxacin)

Table 21: Multiple acquired resistance in *Staphylococcus aureus* (methicillin resistant), by state and territory, 2018

State or territory	Total	Number of antimicrobial categories*												
		0	1	2	%<2	3	4	5	6	7	8	9	10	11	%≥2
NSW	116	36	23	12	61.2	17	14	7	7	0	0	0	0	0	38.8
Vic	59	18	18	9	76.3	7	6	0	1	0	0	0	0	0	23.7
Qld	80	47	15	7	86.3	3	1	1	5	0	1	0	0	0	13.8
SA	40	14	13	8	87.5	2	1	1	1	0	0	0	0	0	12.5
WA	103	53	27	18	95.1	4	1	0	0	0	0	0	0	0	4.9
Tas	9	3	0	3	–†	0	1	1	1	0	0	0	0	0	–†
NT	31	16	9	2	87.1	3	0	1	0	0	0	0	0	0	12.9
ACT	11	3	0	6	81.8	2	0	0	0	0	0	0	0	0	18.2
Total	**449**	**190**	**105**	**65**	**80.2**	**38**	**24**	**11**	**15**	**0**	**1**	**0**	**0**	**0**	**19.8**

* Resistant to one or more agent in three or more antimicrobial categories
† Not applicable (insufficient numbers)

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 22: Multiple acquired resistance in *Staphylococcus aureus* (methicillin susceptible), by state and territory, 2018

State or territory	Total	Number of antimicrobial categories*												
		0	1	2	%<2	3	4	5	6	7	8	9	10	11	%≥2
NSW	462	380	61	16	98.9	3	1	1	0	0	0	0	0	0	1.1
Vic	353	302	37	9	98.6	4	0	0	1	0	0	0	0	0	1.4
Qld	488	394	75	11	98.4	6	0	1	1	0	0	0	0	0	1.6
SA	214	167	36	8	98.6	2	0	1	0	0	0	0	0	0	1.4
WA	383	301	72	9	99.7	1	0	0	0	0	0	0	0	0	0.3
Tas	99	85	13	0	99.0	1	0	0	0	0	0	0	0	0	1.0
NT	46	38	5	3	100	0	0	0	0	0	0	0	0	0	0.0
ACT	99	84	14	1	100	0	0	0	0	0	0	0	0	0	0.0
Total	**2,144**	**1,751**	**313**	**57**	**98.9**	**17**	**1**	**3**	**2**	**0**	**0**	**0**	**0**	**0**	**1.1**

* 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, more than half (58.7%) 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 23). For *K. pneumoniae*, 13.9% were resistant to at least one antimicrobial group (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 24). For *P. aeruginosa*, 16.7% were resistant to at least one antimicrobial group (piperacillin–tazobactam, fluoroquinolones, ceftazidime, aminoglycosides and carbapenems) (Table 25). For *S. aureus*, the most common resistance combination was resistance to methicillin and fluoroquinolones (Table 26).

Table 23: Resistance combinations among *Escherichia coli* tested against aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems (n = 4,508), Australia, 2018

Resistance pattern	Number	% of total*
Fully susceptible	**1,862**	**41.3**
Single resistance	**1,708**	**37.9**
Aminopenicillins	1,626	36.1
Fluoroquinolones	70	1.6
Aminoglycosides	12	0.3
Resistance to two antimicrobial groups	**383**	**8.5**
Aminopenicillins + third-generation cephalosporins	161	3.6
Aminopenicillins + fluoroquinolones	135	3.0
Aminopenicillins + aminoglycosides	83	1.8
Fluoroquinolones + aminoglycosides	4	0.1
Resistance to three antimicrobial groups	**377**	**8.4**
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	201	4.5
Aminopenicillins + fluoroquinolones + aminoglycosides	101	2.2
Aminopenicillins + third-generation cephalosporins + aminoglycosides	74	1.6
Aminopenicillins + third-generation cephalosporins + carbapenems	1	0.0
Resistance to four antimicrobial groups	**175**	**3.9**
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	175	3.9
Resistance to five antimicrobial groups	**3**	**0.1**
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	3	0.1

* Only data from isolates tested against all five antimicrobial groups were included

Table 24: Resistance combinations among *Klebsiella pneumoniae* tested against fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems (n = 1,088), Australia, 2018

Resistance pattern	Number	% of total
Fully susceptible	**937**	**86.1**
Single resistance	**56**	**5.1**
Fluoroquinolones	32	2.9
Third-generation cephalosporins	20	1.8
Aminoglycosides	4	0.4
Resistance to two antimicrobial groups	**24**	**2.2**
Third-generation cephalosporins + fluoroquinolones	14	1.3
Fluoroquinolone + aminoglycosides	6	0.6
Third-generation cephalosporins + aminoglycosides	4	0.4
Resistance to three antimicrobial groups	**62**	**5.7**
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	62	5.7
Resistance to four antimicrobial groups	**9**	**0.8**
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	9	0.8

* Only data from isolates tested against all four antimicrobial groups were included

Table 25: Resistance combinations among *Pseudomonas aeruginosa* tested against piperacillin-tazobactam, ceftazidime, fluoroquinolones, aminoglycosides and carbapenems (n = 725), Australia, 2018

Resistance pattern	Number	% of total
Fully susceptible	**604**	**83.3**
Single resistance	**51**	**7.0**
Fluoroquinolones	22	3.0
Piperacillin-tazobactam	18	2.5
Aminoglycosides	8	1.1
Carbapenems	2	0.3
Ceftazidime	1	0.1
Resistance to two antimicrobial groups	**41**	**5.7**
Piperacillin-tazobactam + ceftazidime	29	4.0
Piperacillin-tazobactam + fluoroquinolones	5	0.7
Fluoroquinolones + aminoglycosides	4	0.6
Fluoroquinolones + carbapenems	2	0.3
Piperacillin-tazobactam + aminoglycosides	1	0.1
Resistance to three antimicrobial groups	**18**	**2.5**
Piperacillin-tazobactam + ceftazidime + fluoroquinolones	9	1.2
Piperacillin-tazobactam + ceftazidime + carbapenems	6	0.8
Fluoroquinolones + aminoglycosides + carbapenems	2	0.3
Piperacillin-tazobactam + fluoroquinolones + aminoglycosides	1	0.1
Resistance to four antimicrobial groups	**9**	**1.2**
Piperacillin-tazobactam + ceftazidime + fluoroquinolones + carbapenems	9	1.2
Resistance to five antimicrobial groups	**2**	**0.3**
Piperacillin-tazobactam + ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	2	0.3

* Only data from isolates tested against all five antimicrobial groups were included

Table 26: Resistance combinations among *Staphylococcus aureus* tested against methicillin, fluoroquinolones and rifampicin (n = 2,666), Australia, 2018

Resistance pattern	N	% of total
Fully susceptible	**2,135**	**80.1**
Single resistance	362	13.6
Methicillin	299	11.2
Fluoroquinolones	58	2.2
Rifampicin	5	0.2
Resistance to two antimicrobial groups	162	6.0
Methicillin + fluoroquinolones	159	7.8
Fluoroquinolones + rifampicin	2	0.1
Methicillin + rifampicin	1	<0.1
Resistance to three antimicrobial groups	7	0.3
Methicillin + fluoroquinolones + rifampicin	7	0.3

* Only data from isolates tested against all three antimicrobial groups were included

Multidrug resistance by onset setting and 30-day all-cause mortality

Multidrug resistances by onset setting (community or hospital) and 30-day all-cause mortality for the most common species are shown in Table 27.

Table 27: Multidrug resistance, by onset setting and 30-day all-cause mortality, 2018

Species	Category	Total		Community onset		Hospital onset	
		Number	Deaths, % (n)	Number	Deaths,% (n)	Number	Deaths, % (n)
Escherichia coli	Total	2,904	9.4 (274)	2,383	8.6 (205)	521	13.2 (69)
	Non-MDR (≤2)	2,072	8.6 (178)	1,753	7.9 (138)	319	12.5 (40)
	MDR (>2)	832	11.5 (96)	630	10.6 (67)	202	14.4 (29)
Enterobacter cloacae complex	Total	301	12.3 (37)	157	12.1 (19)	144	12.5 (18)
	Non-MDR (≤2)	274	12.0 (33)	145	11.0 (16)	129	13.2 (17)
	MDR (>2)	27	14.8 (4)	12	25.0 (3)	15	6.7 (1)
Enterococcus faecalis	Total	435	14.0 (61)	289	13.5 (39)	146	15.1 (22)
	Non-MDR (≤2)	435	14.0 (61)	289	13.5 (39)	146	15.1 (22)
	MDR (>2)	0	n/a	0	n/a	0	n/a
Enterococcus faecium	Total	327	28.1 (92)	92	20.7 (19)	235	31.1 (73)
	Non-MDR (≤2)	135	20.7 (28)	47	17.0 (8)	88	22.7 (20)
	MDR (>2)	192	33.3 (64)	45	24.4 (11)	147	36.1 (53)
Klebsiella pneumoniae	Total	764	12.0 (92)	536	10.4 (56)	228	15.8 (36)
	Non-MDR (≤2)	663	11.2 (74)	485	9.9 (48)	178	14.6 (26)
	MDR (>2)	101	17.8 (18)	51	15.7 (8)	50	20.0 (10)
Staphylococcus aureus[†]	Total	2,057	14.0 (288)	1,598	13.3 (213)	459	18.7 (75)
	Non-MDR (≤2)	1,887	13.6 (257)	1,477	13.1 (193)	410	18.3 (64)
	MDR (>2)	170	18.2 (31)	121	16.5 (20)	49	22.4 (11)
Pseudomonas aeruginosa	Total	521	18.4 (96)	296	18.9 (56)	225	17.8 (40)
	Non-MDR (≤2)	497	18.1 (90)	286	18.9 (54)	211	17.1 (36)
	MDR (>2)	24	25.0 (6)	10	20.0 (2)	14	28.6 (4)

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable

* Insufficient numbers (<10) to calculate percentage

Note: Antimicrobial categories (agents) for each species are listed under Tables 15 to 22. For *Staphylococcus aureus,* anti-staphylococcal β-lactams (cefoxitin) is also included

3.9. Molecular studies

This section describes the results of molecular studies of the resistance 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

Molecular studies were used to examine the resistance of gram-negative organisms to third-generation cephalosporins, quinolones and carbapenems, and to monitor the epidemiology of *E. coli* sequence type 131.

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: the presence of 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. 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 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.

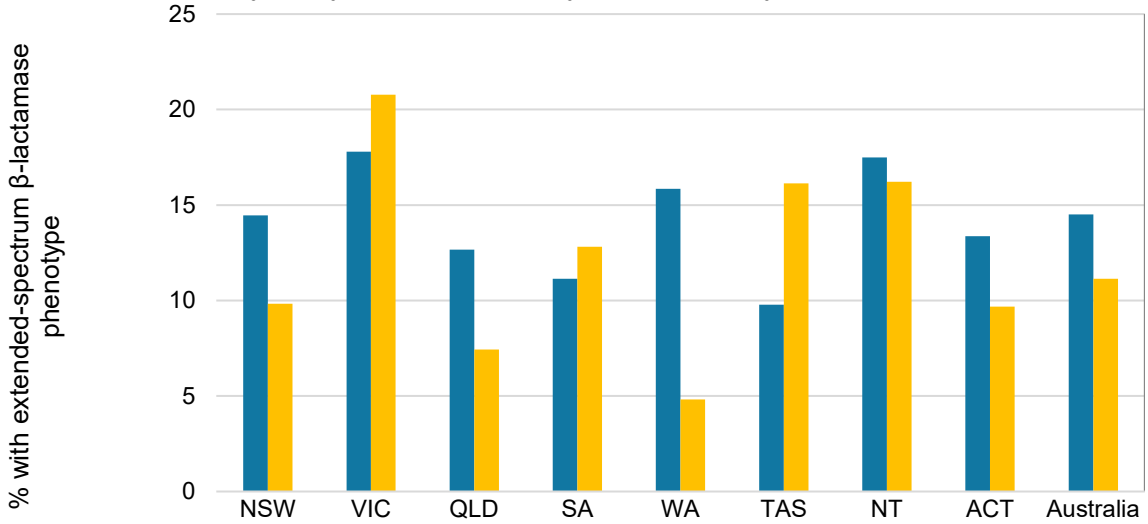
Neither ceftriaxone nor ceftazidime testing will identify ESBL production in *Enterobacter* species because of their intrinsic chromosomal AmpC β-lactamase. In Enterobacter, cefepime MICs of greater than 0.25 mg/L suggest that an isolate of this genus harbours an ESBL.[44] However, because of the susceptibility card range, isolates with a cefepime MIC of greater than 1 mg/L were selected for molecular testing.

Testing included screening for TEM, SHV, CTX-M and plasmid-borne *ampC* genes using molecular methods outlined in Appendix B. TEM screening does not accurately discriminate between TEM-1/2 genes, which encode narrow-spectrum β-lactamases, and TEM genes with higher numbers, which encode ESBLs. Similarly, SHV screening does not discriminate between genes for narrow-spectrum β-lactamases and those that encode ESBLs. SHV-1 is the chromosomally encoded enzyme that gives *K. pneumoniae* its characteristic amoxicillin resistance. *E. coli* isolates containing only TEM genes and *Klebsiella* species containing only SHV genes have not been classified as carrying an ESBL in this analysis. All CTX-M genes encode ESBLs, as in effect do plasmid-borne *ampC* genes.

E. coli and *K. pneumoniae* resistant to ceftriaxone and/or ceftazidime (MIC >1 mg/L), and their variation across states and territories, are shown in Figure 9. The presumptive and confirmed ESBLs by state and territory are shown in Table 28.

ESBL phenotypes were significantly more likely to be found among hospital onset than community onset episodes of *E. coli* bacteraemia (149/701 [21.3%] vs 514/3,868 [13.3%]; P < 0.01), *K. pneumoniae* bacteraemia (57/297 [19.2%] vs 66/807 [8.2%]; P < 0.01), and *E. cloacae* bacteraemia (36/198 [18.2%] vs 20/221 [9.0%]; P < 0.01).

Figure 9. Percentage of *Escherichia coli* and *Klebsiella pneumoniae* with extended-spectrum β-lactamase phenotype, by state and territory, and nationally, 2018



	NSW	VIC	QLD	SA	WA	TAS	NT	ACT	Australia
E. coli, %	14.5	17.8	12.7	11.1	15.9	9.8	17.5	13.4	14.5
K. pneumoniae, %	9.8	20.8	7.4	12.8	4.8	16.1	16.2	9.7	11.1
E. coli (n = 4,569)	177	137	110	45	127	18	28	21	663
K. pneumoniae (n = 1,104)	28	43	20	10	8	5	6	3	123

Table 28: Numbers of isolates with extended-spectrum β-lactamase phenotype, by state and territory, 2018

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,224	770	869	404	801	184	160	157	4,569
ESBL phenotype	177	137	110	45	127	18	28	21	663
Confirmed									
Any ESBL*/number received, n (%)	163/171 (95.3)	126/131 (96.2)	98/108 (90.7)	37/43 (86.0)	121/125 (96.8)	16/18 (88.9)	27/28 (96.4)	20/21 (95.2)	608/645 (94.3)
CTX-M types	130	115	81	25	116	13	26	19	525
Plasmid-borne AmpC	32	17	17	10	11	3	4	2	96
SHV	1	1	1	2	0	0	0	0	5
Klebsiella pneumoniae	285	207	269	78	166	31	37	31	1,104
ESBL phenotype	28	43	20	10	8	5	6	3	123
Confirmed									
Any ESBL*/number received, n (%)	24/27 (88.9)	38/42 (90.5)	18/20 (90.0)	7/9 (n/a)	8/8 (n/a)	5/5 (n/a)	6/6 (n/a)	2/3 (n/a)	108/120 (90.0)
CTX-M types	23	35	10	5	7	4	4	1	89
Plasmid-borne AmpC	1	0	7	3	0	1	1	0	13
TEM	15	33	12	6	7	2	3	2	80
Klebsiella oxytoca	66	52	29	20	34	16	2	11	230
ESBL phenotype	5	5	4	0	3	1	0	2	20
Confirmed									
Any ESBL*/number received	0/5	1/5	0/4	0/0	0/3	0/1	0/0	0/2	1/20 (5.0)
CTX-M types	0	0	0	n/a	0	0	n/a	0	0
SHV	0	1	0	n/a	0	0	n/a	0	1
Proteus mirabilis	74	44	43	27	49	6	8	8	258
ESBL phenotype	4	0	0	0	2	0	0	0	6
Confirmed									
Any ESBL*/number received	3/4	0/0	0/0	0/0	0/2	0/0	0/0	0/0	3/6
CTX-M types	1	n/a	n/a	n/a	0	n/a	n/a	n/a	1
Plasmid-borne AmpC	2	n/a	n/a	n/a	0	n/a	n/a	n/a	2
TEM	1	n/a	n/a	n/a	0	n/a	n/a	n/a	1
Salmonella species (non-typhoidal)	26	16	29	3	15	4	12	1	106
ESBL phenotype	0	0	0	0	0	0	0	0	0

ESBL = extended-spectrum β-lactamase; n/a = not applicable
* Isolates may possess more than one type of ESBL gene
† See text for an explanation of the low proportion of ESBL

Based on the tests performed in this study, ESBLs were more common among *E. coli* (13.3% confirmed) and *K. pneumoniae* (9.8% confirmed) than among other species. For *Enterobacter* species with cefepime MIC greater than 1 mg/L, 24 of 54 *E. cloacae* complex (44%; 5.7% overall) contained an ESBL. Of identified ESBLs, *E. cloacae* contained the following types: TEM and SHV (*n* = 4), CTX-M group 1 and TEM (*n* = 5), CTX-M group 1 only (*n* = 1), CTX-M group 9 and SHV (*n* = 2), SHV only (*n* = 2), CTX-M group 1 and CTX-M Group 9 (*n* = 1), and TEM only (*n* = 9). Eight of 24 *E. cloacae* complex with confirmed ESBLs also contained carbapenemases (bla_{IMP-4} [*n* = 8]).

The majority (96%) of *K. oxytoca* isolates with a ceftriaxone-resistant phenotype were presumably hyperproducers of K1 β-lactamase, the natural chromosomal enzyme in this species, with characteristic resistance to piperacillin–tazobactam and borderline resistance to cefepime, but susceptibility to ceftazidime. This pattern is not typical of other types of gram-negative β-lactamases.

As expected, the CTX-M-type ESBL genes were prominent in *E. coli*. Of 609 confirmed ESBLs, 525 (86.3%; range 67.6–96.3%) had CTX-M types detected by consensus primers targeting CTX-M group 1 (*n* = 250), CTX-M group 9 (*n* = 273), and CTX-M group 1 + group 9 (*n* = 2). Among *K. pneumoniae* with confirmed ESBLs, 89 of 108 (82.4%) contained CTX-M types: CTX-M group 1 (*n* = 79), CTX-M group 9 (*n* = 7), and CTX-M group 1 + group 9 (*n* = 3).

Plasmid-borne AmpC β-lactamases

Plasmid-borne AmpC β-lactamases 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-borne 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 already naturally possess chromosomally encoded AmpC enzymes.

The proportions of *E. coli* and *K. pneumoniae* with elevated cefoxitin MICs were low. Only 51% (93/183) of *E. coli* and 22% (13/59) of *K. pneumoniae* with cefoxitin MIC ≥32 mg/L that were available for molecular confirmation were confirmed to contain plasmid-borne *ampC* genes (Table 29).

The bla_{CMY} gene was found in 61% (57/93) of *E. coli* with plasmid-borne *ampC* genes; bla_{DHA} was found in 85% (11/13) of *K. pneumoniae* with plasmid-borne *ampC* genes.

Carbapenemase genes were detected in seven of 46 cefoxitin-resistant (MIC ≥ 32 mg/L) *K. pneumoniae* (bla_{IMP-4}, *n* = 2; bla_{KPC-2}, *n* = 2; $bla_{OXA-181}$, *n* = 2; bla_{NDM-4}, *n* = 1) and two *E. coli* (bla_{NDM-5}, bla_{OXA-48}) that did not have plasmid-borne *ampC* genes. Seven *E. coli* with a cefoxitin MIC of <32 mg/L also contained bla_{CMY} (*n* = 6) or bla_{DHA} (*n* = 1). One *K. pneumoniae* (bla_{DHA}) and one *P. mirabilis* (bla_{CMY}) also had cefoxitin MIC < 32 mg/L.

Table 29: Numbers of isolates with presumptive plasmid-borne AmpC β-lactamase production, by state and territory, 2018

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,220	770	869	404	801	184	160	157	4,565
Cefoxitin MIC ≥32 mg/L (%)	55 (4.5)	28 (3.6)	34 (3.9)	20 (5.0)	27 (3.4)	8 (4.3)	8 (5.0)	6 (3.8)	186 (4.1)
Confirmed/number received	33/54	17/27	17/33	10/20	9/27	3/8	2/8	2/6	93/183
bla_{CMY}	22	12	10	4	5	1	1	2	57
bla_{DHA}	11	5	7	6	4	2	1	0	36
Klebsiella pneumoniae	283	207	269	78	166	31	37	31	1,102
Cefoxitin MIC ≥32 mg/L (%)	19 (6.7)	12 (5.8)	15 (5.6)	4 (5.1)	4 (2.4)	3 (9.7)	1 (2.7)	4 (12.9)	62 (5.6)
Confirmed/number received	1/16	0/12	7/15	3/4	0/4	1/3	1/1	0/4	13/59
bla_{DHA}	0	0	7	2	0	1	1	0	11
bla_{CMY}	1	0	0	1	0	0	0	0	2

MIC = minimum inhibitory concentration; n/a = not applicable

Carbapenemases

Thirty-one (0.37%) isolates from 27 patients were found to harbour a carbapenemase gene (Table 30). The *bla*$_{IMP-4}$ gene was detected in 14 isolates from 11 patients: *E. cloacae* complex [8, from 5 patients], *K. pneumoniae* [2], *K. aerogenes* [1]*, K. variicola* [1]*, C. freundii* [1]*,* and one *A. radioresistens* which also harboured *bla*$_{OXA-23+OXA-96}$; *bla*$_{OXA-48}$ was detected in two *E. coli* and one *K. pneumoniae*; *bla*$_{OXA-181}$ was detected in two *K. pneumoniae; bla*$_{KPC-2}$ was detected in two *K. pneumoniae,* and *bla*$_{KPC-3}$ in two *K. pneumoniae* from one patient; *bla*$_{NDM-5}$ was detected in two *E. coli* and *bla*$_{NDM-4}$ in one *K. pneumoniae*; *bla*$_{GES-5}$ was detected in three *P. aeruginosa*, and *bla*$_{OXA-23}$ was detected in one *A. baumannii* and one *A. pittii*. Fourteen of 16 Enterobacterales with confirmed metallo-β-lactamases also contained plasmid-mediated quinolone resistance genes (*aac[6']- Ib-cr* alone or with *qnrB* or *qnrA*).

One *E. coli* with *bla*$_{OXA-48}$ had a meropenem MIC = 0.25 mg/L; all other isolates with confirmed carbapenemases had meropenem MICs >1 mg/L.

Three *E. cloacae* and one *P. aeruginosa* demonstrated carbapenemase activity by the carbapenem inactivation method (CIM), but were negative for IMP, VIM, KPC, NDM, OXA-48- like, SIM, GIM, SPM, BIC, DIM, AIM, GES, SME, IMI or FRI carbapenemases. All four isolates contained AmpC genes (ACT-28 [1], MIR-3 [2]), PDC-5 [1]).

Overall prevalence of carbapenemase genes (excluding isolates from the same patient) among Enterobacterales was 0.28% (21/7,512). This consisted of 13 isolates (10 patients) with *bla*$_{IMP-4}$ gene, four (three patients) with *bla*$_{KPC,}$ three with *bla*$_{OXA–48}$, three with *bla*$_{NDM}$ and two with *bla*$_{OXA–181,}$ It was 0.40% (3/742) for *P. aeruginosa* and 3.2% (3/95) for *Acinetobacter* species.

Table 30: Number of carbapenemases and associated resistance genes, by species, and state and territory, 2018

Gene	S/T	Species	ST	MEM MIC (mg/L)	ESBL type*	PMQR gene†	RMT	MCR
bla$_{IMP-4}$ (*n* = 13)	NSW	*E. hormaechei* (*n* = 3)#	114	≥ 16	–§	*aac(6')-Ib-crA, qnrB2, qnrA1*	–§	mcr-9.1
	NSW	*E. hormaechei* (*n* = 1)	66	≥ 16	SHV-12	*aac(6')-Ib-crA, qnrB2*	–§	mcr-9.1
	NSW	*E. hormaechei* (*n* = 1)	108	≥ 16	–§	*qnrB2*	–§	–§
	NSW	*E. cloacae* (*n* = 1)	–§	2	–§	*aac(6')-Ib-crA, qnrB2, qnrA1*	–§	mcr-9.1
	NSW	*E. hormaechei* (*n* = 1)#	114	4	–§	*aac(6')-Ib-crA, qnrA1*	–§	mcr-9.1
	NSW	*K. aerogenes* (*n* = 1)	–§	4	–§	*aac(6')-Ib-crA*	–§	–§
	NSW	*K. variicola* (*n* = 1)	–§	≥ 16	–§	–§	–§	–§
	Qld	*E. hormaechei* (*n* = 1)	527	≥ 16	SHV-12	*aac(6')-Ib-crA, qnrB2*	–§	mcr-9.1
	WA	*K. pneumoniae* (*n* = 1)	45	≥ 16	–§	–§	–§	–§
	ACT	*Citrobacter freundii* (*n* = 1)	8	≥ 16	SHV-12	*aac(6')-Ib-crA, qnrB2*	–§	mcr-9.1
	ACT	*K. pneumoniae* (*n* = 1)	–§	≥ 16	–§	*qnrB2*	–§	–§
bla$_{IMP-4+OXA-23+OXA-96}$(*n* = 1)	Qld	*A. radioresistens* (*n* = 1)	–§	≥ 16	–§	–§	–§	–§
bla$_{OXA-48}$ (*n* = 3)	NSW	*K. pneumoniae* (*n* = 1)	307	8	SHV-28, CTX-M-15	*aac(6')-Ib-crC, qnrB1*	–§	–§
	NSW	*E. coli* (*n* = 1)	405	4	CTX-M-15	–§	–§	–§
	NSW	*E. coli* (*n* = 1)	69	0.25	TEM-33	–§	–§	–§
bla$_{OXA-181}$ (*n* = 2)	NSW	*K. pneumoniae* (*n* = 2)	147	≥ 16	CTX-M-15	*qnrS1*	–§	–§
bla$_{KPC-2}$ (*n* = 2)	Vic	*K. pneumoniae* (*n* = 2)	258	≥ 16	–§	–§	–§	–§
bla$_{KPC-3}$ (*n* = 2)	NSW	*K. pneumoniae* (*n* = 2)**	307	≥ 16	SHV-28, CTX-M-15	*aac(6')-Ib-crC, qnrB1*	–§	–§
bla$_{NDM-4}$ (*n* = 1)	NSW	*K. pneumoniae* (*n* = 1)	15	≥ 16	SHV-28, CTX-M-14, CTX-M 15	*aac(6')-Ib-cr, qnrS1*	–§	–§
bla$_{NDM-5}$ (*n* = 2)	NSW	*E. coli* (*n* = 1)	44	≥ 16	CTX-M-15	*aac(6')-Ib-crC*	–§	–§
	NSW	*E. coli* (*n* = 1)	410	≥ 16	CTX-M-15, CMY-2	*aac(6')-Ib-crC*	–§	–§
bla$_{GES-5}$ (*n* = 3)	NSW	*P. aeruginosa* (*n* = 2)	–§	≥ 16	–§	–§	–§	–§
	SA	*P. aeruginosa* (*n* = 1)	–§	≥ 16	–§	–§	–§	–§
bla$_{OXA-23}$ (*n* = 2)	Qld	*A. baumannii* (n = 1)	2	≥ 16	–§	–§	*armA*	–§
	WA	*A. pittii* (n = 1)	64	≥ 16	–§	–§	–§	–§

ESBL = extended-spectrum β-lactamase; MCR = mobile colistin resistance; MEM = meropenem; MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance; RMT = ribosomal methyltransferase; ST = sequence type; S/T = state or territory

* TEM types, SHV types, CTX-M types, pAmpC

† *aac(6')-Ib-cr*, *qnr*, efflux (*qepA*, *oqxAB*)

§ Not detected

Four *bla*$_{IMP-4}$ from the same patient, collected more than 14 days after the initial positive blood culture

** Two *bla*$_{KPC-3}$ from the same patient

Plasmid-mediated quinolone resistance

Quinolone resistance is most commonly due to mutations in DNA gyrase and topoisomerase IV. More recently, transmissible plasmid-mediated quinolone resistance (PMQR) has emerged in Enterobacterales. PMQR may be due to the presence of *qnr* genes (*qnrA, qnrB, qnrS, qnrC, qnrD); aac(6')-Ib-cr*, coding for a variant aminoglycoside acetyltransferase enzyme; or genes coding for efflux pumps (*qepA*, *oqxAB*).

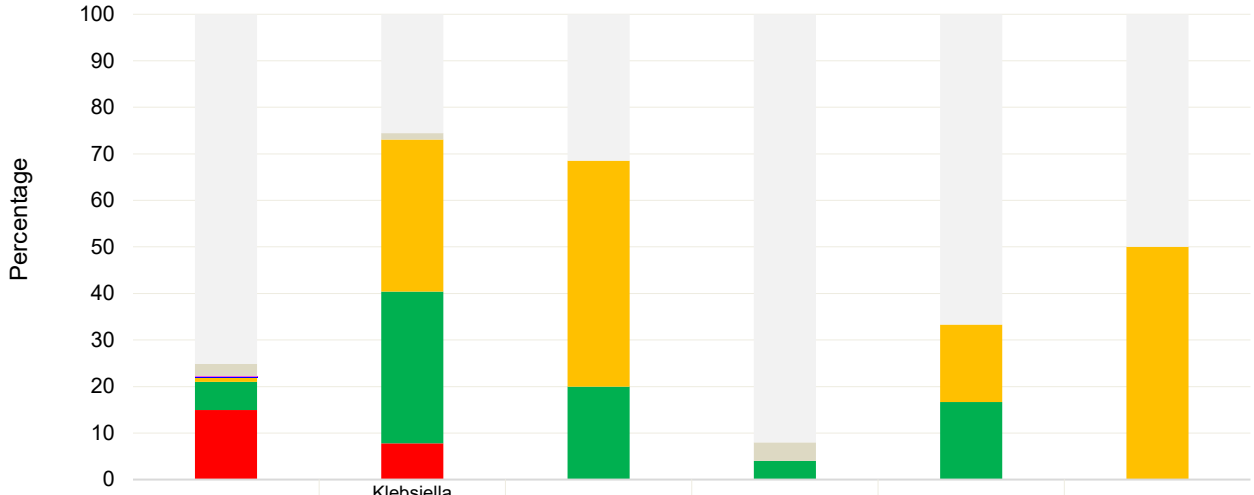
Of isolates with ciprofloxacin MIC greater than 0.25 mg/L, 23% of *E. coli,* 74% of *K. pneumoniae* and 69% of *E. cloacae* were confirmed to contain PMQRs (Table 31). The proportion and type of PMQR determinant found among isolates with ciprofloxacin MIC greater than 0.25 mg/L varied among the different species (Figure 10). The *aac(6')-Ib-cr* gene, with or without *qnr*, was the dominant gene responsible for fluoroquinolone resistance, and was present in five of the six species.

Table 31: Number and percentage of isolates with plasmid-mediated quinolone resistance, by species, and state and territory, 2018

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli									
Percent ciprofloxacin MIC >0.25 mg/L* (*n*)	20.7 (253)	20.1 (155)	14.5 (126)	16.8 (68)	23.6 (189)	10.3 (19)	20.6 (33)	21.0 (33)	19.2 (876)
Confirmed/number received	50/243 (20.6)	40/149 (26.8)	26/124 (21.0)	17/66 (25.8)	47/186 (25.3)	1/18 (5.6)	8/33 (24.2)	5/33 (15.2)	194/852 (22.8)
aac(6')Ib-cr	29	27	19	11	37	0	5	3	131
aac(6')Ib-cr; qnrB	1	2	0	2	2	0	0	0	7
aac(6')Ib-cr; qnrS	0	0	1	0	0	0	0	0	1
aac(6')Ib-cr; qnrB; oqxAB	0	1	0	0	0	0	0	0	1
qnrS	14	8	4	0	7	0	3	2	38
qnrB	5	1	2	4	1	1	0	0	14
qnrA	0	1	0	0	0	0	0	0	1
QepA	1	0	0	0	0	0	0	0	1
Klebsiella pneumoniae									
Percent ciprofloxacin MIC >0.25 mg/L* (*n*)	10.9 (31)	25.1 (52)	7.8 (21)	12.8 (10)	9.0 (15)	12.9 (4)	13.5 (5)	9.7 (3)	12.8 (141)
Confirmed/number received	21/30 (70.0)	40/51 (78.4)	17/21 (81.0)	8/10 (80.0)	8/15 (53.3)	1/4 (25.0)	5/5 (100.0)	3/3 (100.0)	103/139 (74.1)
aac(6')-Ib-cr	4	2	0	0	2	0	2	1	11
aac(6')-Ib-cr + qnrB	4	28	5	5	2	0	2	0	46
qnrS	13	9	4	2	4	1	0	0	33
qnrB	0	1	8	1	0	0	1	2	13
Enterobacter cloacae									
Percent ciprofloxacin MIC >0.25 mg/L* (*n*)	12.1 (14)	4.6 (3)	8.5 (10)	6.7 (2)	7.4 (4)	0.0 (0)	8.3 (1)	–† (1)	8.4 (35)
Confirmed/number received	10/14 (71.4)	2/3 (66.7)	9/10 (90.0)	2/2 (100.0)	1/4 (25.0)	n/a	0/1 (0.0)	0/1 (0.0)	24/35 (68.6)
aac(6')Ib-cr; qnrB	2	0	8	0	0	0	0	0	10
aac(6')Ib-cr; qnrA	2	0	0	1	0	0	0	0	3
aac(6')Ib-cr; qnrA; qnrB	4	0	0	0	0	0	0	0	4
qnrB	2	0	1	0	0	0	0	0	3
qnrS	0	0	0	1	1	0	0	0	2
qnrA	0	2	0	0	0	0	0	0	2

MIC = minimum inhibitory concentration; n/a = not applicable (insufficient numbers)
* Concentration used to select isolates for molecular testing
† Insufficient numbers (< 10) to calculate percentage

Figure 10. Proportion of plasmid-mediated quinolone resistance genes among gram-negative species with ciprofloxacin MIC >0.25 mg/L, 2018



	Escherichia coli (n = 876)	Klebsiella pneumoniae (n = 141)	Enterobacter cloacae complex (n = 35)	Salmonella species (typhoidal) (n = 25)	Klebsiella aerogenes (n = 6)	Citrobacter freundii complex (n = 4)
Not detected	75.1	25.5	31.4	92.0	66.7	50.0
Not available	2.7	1.4	0.0	4.0	0.0	0.0
CR + oqxAB	0.1	0.0	0.0	0.0	0.0	0.0
QepA	0.1	0.0	0.0	0.0	0.0	0.0
CR + Qnr	0.9	32.6	48.6	0.0	16.7	50.0
Qnr	6.1	32.6	20.0	4.0	16.7	0.0
CR	15.0	7.8	0.0	0.0	0.0	0.0

CR = *aac(6')-Ib-cr*

Escherichia coli sequence type 131

Sequence type 131 (O25b-ST131) is the main *E. coli* lineage among extra-intestinal pathogenic *E. coli* worldwide. O25b-ST131 isolates are commonly reported to produce ESBLs, such as CTX-M-15, and almost all O25b-ST-131 isolates with CTX-M-15 are resistant to fluoroquinolones.

Most of the isolates with an ESBL phenotype harboured genes of the CTX-M type (527/645; 81.7%) (Table 32). Fifty-one per cent (128/252) of the *E. coli* with CTX-M group 1 types (CTX-M-15 like) were found to belong to the O25b-ST131 lineage. O25b-ST131 accounted for 62.6% (199/318) of *E. coli* ESBL phenotypes that were ciprofloxacin resistant (MIC >1 mg/L), but only 3.7% (12/327) of ciprofloxacin-susceptible ESBL phenotypes. O25b-ST131 often carried *bla*CTX-M-15 and *aac*(*6')-Ib-cr*.

Table 32: Number of *Escherichia coli* with ESBL phenotype, by O25b-ST131 clone and ciprofloxacin resistance, 2018

		CTX-M types			Ciprofloxacin MIC	
Clone	Total	CTX-M-15-like	CTX-M-15like + CTX-M 14 like	Non-CTX-M-15	>1 mg/L	≤1 mg/L
O25b-ST131	211	128	0	77	199	12
Non-O25b-ST131	434	124	2	196	119	315
Total	645	252	2	273	318	327

ESBL = extended spectrum β-lactamase; MIC = minimum inhibitory concentration

Plasmid-mediated colistin determinants

Because colistin is currently only available on the Phoenix cards, only 1,089 (13.6%) isolates from four laboratories were tested for colistin susceptibility. Excluding intrinsically resistant species, 3/1,006 (0.3%) had colistin MIC >2 mg/L (*E. coli,* n = 2; and *A. radioresistens*, n = 1).

All referred isolates were screened for the presence of plasmid-mediated colistin determinants, *mcr-1*, *mcr-2* and *mcr-3*, regardless of the resistance profile.

Of 1,580 (18.9%) isolates (which excluded intrinsically resistant species) available, mcr-1.1 was detected in 2/575 (0.35%) *E. coli*. These two isolates were from two different institutions in New South Wales. Both isolates were meropenem susceptible, and had colistin MIC = 4 mg/L.

Of interest, eight isolates (from five patients) with IMP-4 carbapenemase (*E. hormaechei* [n = 6, three patients], *E. cloacae* [n = 1], *Citrobacter freundii* [n = 1]) also harboured mcr-9.1 (Table 30). An additional two *E. cloacae* (from one patient) that were CIM positive, but carbapenemase genes were not detected, harboured mcr-10.1. The mcr-9 gene has recently been found among several species of Enterobacterales, and the expression of mcr-9 was inducible by subinhibitory concentrations of colistin.[45]

3.9.2. Molecular epidemiology of *Enterococcus faecium*

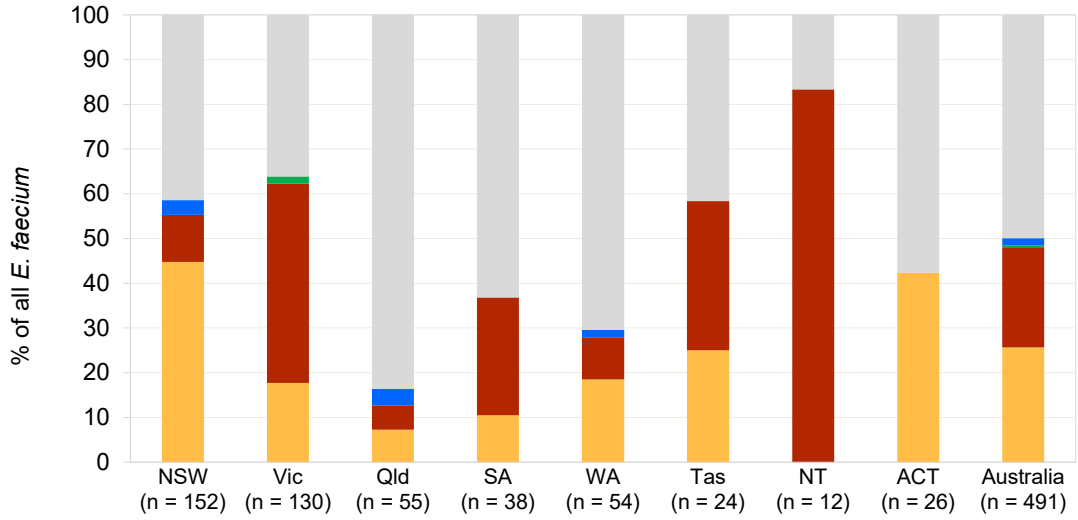
van genes

Results of Polymerase Chain Reaction testing for *vanA* and *vanB* genes were available for 483 (98.3%) of the 491 *E. faecium* isolates. *van* genes were detected in 49.3% (238/483) of *E. faecium*; *vanA* in 126 (26.1%), *vanB* in 110 (22.8%), and *vanA* and *vanB* in two (0.4%) isolates (Figure 11).

For vancomycin-resistant *E. faecium* (MIC > 4 mg/L), *vanA* was detected in 116/220 (52.7%), *vanB* in 102 (46.4%), and *vanA* and *vanB* in two (0.9%).

In 18 of 263 (6.8%) vancomycin-susceptible *E. faecium*; *van* genes were detected: 10 with *vanA* and eight with *vanB*. All isolates had vancomycin MIC ≤ 2 mg/L.

Figure 11: Vancomycin genotype of *Enterococcus faecium* isolates, by state and territory, and nationally, 2018



	NSW (n = 152)	Vic (n = 130)	Qld (n = 55)	SA (n = 38)	WA (n = 54)	Tas (n = 24)	NT (n = 12)	ACT (n = 26)	Australia (n = 491)
not vanA or vanB (n = 245)	41.4	36.2	83.6	63.2	70.4	41.7	16.7	57.7	49.9
Not determined (n = 8)	3.3	0.0	3.6	0.0	1.9	0.0	0.0	0.0	1.6
vanA and vanB (n = 2)	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.4
vanB (n = 110)	10.5	44.6	5.5	26.3	9.3	33.3	83.3	0.0	22.4
vanA (n = 126)	44.7	17.7	7.3	10.5	18.5	25.0	0.0	42.3	25.7

Multilocus sequence type

Of the 491 *E. faecium* isolates reported, 465 (94.7%) were available for typing by whole genome sequencing (Table 33). Based on the MLST, 58 sequence types (STs) were identified. Overall, 74.4% of *E. faecium* could be characterised into six STs: ST17 (n = 88); ST1424, formerly known as M-type 3 (n = 73); ST796 (n = 64); ST1421, formerly known as M-type 1 (n = 55); ST80 (n = 55); and ST262 (n = 11). The *pstS* housekeeping gene is absent in the M-type isolates. M-type 1 was initially identified in 2015. In 2018, there were three M-type single locus variants. There were 32 STs with a single isolate.

ST17 was the predominant ST in Queensland and Western Australia. ST1424 was detected in all states and territories except Western Australian and the Northern Territory and was the predominant ST in New South Wales. ST1421 was detected in all states and territories except South Australia, Western Australia and the Northern Territory. ST796 was the predominant ST in Victoria, and ST262 was found in four states and territories, most commonly in South Australia.

The distribution of vancomycin-resistant *E. faecium* sequence types throughout Australian states and territories is shown in Figure 12.

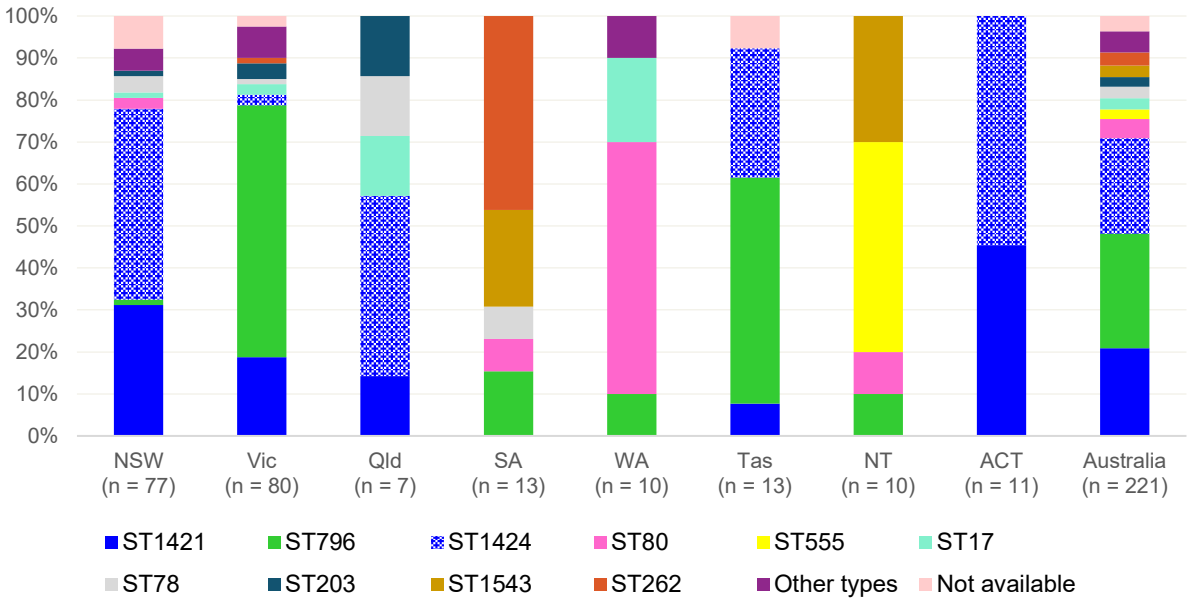
Table 33: *Enterococcus faecium* MLST, by state and territory, 2018

	Percentage, % (*n*)								
MLST	**NSW**	**Vic**	**QLD**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST17	7.2 (10)	9.8 (12)	58.5 (31)	21.1 (8)	46.2 (24)	13.0 (3)	0.0 (0)	0.0 (0)	18.9 (88)
ST1424	38.1 (53)	1.6 (2)	5.7 (3)	2.6 (1)	0.0 (0)	21.7 (5)	0.0 (0)	36.0 (9)	15.7 (73)
ST796*	1.4 (2)	39.8 (49)	0.0 (0)	7.9 (3)	1.9 (1)	34.8 (8)	8.3 (1)	0.0 (0)	13.8 (64)
ST1421	21.6 (30)	12.2 (15)	1.9 (1)	0.0 (0)	0.0 (0)	4.3 (1)	0.0 (0)	32.0 (8)	11.8 (55)
ST80†	8.6 (12)	7.3 (9)	5.7 (3)	13.2 (5)	38.5 (20)	0.0 (0)	16.7 (2)	16.0 (4)	11.8 (55)
ST262	0.0 (0)	0.8 (1)	0.0 (0)	21.1 (8)	1.9 (1)	0.0 (0)	0.0 (0)	4.0 (1)	2.4 (11)
Other types (n = 56)	23.0 (32)	28.5 (35)	28.3 (15)	34.2 (13)	11.5 (6)	26.1 (6)	75.0 (9)	12.0 (3)	25.6 (119)
Total	**139**	**123**	**53**	**38**	**52**	**23**	**12**	**25**	**465**

MLST = multi-locus sequence type; slv = single locus variant(s)

* includes one slv
† Includes two slv

Figure 12: Distribution of vancomycin-resistant *Enterococcus faecium* sequence types, by state and territory, 2018



MLST and *van* genes

The *vanA* gene alone was detected in nine STs; ST1424 (*n* = 53), ST1421 (*n* = 45), ST80 (*n* = 12), ST262 (*n* = 4), ST203 (*n* = 2), and one each of ST18, ST252, ST789, and ST992. The *vanB* gene alone was detected in 12 STs: ST796 (*n* = 62), ST78 (*n* = 8), ST17 (*n* = 7), ST1543 (*n* = 6), ST555 (*n* = 5), ST203 (*n* = 4), ST341 (*n* = 4), ST80 (*n* = 3), ST262 (n = 3), ST252 (n =2), ST1424 (n = 2), and ST233 (*n* = 1) (Table 34). Isolates with both *vanA* and *vanB* genes were found in ST796 (*n* = 1) and ST1421 (*n* = 1).

Table 34: *Enterococcus faecium* MLST harbouring *vanA* and/or *vanB* genes, 2018

MLST	*vanA*, %* (*n*)	*vanB*, %* (*n*)	*vanA* and *vanB*, %* (*n*)	*vanA* or *vanB* not detected, %* (n)	Total, *n*
ST17	0.0 (0)	8.0 (7)	0.0 (0)	92.0 (81)	88
ST1424 (M-type 3)	72.6 (53)	2.7 (2)	0.0 (0)	24.7 (18)	73
ST796†	0.0 (0)	96.9 (62)	1.6 (1)	1.6 (1)	64
ST1421 (M-type 1)	81.8 (45)	0.0 (0)	1.8 (1)	16.4 (9)	55
ST80§	21.8 (12)	5.5 (3)	0.0 (0)	72.7 (40)	55
ST262	36.4 (4)	27.3 (3)	0.0 (0)	36.4 (4)	11
Other types (n = 53)	5.0 (6)	25.8 (31)	0.0 (0)	69.2 (83)	120
Total	**25.8 (120)**	**23.2 (108)**	**0.4 (2)**	**50.6 (236)**	**466**

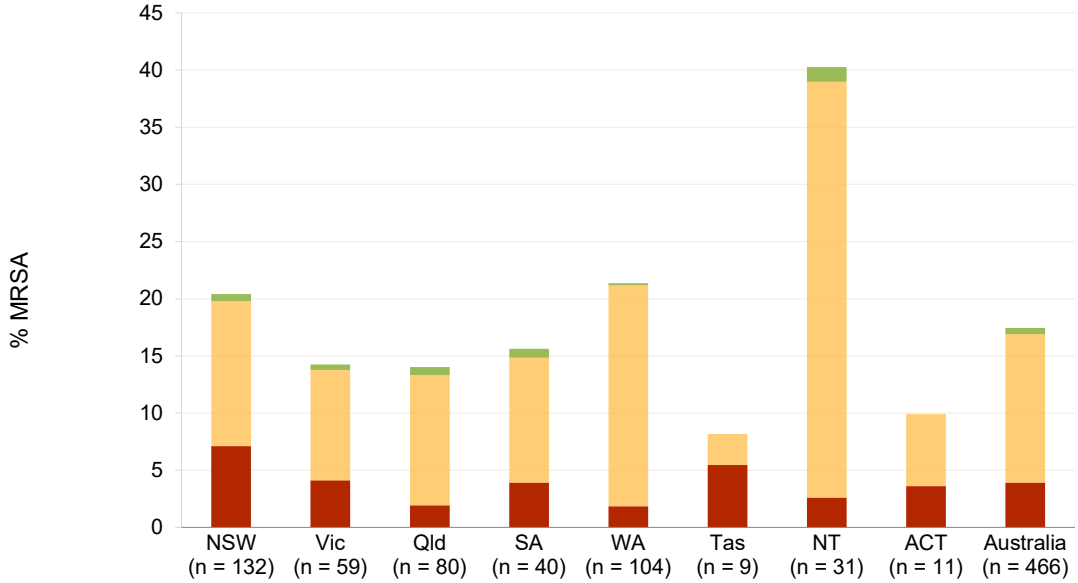
MLST = multi-locus sequence type; slv = single locus variant(s)

* Percentage of total with *van* genes
† includes one slv
§ Includes two slv

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

Of the 466 MRSA reported 452 (97.0%) 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 8.2% in Tasmania to 40.3% in the Northern Territory (Figure 13).

Figure 13: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, 2018



	NSW (n = 132)	Vic (n = 59)	Qld (n = 80)	SA (n = 40)	WA (n = 104)	Tas (n = 9)	NT (n = 31)	ACT (n = 11)	Australia (n = 466)
Not available (n = 14)	0.6	0.5	0.7	0.8	0.2	0.0	1.3	0.0	0.5
Community associated (n = 347)	12.7	9.7	11.4	10.9	19.3	2.7	36.4	6.3	13.0
Healthcare associated (n = 105)	7.1	4.1	1.9	3.9	1.8	5.5	2.6	3.6	3.9

MRSA = methicillin-resistant *Staphylococcus aureus*

Healthcare-associated MRSA

Based on the MLST and SCC*mec* type, four HA-MRSA clones were identified: ST22-IV (EMRSA-15), ST239-III (Aus 2/3 EMRSA), ST5-II (NY/Japan), and ST8-II (Irish EMRSA-1) (Tables 35, 36).

PVL-associated genes were not identified in HA-MRSA. Seven PVL positive ST22-IV isolates were identified; three in New South Wales, two in Victoria, and one each in Queensland and South Australia. 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.

The most frequently isolated HA-MRSA clone, ST22-IV, was identified in all states and territories except the Northern Territory. ST239-III was identified in all states and territories except Western Australia, Tasmania, and the Australian Capital Territory. ST5-II was identified in all states and territories except South Australia, Tasmania and the Australian Capital Territory. ST8-II was only identified in the Australian Capital Territory (Table 37).

Community-associated MRSA

Based on the MLST and SCC*mec* type, 45 CA-MRSA clones were identified. PVL was detected in 12 CA-MRSA clones. Overall 41.8% of CA MRSA were PVL positive (Tables 35, 36).

The most frequently isolated CA-MRSA clone, ST93-IV (Qld CA-MRSA), was isolated in all states except Tasmania (Table 38).

Of the hospital onset MRSA, 63.8% (67/105) were caused by CA-MRSA.

Table 35: MRSA clones, association, place of onset and PVL carriage, 2018

Clone	Clonal complex	Total, *n*	Community onset, % (*n*)*	Hospital onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)†	22	81	63.0 (51)	37.0 (30)	0.0 (0)
ST239-III (Aus2/3 EMRSA)§	8	17	64.7 (11)	35.3 (6)	0.0 (0)
ST5-II (NY/Japan)	5	6	66.7 (4)	33.3 (2)	–** (0)
ST8-II (Irish EMRSA-1)		1	100.0 (1)	0.0 (0)	–** (0)
Total HA-MRSA		105	63.8 (67)	36.2 (38)	0.0 (0)
Community-associated					
ST93-IV (Qld CA-MRSA)§	Singleton	99	88.9 (88)	11.1 (11)	96.0 (95)
ST45-V	45	41	70.7 (29)	29.3 (12)	0.0 (0)
ST5-IV§	5	41	70.7 (29)	29.3 (12)	34.1 (14)
ST1-IV (WA1 MRSA)	1	35	82.9 (29)	17.1 (6)	2.9 (1)
ST30-IV (SWP MRSA)	30	21	90.5 (19)	9.5 (2)	81.0 (17)
ST97-IV		14	85.7 (12)	14.3 (2)	0.0 (0)
ST78-IV (WA2 MRSA)	78	13	76.9 (10)	23.1 (3)	0.0 (0)
ST5-V		8	–** (7)	–** (1)	–** (0)
ST8-IV		8	–** (8)	–** (0)	–** (5)
ST22-IV (PVL positive)		7	–** (6)	–** (1)	–** (7)
ST872-IV		7	–** (6)	–** (1)	–** (0)
ST72-IV		5	–** (3)	–** (2)	–** (0)
ST953-IV		5	–** (2)	–** (3)	–** (0)
Other (*n* = 32)		43	74.4 (32)	25.6 (11)	14.0 (6)
Total CA-MRSA		347	80.7 (280)	19.3 (67)	41.8 (145)
MRSA		**452**	**347**	**105**	

MRSA = methicillin-resistant *Staphylococcus aureus*; PVL = Panton-Valentine leucocidin; slv = single locus variant(s)

* Percentage of the clone
† includes three slv
§ Includes two slv
** Insufficient numbers (<10) to calculate percentage

Table 36: MRSA clones, association, place of onset, 2018

Clone	Clonal complex	Community onset, % (*n*)*	Hospital onset, % (*n*)*	Total, % (*n*)
Healthcare-associated				
ST22-IV (EMRSA-15)†	22	14.7 (51)	28.6 (30)	17.9 (81)
ST239-III (Aus2/3 EMRSA)§	8	3.2 (11)	5.7 (6)	3.8 (17)
ST5-II (NY/Japan)	5	1.2 (4)	1.9 (2)	1.3 (6)
ST8-II (Irish EMRSA-1)		0.3 (1)	0.0 (0)	0.2 (1)
Total HA-MRSA		19.3 (67)	36.2 (38)	23.2 (105)
Community-associated				
ST93-IV (Qld CA-MRSA)§	Singleton	25.4 (88)	10.5 (11)	21.9 (99)
ST45-V	45	8.4 (29)	11.4 (12)	9.1 (41)
ST5-IV§	5	8.4 (29)	11.4 (12)	9.1 (41)
ST1-IV (WA1 MRSA)	1	8.4 (29)	5.7 (6)	7.7 (35)
ST30-IV (SWP MRSA)	30	5.5 (19)	1.9 (2)	4.6 (21)
ST97-IV		3.5 (12)	1.9 (2)	3.1 (14)
ST78-IV (WA2 MRSA)	78	2.9 (10)	2.9 (3)	2.9 (13)
ST5-V		2.0 (7)	1.0 (1)	1.8 (8)
ST8-IV		2.3 (8)	0.0 (0)	1.8 (8)
ST22-IV (PVL positive)		1.7 (6)	1.0 (1)	1.5 (7)
ST872-IV		1.7 (6)	1.0 (1)	1.5 (7)
ST72-IV		0.9 (3)	1.9 (2)	1.1 (5)
ST953-IV		0.6 (2)	2.9 (3)	1.1 (5)
Other (*n* = 32)		9.2 (32)	10.5 (11)	9.5 (43)
Total CA-MRSA		80.7 (280)	63.8 (67)	76.8 (347)
MRSA		**76.8 (347)**	**23.2 (105)**	**452**

MRSA = methicillin-resistant *Staphylococcus aureus*; PVL = Panton-Valentine leucocidin; slv = single locus variant(s)

* Percentage of all MRSA
† includes three slv
§ Includes two slv

Table 37: Healthcare-associated MRSA clones, by state and territory, 2018

Clone	Percentage, % (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15)†	76.1 (35)	88.2 (15)	45.5 (5)	90.0 (9)	–§ (8)	–§ (6)	–§ (0)	–§ (3)	77.1 (81)
ST239-III (Aus2/3 EMRSA)§	19.6 (9)	5.9 (1)	45.5 (5)	10.0 (1)	–§ (0)	–§ (0)	–§ (1)	–§ (0)	16.2 (17)
ST5-II (NY/Japan)	4.3 (2)	5.9 (1)	9.1 (1)	0.0 (0)	–§ (1)	–§ (0)	–§ (1)	–§ (0)	5.7 (6)
ST8-II (Irish EMRSA-1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–§ (0)	–§ (0)	–§ (0)	–§ (1)	1.0 (1)
Total	46	17	11	10	9	6	2	4	105

MRSA = methicillin-resistant *Staphylococcus aureus*; slv = single locus variant(s)

* Includes seven slv
† Included one slv
§ Insufficient numbers (<10) to calculate percentage

Table 38: Major community-associated MRSA clones (> 10 isolates) by state and territory and PVL carriage, 2018

Clone	Percentage, % (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST93-IV (Qld CA-MRSA)*	18.3 (15)	15.0 (6)	26.2 (17)	46.4 (13)	29.8 (28)	–† (0)	67.9 (19)	–† (1)	28.5 (99)
Number PVL positive	12	6	16	13	28	0	19	1	95
Number PVL negative	3	0	1	0	0	0	0	0	4
ST45-V	31.7 (26)	17.5 (7)	1.5 (1)	10.7 (3)	1.1 (1)	–† (0)	3.6 (1)	–† (2)	11.8 (41)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	26	7	1	3	1	0	1	2	41
ST5-IV	7.3 (6)	7.5 (3)	21.5 (14)	7.1 (2)	13.8 (13)	–† (0)	10.7 (3)	–† (0)	11.8 (41)
Number PVL positive	0	3	1	1	6	0	3	0	14
Number PVL negative	6	0	13	1	7	0	0	0	27
ST1-IV	6.1 (5)	12.5 (5)	7.7 (5)	14.3 (4)	11.7 (11)	–† (3)	7.1 (2)	–† (0)	10.1 (35)
Number PVL positive	0	0	0	0	0	1	0	0	1
Number PVL negative	5	5	5	4	11	2	2	0	34
ST30-IV	6.1 (5)	2.5 (1)	13.8 (9)	3.6 (1)	5.3 (5)	–† (0)	0.0 (0)	–† (0)	6.1 (21)
Number PVL positive	4	0	8	1	4	0	0	0	17
Number PVL negative	1	1	1	0	1	0	0	0	4
ST97-IV	3.7 (3)	2.5 (1)	10.8 (7)	0.0 (0)	2.1 (2)	–† (0)	0.0 (0)	–† (1)	4.0 (14)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	3	1	7	0	2	0	0	1	14
ST78-IV	3.7 (3)	0.0 (0)	0.0 (0)	0.0 (0)	10.6 (10)	–† (0)	0.0 (0)	–† (0)	3.7 (13)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	3	0	0	0	10	0	0	0	13
Other clones (n = 39)	23.2 (19)	42.5 (17)	18.5 (12)	17.9 (5)	25.5 (24)	–† (0)	10.7 (3)	–† (3)	23.9 (83)
Number PVL positive	4	5	1	1	6	0	1	0	18
Number PVL negative	15	12	11	4	18	0	2	3	65
Total	**82**	**40**	**65**	**28**	**94**	**3**	**28**	**7**	**347**
PVL positive	20	14	26	16	44	1	23	1	145
PVL negative	62	26	39	12	50	2	5	6	202

CA-MRSA = community-associated methicillin-resistant *Staphylococcus aureus*; MRSA = methicillin-resistant *Staphylococcus aureus*; PVL = Panton-Valentine leucocidin; slv = single locus variant(s)

* includes tw slv
† Insufficient numbers (<10) to calculate percentage

3.10. Trend analysis (2013–2018)

Trend data were available for Enterobacterales for the period 2013 to 2018. *Acinetobacter* species and *P. aeruginosa* were introduced to the program in 2015.

EUCAST interpretive criteria have been used throughout, with the notable exception of amoxicillin–clavulanic acid, as both the Vitek® and Phoenix™ cards used the CLSI formulation for this agent.

Gram-negative species

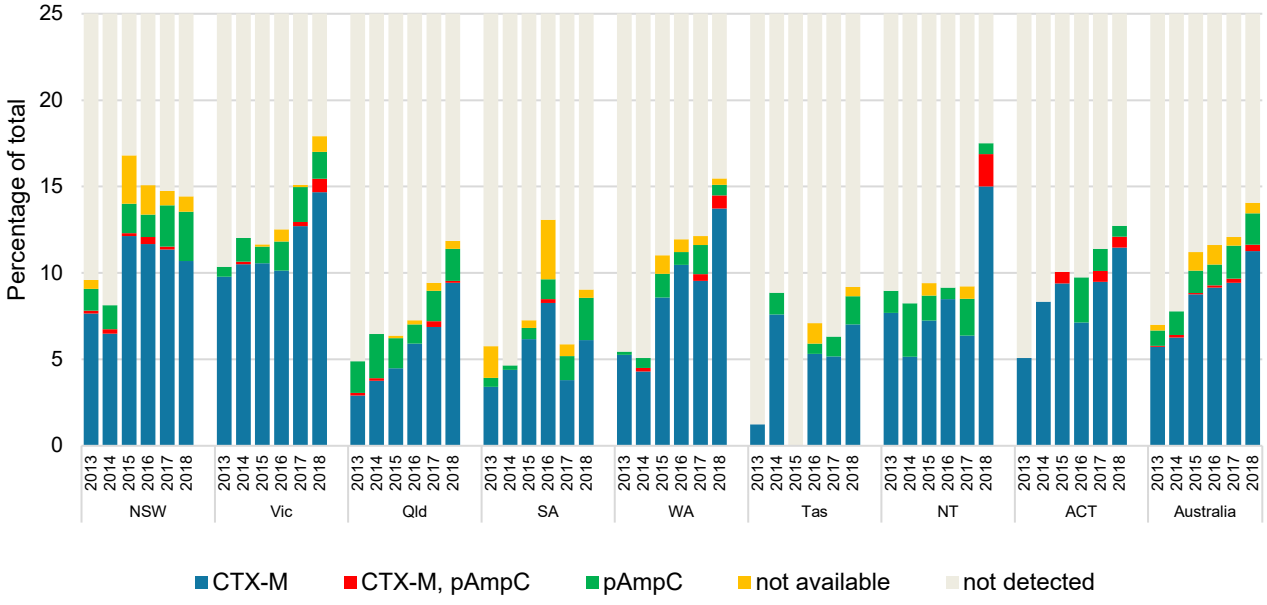
Extended-spectrum β-lactamases

Nationally, there was a significant increase in the proportion of *E. coli* with CTX-M-type (see Section 3.9.1) from 2013 to 2018 (X^2 for linear trend = 102.1, $P < 0.01$), most notably in Western Australia and Queensland (Figure 14). There was also a significant increase in the proportion of plasmid-borne AmpC β-lactamases (X^2 for linear trend = 22.08, $P < 0.01$).

SHV and TEM types were not included in this analysis, because it was not possible to discriminate between genes that encode narrow-spectrum β-lactamases and those that encode ESBLs.

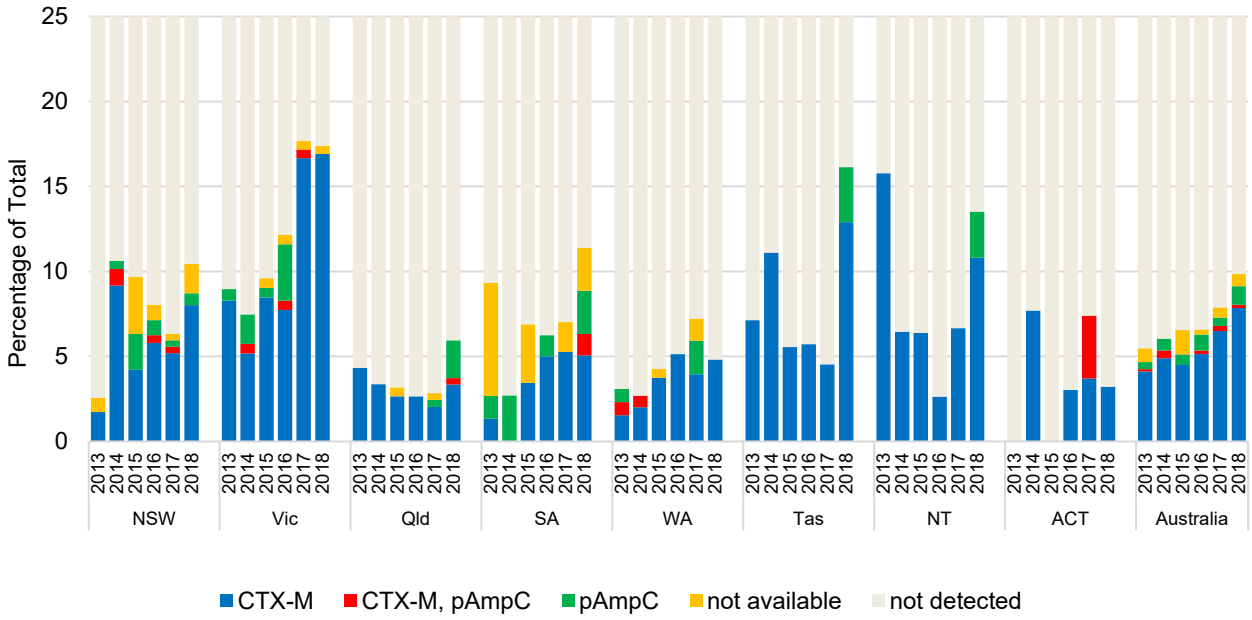
The proportion of *K. pneumoniae* with CTX-M-type or plasmid-borne AmpC β-lactamases has doubled during the period 2013–2018, although regional variations were seen (Figure 15). Most notable was the significant increase in CTX-M types detected from isolates from Victoria (X^2 for linear trend = 17.00, $P < 0.01$).

Figure 14. Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Escherichia coli* by state and territory, and nationally, 2013–2018



Not available = ESBL phenotype, isolate not available for molecular confirmation

Figure 15. Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Klebsiella pneumoniae* by state and territory, and nationally, 2013–2018



Not available = ESBL phenotype, isolate not available for molecular confirmation

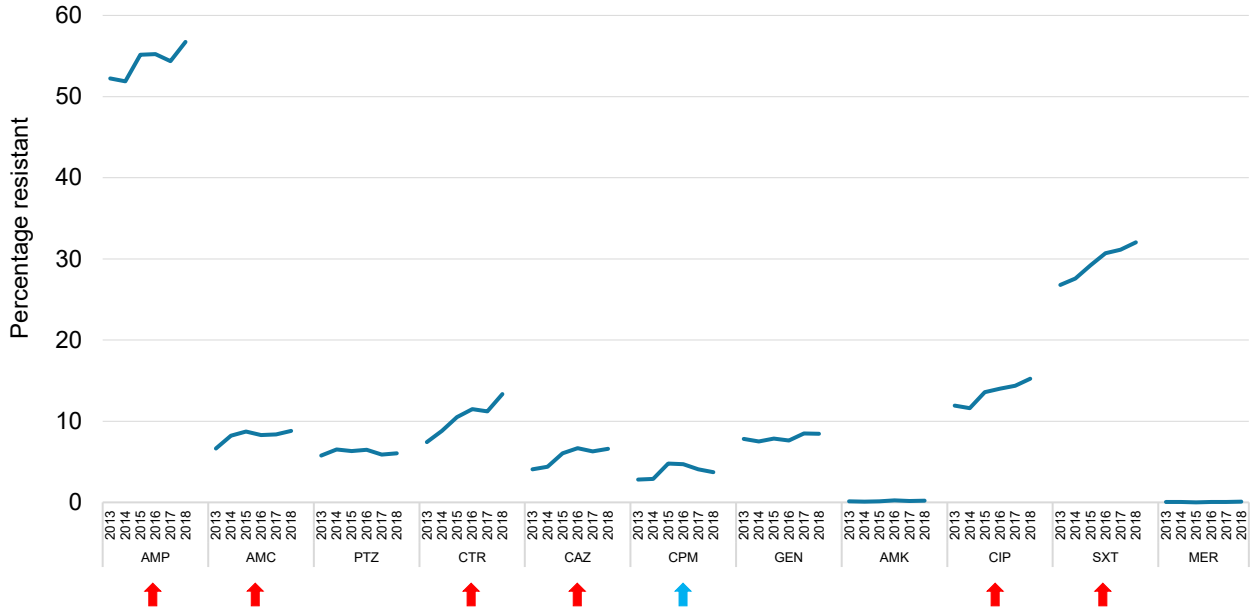
Escherichia coli

Resistance to key anti–gram negative antimicrobial agents showed a steady increase from 2013 to 2018 (Figure 16). There was a significant increase in resistance to ampicillin (X^2 for linear trend = 18.98, $P < 0.01$), amoxicillin–clavulanic acid (X^2 for linear trend = 6.792, $P < 0.01$), ceftriaxone (X^2 for linear trend = 76.53, $P < 0.01$), ceftazidime (X^2 for linear trend = 31.12, $P < 0.01$), cefepime (X^2 for linear trend = 5.844, $P = 0.0156$), ciprofloxacin (X^2 for linear trend = 28.87, $P < 0.01$), and trimethoprim–sulfamethoxazole (X^2 for linear trend = 36.63, $P < 0.01$).

Klebsiella pneumoniae

There were significant increases in resistance to key antimicrobial agents for *K. pneumoniae* over the six-year period 2013–2018 (Figure 17). Key antimicrobial agents included ceftriaxone (X^2 for linear trend = 8.342, $P < 0.01$), ceftazidime (X^2 for linear trend = 4.413, $P = 0.0357$), cefepime (X^2 for linear trend = 4.510, $P = 0.0337$), ciprofloxacin (X^2 for linear trend = 9.247, $P < 0.01$), and trimethoprim–sulfamethoxazole (X^2 for linear trend = 18.34, $P < 0.01$).

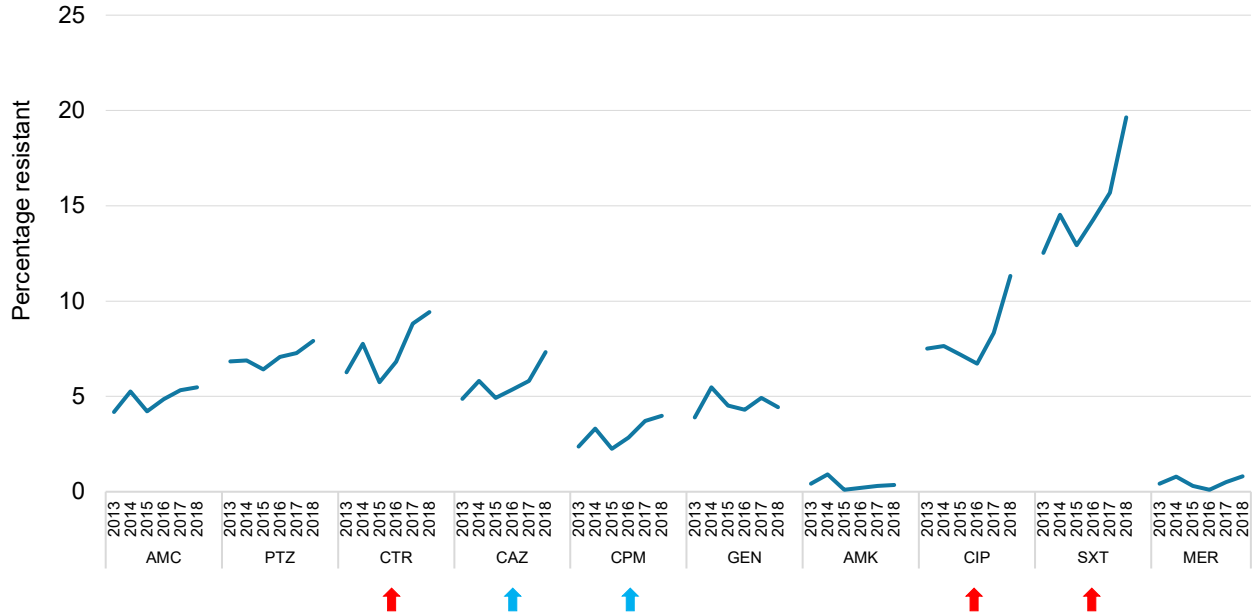
Figure 16. *Escherichia coli* resistance to key antimicrobials (EUCAST), Australia, 2013–2018



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

Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the period 2013 to 2018. Blue arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the period 2013 to 2018.

Figure 17. *Klebsiella pneumoniae* resistance to key antimicrobials (EUCAST), Australia, 2013–2018



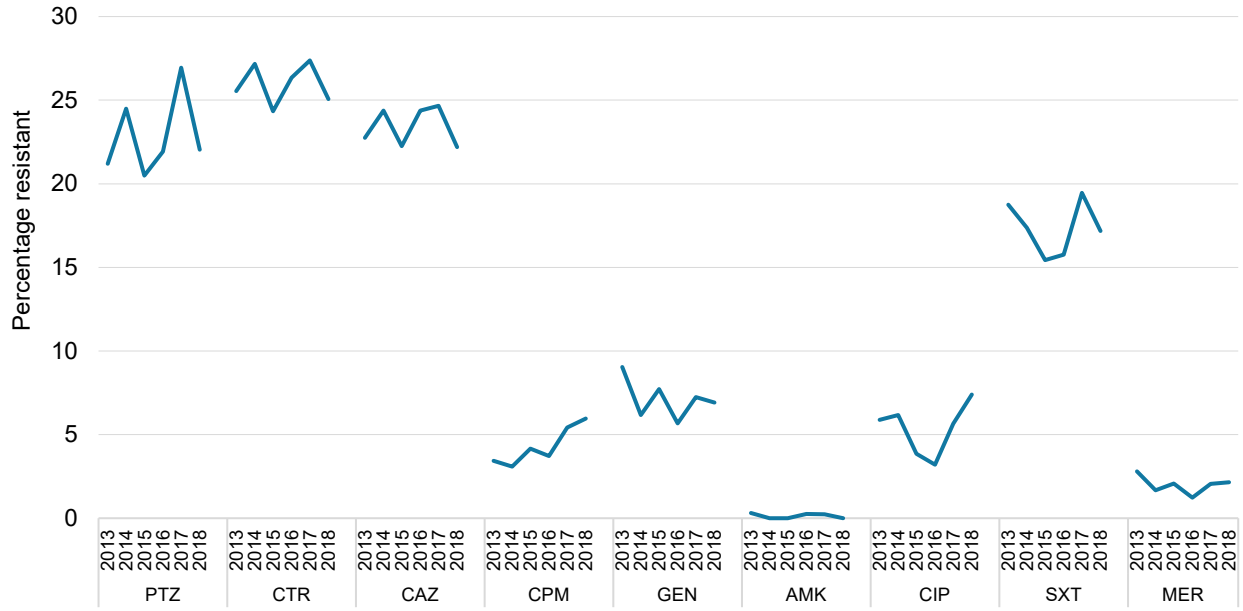
AMC = amoxicillin–clavulanate (2:1 ratio); AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; SXT = trimethoprim–sulfamethoxazole

Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the period 2013 to 2018. Blue arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the period 2013 to 2018.

Enterobacter cloacae complex

There were no significant differences in non-susceptibility to key antimicrobials for *E. cloacae* complex over the six-year period 2013–2018 (Figure 18)

Figure 18. *Enterobacter cloacae* complex resistance to key antimicrobials (EUCAST), Australia, 2013–2018



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

Enterococcus species

The 2018 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 2013–2018 are described below.

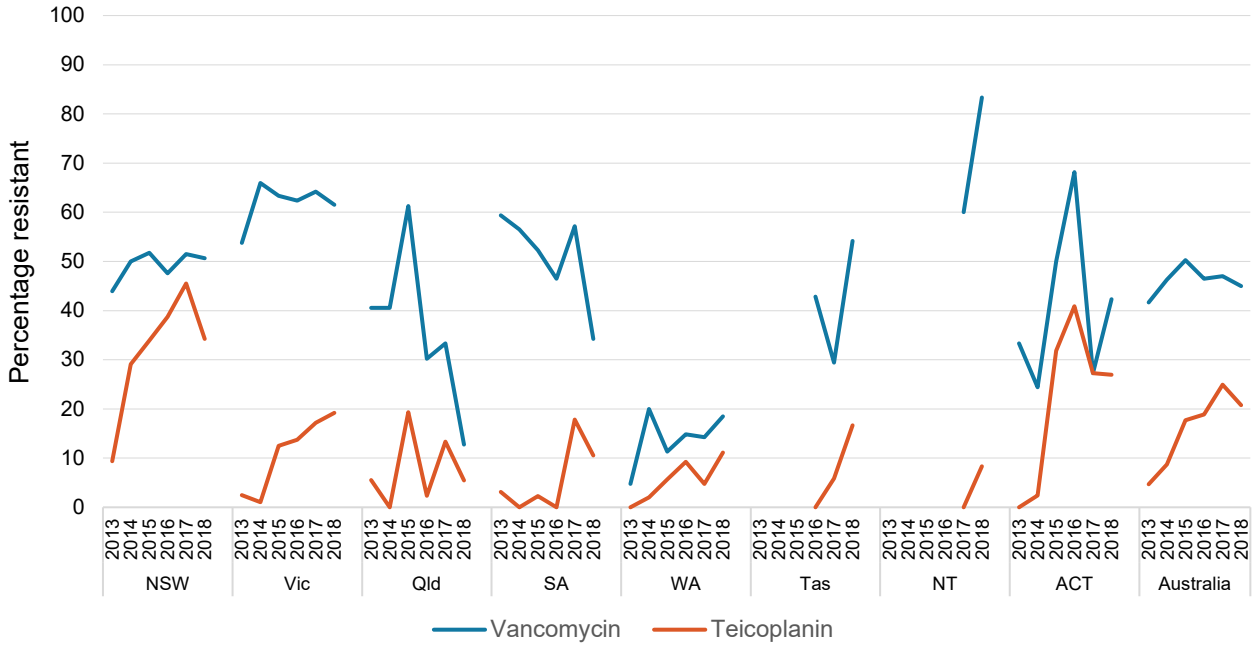
Vancomycin-resistant *Enterococcus faecium*

The proportion of glycoside-resistant *E. faecium* by state and territory is shown in Figure 19.

Regional variations were seen with both vancomycin and teicoplanin resistance. Most notable was a significant decrease in vancomycin resistance in Queensland (X^2 for linear trend = 11.18, P = 0.0008), and increase in Tasmania (X^2 for linear trend = 8.050, P = 0.0046) over the period 2013–2018. Teicoplanin resistance continued to increase in Victoria X^2 for linear trend = 24.12, P < 0.0001), and South Australia X^2 for linear trend = 7.959, P = 0.0048) over the six-year period.

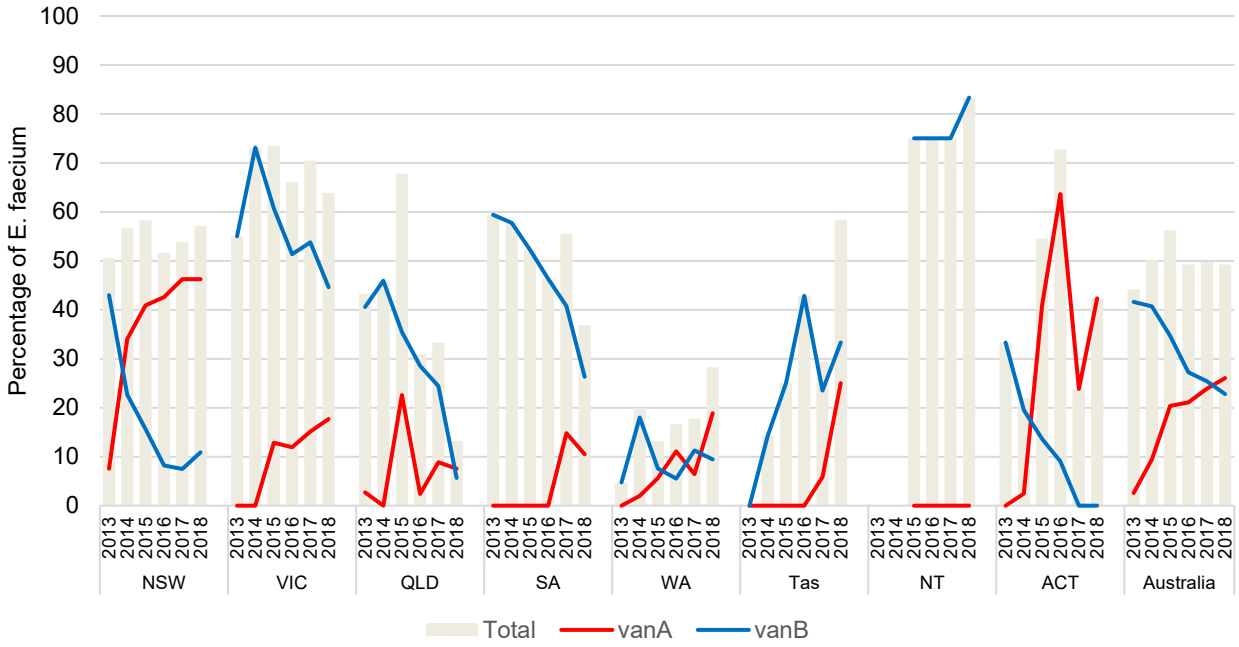
Nationally, there was a significant increase in the proportion of *vanA* genes in *E. faecium* from 2013-2018 (X^2 for linear trend = 90.32, P < 0.001 (Figure 20). This increase was seen in all states and territories, except in Queensland and the Northern Territory. There a decrease in *vanB* genes nationally (X^2 for linear trend = 56.94, P < 0.001) over this period, which was seen in all states and territories except Western Australia, Tasmania and the Northern Territory.

Figure 19. *Enterococcus faecium*, glycopeptide resistance (EUCAST), Australia, 2013–2018



Note: Insufficient numbers to calculate percentage for Tasmania (2013–2015) and the Northern Territory (2013-2017)

Figure 20. Proportion of van genes in *Enterococcus faecium* by state and territory, and nationally, 2013–2018

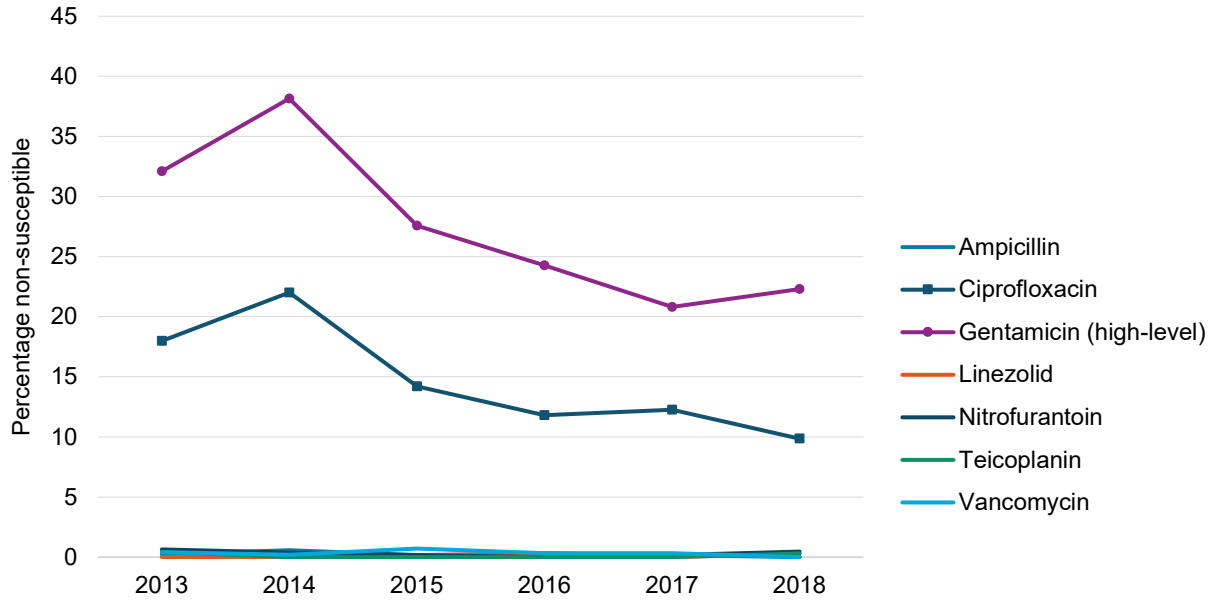


Note: Insufficient numbers (< 10 isolates) to calculate percentage for the Northern Territory (2013-2014)

Enterococcus faecalis

Resistance (EUCAST) to key antimicrobial agents for *E. faecalis* over the six-year period 2013–2018 is shown in Figure 21. The only significant trends over this period was a decrease in ciprofloxacin resistance (χ^2 for linear trend = 30.37, $P < 0.0001$); predominantly seen in New South Wales and South Australia. High-level gentamicin resistance increased slightly in 2018. Detailed data on *E. faecalis* resistance by state and territory are available in Appendix E1.

Figure 21. *Enterococcus faecalis*, non-susceptibility (EUCAST), Australia, 2013–2018



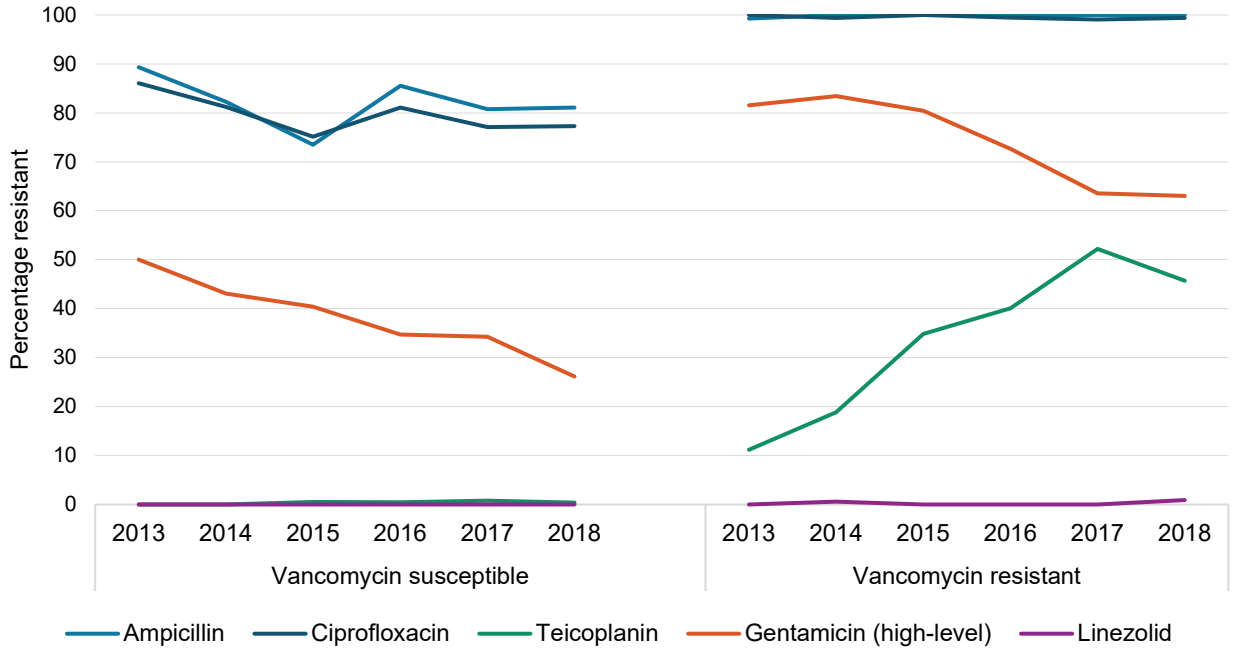
EUCAST = European Committee on Antimicrobial Susceptibility Testing

Enterococcus faecium

For *E. faecium*, there was a significant decrease in gentamicin (high-level) resistance (χ^2 for linear trend = 49.50, $P < 0.0001$) from 2013–2018, and a significant increase in teicoplanin resistance (χ^2 for linear trend = 64.30, $P < 0.0001$) (Figure 22). Teicoplanin-resistant isolates were detected in all states and territories; South Australia and the Australian Capital Territory had significant increase over the six-year period. A decrease in teicoplanin resistance was noted in 2018, predominantly in New South Wales. Two linezolid resistant *E. faecium* were confirmed in 2018, one each in Victoria and the Australian Capital Territory.

Detailed data on *E. faecium* resistance by state and territory are available in Appendix E2.

Figure 22: Non-susceptibility of *Enterococcus faecium* to key antimicrobials (EUCAST), vancomycin susceptibility, Australia, 2013–2018



EUCAST = European Committee on Antimicrobial Susceptibility Testing

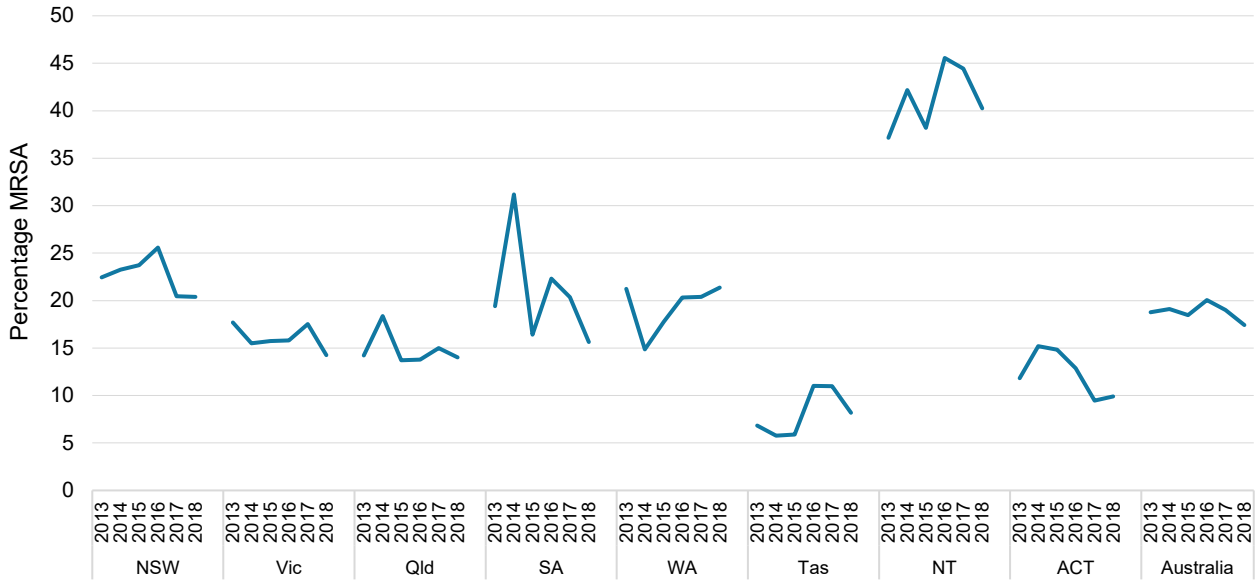
Staphylococcus aureus

A primary objective of the 2018 program 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 2013–2018.

Methicillin-resistant *Staphylococcus aureus*

The proportion of *S. aureus* that was methicillin resistant throughout Australia remained constant over the years 2013–2018, although there were notable variations at state and territory level (Figure 23).

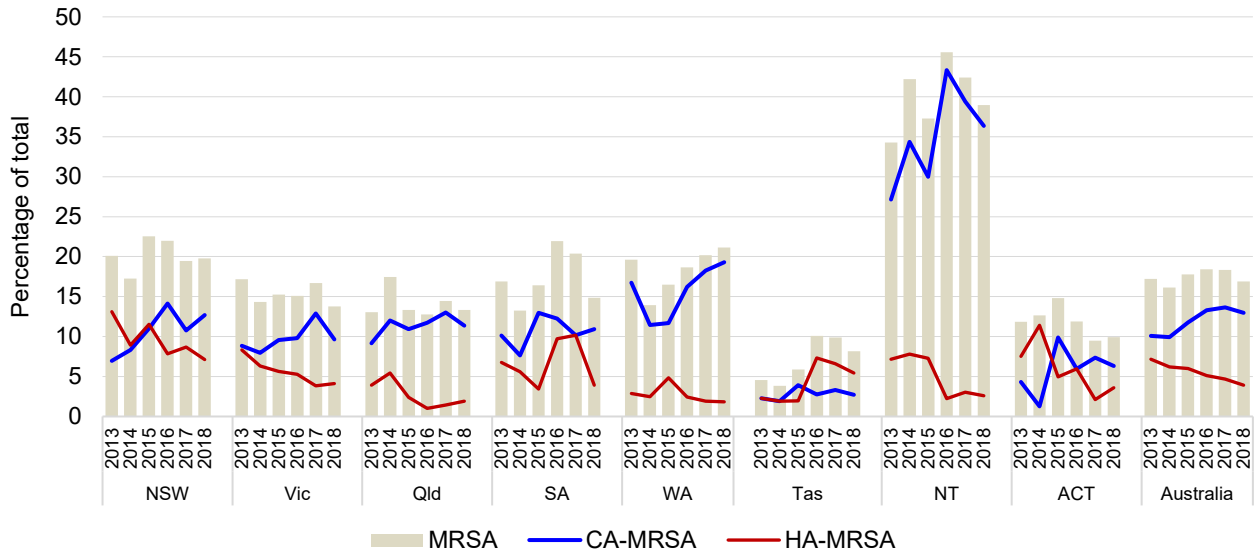
Figure 23: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, 2013–2018



MRSA = methicillin-resistant *Staphylococcus aureus*

There were significant changes in the proportion of CA-MRSA and HA-MRSA over the period 2013-2018. Nationally, there was a significant increase in the proportion of CA-MRSA clones (X^2 for linear trend = 21.44, $P < 0.01$), notably in New South Wales (Figure 24). The proportion of HA-MRSA clones declined nationally (X^2 for linear trend = 31.11, $P < 0.01$), notably in New South Wales, Victoria, and Queensland.

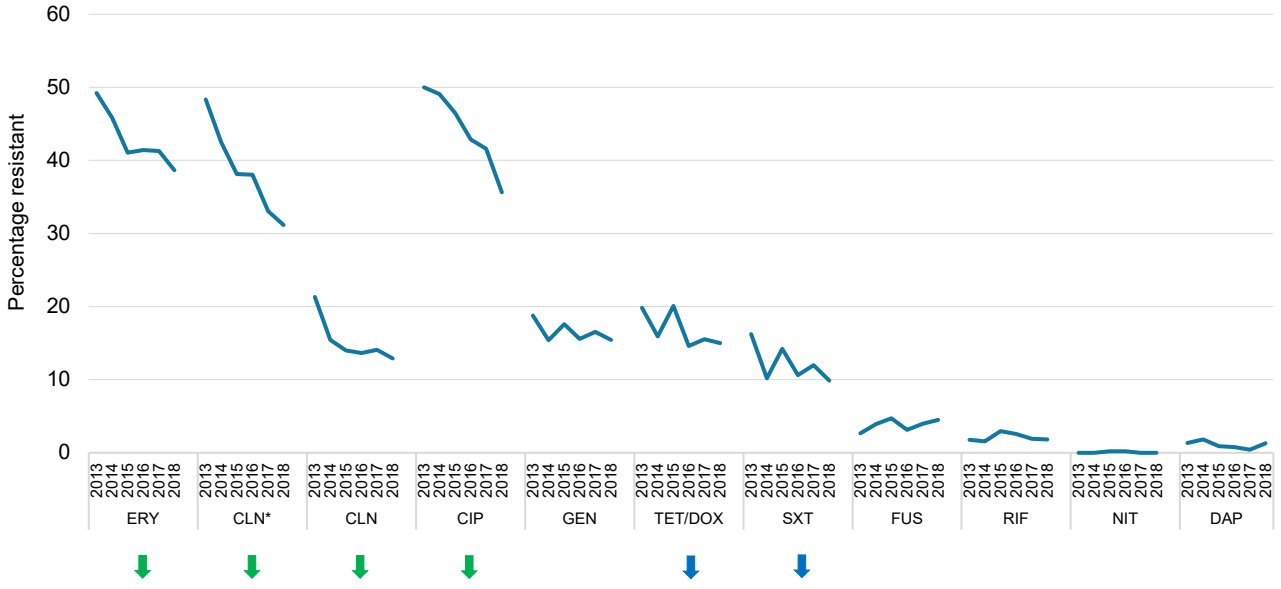
Figure 24: Proportion of methicillin-resistant *Staphylococcus aureus*, by association, state and territory, 2013–2018



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

There was a significant decrease in erythromycin (χ^2 for linear trend = 10.39, $P < 0.01$), clindamycin (χ^2 for linear trend = 9.817, $P < 0.01$), ciprofloxacin (χ^2 for linear trend = 24.15, $P < 0.01$), tetracyclines (χ^2 for linear trend = 4.179, $P = 0.0409$) and trimethoprim–sulfamethoxazole (χ^2 for linear trend = 5.275, $P = 0.0216$) resistant MRSA, 2013–2018 (Figure 25).

Figure 25: Methicillin-resistant *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, 2013–2018



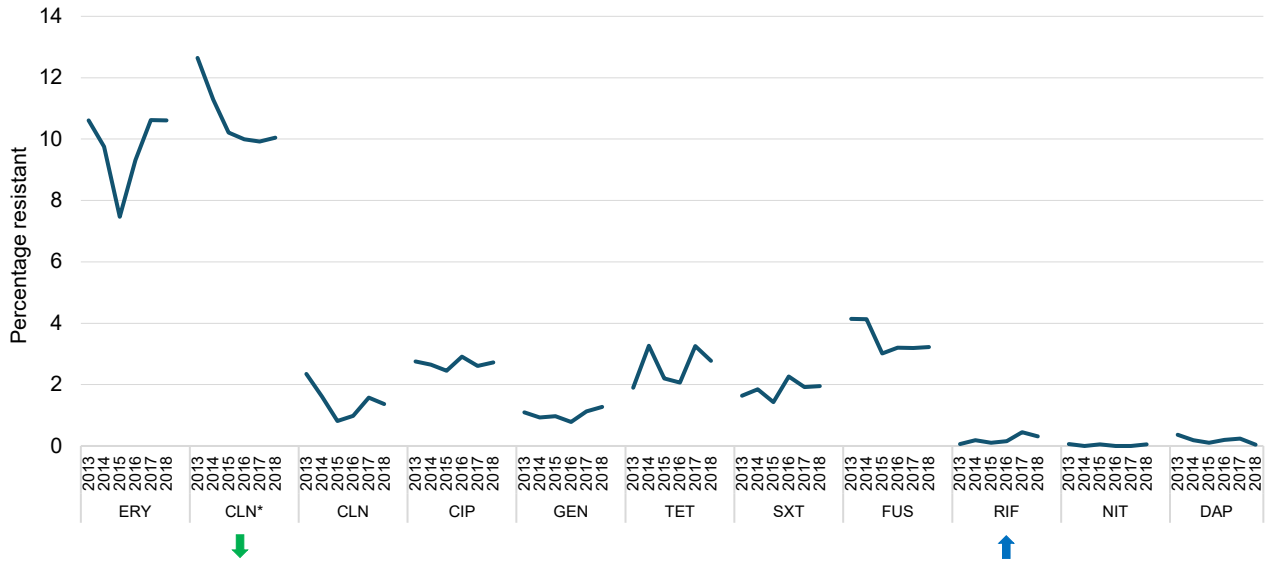
CIP = ciprofloxacin; CLN = clindamycin; CLN* = clindamycin (inducible and constitutive); DAP = daptomycin; ERY = erythromycin; EUCAST = European Committee on Antimicrobial Susceptibility Testing; FUS = fusidic acid; GEN = gentamicin; NIT = nitrofurantoin [CLSI]; RIF = rifampicin; SXT = trimethoprim–sulfamethoxazole,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

Green arrows indicate antimicrobial agents with significant decrease ($P < 0.01$) over the period 2013 to 2018
Blue arrows indicate antimicrobial agents with significant decrease ($0.01 < P < 0.5$) over the period 2013 to 2018

Methicillin-susceptible *Staphylococcus aureus*

There was little change in resistance to key antimicrobials in MSSA between 2017 and 2018. However, there was a significant decline in clindamycin resistant (inducible + constitutive resistance) (χ^2 for linear trend = 7.358, P = 0.0067) MSSA, and an increase in rifampicin resistant (χ^2 for linear trend = 5.558, P = 0.0184) MSSA over the period 2013-2018 (Figure 26).

Figure 26: Methicillin-susceptible *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, 2013–2018



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 = tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™)

Green arrows indicate antimicrobial agents with significant decrease (P < 0.01) over the period 2013 to 2018
Blue arrows indicate antimicrobial agents with significant decrease (0.01 < P < 0.5) over the period 2013 to 2018

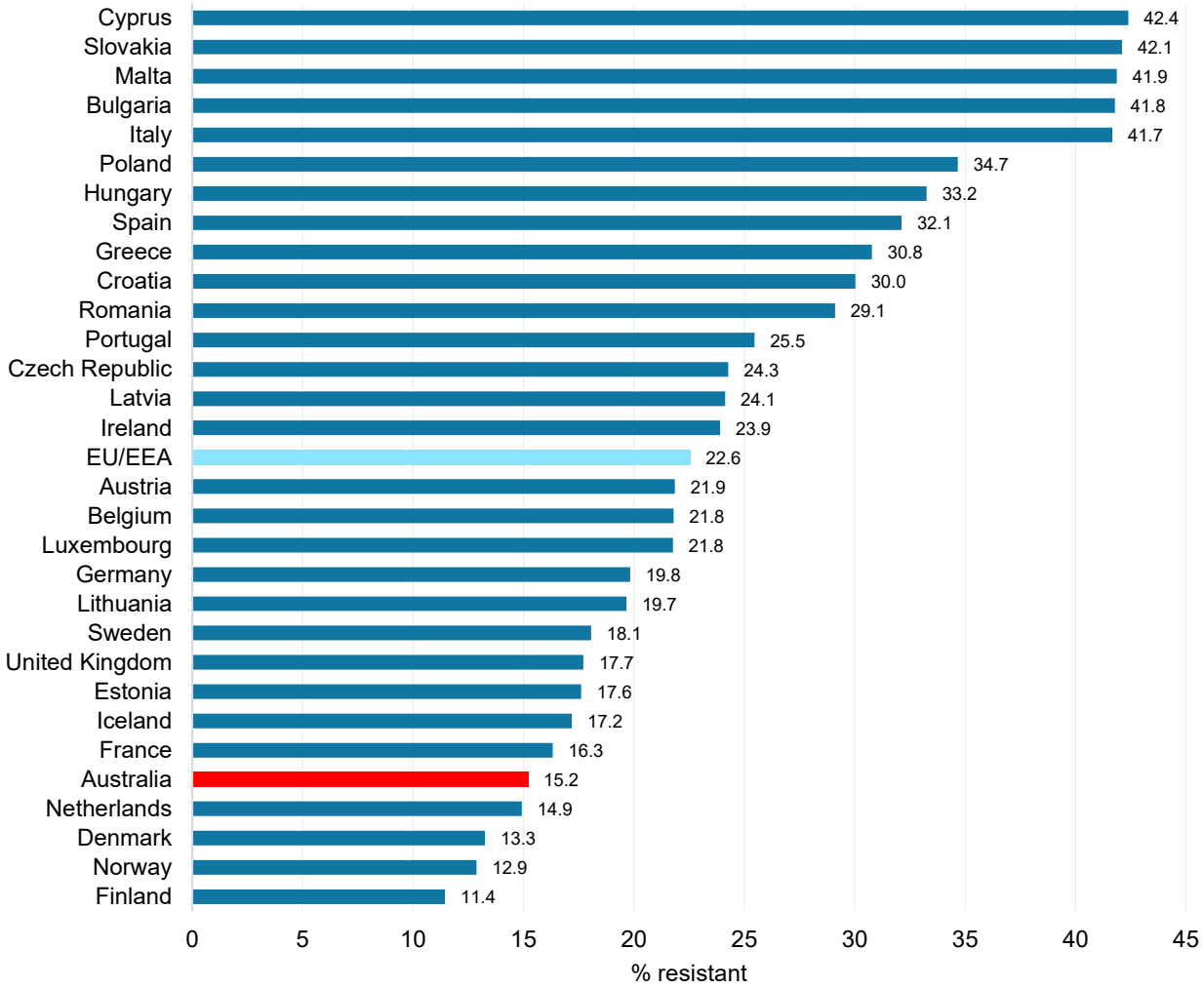
4. International comparisons

Data from AGAR can be compared with data from the European Antimicrobial Resistance Surveillance Network (EARs-Net) program,[46] as both programs examine resistance in bacterial pathogens found in blood culture.

Rates of resistance to fluoroquinolone in *E. coli* and *K. pneumoniae* (represented by resistance to ciprofloxacin) remain very low in Australia compared with most European countries (Figures 25 and 26). Australia now ranks towards the middle in rates of resistance to third-generation cephalosporins in *E. coli*, and is now above that of the European Union and European Economic Area average. Third-generation resistance in *K. pneumoniae* is low by comparison (Figures 27 and 28).

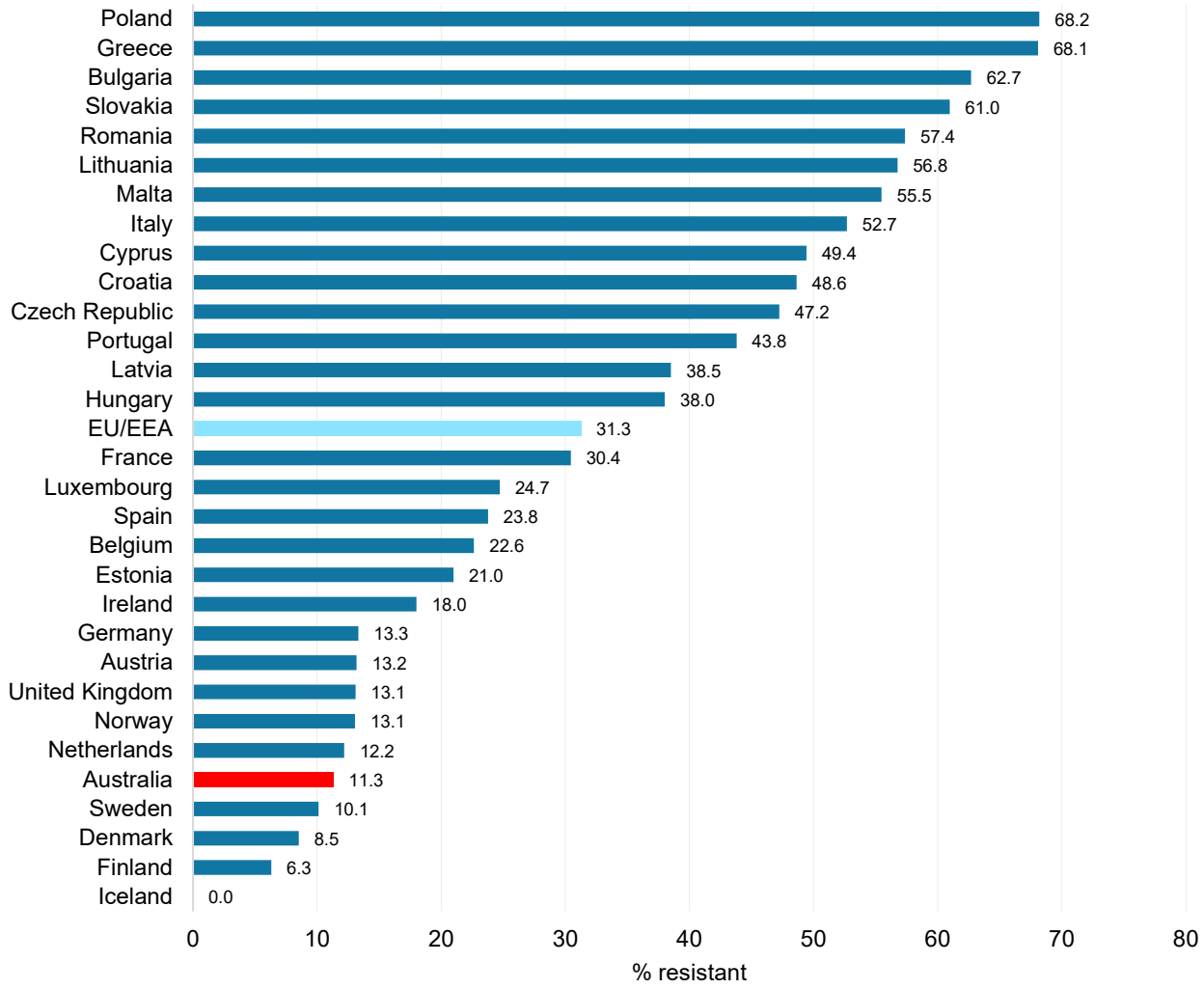
Australia ranks in the top half in rates of resistance to methicillin in *S. aureus* (Figure 29), and higher than all European countries except Cyprus in rates of resistance to vancomycin in *E. faecium* (Figure 30).

Figure 25: Comparison of *Escherichia coli* rates of resistance to ciprofloxacin in Australia and European countries, blood culture isolates, 2018



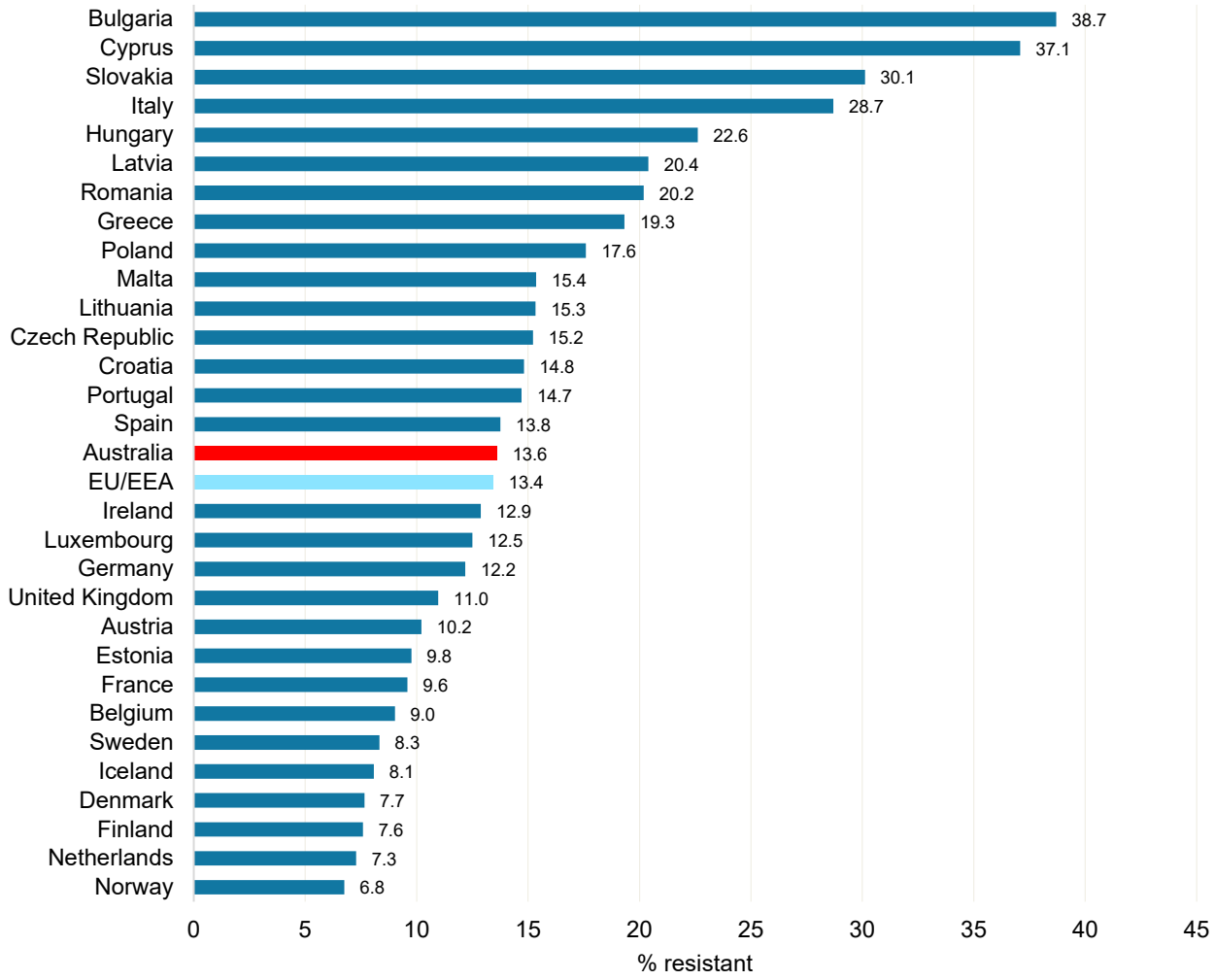
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 26: Comparison of *Klebsiella pneumoniae* rates of resistance to ciprofloxacin in Australia and European countries, blood culture isolates, 2018



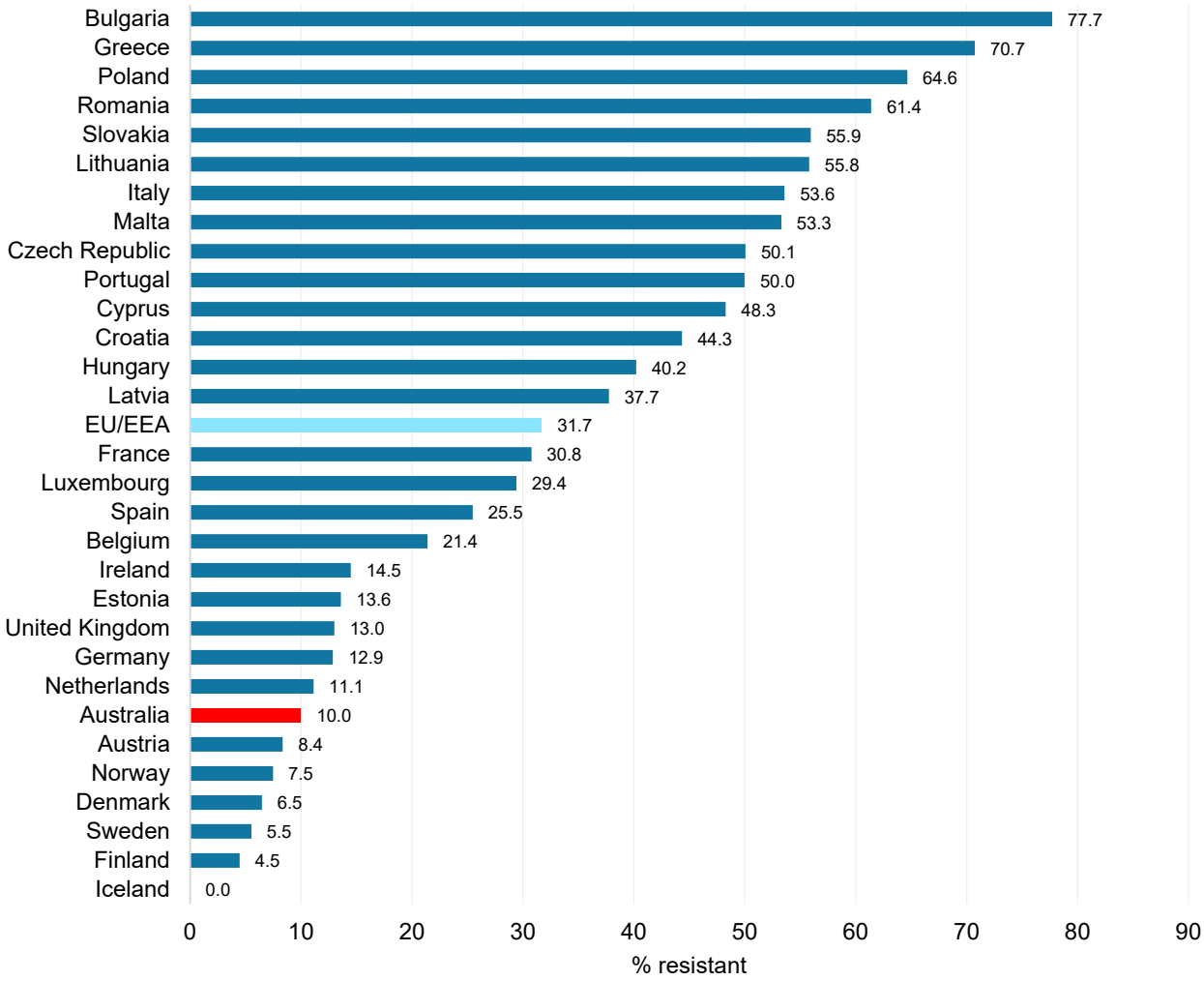
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 27: Comparison of *Escherichia coli* rates of resistance to third-generation cephalosporins in Australia and European countries, blood culture isolates, 2018



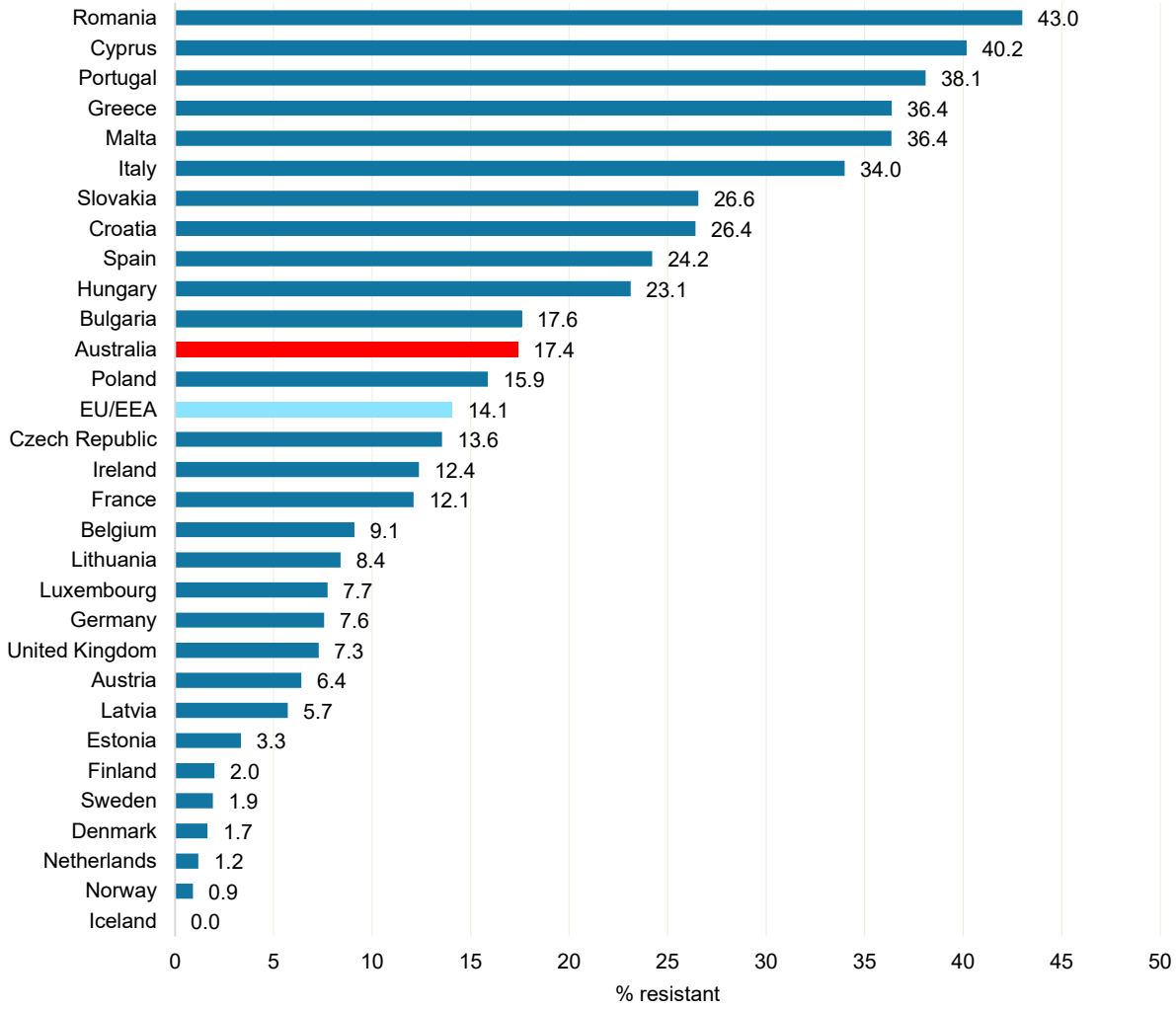
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 28: Comparison of *Klebsiella pneumoniae* rates of resistance to third-generation cephalosporins in Australia and European countries, blood culture isolates, 2018



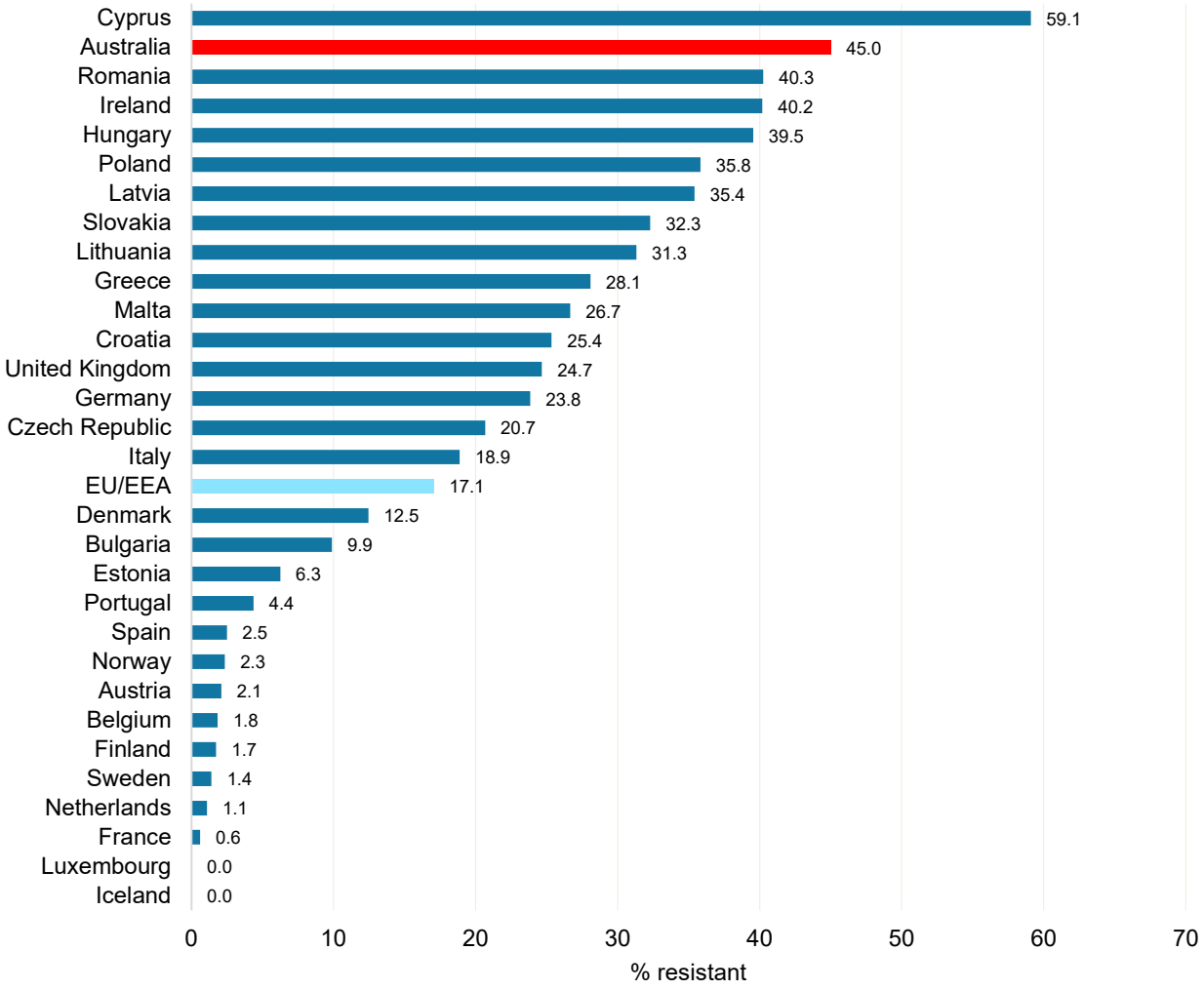
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 29: Comparison of *Staphylococcus aureus* rates of resistance to methicillin in Australia and European countries, blood culture isolates, 2018



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

Figure 30: Comparison of *Enterococcus faecium* rates of resistance to vancomycin in Australia and European countries, blood culture isolates, 2018



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

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 36 large hospitals across 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 both the Vitek® and Phoenix™ cards used, interpretation using EUCAST guidelines for this agent was not possible
- 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 is classified into hospital and community onset infections; healthcare-associated community onset infections may be included in the community onset group.

6. Discussion and conclusions

AGAR data show that in 2018, 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, skin and skin structure and device-related infection without metastatic focus. Strategies to reduce blood stream infections should take this information on clinical manifestation into account.

AGAR data show a longitudinal trend of increasing *E. coli* non-susceptibility to key anti-gram negative antimicrobial agents, including ceftriaxone and ciprofloxacin. Rates of non-susceptibility to amoxicillin–clavulanic acid in *E. coli* (22.4%) are no longer substantially different from rates of non-susceptibility to ciprofloxacin (19.2%). The steady rise in resistance to fluoroquinolones is more striking in hospital onset bacteraemia, with a change from 16.1% to 23.8% between 2013 and 2018. In *K. pneumoniae*, rates of non-susceptibility to amoxicillin–clavulanic acid and ciprofloxacin, were lower than for *E. coli,* and were 11.8% and 12.8%, respectively, in 2018.

Emerging fluoroquinolone resistance in Australia is a concern. A little over a decade ago, ciprofloxacin-resistance rates were consistently between 1%–4%.[26, 47] 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 antibiotics, can no longer be considered as a broadly reliable antibiotic choice in empiric management of gram-negative infection. The mechanism responsible for fluoroquinolone resistance involved the *aac(6’)-Ib-cr* gene and this was much more common than carriage of *qnr* genes. Despite this concerning increase, the percentage of fluoroquinolone-resistant *E. coli* in Australia (see Table 25) remains low in comparison to most European countries.[48] 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 is driving this resistance.

Fluoroquinolone resistance in *E. coli* can also be linked to the emergence of O25b-ST131. O25b-ST131 is an international clone associated with third-generation cephalosporin and fluoroquinolone resistance, as well as increased virulence. In 2018, ESBL phenotypes were found in 14.5% of *E. coli* and 11.1% of *K. pneumoniae* isolates submitted to AGAR; O25b-ST131 accounted for 63% of *E. coli* ESBL phenotypes that were ciprofloxacin resistant. This reflects the dynamics of clonal spread of resistance, leading to rapid international, and now Australian, emergence of clones such as O25b-ST131. It shows how quickly resistance successes can be undermined, and also demonstrates the value of regular surveillance in identifying rapid changes in resistance.

When ESBLs first arose globally, they were more common in hospital onset infections in *K. pneumoniae* (TEM, SHV); as a result, there is a perception that ESBLs are primarily a hospital problem. However, this is no longer the case, with 78.0% of ESBL *E. coli* bacteraemias being 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.[49] 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 antibiotics. The AGAR data suggest that customised patient risk assessment may be required in empirical treatment decisions. Rates of *E. coli* resistance to ceftriaxone continue to rise in hospital onset bacteraemia (from 13.0% in 2016 to 19.8% in 2018), however community onset ceftriaxone resistance has remained steady (11.1% in 2016 and 12.3% in 2018).

To date, carbapenemase-producing Enterobacterales (CPE) remain uncommon (0.09% in *E. coli* and 0.9% in *K. pneumoniae*). The overall low rates of CPE bacteraemia are encouraging; however, some organisms harbour them more commonly; 4.1% of *Enterobacter cloacae* complex infections harbour a carbapenemase in hospital onset infections. Examining previous and current AGAR surveys, most CPEs are endemic in origin.[50, 51] Fourteen of the 31 CPEs were due to the IMP-4 gene, predominantly from New South Wales and the Australian Capital Territory. No IMP-4 positive isolates were reported from Victoria, South Australia, Tasmania and the Northern Territory. The 17 non-IMP-4 isolates (15 patients) are thought to be introductions of individual CPEs into hospitals by patients who acquired the isolates overseas; these isolates have the potential for secondary local transmission, as occurred recently in Victoria with KPC-producing *K. pneumoniae*.[52] This reinforces the importance of infection control programs and adherence to carbapenemase management guidelines to limit transmission of CPE.[3]

Colistin susceptibility testing cannot be performed on the current Vitek® susceptibility cards. Two *E. coli* harbouring mobile colistin resistance genes (mcr-1.1) were detected from all isolates referred for molecular testing. Whole genome sequencing of isolates with carbapenemase activity detected a further eight Enterobacterales (from five patients) with IMP-4 and mcr-9.1 genes. In addition, two CIM positive, carbapenemase gene negative *E. cloacae* harboured mcr-10.1.

E. faecium bacteraemia has significant clinical consequences and resource implications, due to increased length of hospital stay. Bacteraemia episodes from all causes contributed to increased length of hospital stay; the average length of stay in all Australian public hospitals in 2017–8 was 5.3 days.[53] Thirty-day all-cause mortality due to *E. faecium* in 2018 was high (27.2%); there were significant differences in 30-day all-cause mortality between community and hospital onset cases, but no significant difference between vancomycin-susceptible and resistant isolates. The increasing trend in antimicrobial resistant hospital onset sepsis may be a contributing factor to an increase in 30-day all-cause mortality. The 30-day all-cause mortality associated with *E. coli*, *K. pneumoniae* and *E. faecium* hospital onset infections exceeds community onset infections.

The emergence of penicillin-resistant clonal complex 17 *E. faecium* bacteraemia is a worldwide phenomenon. In addition to penicillin resistance, the isolates are often multidrug resistant, with high-level gentamicin resistance and vancomycin resistance. The limited therapeutic options may be a factor in the differing 30-day all-cause mortality between *E. faecium* (27.2%) and *E. faecalis* (14.9%).

In the 2018 survey, 49.3% of *E. faecium* harboured *vanA* or *vanB* genes, or both. 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 2017 survey, 50% of vancomycin-resistant *E. faecium* bacteraemias were due to *vanA*; increasing to 52.5% in 2018. This type of vancomycin resistance has emerged rapidly in the past six 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 2017, the European Union/European Economic Area (EU/EEA) population-weighted mean percentage was 14.9%; most other countries are below 35%, except for Cyprus (43.9%), Ireland (38.2%), and Lithuania (36.3%).[48]

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, such as third-generation cephalosporins, are widely used in Australia.

The overall rates of MRSA decreased from 19.0% in 2017[54] to 17.4% in the 2018 study. This compares with the 2017 EU/EEA population-weighted mean MRSA percentage of 16.9%, ranging from 1.0% in Norway to 44.4% in Romania.[48]

The rate of community onset SABs that are methicillin-resistant is increasing. Additionally, CA-MRSA clones are an increasing source of hospital onset bacteraemia (particularly ST45-V, ST5-IV, and ST96-IV). 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 blood stream infections in the Australian setting.

The rapidly changing picture of MRSA in Australia, drawing from 15 years of AGAR surveillance, is further explored in *MRSA: A tale of three types*.[55] This technical paper will be updated as appropriate by AGAR and the Commission to provide further information on the issue.

It should be noted that outbreaks of multidrug-resistant organisms occur in hospitals and other institutional care settings, and substantial transmission occurs before invasive bloodstream infections develop. AGAR data may therefore underestimate local or regional spread of 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 APAS and 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
ESBL	extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
MIC	minimum inhibitory concentration

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Participating members of AGAR:

Institution	AGAR members
Alfred Hospital, Vic	Denis Spelman and Chris Lee
Alice Springs Hospital, NT	James McLeod
Austin Hospital, Vic	Marcel Leroi and Elizabeth Grabsch
Australian Clinical Labs, Murdoch, WA	Sudha Pottumarthy-Boddu and Fay Kappler
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John Hunter Hospital, NSW	Rod Givney and Kimberly Ross
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Monash Health (Monash Medical Centre), Vic	Tony Korman and Despina Kotsanas
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Pathology Queensland, Central Laboratory, Qld	Graeme Nimmo and Narelle George
Pathology Queensland, Gold Coast Hospital, Qld	Petra Derrington and Cheryl Curtis
Pathology Queensland, Prince Charles Hospital, Qld	Robert Horvath and Laura Martin
Pathology Queensland, Princess Alexandra Hospital, Qld	Naomi Runnegar and Joel Douglas
Pathology Queensland, Queensland Children's Hospital, Qld	Clare Nourse
PathWest Laboratory Medicine – Remote WA	Michael Leung
PathWest Laboratory Medicine – WA, Fiona Stanley Hospital	David McGechie and Denise Daley
PathWest Laboratory Medicine – WA, Perth Children's Hospital	Chris Blyth
PathWest Laboratory Medicine – WA, Queen Elizabeth II Hospital	Ronan Murray and Jacinta Bowman
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Reference laboratories

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AGAR also gratefully acknowledges Ms Yung Thin Lee and Dr Stanley Pang at the Antimicrobial Resistance and Infectious Disease Laboratory, School of Veterinary Life Science, Murdoch University, Western Australia for performing the whole genome sequencing on *E. faecium* and MRSA isolates.

Appendix A. Study design

Thirty-six institutions participated in the 2018 survey. All states and territories were represented. The laboratories 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 that participated in AGAR obtained basic laboratory information for each patient episode plus varying demographic information, depending on the level at which they are enrolled in the program. There are two levels of enrolment: Bronze and Silver (Tables A1). 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 30 days and date of death.

Table A1: Level of participation of laboratories that contributed data on gram-negative* bacteraemia, by state and territory, 2018

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	8	2	6
Victoria	6	0	6
Queensland	7	1	6
South Australia	3	2	1
Western Australia	7	3	4
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	36	9	27

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

Table A2: Level of participation of laboratories that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2017

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	8	1	7
Victoria	6	0	6
Queensland	7	1	6
South Australia	3	0	3
Western Australia	7	3	4
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	36	6	30

Table A3: Level of participation of laboratories that contributed data on enterococcal bacteraemia, by state and territory, 2017

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	8	1	7
Victoria	6	0	6
Queensland	7	0	7
South Australia	2	0	2
Western Australia	7	3	4
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	35	5	30

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* = 32) and Phoenix (BD) (*n* = 4), which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution. Commercially available Vitek 2 AST-N246 and AST-N247 cards or Phoenix NMIC-404 and NMIC-422 cards were used by all participants throughout the survey period.

The CLSI M100-A29[28] and the EUCAST v9.0[29] breakpoints from January 2019 were used in the analysis. For analysis of cefazolin, breakpoints of ≤4 mg/L for susceptible and ≥8 mg/L for resistant were applied, because of the restricted MIC range available on the commercial cards (recognising that the January 2019 breakpoint is susceptible ≤2 mg/L).

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 v8.0†		
	S	SDD	I	R	S	I	R
Benzylpenicillin							
Enterococcus spp.	≤8		–§	≥16	–#	–#	–#
Staphylococcus aureus	≤0.12		–§	≥0.25	≤0.125	–§	>0.125
Amikacin							
Acinetobacter spp.	≤16		32	≥64	≤8	16	>16
Enterobacterales	≤16		32	≥64	≤8	16	>16
Pseudomonas spp.	≤16		32	≥64	≤8	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	≤1	2–16	>16
Cefazolin (Australian)‡	≤2		4	≥8	≤2	4	>4
Cefepime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤2	4–8	–§	≥16	≤1	2–4	>4

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v8.0†		
	S	SDD	I	R	S	I	R
Pseudomonas spp.	≤8		16	≥32	8	–§	>8
Cefalexin	–#		–#	–#	≤16	–§	>16
Cefalotin	≤8		16	≥32	–#	–#	–#
Cefoxitin	≤8		16	≥32	–#	–#	–#
Ceftazidime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤8	–§	>8
Ceftriaxone							
Acinetobacter spp.	≤8		16–32	≥64	–#	–#	–#
Enterobacterales	≤1		2	≥4	≤1	2	>2
Chloramphenicol (Phoenix card)	≤8		16	≥32	≤8	–§	≥16
Ciprofloxacin							
Acinetobacter spp.	≤1		2	≥4	**≤0.06**	**0.125–1§**	**>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
Staphylococcus aureus	≤1		2	≥4	≤1	–§	>1
Pseudomonas spp.	**≤0.5**		**1**	**≥2**	≤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	–§	>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	1	>1
Erythromycin							
Enterococcus spp.	≤0.5		1–4	≥8	–#	–#	–#
Staphylococcus aureus	≤0.5		1–4	≥8	≤1	2	>2
Fosfomycin (Phoenix card)	≤64		128	≥256	≤32	–§	>32
Fusidic acid							
Staphylococcus aureus	–#		–#	–#	≤1	–§	>1
Gentamicin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	>4
Enterobacterales	≤4		8	≥16	≤2	4	>4
Pseudomonas spp.	≤4		8	≥16	≤4	–§	>4

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v8.0†		
	S	SDD	I	R	S	I	R
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.	-		-	-	≤4	8	>8
Pseudomonas spp.	≤2		4	≥8	**≤4**	**–§**	**>4**
Linezolid							
Enterococcus spp.	≤2		4	≥8	≤4	–§	>4
Staphylococcus aureus	≤4		–§	≥8	≤4	–§	>4
Meropenem							
Acinetobacter spp.	≤2		4	≥8	≤2	4–8	>8
Enterobacterales	≤1		2	≥4	≤2	4–8	>8
Pseudomonas spp.	≤2		4	≥8	≤2	4–8	>8
Nitrofurantoin							
Enterobacterales	≤32		64	≥128	≤64††	–§	>64
Enterococcus spp.	≤32		64	≥128	≤64††	–§	>64
Staphylococcus aureus	≤32		64	≥128	–#	–#	–#
Norfloxacin							
Enterobacterales	**–#**		**–#**	**–#**	≤0.5	1	>1
Pseudomonas spp.	**–#**		**–#**	**–#**	–#	–#	–#
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	16	>16
Pseudomonas spp.	≤16/4		32/4–64/4	≥128/4	≤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–clavulanic acid							
Acinetobacter spp.	≤16/2		32/2–64/2	≥128/2	–#	–#	–#
Enterobacterales	≤16/2		32/2–64/2	≥128/2	≤8	16	>16

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v8.0†		
	S	SDD	I	R	S	I	R
Pseudomonas spp.	≤16/2		32/2–64/2	≥128/2	≤16	–§	>16
Tigecycline (Phoenix card)	–#		–#	–#	≤1	2	≥4
Tobramycin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	>4
Enterobacterales	≤4		8	≥16	≤2	4	>4
Pseudomonas spp.	≤4		8	≥16	≤4	–§	>4
Trimethoprim							
Enterobacterales	≤8		–§	≥16	≤2	4	>4
Enterococcus spp.	–#		–#	–#	≤0.03	0.06–1	>1
Staphylococcus aureus	≤8		–§	≥16	≤2	4	>4
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
Enterococcus spp.	–#		–#	–#	**≤1§§§**	**–§**	**>1§§§**
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; R = resistant; S = sensitive; SDD = sensitive dose dependent

Note: Information in blue boldface type is new or modified since 2018

* The breakpoints selected to identify resistance are described in *Performance Standards for Antimicrobial Susceptibility Testing: Twenty-seventh informational supplement*, CLSI document M100-S29, January 2019.
† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 9.0, 2019 (www.eucast.org)
§ No category defined
# No guidelines for indicated species
** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanic acid at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines. All cards used in this study have a 2:1 ratio; therefore, no EUCAST categories can be determined.
‡ 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.
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 ECOFF to categorise isolates as wild type or non-wild type for both *E. faecalis* and *E. faecium* is 1 mg/L

Molecular confirmation of resistance

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 isolates with ciprofloxacin MIC >0.25 mg/L; all isolates with meropenem MIC >0.25 mg/L; and all isolates with amikacin MIC >32 mg/L were referred to a central laboratory (the Australian Centre for Antimicrobial Resistance Ecology) for molecular confirmation of resistance.

All referred isolates were screened using real-time polymerase chain reaction (PCR) platform (LC-480) and published primers for the presence of *bla*$_{TEM}$ and *bla*$_{SHV}$, CTX-M-type genes (groups 1, 2, 9, 8/25), plasmid-borne AmpC (*bla*$_{CIT}$, *bla*$_{DHA}$, *bla*$_{EBC}$, *bla*$_{ACC}$, *bla*$_{FOX}$, *bla*$_{MOX}$), and carbapenemases genes (*bla*$_{IMP}$, *bla*$_{NDM}$, *bla*$_{KPC}$, *bla*$_{OXA-48-like}$, *bla*$_{VIM}$, *bla*$_{GES}$, *bla*$_{SME}$, *bla*$_{IMI}$).[30-32]

PCRs were also used to detect *bla*$_{IMP}$ types, known plasmid-mediated quinolone resistance mechanisms (*qnr*, efflux [*qepA*, *oqxAB*] and *aac* (*6')-Ib-cr*), aminoglycoside ribosomal methyltransferases (armA, rmtB, rmtC, rmtF), and mobile colistin resistance genes (mcr-1, mcr-2, mcr-3)[33-38]. All referred *E. coli* were examined for membership of the O25b-ST131 clone.[39] All isolates with demonstrated carbapenemase activity and any amikacin resistant isolates were also screened for OXA-23-like, -24, and -58 carbapenemases.[40]

All gram-negative isolates with carbapenemase activity, *E. faecium* and MRSA were subjected to whole genome sequencing using the Illumina MiSeq platform. Data were analysed using the Nullarbor bioinformatic pipeline.[41] The pipeline was used to identify the multi-locus sequence type and the resistome.

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
- Age ≥100 or <0 years
- Date of collection > discharge date
- Discharge date < date of admission
- Date of admission < date of birth
- Date of admission < date of collection + two days.

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. Similarly, non-resistant (NR) refers to both susceptible and intermediate.

Table C1: Susceptibility (CLSI and EUCAST) to antimicrobial agents in indicator species of national priority, by state and territory, 2018

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	4	23	1	8	3	11	1	61
	%R	0.0, 0.0	n/a	4.3, 4.3	n/a	n/a	n/a	0.0, 0.0	n/a	3.3, 3.3
Enterobacter cloacae complex	n	116	65	117	30	54	14	12	9	417
	%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	n/a	0.0, 0.0
Escherichia coli	n	1,224	770	867	404	801	184	160	157	4,567
	%R	0.0, 0.2	0.0, 0.4	0.0, 0.2	0.0, 0.0	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.2
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%R	0.0, 0.0	3.7, 3.7	0.0, 0.0	0.0, 9.1	0.0, 0.0	n/a	n/a	n/a	0.8, 1.6
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%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	n	286	207	269	78	166	31	37	31	1,105
	%R	0.0, 0.0	0.5, 1.0	0.0, 0.0	1.3, 1.3	0.0, 0.0	3.2, 3.2	0.0, 0.0	0.0, 0.0	0.3, 0.4
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%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	227	77	178	65	104	27	20	32	730
	%R	0.4, 0.9	0.0, 0.0	0.0, 0.6	1.5, 6.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.1, 3.1	0.4, 1.1
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%R	0.0, 0.0	0.0, 0.0	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	6	14	8	1	10	1	1	4	45
	%R	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Amoxicillin–clavulanic acid										
Escherichia coli	n	1,190	770	867	404	801	184	160	157	4,533
	%I	13.9, –†	16.2, –†	12.6, –†	12.1, –†	12.5, –†	12.0, –†	14.4, –†	13.4, –†	13.6, –†
	%R	8.7, –†	10.9, –†	7.6, –†	7.7, –†	8.2, –†	8.7, –†	12.5, –†	8.3, –†	8.8, –†
Klebsiella oxytoca	n	65	52	29	20	34	16	2	11	229

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%I	4.6, –†	5.8, –†	0.0, –†	0.0, –†	0.0, –†	6.3, –†	n/a	9.1, –†	3.5, –†
	%R	6.2, –†	9.6, –†	24.1, –†	0.0, –†	8.8, –†	6.3, –†	n/a	9.1, –†	9.2, –†
Klebsiella pneumoniae	n	276	207	269	78	166	31	37	31	1,095
	%I	5.8, –†	11.6, –†	4.1, –†	7.7, –†	3.6, –†	0.0, –†	10.8, –†	6.5, –†	6.3, –†
	%R	4.7, –†	9.2, –†	4.8, –†	7.7, –†	1.8, –†	3.2, –†	5.4, –†	9.7, –†	5.5, –†
Proteus mirabilis	n	73	43	43	27	49	6	8	8	257
	%I	2.7, –†	7.0, –†	4.7, –†	3.7, –†	12.2, –†	n/a	n/a	n/a	5.8, –†
	%R	4.1, –†	4.7, –†	2.3, –†	0.0, –†	2.0, –†	n/a	n/a	n/a	2.7, –†
Salmonella species (non-typhoidal)	n	21	16	29	3	15	4	12	1	101
	%I	9.5, –†	0.0, –†	0.0, –†	n/a	0.0, –†	n/a	0.0, –†	n/a	2.0, –†
	%R	0.0, –†	0.0, –†	3.4, –†	n/a	0.0, –†	n/a	0.0, –†	n/a	1.0, –†
Salmonella species (typhoidal)	n	6	14	8	1	10	1	1	4	45
	%I	n/a	0.0, –†	n/a	n/a	0.0, –†	n/a	n/a	n/a	2.2, –†
	%R	n/a	0.0, –†	n/a	n/a	0.0, –†	n/a	n/a	n/a	0.0, –†
Ampicillin										
Enterococcus faecalis	n	211	117	131	57	91	31	11	26	675
	%I	–§, 0.0	–§, 0.0	–§, 1.0	–§, 0.0	–§, 0.0	–§, 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	0.0, 0.0	0.0, 0.0	0.0, 0.0
Enterococcus faecium	n	152	130	55	38	54	24	12	26	491
	%I	–§, 0.0	–§, 0.8	–§, 0.0	–§, 0.0	–§, 0.0	–§, 0.0	n/a	–§, 0.0	–§, 0.2
	%R	89.5, 89.5	95.4, 95.4	74.5, 74.5	84.2, 84.2	90.7, 90.7	91.7, 91.7	91.7, 91.7	92.3, 92.3	89.4, 89.4
Escherichia coli	n	1,224	770	866	405	801	184	160	157	4,567
	%I	1.9, –§	2.7, –§	2.2, –§	1.2, –§	2.2, –§	1.1, –§	1.9, –§	1.9, –§	2.1, –§
	%R	53.8, 55.9	62.2, 64.9	52.4 54.6	47.9, 49.1	54.1, 56.3	44.6, 45.7	68.1, 70.0	54.8, 56.7	54.7, 56.8
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%I	0.0, –§	0.0, –§	2.3, –§	0.0, –§	4.1, –§	n/a	n/a	n/a	1.2, –§
	%R	17.6, 17.6	27.9, 27.9	9.3, 11.6	14.8, 14.8	18.4, 22.4	n/a	n/a	n/a	17.1, 18.2
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%I	0.0, –§	0.0, –§	0.0, –§	n/a	0.0, –§	n/a	0.0, –§	n/a	0.0, –§
	%R	19.2, 19.2	0.0, 0.0	3.4, 3.4	n/a	6.7, 6.7	n/a	16.7, 16.7	n/a	8.5, 8.5
Salmonella species (typhoidal)	n	6	14	8	1	10	1	1	4	45
	%I	n/a	0.0,	n/a	n/a	0.0,	n/a	n/a	n/a	0.0, –§

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
			–[§]			–[§]				
	%R	n/a	7.1, 7.1	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	4.4, 4.4
Benzylpenicillin										
Enterococcus faecalis	n	208	117	131	54	91	16	11	26	654
	%R/–[#]	1.4, –[#]	0.9, –[#]	0.8, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.8, –[#]
Enterococcus faecium	n	149	129	54	37	54	17	12	26	478
	%R/–[#]	89.3, –[#]	95.3, –[#]	77.8, –[#]	83.8, –[#]	90.7, –[#]	94.1, –[#]	91.7, –[#]	92.3, –[#]	89.7, –[#]
Staphylococcus aureus	n	646	413	569	254	487	110	77	111	2,667
	%R	80.3, 80.3	79.2, 79.2	80.1, 80.1	79.1, 79.1	77.2, 77.2	74.5, 74.5	93.5, 9.35	64.9, 64.9	78.9, 78.9
Cefazolin										
Enterobacter cloacae complex	n	112	65	117	30	54	16	12	9	415
	%R	97.3, 97.3	96.9, 96.9	96.6, 96.6	100.0, 100.0	94.4, 94.4	100.0, 100.0	100.0, 100.0	n/a	97.1, 97.1
Escherichia coli	n	1,190	770	869	404	801	184	160	157	4,535
	%R	26.1, 26.1	29.6, 29.6	21.9, 21.9	18.8, 18.8	25.7, 25.7	15.2, 15.2	33.8, 33.8	21.0, 21.0	24.8, 24.8
Klebsiella aerogenes	n	36	27	18	11	20	4	3	4	123
	%R	77.8, 77.8	85.2, 85.2	94.4, 94.4	100.0, 100.0	75.0, 75.0	n/a	n/a	n/a	84.6, 84.6
Klebsiella oxytoca	n	63	52	29	20	34	16	2	11	227
	%R	66.7, 66.7	65.4, 65.4	72.4, 72.4	50.0, 50.0	55.9, 55.9	56.3, 56.3	n/a	45.5, 45.5	62.1, 62.1
Klebsiella pneumoniae	n	276	207	269	78	166	31	37	31	1,095
	%R	14.1, 14.1	23.7, 23.7	11.9, 11.9	19.2, 19.2	4.8, 4.8	16.1, 16.1	18.9, 18.9	12.9, 12.9	14.5, 14.5
Proteus mirabilis	n	73	43	43	27	49	6	8	8	257
	%R	16.4, 16.4	27.9, 27.9	11.6, 11.6	14.8, 14.8	20.4, 20.4	n/a	n/a	n/a	18.7, 18.7
Cefepime										
Acinetobacter baumannii	n	8	4	23	1	8	2	11	0	57
	%I	0.0, -	n/a	4.3, -	n/a	n/a	n/a	0.0, -	n/a	3.5, -
	%R	0.0, -	n/a	8.7, -	n/a	n/a	n/a	0.0, -	n/a	5.3, -
Enterobacter cloacae complex	n	116	65	117	30	54	16	12	9	419
	%SDD/I	5.2, 8.6	3.1, 12.3	5.1, 2.6	13.3, 13.3	1.9, 3.7	6.3, 25.0	16.7, 0.0	n/a	5.3, 7.4
	%R	4.3, 7.8	6.2, 6.2	4.3, 7.7	0.0, 3.3	0.0, 0.0	0.0, 0.0	0.0, 16.7	n/a	3.3, 6.0
Escherichia coli	n	1,224	770	869	404	801	184	160	157	4,569
	%SDD/I	1.2, 5.2	1.8, 9.7	1.3, 6.5	2.0, 3.0	2.6, 9.2	1.1, 3.8	3.1, 8.8	0.6, 6.4	1.7, 6.8
	%R	4.2, 4.8	2.6, 3.6	2.2, 2.6	3.0, 3.7	2.7, 3.7	1.1, 1.6	1.9, 4.4	1.9, 2.5	2.9, 3.7
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%SDD/I	7.9, 2.6	0.0, 0.0	0.0, 0.0	0.0, 9.1	5.0, 5.0	n/a	n/a	n/a	3.2, 2.4

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	5.3, 10.5	3.7, 3.7	0.0, 0.0	9.1, 9.1	0.0, 0.0	n/a	n/a	n/a	3.2, 4.8
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%SDD/I	0.0, 1.5	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, 0.4
	%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	n	285	207	269	78	166	31	37	31	1,104
	%SDD/I	0.7, 2.5	4.3, 9.2	0.0, 2.6	1.3, 1.3	1.2, 3.6	0.0, 6.5	0.0, 2.7	0.0, 3.2	1.3, 4.0
	%R	4.9, 5.6	4.8, 7.2	0.4, 0.4	6.4, 6.4	0.0, 1.2	3.2, 3.2	8.1, 8.1	3.2, 3.2	3.2, 4.0
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%SDD/I	0.0, 2.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
	%R	1.4, 1.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.0, 2.0	n/a	n/a	n/a	0.8, 0.8
Pseudomonas aeruginosa	n	227	77	178	65	104	27	20	32	730
	%I	4.0, 0.0	2.6, 0.0	1.1, 0.0	7.7, 0.0	1.9, 0.0	3.7, 0.0	0.0, 0.0	3.1, 0.0	3.0, 0.0
	%R	2.6, 6.6	3.9, 6.5	2.2, 3.4	1.5, 9.2	0.0, 1.9	14.8, 18.5	0.0, 0.0	3.1, 6.3	2.6, 5.6
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%SDD/I	0.0, 0.0	0.0, 0.0	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	0.0, 0.0	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	6	14	8	1	10	1	1	4	45
	%SDD/I	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	2.2, 2.2
Cefoxitin										
Escherichia coli	n	1,220	770	869	404	801	184	160	157	4,565
	%R/ecoff	4.5, 7.1	3.6, 7.5	3.9, 6.2	5.0, 6.9	3.4, 7.5	4.3, 7.6	5.0, 8.1	3.8, 9.6	4.1, 7.2
Klebsiella oxytoca	n	65	52	29	20	34	16	2	11	229
	%R/ecoff	0.0, 1.5	0.0, 1.9	3.4, 6.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 9.1	0.4, 2.2
Klebsiella pneumoniae	n	283	207	269	78	166	31	37	31	1,102
	%R/ecoff	6.7, 10.6	5.8, 9.2	5.6, 6.3	5.1, 7.7	2.4, 3.6	9.7, 9.7	2.7, 5.4	12.9, 12.9	5.6, 7.9
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%R/ecoff	1.4, 2.7	0.0, 2.3	2.3, 2.3	0.0, 3.7	0.0, 0.0	n/a	n/a	n/a	0.8, 1.9
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%R/ecoff	0.0, 0.0	0.0, 0.0	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	6	14	8	1	10	1	1	4	45
	%R/ecoff	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Ceftazidime										

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Acinetobacter baumannii complex	n	6	4	23	1	8	2	11	1	56
	%I	n/a	n/a	13.0, –§	n/a	n/a	n/a	0.0, –§	n/a	10.7, –§
	%R	n/a	n/a	8.7, –§	n/a	n/a	n/a	0.0, –§	n/a	3.6, –§
Enterobacter cloacae complex	n	116	65	117	30	54	16	12	9	419
	%I	0.9, 1.7	0.0, 1.5	0.9, 2.6	0.0, 6.7	0.0, 3.7	0.0, 0.0	0.0, 0.0	n/a	0.5, 2.4
	%R	25.0, 25.9	30.8, 30.8	14.5, 15.4	23.3, 23.3	14.8, 14.8	31.3, 31.3	33.3, 33.3	n/a	21.7, 22.2
Escherichia coli	n	1,224	770	869	404	801	184	160	157	4,569
	%I	0.9, 6.1	0.1, 6.5	0.5, 5.7	2.2, 4.5	0.6, 6.5	0.0, 4.9	0.6, 6.9	0.0, 8.3	0.7, 6.1
	%R	5.6, 6.5	8.2, 8.3	5.6, 6.1	4.0, 6.2	6.5, 7.1	3.8, 3.8	5.0, 5.6	4.5, 4.5	5.9, 6.6
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%I	0.0, 0.0	3.7, 0.0	0.0, 0.0	0.0, 18.2	5.0, 0.0	n/a	n/a	n/a	1.6, 2.4
	%R	36.8, 36.8	37.0, 40.7	27.8, 27.8	18.2, 18.2	5.0, 10.0	n/a	n/a	n/a	28.0, 29.6
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%I	0.0, 0.0	0.0, 1.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.4
	%R	0.0, 0.0	1.9, 1.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
Klebsiella pneumoniae	n	286	207	269	78	166	31	37	31	1,105
	%I	1.0, 1.7	2.9, 7.2	1.1, 2.2	0.0, 1.3	0.0, 1.8	0.0, 6.5	5.4, 2.7	0.0, 3.2	1.3, 3.1
	%R	6.3, 7.3	9.2, 12.1	3.7, 4.8	11.5, 11.5	2.4, 2.4	6.5, 6.5	8.1, 13.5	6.5, 6.5	6.1, 7.3
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%I	0.0, 1.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.0, 0.0	n/a	n/a	n/a	0.4, 0.4
	%R	2.7, 2.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.0, 4.1	n/a	n/a	n/a	1.2, 1.6
Pseudomonas aeruginosa	n	227	77	178	65	104	27	20	32	730
	%I	4.8, 0.0	2.6, 0.0	2.2, 0.0	3.1, 0.0	1.0, 0.0	11.1, 0.0	5.0, 0.0	6.3, 0.0	3.6, 0.0
	%R	5.7, 10.6	6.5, 9.1	3.9, 6.2	4.6, 7.7	1.0, 1.9	11.1, 22.2	0.0, 5.0	3.1, 9.4	4.5, 8.1
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%I	0.0, 0.0	0.0, 0.0	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	0.0, 0.0	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	6	14	8	1	10	1	1	4	45
	%I	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	2.2, 2.2
Ceftriaxone										
Acinetobacter	n	3	4	23	1	8	4	11	1	55

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
baumannii complex	%I	n/a	n/a	78.3, –§	n/a	n/a	n/a	100.0, –§	n/a	83.6, –§
	%R	n/a	n/a	13.0, –§	n/a	n/a	n/a	0.0, –§	n/a	7.3, –§
Enterobacter cloacae complex	n	116	65	117	30	54	16	12	9	419
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.7, 3.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.5
	%R	26.7, 26.7	35.4, 35.4	19.7, 19.7	30.0, 30.0	16.7, 16.7	31.3, 31.3	33.3, 33.3	n/a	25.1, 25.1
Escherichia coli	n	1,224	770	869	404	801	184	160	157	4,569
	%I	0.0, 0.0	0.0, 0.0	0.1, 0.1	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.6, 0.6	0.1, 0.1
	%R	13.3, 13.3	17.1, 17.1	11.2, 11.2	8.2, 8.2	15.5, 15.5	7.1, 7.1	17.5, 17.5	12.7, 12.7	13.4, 13.4
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%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	36.8, 36.8	40.7, 40.7	27.8, 27.8	27.3, 27.3	10.0, 10.0	n/a	n/a	n/a	30.4, 30.4
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%I	1.5, 1.5	1.9, 1.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.9, 0.9
	%R	6.1, 6.1	7.7, 7.7	13.8, 13.8	0.0, 0.0	8.8, 8.8	6.3, 6.3	n/a	18.2, 18.2	7.8, 7.8
Klebsiella pneumoniae	n	285	207	269	78	166	31	37	31	1,104
	%I	0.0, 0.0	0.5, 0.5	0.0, 0.0	1.3, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
	%R	8.8, 8.8	19.8, 19.8	4.1, 4.1	10.3, 10.3	4.8, 4.8	12.9, 12.9	13.5, 13.5	6.5, 6.5	9.4, 9.4
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%I	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	0.4, 0.4
	%R	4.1, 4.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.0, 2.0	n/a	n/a	n/a	1.6, 1.6
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%I	0.0, 0.0	0.0, 0.0	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	0.0, 0.0	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	6	14	8	1	10	1	1	4	45
	%I	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	2.2, 2.2
Ciprofloxacin										
Acinetobacter baumannii complex	n	10	4	23	1	8	5	11	1	63
	%I**	0.0, 100	n/a	4.3, 91.3	n/a	n/a	n/a	18.2, 81.8	n/a	6.3, 92.1
	%R	0.0, 0.0	n/a	4.3, 8.7	n/a	n/a	n/a	0.0, 18.2	n/a	1.6, 7.9
Enterococcus faecalis	n	172	94	120	44	91	16	11	0	548
	%NS/R**	16.3,	13.8,	9.2,	15.9,	8.8,	18.8,	9.1,	n/a	13.0, 9.9

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		12.2	12.8	6.7	11.4	4.4	18.8	9.1		
Enterococcus faecium	n	140	86	51	30	54	17	12	0	390
	%NS/R**	90.7, 86.4	94.2, 93.0	80.4, 70.6	90.0, 86.7	94.4, 90.7	100, 94.1	91.7, 91.7	n/a	90.0, 86.9
Staphylococcus aureus	n	646	413	569	255	487	110	77	111	2,668
	%NS	13.9, 13.9	10.4, 10.4	4.2, 4.2	6.7, 6.7	6.8, 6.8	8.2, 8.2	3.9, 3.9	6.3, 6.3	8.5, 8.5
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%NS/R	58.3, 58.3	49.2, 49.2	18.7, 18.8	30.0, 30.0	18.3, 18.3	n/a	6.5, 6.5	54.5, 54.5	35.6, 35.6
Methicillin-susceptible *S. aureus*	n	514	354	489	215	383	101	46	100	2,202
	%NS/R	2.6, 2.5	4.0, 4.0	1.8, 1.8	2.3, 2.3	3.7, 3.7	3.0, 3.0	2.2, 2.2	1.0, 1.0	2.7, 2.7
Acinetobacter baumannii complex	n	10	4	23	1	8	5	11	1	63
	%I	0.0, 100.0	n/a	4.3, 91.3	n/a	n/a	n/a	18.2, 81.8	n/a	6.3, 92.1
	%R	0.0, 0.0	n/a	4.3, 8.7	n/a	n/a	n/a	0.0, 18.2	n/a	1.6, 7.9
Enterobacter cloacae complex	n	116	65	117	30	54	16	12	9	419
	%I	0.0, 0.0	0.0, 0.0	0.9, 0.9	3.3, 3.3	3.7, 3.7	0.0, 0.0	0.0, 0.0	n/a	1.0, 1.0
	%R	12.1, 12.1	4.6, 4.6	7.7, 7.7	3.3, 3.3	3.7, 3.7	0.0, 0.0	8.3, 8.3	n/a	7.4, 7.4
Escherichia coli	n	1,224	770	869	404	801	184	160	157	4,569
	%I	4.8, 4.8	2.1, 2.1	4.1, 4.1	5.2, 5.2	3.1, 3.1	2.7, 2.7	8.1, 8.1	3.2, 3.2	3.9, 3.9
	%R	15.8, 15.8	18.1, 18.1	10.4, 10.4	11.6, 11.6	20.5, 20.5	7.6, 7.6	12.5, 12.5	17.8, 17.8	15.2, 15.2
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%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	14.8, 14.8	5.6, 5.6	0.0, 0.0	5.0, 5.0	n/a	n/a	n/a	4.8, 4.8
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%I	0.0, 0.0	1.9, 1.9	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	1.5, 1.5	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
Klebsiella pneumoniae	n	285	207	269	78	166	31	37	31	1,104
	%I	1.1, 1.1	0.5, 0.5	2.2, 2.2	3.8, 3.8	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.4, 1.4
	%R	9.8, 9.8	24.6, 24.6	5.6, 5.6	9.0, 9.0	7.2, 7.2	12.9, 12.9	13.5, 13.5	9.7, 9.7	11.3, 11.3
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%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	7.0, 7.0	0.0, 0.0	0.0, 0.0	2.0, 2.0	n/a	n/a	n/a	2.7, 2.7
Pseudomonas aeruginosa	n	227	77	178	65	104	27	20	32	730
	%I	4.4, 0.0	1.3, 0.0	2.2, 0.0	12.3, 0.0	2.9, 0.0	7.4, 0.0	5.0, 0.0	3.1, 0.0	4.1, 0.0
	%R	4.0,	3.9,	2.8,	7.7,	1.0,	11.1,	0.0,	0.0,	3.6, 7.7

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		8.4	5.2	5.1	20.0	3.8	18.5	5.0	3.1	
Salmonella species (non-typhoidal)	n	26	15	29	3	15	4	12	1	105
	%I	–[**], –[§]	–[**], –[§]	–[**], –[§]	n/a	–[**], –[§]	n/a	–[**], –[§]	n/a	–[**], –[§]
	%R	30.8, 53.8	0.0, 0.0	3.4, 3.4	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	8.6, 14.3
Salmonella species (typhoidal)	n	6	12	8	1	10	1	1	4	43
	%I	n/a	–[**], –[§]	n/a	n/a	–[**], –[§]	n/a	n/a	n/a	–[**], –[§]
	%R	n/a	50.0, 50.0	n/a	n/a	80.0, 90.0	n/a	n/a	n/a	46.5, 58.1
Clindamycin (inducible + constitutive resistance)										
Staphylococcus aureus	n	646	412	569	255	468	110	77	111	2,666
	%R	14.9, 14.9	12.6, 12.6	13.5, 13.6	7.5, 7.5	16.7, 16.7	11.8, 11.8	24.7, 24.7	8.1, 8.1	13.7, 13.7
Methicillin-resistant *S. aureus*	n	132	59	80	40	103	9	31	11	465
	%NS	35.6, 35.6	30.5, 30.5	27.5, 27.5	17.5, 17.5	29.1, 29.1	n/a	38.7, 38.7	36.4, 36.4	31.2, 31.2
Methicillin-susceptible *S. aureus*	n	514	353	489	215	383	101	46	100	2,201
	%NS	9.5, 9.5	9.6, 9.6	11.2, 11.2	5.6, 5.6	13.3, 13.3	7.9, 7.9	15.2, 15.2	5.0, 5.0	10.0, 10.0
Daptomycin										
Enterococcus faecalis	n	211	117	131	57	91	29	11	26	673
	%R	0.5, –[#]	0.0, –[#]	0.0, –[#]	1.8, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.3, –[#]
Enterococcus faecium	n	50	0[§§]	0[§§]	30	0[§§]	0[§§]	0[§§]	0[§§]	80
	%R	2.0, –[#]	n/a	n/a	3.3, –[#]	n/a	n/a	n/a	n/a	2.5, –[#]
Staphylococcus aureus	n	647	413	571	256	487	110	77	111	2,672
	%NS/R	0.2, 0.2	0.2, 0.2	0.2, 0.2	0.4, 0.4	0.2, 0.2	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.3, 0.3
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%NS	0.8, 0.8	1.7, 1.7	1.3, 1.3	0.0, 0.0	1.0, 1.0	n/a	0.0, 0.0	0.0, 0.0	1.3, 1.3
Methicillin-susceptible *S. aureus*	n	515	354	491	216	383	101	46	100	2,206
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	<0.0, <0.0
Erythromycin										
Staphylococcus aureus	n	579	413	569	254	487	110	77	110	2,599
	%NS	24.7, 19.2	25.7, 10.9	20.2, 13.2	31.1, 19.7	18.9 17.5	11.8, 10.9	24.7, 23.4	10.0, 9.1	22.2, 15.6
Methicillin-resistant *S. aureus*	n	116	59	80	40	104	9	31	11	450
	%NS	52.6, 48.3	45.8, 30.5	32.5, 31.3	47.5, 47.5	33.7 32.7	n/a	38.7, 38.7	45.5, 45.5	42.2, 38.7
Methicillin-susceptible *S. aureus*	n	463	354	489	214	383	101	46	99	2,149
	%NS	17.7 11.9	22.3, 7.6	18.2, 10.2	28.0, 14.5	14.9, 13.3	7.9, 6.9	15.2, 13.0	6.1, 5.1	18.1, 10.8
Fusidic acid										
Staphylococcus aureus	n	646	413	569	255	487	110	77	111	2,668

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	–#, 2.2	–#, 2.4	–#, 5.3	–#, 4.7	–#, 2.5	–#, 4.5	–#, 3.9	–#, 5.4	–#, 3.4
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%R	–#, 2.3	–#, 5.1	–#, 2.5	–#, 5.0	–#, 3.8	n/a	–#, 9.7	–#, 9.1	–#, 4.5
Methicillin-susceptible *S. aureus*	N	514	354	489	215	383	101	46	100	2,202
	%R	–#, 2.1	–#, 2.0	–#, 5.7	–#, 4.7	–#, 2.1	–#, 2.0	–#, 0.0	–#, 5.0	–#, 3.2
Gentamicin										
Acinetobacter baumannii complex	n	10	4	23	1	8	5	11	1	63
	%R	0.0, 0.0	n/a	4.3, 4.3	n/a	n/a	n/a	0.0, 0.0	n/a	3.2, 3.2
Enterobacter cloacae complex	n	116	65	117	30	54	16	12	9	419
	%R	10.3, 12.1	3.1, 6.2	6.8, 6.8	3.3, 3.3	0.0, 0.0	6.3, 6.3	8.3, 8.3	n/a	6.0, 6.9
Escherichia coli	n	1,225	770	869	404	801	184	160	157	4,570
	%R	8.5, 8.8	7.7, 7.8	6.8, 7.0	7.7, 7.9	10.4, 10.6	3.8, 3.8	13.8, 13.8	6.4, 7.0	8.2, 8.4
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%R	5.3, 5.3	3.7, 7.4	0.0, 0.0	18.2, 18.2	0.0, 0.0	n/a	n/a	n/a	4.0, 4.8
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%R	0.0, 0.0	0.0, 1.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.4
Klebsiella pneumoniae	n	286	207	269	78	166	31	37	31	1,105
	%R	4.2, 4.2	4.3, 4.3	2.6, 3.0	9.0, 9.0	3.6, 3.6	6.5, 6.5	5.4, 5.4	9.7, 9.7	4.3, 4.4
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%R	1.4, 1.4	0.0, 2.3	0.0, 2.3	3.7, 3.7	2.0, 2.0	n/a	n/a	n/a	1.2, 1.9
Pseudomonas aeruginosa	n	227	78	178	65	104	27	20	31	730
	%R	1.3, 2.2	0.0, 0.0	0.6, 2.8	1.5, 4.6	0.0, 1.0	0.0, 3.7	0.0, 5.0	0.0, 0.0	0.7, 2.2
Staphylococcus aureus	n	646	413	569	255	487	110	77	111	2,668
	%R	4.2, 8.2	1.0, 2.7	1.9, 2.5	1.6, 3.9	0.2, 0.8	0.0, 0.0	3.9, 6.5	0.9, 2.7	1.9, 3.7
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%R	18.2, 33.3	5.1, 11.9	11.3, 12.5	10.0, 12.5	1.0, 1.0	n/a	6.5, 6.5	9.1, 27.3	9.4, 15.5
Methicillin-susceptible *S. aureus*	n	514	354	489	215	383	101	46	100	2,202
	%R	0.6, 1.8	0.3, 1.1	0.4, 0.8	0.0, 2.3	0.0, 0.8	0.0, 0.0	2.2, 6.5	0.0, 0.0	0.3, 1.3
Linezolid										
Enterococcus faecalis	n	211	117	131	57	91	31	11	26	675
	%NS/R	0.0, 0.0	0.9, 0.9	0.8, 0.0	1.8, 0.0	1.1, 1.1	3.2, 0.0	0.0, 0.0	0.0, 0.0	0.7, 0.3
Enterococcus faecium	n	152	130	54	38	54	24	12	26	490
	%NS/R	0.7, 0.0	0.8, 0.8	0.0, 0.0	0.0, 0.0	1.9, 0.0	0.0, 0.0	0.0, 0.0	3.8, 3.8	0.8, 0.4
Staphylococcus aureus	n	647	413	571	256	487	110	77	111	2,672
	%NS/R	0.0,	0.0,	0.0,	0.0,	0.0,	0.0,	0.0,	0.0,	0.0, 0.0

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%NS/R	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	0.0, 0.0
Methicillin-susceptible *S. aureus*	n	515	354	491	216	383	101	46	100	2,206
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Meropenem										
Acinetobacter baumannii complex	n	10	4	23	1	8	5	11	1	63
	%I	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	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	4.3, 4.3	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	3.2, 3.2
Enterobacter cloacae complex	n	116	64	117	30	54	16	12	9	418
	%I	1.7, 0.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 8.3	n/a	0.5, 0.5
	%R	5.2, 4.3	1.6, 1.6	2.6, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	8.3, 0.0	n/a	2.6, 2.2
Escherichia coli	n	1,224	770	869	404	801	183	160	157	4,568
	%I	0.1, 0.2	0.0, 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	0.0, 0.0
	%R	0.4, 0.2	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%I	0.0, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
	%R	7.9, 5.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	2.4, 1.6
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%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	n	285	207	269	78	166	31	37	31	1,104
	%I	0.0, 0.4	0.0, 0.5	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, 0.2
	%R	2.1, 1.8	1.4, 1.0	0.0, 0.0	0.0, 0.0	0.6, 0.6	0.0, 0.0	0.0, 0.0	3.2, 3.2	1.0, 0.8
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.7, 0.0	0.0, 0.0	n/a	n/a	n/a	0.4, 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	226	77	178	65	104	27	20	32	729
	%I	3.5, 4.0	1.3, 1.3	3.4, 5.7	3.1, 7.7	2.9, 3.8	11.1, 14.8	0.0, 0.0	0.0, 0.0	3.2, 4.5
	%R	4.4, 4.0	6.5, 6.5	4.5, 2.3	7.7, 3.1	1.9, 1.0	11.1, 7.4	0.0, 0.0	0.0, 0.0	4.5, 3.2
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%I	0.0, 0.0	0.0, 0.0	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,	0.0,	n/a	0.0,	n/a	0.0,	n/a	0.0, 0.0

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.0	0.0	0.0		0.0		0.0		
Salmonella species (typhoidal)	n	6	14	8	1	10	1	1	4	45
	%I	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Mupirocin (high-level)										
Staphylococcus aureus	n	645	412	568	250	487	110	76	111	2,659
	%R	0.6, –[#]	1.2, –[#]	4.2, –[#]	0.8, –[#]	0.0, –[#]	0.9, –[#]	1.3, –[#]	0.0, –[#]	1.4, –[#]
Methicillin-resistant *S. aureus*	n	132	58	80	40	104	9	30	11	464
	%R	1.5, –[#]	1.7, –[#]	5.0, –[#]	2.5, –[#]	0.0, –[#]	n/a	3.3, –[#]	0.0, –[#]	1.9, –[#]
Methicillin-susceptible *S. aureus*	n	513	354	488	210	383	101	46	100	2,195
	%R	0.4, –[#]	1.1, –[#]	4.1, –[#]	0.5, –[#]	0.0, –[#]	1.0, –[#]	0.0, –[#]	0.0, –[#]	1.3, –[#]
Nitrofurantoin										
Enterococcus faecalis	n	208	116	131	55	90	31	11	26	668
	%R	0.5, 0.5	0.0, 0.0	0.0, 0.0	1.8, 1.8	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.4, 0.4
Enterococcus faecium	n	140	129	38	37	54	17	12	26	453
	%R	72.9, –[§]	35.7, –[§]	84.2, –[§]	70.3, –[§]	50.0, –[§]	35.3, –[§]	33.3, –[§]	76.9, –[§]	58.1, –[§]
Enterobacter cloacae complex	n	102	65	117	30	54	16	12	9	405
	%R	26.5, –[§]	16.9, –[§]	12.8, –[§]	23.3, –[§]	11.1, –[§]	6.3, –[§]	16.7, –[§]	n/a	17.3, –[§]
Escherichia coli	n	1,223	770	869	404	801	184	160	157	4,568
	%R	1.0, 0.0	0.8, 0.0	1.2, 0.0	0.5, 0.0	0.9, 0.0	1.1, 0.0	0.0, 0.0	0.6, 0.0	0.9, 0.0
Klebsiella (*Enterobacter*) *aerogenes*	n	29	27	18	11	20	4	3	4	116
	%R	20.7, –[§]	40.7, –[§]	27.8, –[§]	0.0, –[§]	35.0, –[§]	n/a	n/a	n/a	30.2, –[§]
Klebsiella oxytoca	n	54	52	29	20	34	16	2	11	218
	%R	0.0, –[§]	1.9, –[§]	3.4, –[§]	0.0, –[§]	5.9, –[§]	0.0, –[§]	n/a	0.0, –[§]	1.8, –[§]
Klebsiella pneumoniae	n	251	207	269	78	166	31	37	31	1,070
	%R	32.7, –[§]	41.5, –[§]	31.2, –[§]	28.2, –[§]	45.2, –[§]	19.4, –[§]	29.7, –[§]	54.8, –[§]	35.8, –[§]
Proteus mirabilis	n	62	43	43	27	49	6	8	0	238
	%R	91.9, –[§]	97.7, –[§]	95.3, –[§]	81.5, –[§]	98.0, –[§]	n/a	n/a	n/a	94.1, –[§]
Salmonella species (non-typhoidal)	n	23	16	29	3	15	4	12	0	102
	%R	13.0, –[§]	6.3, –[§]	3.4, –[§]	n/a	6.7, –[§]	n/a	25.0, –[§]	n/a	8.8, –[§]
Salmonella species (typhoidal)	n	6	14	8	1	10	1	1	0	41
	%R	n/a	0.0, –[§]	n/a	n/a	0.0, –[§]	n/a	n/a	n/a	2.4, –[§]
Oxacillin/methicillin										
Staphylococcus aureus	n	647	414	571	256	487	110	77	111	2,673
	%R	20.4, 20.4	14.3, 14.3	14.0, 14.0	15.6, 15.6	21.4, 21.4	8.2, 8.2	40.3, 40.3	9.9, 9.9	17.4, 17.4

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Piperacillin–tazobactam										
Acinetobacter baumannii complex	n	10	4	23	1	8	2	11	1	60
	%R	20.0, _[#]	n/a	13.0, _[#]	n/a	n/a	n/a	0.0, –[#]	n/a	15.0, –[#]
Enterobacter cloacae complex	n	116	64	114	30	52	16	12	9	413
	%R	21.6, 25.0	25.0, 26.6	12.3, 16.7	10.0, 23.3	17.3, 19.2	31.3, 31.3	16.7, 16.7	n/a	18.2, 22.0
Escherichia coli	n	1,219	766	865	402	797	181	160	156	4,546
	%R	3.4, 6.8	4.4, 8.7	2.8, 5.3	2.0, 3.5	1.9, 4.6	2.8, 3.9	1.3, 6.9	4.5, 5.8	3.0, 6.0
Klebsiella (*Enterobacter*) *aerogenes*	n	38	27	18	11	20	4	3	4	125
	%R	28.9, 34.2	37.0, 40.7	16.7, 27.8	27.3, 36.4	10.0, 15.0	n/a	n/a	n/a	24.8, 31.2
Klebsiella oxytoca	n	66	51	29	20	34	16	2	11	229
	%R	9.1, 10.6	9.8, 9.8	17.2, 20.7	0.0, 0.0	8.8, 8.8	6.3, 6.3	n/a	18.2, 18.2	9.6, 10.5
Klebsiella pneumoniae	n	283	207	267	78	165	31	37	31	1,099
	%R	5.7, 8.5	4.8, 12.1	3.7, 6.4	5.1, 6.4	1.2, 4.8	6.5, 6.5	2.7, 8.1	6.5, 9.7	4.3, 7.9
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%R	0.0, 1.4	0.0, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
Pseudomonas aeruginosa	n	225	77	178	65	103	27	20	32	727
	%R	5.3, 13.3	7.8, 13.0	5.1, 10.1	3.1, 7.7	1.0, 4.9	18.5, 29.6	5.0, 5.0	3.1, 12.5	5.1, 11.1
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%R	0.0, 0.0	0.0, 0.0	0.0, 3.4	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.9
Salmonella species (typhoidal)	n	6	13	8	1	10	1	1	4	44
	%R	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 2.3
Rifampicin										
Staphylococcus aureus	n	646	413	569	255	487	108	77	111	2,666
	%NS	0.9, 0.9	0.2, 0.2	0.5, 0.5	0.0, 0.4	0.4, 0.4	2.8, 2.8	0.0, 0.0	0.0, 0.0	0.6, 0.6
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%NS	2.3, 2.3	0.0, 0.0	2.5, 2.5	0.0, 2.5	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	1.7, 1.9
Methicillin-susceptible *S. aureus*	n	514	354	489	215	383	99	46	100	2,200
	%NS	0.6, 0.6	0.3, 0.3	0.2, 0.2	0.0, 0.0	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.5
Teicoplanin										
Enterococcus faecalis	n	211	117	131	57	91	31	11	26	675
	%NS/R	0.0, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.3
Enterococcus faecium	n	152	130	55	38	54	24	12	26	491
	%NS/R	30.9, 34.2	17.7, 19.2	5.5, 5.5	10.5, 10.5	11.1, 11.1	16.7, 16.7	8.3, 8.3	26.9, 26.9	19.3, 20.8
Staphylococcus aureus	n	647	413	571	256	487	110	77	111	2,672
	%NS/R	0.0, 0.2	0.0, 0.0	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Tetracycline/doxycycline										
Enterococcus faecalis	n	162	94	98	32	91	16	11	0§§	504
	%NS	72.8, _#	69.1, _#	77.6, _#	78.1, _#	80.2, _#	62.5, _#	90.9, _#	n/a	74.8, –#
Enterococcus faecium	n	141	115	39	30	54	17	12	0§§	408
	%NS	48.9, _#	73.9, _#	79.5, _#	20.0, _#	77.8, _#	70.6, _#	91.7, _#	n/a	62.7, –#
Staphylococcus aureus	n	646	413	569	255	487	110	77	111	2,668
	%R	6.5, 8.0	4.8, 4.8	4.2, 4.2	0.8, 2.4	3.5, 3.5	0.9, 0.9	3.9, 3.9	7.2, 7.2	4.4, 4.9
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%R	22.0, 26.5	20.3, 20.3	10.0, 10.0	0.0, 5.0	6.7, 6.7	n/a	9.7, 9.7	27.3, 27.3	13.3, 15.0
Methicillin-susceptible *S. aureus*	n	514	354	489	215	383	101	46	100	2,202
	%R	2.5, 3.3	2.3, 2.3	3.3, 3.3	0.9, 1.9	2.6, 2.6	1.0, 1.0	0.0, 0.0	5.0, 5.0	2.5, 2.8
Ticarcillin–clavulanic acid										
Acinetobacter baumannii complex	n	3	4	22	0	8	2	11	1	51
	%R	n/a	n/a	4.5, 0.0	n/a	n/a	n/a	0.0, 0.0	n/a	3.9, 0.0
Enterobacter cloacae complex	n	85	65	115	6	54	16	12	9	362
	%R	28.2, 28.2	26.2, 29.2	17.4, 23.5	n/a	18.5, 20.4	25.0, 31.3	16.7, 25.0	n/a	21.5, 24.9
Escherichia coli	n	891	769	844	179	801	184	160	157	3,985
	%R	10.3, 20.8	11.7, 20.7	6.6, 13.4	8.9, 15.1	7.2, 16.5	3.8, 13.6	11.9, 19.4	8.9, 17.8	8.8, 17.6
Klebsiella (*Enterobacter*) *aerogenes*	n	28	27	17	4	20	4	3	4	107
	%R	32.1, 35.7	29.6, 37.0	29.4, 29.4	n/a	20.0, 25.0	n/a	n/a	n/a	28.0, 32.7
Klebsiella oxytoca	n	52	52	27	9	34	16	2	11	203
	%R	5.8, 9.6	5.8, 11.5	22.2, 22.2	n/a	8.8, 8.8	6.3, 6.3	n/a	18.2, 18.2	8.9, 11.3
Klebsiella pneumoniae	n	196	207	255	27	166	31	37	31	950
	%R	6.6, 9.2	9.2, 20.3	4.3, 8.6	11.1, 11.1	2.4, 4.2	0.0, 12.9	5.4, 16.2	12.9, 16.1	5.9, 11.3
Proteus mirabilis	n	59	43	42	12	49	6	8	8	227
	%R	0.0, 0.0	2.3, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.4, 0.4
Pseudomonas aeruginosa	n	150	77	170	21	103	27	20	32	600
	%R	14.0, 54.7	18.2, 58.4	15.3, 62.4	4.8, 61.9	2.9, 42.7	33.3, 77.8	5.0, 60.0	12.5, 53.1	13.2, 56.7
Salmonella species (non-typhoidal)	n	11	16	28	2	15	4	12	1	89
	%R	0.0, 9.1	0.0, 0.0	3.6, 3.6	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.1, 2.2
Salmonella species (typhoidal)	n	6	14	7	1	10	1	1	4	44
	%R	n/a	0.0, 7.1	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	2.3, 4.5
Tobramycin										
Acinetobacter baumannii complex	n	10	4	23	1	8	5	11	1	63
	%R	0.0,	n/a	4.3,	n/a	n/a	n/a	0.0,	n/a	3.2, 3.2

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.0		4.3				0.0		
Enterobacter cloacae complex	n	116	65	117	30	54	16	12	9	419
	%R	5.2, 12.9	0.0, 6.2	8.5, 9.4	3.3, 3.3	0.0, 0.0	6.3, 6.3	0.0, 8.3	n/a	4.3, 7.9
Escherichia coli	n	1,224	770	869	404	801	184	160	157	4,569
	%R	3.2, 9.1	4.4, 9.2	2.3, 7.1	3.5, 9.2	4.7, 12.4	0.0, 3.3	3.1, 16.9	0.0, 6.4	3.3, 9.3
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%R	5.3, 5.3	7.4, 7.4	0.0, 0.0	18.2, 18.2	0.0, 0.0	n/a	n/a	n/a	4.8, 4.8
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%R	0.0, 0.0	0.0, 1.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.4
Klebsiella pneumoniae	n	286	207	269	78	166	31	37	31	1,105
	%R	1.4, 4.2	9.2, 19.3	1.9, 2.6	5.1, 7.7	1.8, 4.2	3.2, 6.5	8.1, 13.5	3.2, 9.7	3.6, 7.4
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%R	1.4, 1.4	0.0, 2.3	0.0, 0.0	0.0, 3.7	2.0, 2.0	n/a	n/a	n/a	0.8, 1.6
Pseudomonas aeruginosa	n	227	77	178	65	104	27	20	32	730
	%R	0.9, 0.9	0.0, 0.0	0.0, 0.0	3.1, 3.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.5
Trimethoprim										
Enterobacter cloacae complex	n	115	65	117	30	54	16	12	9	418
	%R	20.9, 20.9	21.5, 21.5	20.5, 20.5	10.0, 13.3	11.1, 13.0	6.3, 6.3	16.7, 16.7	n/a	18.4, 18.9
Escherichia coli	n	1,220	770	869	404	801	184	160	157	4,565
	%R	35.3, 35.7	36.8, 37.3	33.5, 33.6	30.0, 30.0	37.2, 37.5	24.5, 24.5	43.8, 44.4	28.7, 28.7	34.7, 35.0
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%R	2.6, 2.6	11.1, 14.8	0.0, 0.0	18.2, 18.2	10.0, 10.0	n/a	n/a	n/a	7.2, 8.0
Klebsiella oxytoca	n	65	52	29	20	34	16	2	11	229
	%R	3.1, 3.1	9.6, 9.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	3.1, 3.1
Klebsiella pneumoniae	n	283	207	269	78	166	31	37	31	1,102
	%R	23.0, 23.3	30.9, 31.4	19.0, 19.0	23.1, 26.9	11.4, 13.9	19.4, 22.6	21.6, 21.6	22.6, 22.6	21.6, 22.5
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%R	10.8, 10.8	27.9, 27.9	16.3, 16.3	18.5, 18.5	16.3, 16.3	n/a	n/a	n/a	17.1, 17.1
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%R	11.5, 11.5	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	2.8, 2.8
Salmonella species (typhoidal)	n	6	14	8	1	10	1	1	4	45
	%R	n/a	7.1, 7.1	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	4.4, 4.4
Trimethoprim–sulfamethoxazole										
Acinetobacter baumannii complex	n	10	4	23	1	8	5	11	1	63
	%R	0.0,	n/a	17.4,	n/a	n/a	n/a	27.3,	n/a	12.7,

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.0		17.4				27.3		12.7
Enterobacter cloacae complex	n	116	65	117	30	54	16	12	9	419
	%R	19.8, 19.8	20.0, 20.0	19.7, 19.7	10.0, 10.0	7.4, 7.4	6.3, 6.3	16.7, 16.7	n/a	17.2, 17.2
Escherichia coli	n	1,225	769	868	403	801	183	160	157	4,566
	%R	32.9, 32.7	35.0, 34.9	31.3, 31.3	27.3, 26.8	33.8, 33.8	21.3, 21.3	39.4, 39.4	25.5, 25.5	32.1, 32.0
Klebsiella aerogenes	n	38	27	18	11	20	4	3	4	125
	%R	2.6, 2.6	3.7, 3.7	0.0, 0.0	18.2, 18.2	10.0, 10.0	n/a	n/a	n/a	5.6, 5.6
Klebsiella oxytoca	n	66	52	29	20	34	16	2	11	230
	%R	3.0, 3.0	9.6, 9.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	3.0, 3.0
Klebsiella pneumoniae	n	286	207	269	78	166	31	37	31	1,105
	%R	21.7, 20.6	30.0, 28.5	17.5, 17.1	23.1, 21.8	10.8, 10.2	16.1, 16.1	18.9, 18.9	22.6, 22.6	20.5, 19.6
Proteus mirabilis	n	74	43	43	27	49	6	8	8	258
	%R	9.5, 9.5	25.6, 25.6	11.6, 11.6	14.8, 14.8	16.3, 16.3	n/a	n/a	n/a	14.3, 14.3
Salmonella species (non-typhoidal)	n	26	16	29	3	15	4	12	1	106
	%R	11.5, 11.5	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	2.8, 2.8
Salmonella species (typhoidal)	n	6	14	8	1	10	1	1	4	45
	%R	n/a	7.1, 7.1	n/a	n/a	0.0, 0.0	n/a	n/a	n/a	4.4, 4.4
Staphylococcus aureus	n	645	413	568	255	487	110	77	111	2,666
	%R	4.8, 4.0	4.6, 4.4	3.7, 3.5	3.1, 3.1	2.3, 2.3	1.8, 1.8	5.2, 3.9	1.8, 0.9	3.7, 3.3
Methicillin-resistant *S. aureus*	n	132	59	80	40	104	9	31	11	466
	%R	9.8, 9.1	18.6, 16.9	12.5, 12.5	10.0, 10.0	6.7, 6.7	n/a	12.9, 9.7	0.0, 0.0	10.5, 9.9
Methicillin-susceptible *S. aureus*	n	513	354	488	215	383	101	46	100	2,200
	%R	3.5, 2.7	2.3, 2.3	2.3, 2.0	1.9, 1.9	1.0, 1.0	2.0, 2.0	0.0, 0.0	2.0, 1.0	2.2, 2.0
Vancomycin										
Enterococcus faecalis	n	211	117	131	57	91	31	11	26	675
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Enterococcus faecium	n	152	130	55	38	54	24	12	26	490
	%NS/R	50.7, 50.7	61.5, 61.5	12.7, 12.7	34.2, 34.2	18.5, 18.5	54.2, 54.2	83.3, 83.3	42.3, 42.3	45.0, 45.0
Staphylococcus aureus	n	647	413	571	256	487	110	77	111	2,672
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

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

* 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. All cards used in this study have a 2:1 ratio; therefore, no EUCAST categories can be determined.

§ No category defined
# No breakpoints defined for indicated species
** The ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible and intermediate (EUCAST) categories for *Acinetobacter* species; intermediate and resistant categories (EUCAST) for *Enterococcus* species; and susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species.

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

The most problematic pathogens are those with multiple acquired resistances. Although there is no agreed benchmark for the definition of multidrug resistance, acquired resistance to more than three agents has been chosen to define multidrug resistance in this survey. 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–D12 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 multidrug resistance. The agents included for each species are listed in the notes after each table. EUCAST breakpoints were used throughout the analysis. For cefazolin, the EUCAST-approved Australian National Advisory Committee guidelines were used. For amoxicillin–clavulanic acid, CLSI breakpoints were used, because both the Vitek and Phoenix cards used the CLSI formulation for this agent.

Table D1: Multiple acquired resistance in *Acinetobacter baumannii* complex, by state and territory, 2018

State or territory		Number of categories (non-multidrug resistant)				Number of categories (multidrug resistant)		
	Total	0	1	2	%	3	4	%
NSW	10	10	0	0	–*	0	0	–*
Vic	4	3	0	1	–*	0	0	–*
Qld	23	18	4	0	–*	0	1	–*
SA	1	1	0	0	–*	0	0	–*
WA	8	7	1	0	–*	0	0	–*
Tas	5	4	1	0	–*	0	0	–*
NT	11	8	1	2	–*	0	0	–*
ACT	1	1	0	0	–*	0	0	–*
Total	**63**	**52**	**7**	**3**	**98.4**	**0**	**1**	**1.6**

Resistant to one or more agent in three or more antimicrobial categories

* Not applicable (insufficient numbers)

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. nosocomialis* (*n* = 1), and *A. pittii* (*n* = 1)

Table D2: Multiple acquired resistance in *Citrobacter koseri,* by state and territory, 2018

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	19	17	0	1	–*	1	0	0	0	0	0	0	–*
Vic	12	11	0	0	–*	1	0	0	0	0	0	0	–*
Qld	11	11	0	0	–*	0	0	0	0	0	0	0	–*
SA	4	4	0	0	–*	0	0	0	0	0	0	0	–*
WA	14	12	2	0	–*	0	0	0	0	0	0	0	–*
Tas	1	1	0	0	–*	0	0	0	0	0	0	0	–*
NT	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
ACT	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**61**	**56**	**2**	**1**	**96.7**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**3.3**

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), 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, 2018

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	30	20	3	5	93.3	1	0	1	0	6.7
Vic	15	9	2	4	–*	0	0	0	0	–*
Qld	19	17	1	1	–*	0	0	0	0	–*
SA	4	2	0	2	–*	0	0	0	0	–*
WA	12	10	0	2	–*	0	0	0	0	–*
Tas	2	1	1	0	–*	0	0	0	0	–*
NT	1	1	0	0	–*	0	0	0	0	–*
ACT	6	4	0	1	–*	0	0	0	1	–*
Total	**89**	**64**	**7**	**15**	**96.6**	**1**	**0**	**1**	**1**	**3.4**

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
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. youngae* (n = 4), *C. braakii* (n = 4), *C. werkmanii* (n = 3), and *C. sedlakii* (n = 2).

Table D4: Multiple acquired resistance in *Enterococcus faecium* (vancomycin resistant) by state and territory, 2018

State or territory	Total	Number of categories				
		0	1	2	3	4
NSW	72	0	0	29	43	0
Vic	48	0	0	18	30	0
Qld	7	0	0	4	3	0
SA	12	0	0	2	10	0
WA	10	0	0	8	2	0
Tas	11	0	0	1	10	0
NT	10	0	0	1	9	0
ACT	0	n/a	n/a	n/a	n/a	n/a
Total	**170**	**0**	**0**	**63**	**107**	**0**

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin (high level), fluoroquinolones (ciprofloxacin), oxazolidinones (linezolid), and penicillins (ampicillin)

Table D5: Multiple acquired resistance in *Enterococcus faecium* (vancomycin susceptible) by state and territory, 2018

State or territory	Total	Number of categories				
		0	1	2	3	4
NSW	68	15	2	18	33	0
Vic	38	5	1	21	11	0
Qld	43	13	1	26	3	0
SA	18	3	1	13	1	0
WA	44	4	1	36	3	0
Tas	6	1	0	3	2	0
NT	2	1	0	0	1	0
ACT	0	n/a	n/a	n/a	n/a	n/a
Total	**219**	**42**	**6**	**117**	**54**	**0**

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin (high level), fluoroquinolones (ciprofloxacin), oxazolidinones (linezolid), and penicillins (ampicillin)

Table D6: Multiple acquired resistance in *Klebsiella (Enterobacter) aerogenes*, by state and territory, 2018

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	36	22	1	10	91.7	1	2	0	0	8.3
Vic	27	15	1	7	–*	3	0	1	0	–*
Qld	18	12	1	5	–*	0	0	0	0	–*
SA	11	6	1	2	–*	1	1	0	0	–*
WA	20	14	4	2	–*	0	0	0	0	–*
Tas	4	3	1	0	–*	0	0	0	0	–*
NT	3	2	1	0	–*	0	0	0	0	–*
ACT	4	2	0	1	–*	1	0	0	0	–*
Total	**123**	**76**	**10**	**27**	**91.9**	**6**	**3**	**1**	**0**	**8.1**

Resistant to one or more agent in three or more antimicrobial categories

* 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), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim-sulfamethoxazole).

Table D7: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, 2018

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	63	19	39	1	93.7	0	2	2	0	0	0	0	6.3
Vic	51	17	24	4	88.2	1	5	0	0	0	0	0	11.8
Qld	29	7	15	0	–*	3	4	0	0	0	0	0	–*
SA	20	10	10	0	–*	0	0	0	0	0	0	0	–*
WA	34	15	16	0	91.2	0	3	0	0	0	0	0	8.8
Tas	16	7	8	0	–*	0	1	0	0	0	0	0	–*
NT	2	1	1	0	–*	0	0	0	0	0	0	0	–*
ACT	11	6	2	1	–*	1	1	0	0	0	0	0	–*
Total	**226**	**82**	**115**	**6**	**89.8**	**5**	**16**	**2**	**0**	**0**	**0**	**0**	**10.2**

Resistant to one or more agent in three or more antimicrobial categories

* Not applicable (insufficient numbers)

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 D8: Multiple acquired resistance in *Morganella morganii*, by state and territory, 2018

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	25	16	9	0	–*	0	0	0	0	0	–*
Vic	16	4	9	2	–*	1	0	0	0	0	–*
Qld	16	4	11	1	–*	0	0	0	0	0	–*
SA	10	9	1	0	–*	0	0	0	0	0	–*
WA	8	1	6	1	–*	0	0	0	0	0	–*
Tas	4	0	1	2	–*	1	0	0	0	0	–*
NT	1	1	0	0	–*	0	0	0	0	0	–*
ACT	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**80**	**35**	**37**	**6**	**97.5**	**2**	**0**	**0**	**0**	**0**	**2.5**

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), and penicillins + β-lactamase inhibitor (amoxicillin-clavulanic acid, CLSI).

Table D9: Multiple acquired resistance in *Proteus mirabilis*, by state and territory, 2018

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)								
	Total	0	1	2	%	3	4	5	6	7	8	9	10	%
NSW	73	53	9	7	94.5	1	1	0	0	2	0	0	0	5.5
Vic	43	24	7	3	79.1	8	0	0	1	0	0	0	0	20.9
Qld	43	36	2	0	88.4	4	1	0	0	0	0	0	0	11.6
SA	27	19	3	4	–*	1	0	0	0	0	0	0	0	–*
WA	49	33	5	7	91.8	3	0	0	1	0	0	0	0	8.2
Tas	6	3	3	0	–*	0	0	0	0	0	0	0	0	–*
NT	8	4	2	2	–*	0	0	0	0	0	0	0	0	–*
ACT	8	7	1	0	–*	0	0	0	0	0	0	0	0	–*
Total	**257**	**179**	**32**	**23**	**91.1**	**17**	**2**	**0**	**2**	**2**	**0**	**0**	**0**	**8.9**

Resistant to one or more agent in three or more antimicrobial categories

* Not applicable (insufficient numbers)

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 D10: Multiple acquired resistance in *Salmonella* species (non-typhoidal), by state and territory, 2018

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	21	11	8	0	–*	1	1	0	0	0	0	0	–*
Vic	15	15	0	0	–*	0	0	0	0	0	0	0	–*
Qld	29	28	0	0	–*	0	0	0	1	0	0	0	–*
SA	3	3	0	0	–*	0	0	0	0	0	0	0	–*
WA	15	14	1	0	–*	0	0	0	0	0	0	0	–*
Tas	4	4	0	0	–*	0	0	0	0	0	0	0	–*
NT	12	10	2	0	–*	0	0	0	0	0	0	0	–*
ACT	1	1	0	0	–*	0	0	0	0	0	0	0	–*
Total	**100**	**86**	**11**	**0**	**97.0**	**1**	**1**	**0**	**1**	**0**	**0**	**0**	**3.0**

MDR = 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 D11: Multiple acquired resistance in *Salmonella* species (typhoidal), by state and territory, 2018

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)							
	Total	0	1	2	%	3	4	5	6	7	8	9	%
NSW	6	4	2	0	–*	0	0	0	0	0	0	0	–*
Vic	12	5	6	0	–*	0	1	0	0	0	0	0	–*
Qld	8	5	3	0	–*	0	0	0	0	0	0	0	–*
SA	1	0	1	0	–*	0	0	0	0	0	0	0	–*
WA	10	1	9	0	–*	0	0	0	0	0	0	0	–*
Tas	1	1	0	0	–*	0	0	0	0	0	0	0	–*
NT	1	0	1	0	–*	0	0	0	0	0	0	0	–*
ACT	4	1	2	0	–*	0	0	0	0	1	0	0	–*
Total	**43**	**17**	**24**	**0**	**95.3**	**0**	**1**	**0**	**0**	**1**	**0**	**0**	**4.7**

MDR = 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 D12: Multiple acquired resistance in *Serratia marcescens*, by state and territory, 2018

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	63	20	37	5	98.4	1	0	0	0	0	1.6
Vic	33	10	19	2	93.9	0	2	0	0	0	6.1
Qld	42	11	30	1	100	0	0	0	0	0	0.0
SA	14	2	8	2	–*	2	0	0	0	0	–*
WA	6	2	4	0	–*	0	0	0	0	0	–*
Tas	2	0	2	0	–*	0	0	0	0	0	–*
NT	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
ACT	5	0	4	1	–*	0	0	0	0	0	–*
Total	**165**	**45**	**104**	**11**	**97.0**	**3**	**2**	**0**	**0**	**0**	**3.0**

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

* 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), and penicillins + β-lactamase inhibitor (amoxicillin-clavulanic acid, CLSI).

Appendix E. *Enterococcus* resistance by species and state or territory, 2013-2018

Table E1: *Enterococcus faecalis*, resistant (EUCAST), by state and territory, 2013–2018

Antimicrobial	Year	Number tested	Percentage resistant, % (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ampicillin	2013	477	0.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.2 (1)
	2014	522	0.0 (0)	0.0 (0)	2.0 (2)	2.0 (1)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.6 (3)
	2015	561	0.0 (0)	0.0 (0)	1.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.2 (1)
	2016	592	0.0 (0)	0.0 (0)	0.0 (0)	2.0 (1)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.2 (1)
	2017	601	0.0 (0)	0.0 (0)	1.0 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.2 (1)
	2018	675	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)
Vancomycin	2013	477	0.8 (1)	0.9 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.4 (2)
	2014	523	0.0 (0)	0.0 (0)	1.0 (1)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.2 (1)
	2015	561	1.3 (2)	0.9 (1)	0.0 (0)	0.0 (0)	0.0 (0)	8.3 (1)	0.0 (0)	0.0 (0)	0.7 (4)
	2016	592	0.0 (0)	0.8 (1)	0.0 (0)	1.9 (1)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.3 (2)
	2017	601	0.0 (0)	1.7 (2)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.3 (2)
	2018	675	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)
Teicoplanin	2013	476	0.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	9.1 (1)	–* (0)	0.0 (0)	0.4 (2)
	2014	521	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)
	2015	558	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)
	2016	592	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)
	2017	601	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)
	2018	675	0.5 (1)	0.0 (0)	0.0 (0)	0.0 (0)	1.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.3 (2)
Ciprofloxacin	2013	439	24.6 (30)	11.3 (12)	14.9 (11)	37.8 (14)	9.9 (7)	na	–* (1)	17.4 (4)	18.0 (79)
	2014	477	23.1 (31)	20.0 (24)	15.7 (14)	37.5 (12)	11.1 (7)	na	–* (3)	42.4 (14)	22.0 (105)
	2015	521	14.8 (22)	15.5 (17)	9.6 (8)	25.6 (11)	8.8 (8)	na	14.8 (3)	14.3 (5)	14.2 (74)
	2016	559	14.5 (22)	11.5 (15)	8.2 (7)	15.7 (8)	8.0 (7)	21.4 (3)	–* (0)	12.1 (4)	11.8 (66)
	2017	546	10.8 (20)	13.6 (16)	16.8 (16)	22.6 (7)	5.5 (5)	6.3 (1)	–* (1)	na	12.3 (67)
	2018	548	12.2 (21)	12.8 (12)	6.7 (8)	11.4 (5)	4.4 (4)	18.8 (3)	9.1 (1)	na	9.9 (54)
Nitrofurantoin	2013	468	0.8 (1)	0.0 (0)	0.0 (0)	2.3 (1)	0.0 (0)	9.1 (1)	–* (0)	0.0 (0)	0.6 (3)
	2014	521	0.0 (0)	0.0 (0)	1.0 (1)	2.0 (1)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.4 (2)
	2015	558	0.0 (0)	0.0 (0)	1.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.2 (1)

Antimicrobial	Year	Number tested	Percentage resistant, % (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	2016	591	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)
	2017	595	0.0 (0)	0.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.2 (1)
	2018	668	0.5 (1)	0.0 (0)	0.0 (0)	1.8 (1)	1.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.4 (3)
Gentamicin (high-level)	2013	408	40.0 (34)	34.0 (36)	27.6 (24)	31.6 (6)	28.2 (20)	18.2 (2)	–* (2)	30.4 (7)	32.1 (131)
	2014	519	42.4 (56)	38.7 (46)	34.3 (35)	35.3 (18)	28.6 (18)	30.8 (4)	–* (3)	54.5 (18)	38.2 (198)
	2015	544	29.3 (41)	27.4 (29)	25.5 (24)	28.1 (16)	23.3 (21)	25.0 (3)	40.0 (4)	34.3 (12)	27.6 (150)
	2016	589	28.2 (42)	22.3 (29)	28.6 (28)	29.4 (15)	16.1 (14)	14.8 (4)	–* (2)	22.5 (9)	24.3 (143)
	2017	591	16.7 (31)	19.7 (23)	21.2 (21)	35.5 (11)	22.5 (20)	19.4 (6)	10.0 (1)	35.7 (10)	20.8 (123)
	2018	610	24.1 (47)	23.4 (22)	16.9 (210	24.4 (11)	21.1 (19)	16.1 (5)	18.2 (2)	38.5 (10)	22.3 (136)
Linezolid	2013	477	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))
	2014	522	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)
	2015	561	0.0 (0)	0.0 (0)	1.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0	0.2 (1)
	2016	591	0.0 (0)	0.0 (0)	2.0 (2)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.3 (2)
	2017	601	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)
	2018	675	0.0 (0)	0.9 (1)	0.0 (0)	0.0 (0)	1.1 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.3 (2)

EUCAST = European Committee on Antimicrobial Susceptibility Testing; na = not applicable (no isolates tested)

Note: Shaded cells indicate a significant trend (P <0.01)

* Insufficient numbers to calculate percentage (< 10 isolates)

Table E2: *Enterococcus faecium*, non-susceptible (EUCAST), by state and territory, 2013–2018

Antimicrobial	Year	Number tested	Percentage non-susceptible (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ampicillin	2013	321	90.7 (97)	93.8 (75)	88.9 (32)	96.9 (31)	97.6 (41)	–* (5)	–* (3)	100 (16)	93.5 (300)
	2014	379	89.3 (92)	93.6 (88)	86.5 (32)	89.1 (41)	94.0 (47)	–* (5)	–* (0)	92.7 (38)	90.5 (343)
	2015	400	86.1 (99)	90.0 (108)	83.3 (25)	93.2 (41)	79.2 (42)	–* (4)	–* (7)	95.5 (21)	86.8 (347)
	2016	412	92.7 (114)	89.9 (98)	90.7 (39)	97.7 (42)	92.6 (50)	92.9 (13)	–* (4)	90.9 (20)	92.2 (380)
	2017	481	89.2 (149)	93.3 (125)	95.6 (43)	85.7 (24)	81.0 (51)	88.2 (15)	–* (4)	95.5 (21)	89.8 (432)
	2018	491	89.5 (136)	96.2 (125)	74.5 (41)	84.2 (32)	90.7 (49)	91.7 (22)	91.7 (11)	92.3 (24)	89.6 (440)
Vancomycin	2013	324	43.9 (47)	53.8 (43)	40.5 (15)	59.4 (19)	4.8 (2)	–* (0)	–* (3)	33.3 (6)	41.7 (135)
	2014	380	50.0 (52)	66.0 (62)	40.5 (15)	56.5 (26)	20.0 (10)	–* (1)	–* (0)	24.4 (10)	46.3 (176)
	2015	402	51.7 (60)	63.3 (76)	61.3 (19)	52.3 (23)	11.3 (6)	–* (1)	–* (6)	50.0 (11)	50.2 (202)
	2016	413	47.6 (59)	62.4 (68)	30.2 (13)	46.5 (20)	14.8 (8)	42.9 (6)	–* (3)	68.2 (15)	46.5 (192)

Antimicrobial	Year	Number tested	Percentage non-susceptible (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	2017	481	51.5 (86)	64.2 (86)	33.3 (15)	57.1 (16)	14.3 (9)	29.4 (5)	–* (3)	27.3 (6)	47.0 (226)
	2018	491	50.7 (77)	61.5 (80)	12.7 (7)	34.2 (13)	18.5 (10)	54.2 (13)	83.3 (10)	42.3 (11)	45.0 (221)
Teicoplanin	2013	321	9.3 (10)	2.5 (2)	5.6 (2)	3.1 (1)	0.0 (0)	–* (0)	–* (0)	0.0 (0)	4.7 (15)
	2014	377	29.1 (30)	1.1 (1)	0.0 (0)	0.0 (0)	2.0 (1)	–* (0)	–* (0)	2.4 (1)	8.8 (33)
	2015	401	33.9 (39)	12.5 (15)	19.4 (6)	2.3 (1)	5.7 (3)	–* (0)	–* (0)	31.8 (7)	17.7 (71)
	2016	413	38.7 (48)	13.8 (15)	2.3 (1)	0.0 (0)	9.3 (5)	0.0 (0)	–* (0)	40.9 (9)	18.9 (78
	2017	481	45.5 (76)	17.2 (23)	13.3 (6)	17.9 (5)	4.8 (3)	5.9 (1)	–* (0)	27.3 (6)	24.9 (120)
	2018	491	34.2 (52)	19.2 (25)	5.5 (3)	10.5 (4)	11.1 (6)	16.7 (4)	8.3 (1)	26.9 (7)	20.8 (102)
Gentamicin (high-level)	2013	271	77.1 (64)	51.3 (41)	77.8 (28)	–* (2)	31.0 (13)	–* (3)	–* (3)	87.5 (14)	62.0 (168)
	2014	377	70.6 (72)	57.4 (54)	69.4) (25)	67.4 (31)	40.0 (20)	–* (1)	–* (0)	73.2 (30)	61.8 (233)
	2015	387	65.7 (67)	59.2 (71)	63.3 (19)	81.8 (36)	26.4 (14)	–* (2)	–* (6)	86.4 (19)	60.5 (234)
	2016	403	70.1 (82)	39.8 (43)	38.1 (16)	71.4 (30)	24.1 (13)	57.1 (8)	–* (4)	72.7 (16)	52.6 (212)
	2017	473	64.8 (107)	42.3 (55)	36.4 (16)	53.6 (15)	17.5 (11)	37.5 (6)	–* (3)	68.2 (15)	48.2 (228)
	2018	425	55.2 (79)	46.5 (40)	14.0 (7)	36.7 (11)	11.1 (6)	62.5 (15)	83.3 (10)	42.3 (11)	42.1 (179)
Linezolid	2013	321	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	–* (0)	0.0 (0)	0.0 (0)
	2014	378	1.0 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	–* (0)	0.0 (0)	0.3 (1)
	2015	400	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	–* (0)	0.0 (0)	0.0 (0)
	2016	408	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))
	2017	481	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)
	2018	490	0.0 (0)	0.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	3.8 (1)	0.4 (2)

EUCAST = European Committee on Antimicrobial Susceptibility Testing

Note: Shaded cells indicate a significant trend (P <0.01)

* Insufficient numbers to calculate percentage (< 10 isolates)

References

1. Australian Commission on Safety and Quality in Health Care. Preventing and Controlling Healthcare-Associated Infection Standard Sydney: ACSQHC; [Available from: https://www.safetyandquality.gov.au/standards/nsqhs-standards/preventing-and-controlling-healthcare-associated-infection-standard.
2. Australian Government Department of Health, Australian Government Department of Agriculture. Responding to the threat of antimicrobial resistance: Australia's first National Antimicrobial Resistance Strategy 2015-2019. Canberra; 2015.
3. Australian Commission on Safety and Quality in Health Care. Recommendations for the control of carbapenemase-producing Enterobacteriaceae. 2017.
4. Ferguson JK, Munnoch SA, Kozierowski K, Chiu S, Oldmeadow C. Reduced VRE and MRSA colonisation and infection following sustained reduction in broad spectrum antibiotic use in a large tertiary hospital. Med J Aust. 2019;211(3):126-7.
5. Mitchell BG, Hall L, White N, Barnett AG, Halton K, Paterson DL, et al. An environmental cleaning bundle and health-care-associated infections in hospitals (REACH): a multicentre, randomised trial. Lancet Infect Dis. 2019;19(4):410-8.
6. National Health and Medical Research Council. Australian Guidelines for the Prevention and Control of Infection in Healthcare (2019). Canberra: NHMRC; 2019.
7. Health S. The National Antimicrobial Utilisation Surveillance Program Adelaide: SA Health; [Available from: https://www.sahealth.sa.gov.au/wps/wcm/connect/public+content/sa+health+internet/clinical+resources/clinical+programs/antimicrobial+stewardship/national+antimicrobial+utilisation+surveillance+program+nausp.
8. Antibiotic Expert Groups. Therapeutic guidelines: antibiotic. Melbourne: Therapeutic Guidelines Limited; 2014.
9. 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):163-70.
10. 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):145-51.
11. Murray BE. The life and times of the Enterococcus. Clin Microbiol Rev. 1990;3(1):46-65.
12. 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):323-31.
13. 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):462-3.
14. 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.
15. 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):392-7.
16. 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):73-5.
17. Laupland KB. Incidence of bloodstream infection: a review of population-based studies. Clin Microbiol Infect. 2013;19(6):492-500.
18. Johnson AP, Pearson A, Duckworth G. Surveillance and epidemiology of MRSA bacteraemia in the UK. J Antimicrob Chemother. 2005;56(3):455-62.

19. 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):208-22.
20. 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):257-63.
21. Collignon P, Nimmo GR, Gottlieb T, Gosbell IB, Australian Group on Antimicrobial R. *Staphylococcus aureus* bacteremia, Australia. Emerg Infect Dis. 2005;11(4):554-61.
22. 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.
23. 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):242-51.
24. 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):362-86.
25. 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):368-73.
26. 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.
27. 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):E309-19.
28. CLSI. Performance Standards for Antimicrobial Susceptibility Testing. CLSI document M100S. 29th ed. Wayne, PA: Clinical and Laboratory Standards Institute; 2019.
29. The European Committee on Antimicrobial Susceptibility Testing (EUCAST). Breakpoint tables for interpretation of MICs and zone diameters. Version 9.0, valid from 2019-01-01: http://www.eucast.org.
30. Ellington MJ, Findlay J, Hopkins KL, Meunier D, Alvarez-Buylla A, Horner C, et al. Multicentre evaluation of a real-time PCR assay to detect genes encoding clinically relevant carbapenemases in cultured bacteria. Int J Antimicrob Agents. 2016;47(2):151-4.
31. Roschanski N, Fischer J, Guerra B, Roesler U. Development of a multiplex real-time PCR for the rapid detection of the predominant beta-lactamase genes CTX-M, SHV, TEM and CIT-type AmpCs in Enterobacteriaceae. PLoS One. 2014;9(7):e100956.
32. Swayne R, Ellington MJ, Curran MD, Woodford N, Aliyu SH. Utility of a novel multiplex TaqMan PCR assay for metallo-beta-lactamase genes plus other TaqMan assays in detecting genes encoding serine carbapenemases and clinically significant extended-spectrum beta-lactamases. Int J Antimicrob Agents. 2013;42(4):352-6.
33. Ciesielczuk H, Hornsey M, Choi V, Woodford N, Wareham DW. Development and evaluation of a multiplex PCR for eight plasmid-mediated quinolone-resistance determinants. J Med Microbiol. 2013;62(Pt 12):1823-7.
34. Corrêa LL, Montezzi LF, Bonelli RR, Moreira BM, Picão RC. Revised and updated multiplex PCR targeting acquired 16S rRNA methyltransferases. International Journal of Antimicrobial Agents. 2014;43(5):479-81.
35. Doi Y, Arakawa Y. 16S Ribosomal RNA Methylation: Emerging Resistance Mechanism against Aminoglycosides. Clinical Infectious Diseases. 2007;45(1):88-94.
36. Liu YY, Wang Y, Walsh TR, Yi LX, Zhang R, Spencer J, et al. Emergence of plasmid-mediated colistin resistance mechanism MCR-1 in animals and human beings in China: a microbiological and molecular biological study. Lancet Infect Dis. 2016;16(2):161-8.
37. Mendes RE, Kiyota KA, Monteiro J, Castanheira M, Andrade SS, Gales AC, et al. Rapid detection and identification of metallo-beta-lactamase-encoding genes by multiplex real-time PCR assay and melt curve analysis. J Clin Microbiol. 2007;45(2):544-7.
38. Yin W, Li H, Shen Y, Liu Z, Wang S, Shen Z, et al. Novel Plasmid-Mediated Colistin Resistance Gene mcr-3 in Escherichia coli. MBio. 2017;8(3).

39. Dhanji H, Doumith M, Clermont O, Denamur E, Hope R, Livermore DM, et al. Real-time PCR for detection of the O25b-ST131 clone of *Escherichia coli* and its CTX-M-15-like extended-spectrum beta-lactamases. Int J Antimicrob Agents. 2010;36(4):355-8.
40. Woodford N, Ellington MJ, Coelho JM, Turton JF, Ward ME, Brown S, et al. Multiplex PCR for genes encoding prevalent OXA carbapenemases in *Acinetobacter* spp. Int J Antimicrob Agents. 2006;27(4):351-3.
41. Seemann T, Goncalves da Silva A, Bulach DM, Schultz MB, Kwong JC, Howden BP. *Nullarbor* Github [Available from: https://github.com/tseemann/nullarbor.
42. Australian Commission on Safety and Quality in Health Care (ACSQHC). AURA 2017: second Australian report on antimicrobial use and resistance in human health. Sydney: ACSQHC; 2017.
43. 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):268-81.
44. Bell JM, Turnidge JD, Jones RN, Participants SA-P. Prevalence of extended-spectrum beta-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):3989-93.
45. 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).
46. European Centre for Disease Prevention and Control. Data from the ECDC Surveillance Atlas - Antimicrobial resistance Stockholm: ECDC; 2019 [Available from: https://www.ecdc.europa.eu/en/antimicrobial-resistance/surveillance-and-disease-data/data-ecdc.
47. 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. 2007;31:106-12.
48. European Centre for Disease Prevention and Control. Surveillance of antimicrobial resistance in Europe – Annual report of the European Antimicrobial Resistance Surveillance Network (EARS-Net) 2017. Stockholm: ECDC; 2018.
49. Australian Commission on Safety and Quality in Health Care. Australian Passive Antimicrobial Resistance Surveillance. First report: multi-resistant organisms. Sydney; 2018.
50. Australian Commission on Safety and Quality in Health Care. AURA 2016 – First Australian report on antimicrobial use and resistance in human health. Sydney; 2016.
51. Australian Group for Antimicrobial Resistance. The Evolution of Carbapenemases in Major Gram-negative Bacteria in Australia. 2016.
52. Chang LW, Buising KL, Jeremiah CJ, Cronin K, Poy Lorenzo YS, Howden BP, et al. Managing a nosocomial outbreak of carbapenem-resistant *Klebsiella pneumoniae*: an early Australian hospital experience. Internal medicine journal. 2015;45(10):1037-43.
53. Australian Institute of Health and Welfare. Admitted patient care 2017–18: Australian hospital statistics. Canberra: AIHW; 2019.
54. Coombs G, Bell JM, Daley D, Collignon P, Cooley L, Gottlieb T, et al. Australian Group on Antimicrobial Resistance: Sepsis Outcome Programs 2017 report. Sydney: Australian Commission on Safety and Quality in Health Care; 2019.
55. Turnidge J, Coombs, G., Daley, D., Nimmo, G., Australian Group on Antimicrobial Resistance (AGAR) participants, 2000–14. MRSA: A Tale of Three Types 15 years of survey data from AGAR. Australian Commission on Safety and Quality in Health Care, Sydney; 2016.