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Antimicrobial Use and Resistance in Australia

AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Sepsis Outcome Programs

2019 report

AGAR

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Overview

The Australian Group on Antimicrobial Resistance (AGAR), which is auspiced by the Australian Society for Antimicrobials (ASA), conducts targeted surveillance of selected pathogens in Australia. AGAR is a longstanding collaboration of clinicians and scientists from major microbiology laboratories across Australia. The group commenced in 1985 with participation from 13 teaching hospitals. It has subsequently grown to involve 39 institutions across Australia, including four private laboratories (Table 1).

AGAR collects data on antimicrobial resistance (AMR) in bacteria that cause life-threatening infections and analyses and reports on these as part of the Antimicrobial Use and Resistance in Australia (AURA) Surveillance System. This data 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).

Antimicrobial resistance 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.

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

The AURA Surveillance System is coordinated by the Australian Commission on Safety and Quality in Health Care (the Commission). AURA provides essential information used in the development and implementation of strategies to prevent and limit the spread of AMR and encourage the appropriate use of antimicrobials in hospitals, aged care facilities and community healthcare settings. AURA also supports the National Safety and Quality Health Service (NSQHS) Standards[1] and Australia's National Antimicrobial Resistance Strategy.[2] Funding for AURA is provided by the Australian Government Department of Health and state and territory health departments.

The NSQHS Standards require 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 healthcare facilities in meeting the requirements of the NSQHS Standards. To ensure that patients receive the best possible care, the Commission will continue to support states and territories and the private health sector in utilising AGAR data to refine and strengthen their approaches to infection prevention and control, antimicrobial stewardship and antimicrobial treatment.

Geoff Coombs
AGAR Chairperson

Key findings and implications for health care; 2019

A. Key findings

Gram-negative species

- A total of 8,857 episodes of gram-negative bacteraemia were reported, including *Enterobacterales* (90.1%), *Pseudomonas aeruginosa* (8.6%) and *Acinetobacter* species (1.2%). Three genera – *Escherichia* (61.6%), *Klebsiella* (19.8%) and *Enterobacter* (5.5%) – contributed 86.9% of all *Enterobacterales* bacteraemias
- The all-cause 30-day mortality for gram-negative bacteraemia was 12.2% (10.6% in *Escherichia coli*, 16.5% in *P. aeruginosa*)
- Urinary tract infection was the most frequent source of sepsis for *Enterobacterales* (44.8%) and *P. aeruginosa* (22.9%)
- 83% of all *E. coli* bacteraemia cases were community onset. Over 11.9% of these isolates were ceftriaxone resistant
- There was a significant difference in 30-day all-cause mortality between community- and hospital onset (9.3% versus 16.2%) *E. coli* bacteraemia episodes
- In 2019, extended-spectrum β-lactamase (ESBL) phenotypes were found in 14.5% of *E. coli* and 10.3% of *Klebsiella pneumoniae* complex, and were more common in hospital onset patients
- A $bla_{CTX\text{-}M}$ type gene was present in 73.7% of *E. coli* with an ESBL phenotype
- Increasing fluoroquinolone resistance in *E. coli* was most striking in hospital onset bacteraemia, increasing from 13.7% to 21.3% between 2013 and 2019; by comparison community onset bacteraemia resistance increased from 10.9% to 14.9% over the same period
- The low rates of carbapenemase-producing *Enterobacterales* (CPE) bacteraemia are encouraging (0.3% overall, mostly carrying $bla_{IMP\text{-}4}$). For *K. pneumoniae* complex the figure is higher at 1.1% (community-onset 0.6%, hospital-onset 2.5%); and for *Enterobacter cloacae* complex 1.9% overall (community-onset 2.4%, hospital-onset 1.1%)
- The rate of colistin resistance - when tested for, but excluding species with intrinsic resistance, was 0.4% (4/1,023). Among all referred isolates, one *E. coli* isolate was found to contain *mcr-1.* The patient attended an institution in Western Australia.

Enterococcus species

- A total of 1,361 episodes of enterococcal bacteraemia were reported; the majority (95.2%) of enterococcal bacteraemia episodes were caused by *Enterococcus faecalis* or *E. faecium*
- The majority of *E. faecalis* bacteraemia were community onset (69.7%), while in *E. faecium* bacteraemia only 30.2% were community onset
- The most frequent source of sepsis or clinical manifestation for *E. faecalis* was urinary tract infection (23.1%); for *E. faecium*, biliary tract infection (including cholangitis) (20.7%) and intra-abdominal infection other than biliary tract (19.2%) were the most common associations
- The combined 30-day all-cause mortality for *E. faecalis* and *E. faecium* was 19.9%; the 30-day all-cause mortality for *E. faecium* bacteraemia was higher, particularly in hospital onset vancomycin-susceptible (27.6%) and vancomycin-resistant (32.4%) isolates
- There was a significant difference in 30-day all-cause mortality between *E. faecalis* (13.7%) and *E. faecium* (26.4%)
- The length of stay following enterococcal bacteraemia was more than 30 days for 22.7% of patients
- Overall, 45.4% of *E. faecium* harboured *vanA* or *vanB* genes or both, with 48.2% of vancomycin-resistant *E. faecium* bacteraemias due to *vanA*-harbouring isolates. This type of vancomycin resistance has emerged rapidly in the past seven years and is now the dominant genotype in the Australian Capital Territory, New South Wales, and Tasmania).

- Of bloodstream infections caused by *E. faecium*, 41.6% were phenotypically vancomycin resistant, and 45.2% of *E. faecium* harboured *vanA* and/or *vanB* genes (*vanA* 22.4%, *vanB* 22.7%, both 0.2%)
- There were 77 *E. faecium* multilocus sequence types (STs), of which ST1424, ST17, ST796, ST80, ST1421, and ST78 were the six most frequently identified
- *vanA* genes were detected in 12 STs, and *vanB* genes were detected in 12 STs; one ST 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, Greece and Poland.

Staphylococcus aureus

- A total of 3,157 *Staphylococcus aureus* bacteraemia episodes were reported, 79.8% of which were community onset. Almost one in five of all episodes were methicillin resistant (18.5%)
- The 30-day all-cause mortality was 14.3%. Mortality for methicillin-resistant *S. aureus* (MRSA) (14.0%) and methicillin-susceptible *S. aureus* (MSSA) (14.3%) were similar; likewise, between hospital onset (14.8%) and community onset (14.1%) bacteraemia
- Skin and skin structure infections (21.1%) and osteomyelitis/septic arthritis (20.4%) and were the most common principal clinical manifestations
- The hospital length of stay was more than 30 days in 24.2% of patients (26.3% in MRSA, 23.8% in MSSA)
- In MRSA, resistance to erythromycin, and clindamycin, has continued to decline overall, largely due to the substantial decline in the multi-resistant ST239-III clone
- Community-associated methicillin-resistant *S. aureus* (CA-MRSA) strains were the dominant cause of MRSA bacteraemia
- Three 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
- Sixty-one CA-MRSA clones were identified; the dominant CA-MRSA clone was ST93-IV (Queensland clone)
- Overall, 41.1% of CA-MRSA isolates harboured the PVL associated genes
- The Queensland clone of CA-MRSA (ST93-IV), which harbours the PVL associated genes, was seen in all states and territories except Tasmania and the Australian Capital Territory; it is now the most common CA-MRSA clone in 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 2019. AGAR has increased the number of laboratories from 25 in 2013 to 36 in 2018 and 39 in 2019. In addition, the relative distribution of sites has changed with the addition of three more paediatric and/or obstetric institutions from 2017, an additional site in 2019; 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.

Gram-negative resistance

Relative to 2018, the percentage resistance in *E. coli* either declined or remained steady for almost two-thirds of the antimicrobial agents tested, including β-lactam inhibitor combinations and third-generation cephalosporins. There was a slight increase in percentage resistance to aminoglycosides and fluoroquinolones. For *K. pneumoniae* complex there was an increase in percentage resistance to β-lactam inhibitor combinations and gentamicin resistance, and a slight decline in resistance to third-generation cephalosporins and fluoroquinolones.

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

Increasing resistance to third-generation cephalosporins and fluoroquinolones in *E. coli* strains in the community is of concern, given that access to these agents on the Pharmaceutical Benefits Scheme is quite restricted. It is likely that high community use of unrestricted agents to which these strains are co-resistant such as amoxicillin and cefalexin, is fuelling this increase.

Prevalence of extended spectrum beta-lactamases (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 2019, with little change compared to 2018. This phenotype is more common in hospital onset compared to community onset *E. coli* infection, with 1 in 5 (22.2%) demonstrating this pattern in hospital onset infection compared to 13.0% for community onset isolates. In hospital onset *K. pneumoniae* complex isolates, this phenotype is more than double that of community onset isolates (17.4% versus 7.6%). 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 gram-negative organisms

Carbapenem resistance attributable to acquired carbapenemase genes is still uncommon in patients with bacteraemia in Australia, although five different types (IMP, NDM, OXA-48-like, OXA-23, and GES-5) were detected in isolates from just over one-third (14/39, 36%) of the contributing institutions. Invasive CPE infections are particularly notable in Victoria (11/1,500, 0.73%) and New South Wales (8/2,275, 0.35%), compared to other states and territories. Almost 2 in 3 (7/24, 64%) of CPE from Victoria were from one institution. Queensland (*n* = 3) and Western Australia (*n* = 2) were the only other states and territories where CPE were found.

Guidance 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* Enterobacteriaceae: *A guide for acute care health facilities*.[3]

Changing patterns in *Enterococcus* species

Total numbers of enterococcal bacteraemias identified by AGAR, excluding those from three institutions that contributed in 2019 only, were constant (1,242 compared to 1,248 in 2018). However, there was an increase in the proportion of *E. faecium* (547 versus 491, up 11.9%) and a decrease in the proportion of *E. faecalis* (635 versus 676, down 5.6%). The number of vancomycin-resistant *E. faecium* (VRE) isolates was stable; 247 in 2019, compared to 221 in 2018. There was a reduction in overall vancomycin resistance rates in *E. faecium* from 45.0% to 40.8%, down 9.4%. VRE as a proportion of all enterococcal isolates remained steady at 18.0% (17.7% in 2018). The overall contribution of *vanA* and *vanB* genes to VRE is now equal. However, *vanA*-harbouring types are dominant in New South Wales and the Australian Capital Territory, whilst *vanB*-harbouring types are dominant in Victoria and the Northern Territory.

The gradual shift to *vanA*-harbouring *E. faecium* will mean the loss of a valuable treatment choice, namely teicoplanin, which is active only against *vanB*-harbouring types. Optimising all VRE control mechanisms will be required to control Australia's resistance in *E. faecium*.

Methicillin resistance in *Staphylococcus aureus*

Methicillin resistance in *S. aureus*, excluding isolates from three institutions that contributed in 2019 only, has increased by 1.2 percentage points, from 17.4% to 18.6% (up 6.9%). The rate of resistance increased in hospital-onset infections (from 19.5% to 22.3%, up 14.4%) whilst community MRSA rates remained stable at 17.6%. The increase in hospital-onset infections (110 to 129) was attributed to an increase in the community-associated ST93-IV (11 to 16) and ST45-V (12 to 15), predominantly occurring in Victoria (ST45-V) and Queensland (ST93-IV). Increases in community-associated clones were also seen in community-onset infections due to ST93-IV and ST5-IV. ST93-IV increased from 85 cases in 2018 to 113 cases in 2019, predominantly because of increases in Western Australia and Queensland. ST5-IV cases increased to 43 from 29 in 2018, notably in New South Wales. Strategies for control of MRSA community need to be actively sought.

Epidemiology of clinical manifestations

Urinary tract infection remains the most common manifestation associated with blood stream infection in *Enterobacterales*, *P. aeruginosa*, and *E. faecalis* episodes. In 2019, biliary and non-biliary intra-abdominal infections were the most common clinical manifestations associated with *E. faecium*, in contrast to 2018 when it was febrile neutropenia.

Device-related blood stream infections accounted for 9.1% (1,038/11,362) of bacteraemia across all the AGAR surveillance programs in 2019. The rate in 2018 was 9.9%. The decrease was more notable among enterococcal episodes (11.4% compared to 13.2% in 2018) and staphylococcal episodes (18.9% versus 20.4%). Total numbers are dominated by gram-negative (*n* = 378) bacteria and *S. aureus* (*n* = 518) infections.

Gram-negative infections commonly arise from urinary infections associated with the use of indwelling catheter, urinary stent or biliary stent infections. In contrast, *S. aureus* bacteraemia is commonly associated with intra-vascular catheters and/or devices and prosthetic joints. Continuing attention to the National Safety and Quality Health Service (NSQHS) Standards on optimum medical device management[4] is required in all institutions.

Variation across states and territories

Resistance rates vary considerably across states and territories. Methicillin resistance in *S. aureus* ranged from 11.9% in Tasmania to 56.3% in the Northern Territory. *E. coli* resistance to third-generation cephalosporins ranged from 7.0% in Tasmania to 16.9% in Victoria. Aminoglycoside resistance varied from 7.0% in Tasmania to 18.5% in the Northern Territory. Fluoroquinolone-resistance varied from 10.4% in Queensland to 20.5% in the Australian Capital Territory. For

K. pneumoniae complex, third-generation cephalosporin resistance was lowest in Western Australia and Queensland (4.4%), but accounted for almost one in six isolates in Victoria (16.0%) where aminoglycoside resistance was also highest (14.2%). Rates of vancomycin resistance in *E. faecium* ranged from 5.4% in Western Australia to 66.5% in Victoria. Teicoplanin resistance was more common in New South Wales (32.5%) and Tasmania (24.0%). Optimising local treatment guidelines is essential to minimise the overuse of broad-spectrum antimicrobials 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. Organisms such as *E. cloacae* complex, *P. aeruginosa* and *Acinetobacter* species were evenly distributed between community- and hospital-onset infections, whilst others such as *E. coli* and *S. aureus* were more commonly community onset. *Enterococcus faecium* (69.8%) was more commonly hospital onset than *E. faecalis* (30.3%). Vancomycin-resistant *E. faecium* blood stream infections accounted for 7.2% (52/720) of all community-onset enterococcal blood stream infections, compared to 30.4% (195/641) in hospital-onset disease. These variations have implications for choice of empiric antimicrobial therapy and guidelines in community- versus hospital-onset infections, and also need to take into account infections in aged care home residents (which are included in the community-onset group in the AGAR data, but not distinguished as such).

International comparisons

Australia has relatively lower rates of resistance in 2019, compared to European data available at the time of publication, for fluoroquinolone resistance in *E. coli* and *K. pneumoniae*, and third-generation cephalosporin resistance in *K. pneumoniae*. Australia's ranking for resistance to third-generation cephalosporins in *E. coli* is now similar the EU/EEA average in this resistance pattern. Australia continues to be ranked in the top half for methicillin resistance in *S. aureus*, and Australia reports higher VRE rates than any almost all European Union countries.

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[5] 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 antimicrobial stewardship (AMS) services. Antibiograms are tables of antimicrobial susceptibilities that are used to inform local empirical and therapeutic antimicrobial recommendations and formulary management. This work captures geographic variation.
- Adapt national prescribing practices to local resistance patterns and regular review of prescribing guidance by local AMS services; this will support the use of broad-spectrum antibiotics where necessary, whilst limiting their use in areas where their use is not justified due to lower rates of resistance.
- Promote incorporation of concepts of geographical variation in AMR into clinical practice; particularly to support clinicians who regularly work in a range of settings.
- 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.
- Contribute to the AURA Surveillance System and ensure that AMR and antimicrobial use data are readily available to inform antimicrobial stewardship

and infection prevention and control programs

- Promote effective infection prevention and control measures, such as those included in the *Recommendations for the Control of Carbapenemase-Producing* Enterobacteriaceae: *A guide for acute care health facilities* [3], to limit the transmission of CPE
- 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 in relation to invasive medical devices.

1. Background and objectives

This fourth report on sepsis outcome programs operated by the Australian Group on Antimicrobial Resistance (AGAR) presents analyses of antimicrobial resistance (AMR) associated with episodes of bacteraemia (blood stream infection) that were reported by 39 participating Australian public and private laboratories across Australia in 2019.

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

The 39 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 broadened over time to include studies on *Escherichia coli*, *Enterobacter* species, *Klebsiella* species, *Haemophilus influenzae, Streptococcus pneumoniae* and *Enterococcus* species. It now concentrated on the three groups of pathogens within the listed programs.

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

Table 1: Hospitals that contributed to AGAR, by state and territory, 2019

State or territory	Hospital
New South Wales	Concord Repatriation General Hospital
	John Hunter Hospital
	Liverpool Hospital
	Nepean Hospital
	Royal North Shore Hospital
	Royal Prince Alfred Hospital
	St Vincent's Hospital, Sydney
	Sydney Children's Hospital
	Westmead Hospital
	Wollongong Hospital
Victoria	Alfred Hospital
	Austin Hospital (Austin Health)
	Monash Children's Hospital*
	Monash Medical Centre (Dandenong Hospital)*
	Monash Medical Centre (Monash Health)
	Royal Women's and Children's Hospital
	St Vincent's Hospital
Queensland	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 Monash Medical Centre (Monash Health)
† Microbiology services provided by Pathology Queensland Central Laboratory
§ Microbiology services provided by Sullivan Nicolaides Pathology
# Microbiology services provided by SA Pathology, Royal Adelaide Hospital
** Microbiology services provided by PathWest Laboratory Medicine WA, 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 infections are less common in the community, but of high importance because of their intrinsic resistance to several 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 reclassified as *Enterobacterales*) Sepsis Outcome Program (EnSOP), which focused on the prospective collection of resistance and demographic data on all isolates from patients with documented bacteraemia. In 2015, *Pseudomonas aeruginosa* and *Acinetobacter* species were added, and the program evolved into the Gram-negative Sepsis Outcome Program (GNSOP).

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

The objectives of the 2019 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.

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.[6, 7] Although in the 1970s healthcare-associated enterococcal infections were primarily due to *Enterococcus faecalis*, there has been a steady increase in prevalence of *E. faecium* nosocomial infections.[8-10] Worldwide, the increase in nosocomial *E. faecium* infections has primarily been due to the expansion of polyclonal hospital-adapted clonal complex (CC) 17 isolates. While innately resistant to many classes of antimicrobials, *E. faecium* CC17 has demonstrated a remarkable capacity to evolve new antimicrobial resistances. In 2009, the Infectious Diseases Society of America highlighted *E. faecium* as one of the key problem bacteria or ESKAPE (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, P. aeruginosa,* and *Enterobacter* species) pathogens requiring new therapies.[11]

AGAR began surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[12] In 2011, AGAR commenced the Australian Enterococcal Sepsis Outcome Program (AESOP).[13]

In order to provide data to support improved antimicrobial prescribing and patient care, the objective of AESOP 2019 was to determine the proportion of *E. faecalis* and *E. faecium* bacteraemia isolates demonstrating antimicrobial resistance with particular emphasis on:

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

1.3. Australian Staphylococcal Sepsis Outcome Program

Globally *Staphylococcus aureus* is one of the most frequent causes of hospital-acquired and community-acquired blood stream infections.[14] 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.[15]

Despite standardised treatment protocols for SAB, including prolonged antimicrobial therapy and prompt source control[16], mortality can range from as low as 2.5% to as high as 40%.[17-19] Mortality rates are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[20, 21] 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.[22]

AGAR began surveillance of antimicrobial resistance in *S. aureus* in 1986.[23] In 2013, AGAR commenced the Australian Staphylococcal Sepsis Outcome Program (ASSOP).[24]

The primary objective of ASSOP 2019 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-nine institutions, in each state and territory of Australia, were enrolled in the 2019 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 2019 to 31 December 2019. 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*; *Klebsiella pneumoniae* complex comprises *K. pneumoniae*, *K. quasipneumoniae* and *K. variicola*; and *Citrobacter freundii* comprises all species of the *C. freundii* complex (*C. freundii*, *C. braakii*, *C. gillenii*, *C. murliniae*, *C. rodenticum*, *C. sedlakii*, *C. werkmanii* and *C. youngae*). *Klebsiella aerogenes* was previously known as *Enterobacter aerogenes*.

2.3. Susceptibility testing

Susceptibility testing of isolates is described in Appendix B. The analysis used breakpoints from the Clinical and Laboratory Standards Institute (CLSI) M100–A30[25] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v10.0.[26]

2.4. PCR screening and whole genome sequencing

E. coli, *Klebsiella* spp., *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone MIC >1 mg/L, or cefoxitin MIC >8 mg/L; any other *Enterobacterales* with cefepime MIC >1 mg/L; *Enterobacterales* with ciprofloxacin MIC >0.25 mg/L; all isolates with meropenem MIC >0.25 mg/L; all isolates with amikacin MIC >32 mg/L, and all isolates with colistin MIC > 4 mg/L were referred to a central laboratory (Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research) and underwent PCR to detect selected resistance genes (Centre for Infectious Diseases and Microbiology Laboratory Services, ICPMR, Westmead Hospital) and/or whole genome sequencing (Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, CIDMLS, ICPMR, Westmead Hospital).

The following isolates were subjected to whole genome sequencing:

- all isolates with meropenem MIC >0.25 mg/L (*Enterobacterales*) or MIC >4 mg/L (*P. aeruginosa* and *Acinetobacter* species)
- *mcr* positive isolates
- all referred isolates of *P. aeruginosa*
- all referred isolates of *Acinetobacter* species
- all referred *Salmonella* species
- representatives of bacterial species (mainly *E. coli* and *K. pneumoniae*) by phenotype, genotype and region.

All *E. faecium* and methicillin-resistant *S. aureus* (MRSA) were subjected to whole genome sequencing using the Illumina NextSeq platform. Data were analysed using the Nullarbor bioinformatic pipeline.[27] The pipeline was used to identify the multi-locus sequence type, *van* gene (*E. faecium*), SCC*mec* (MRSA) and Panton-Valentine leucocidin (MRSA).

2.5. Statistical analysis

Confidence intervals of proportions, Fisher's exact test for categorical variables, and chi-square test for trend were calculated, if appropriate, using GraphPad Prism version 8.4.2 for Windows (GraphPad Software, La Jolla, California).

3. Results

3.1. Isolates recovered

During 2019, a total of 13,375 bloodstream isolates were reported from 39 participating institutions. Overall, the proportion of isolates from children (<18 years) was 5.7%. The proportion of *S. aureus* isolates from children was 8.3%, *Enterococcus* spp. 4.8%, *Enterobacterales* 4.9%, *P. aeruginosa* 3.7% and *Acinetobacter* spp. 12.7%.

A total of 8,857 gram-negative bloodstream isolates (55 species/complex, 21 genera) were reported. *Enterobacterales* accounted for 90.1%, followed by *P. aeruginosa* (8.6%) and *Acinetobacter* species (1.2%). Of the *Enterobacterales*, three genera – *Escherichia* (61.6%), *Klebsiella* (19.8%) and *Enterobacter* (5.5%) – contributed 86.9% of all isolates. Overall, the top 10 species by rank were *E. coli* (55.5%), *K. pneumoniae* complex (13.5%), *P. aeruginosa* (8.6%), *E. cloacae* complex (4.8%), *Proteus mirabilis* (3.0%), *K. oxytoca* (2.7%), *Serratia marcescens* (2.4%), *K. aerogenes* (1.5%), *Salmonella* species (non- typhoidal) (1.4%), and *Morganella morganii* (1.1%). These 10 species comprised 94.5% of all isolates (Table 2). *Salmonella* spp. and *Enterobacter cloacae* complex episodes were more common among children than adults (15.7% versus 1.7%, and 9.9% versus 4.6% respectively).

There were 1,361 episodes of enterococcal bacteraemia. *E. faecalis* and *E. faecium* accounted for 95.2% of all enterococcal isolates (Table 2).

Of 3,157 SAB episodes, 583 (18.5%; 95% confidence interval [CI] 17.2-19.9) were methicillin resistant, ranging from 11.9% (95% CI 7.4-18.4) in Tasmania to 56.3% (95% CI: 44.1-67.7) in the Northern Territory (Table 2). There was little difference in the proportion of MRSA among children (19.5%, 95% CI: 15.1-24.7) and adults (18.4%, 95% CI: 17.0-19.8)

Table 2: Number of each species recovered, by state and territory, 2019

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Gram-negative species*	2,536	1,640	1,639	790	1,266	363	313	310	8,857
Escherichia coli	1,390	928	818	441	739	201	209	188	4,914
Klebsiella pneumoniae complex†	351	212	249	89	160	51	45	36	1,193
Pseudomonas aeruginosa	244	121	175	68	98	19	16	23	764
Enterobacter cloacae complex	118	93	95	33	48	20	14	6	427
Proteus mirabilis	79	46	38	37	39	14	2	12	267
Klebsiella oxytoca	59	55	35	26	32	17	4	11	239
Serratia marcescens	75	32	57	8	26	6	2	8	214
Klebsiella aerogenes	43	32	14	5	19	5	7	4	129
Salmonella species (non-typhoidal)	32	17	39	3	27	5	3	1	127
Morganella morganii	35	10	20	11	10	6	1	3	96
Salmonella species (typhoidal)	20	31	13	2	7	1	1	7	82
Citrobacter freundii complex	29	13	9	7	14	5	0	0	77
Acinetobacter baumannii complex	6	11	28	5	8	1	3	0	62
Citrobacter koseri	14	7	16	4	17	1	1	2	62
Raoultella ornithinolytica	7	3	2	3	3	2	0	0	20
Klebsiella species	4	5	3	5	2	0	0	0	19
Acinetobacter species	3	4	0	2	4	1	0	0	14
Acinetobacter ursingii	1	3	1	3	0	1	1	3	13
Providencia rettgeri	3	1	5	2	0	1	0	1	13
Acinetobacter lwoffii	4	1	1	1	2	1	2	0	12
Pantoea agglomerans	4	1	1	4	2	0	0	0	12

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Enterobacter species	0	0	0	11	0	0	0	0	11
Other species (*n* = 33)	15	14	20	20	9	5	2	5	90
Enterococcus species	444	307	201	112	150	69	20	58	1,361
Enterococcus faecalis	218	128	124	65	80	41	7	36	699
vancomycin resistant, percent§	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
vancomycin susceptible, percent§	99.5	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9
Enterococcus faecium	209	165	64	45	56	25	13	19	596
vancomycin resistant, percent§	43.5	66.5	15.9	31.1	5.4	40.0	46.2	21.1	41.6
vancomycin susceptible, percent§	56.5	33.5	84.1	68.9	94.6	60.0	53.8	78.9	58.4
Other enterococcal species	17	14	13	2	14	3	0	3	66
Enterococcus casseliflavus	4	7	6	1	3	0	0	1	22
Enterococcus gallinarum	6	4	2	1	6	1	0	1	21
Enterococcus avium	6	2	1	0	2	2	0	0	13
Enterococcus raffinosus	0	1	2	0	0	0	0	0	3
Enterococcus durans	1	0	1	0	0	0	0	1	3
Enterococcus hirae	0	0	1	0	2	0	0	0	3
Enterococcus species	0	0	0	0	1	0	0	0	1
Staphylococcus aureus	907	546	647	238	499	135	64	121	3,157
methicillin resistant, percent	19.4	16.7	15.8	15.1	21.2	11.9	56.3	16.5	18.5
methicillin susceptible, percent	80.6	83.3	84.2	84.9	78.8	88.1	43.7	83.5	81.5

* *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
† *Klebsiella pneumoniae* complex Includes *K. variicola* (*n* = 55) and *K. quasipneumoniae* (*n* = 4)
§ Vancomycin susceptibility was not available for two *E. faecium* (one each from Vic and Qld) and one *E. faecalis* from SA

3.2. Place of onset of bacteraemia

Almost all patients with bacteraemia were admitted to hospital (gram-negative species, 98.4%; *Enterococcus* species, 99.1%; *S. aureus*, 98.1%).

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, 76.5% of all episodes were community onset, with differences seen between *Enterobacterales* (78.6%), *Acinetobacter* species (63.6%) and *P. aeruginosa* (56.2%). The proportion of *Enterobacterales* that were community onset was significantly lower among children (70.3%, 275/391) than adults (79.1%, 6,002/7,592) (P < 0.01), most notable among *K. pneumoniae* complex (children: 50.0% versus adults: 74.0%).

Episodes involving *E. faecalis* and 'other' *Enterococcus* species were predominantly community onset (69.7%, 95% CI: 66.2-73.0 for *E. faecalis*). However, *E. faecium* episodes were predominantly hospital onset (69.8%; 95% CI: 66.0-73.3). The proportion of *E. faecalis* that were community onset was significantly lower among children (45.5%, 20/44) than adults (71.3%, 467/655) (P =< 0.01).

Most SABs were community onset (79.8%; 95% CI 78.4-81.2). The proportion of MRSA episodes that were community onset was significantly higher among children (90.2%, 46/51) than adults (73.7%, 392/532) (P = 0.01).

Table 3: Species recovered, by place of onset, 2019

Organism	Community onset % (*n*)	Hospital onset % (*n*)	Total, 100%
Enterococcus species	52.9 (720)	47.1 (641)	1,361
Enterococcus faecalis	69.7 (487)	30.3 (212)	699
Vancomycin resistant	0.0 (0)	>99.9 (1)	1
Vancomycin susceptible	69.9 (487)	30.1 (210)	697
Enterococcus faecium	30.2 (180)	69.8 (416)	596
Vancomycin resistant	21.1 (52)	78.9 (195)	247
Vancomycin susceptible	36.3 (126)	63.7 (221)	347
Other *Enterococcus* species (*n* = 7)	80.3 (53)	19.7 (13)	66
Gram-negative species*	76.5 (6,776)	23.5 (2,081)	8,857
Escherichia coli	83.3 (4,093)	16.7 (821)	4,914
Klebsiella pneumoniae complex	73.0 (871)	27.0 (322)	1,193
Pseudomonas aeruginosa	56.2 (429)	43.8 (335)	764
Enterobacter cloacae complex	57.4 (245)	42.6 (182)	427
Proteus mirabilis	84.3 (225)	15.7 (42)	267
Klebsiella oxytoca	72.4 (173)	27.6 (66)	239
Serratia marcescens	48.1 (103)	51.9 (111)	214
Klebsiella aerogenes	62.0 (80)	38.0 (49)	129
Salmonella species (non-typhoidal)	96.1 (122)	3.9 (5)	127
Morganella morganii	68.8 (66)	31.3 (30)	96
Salmonella species (typhoidal)	100.0 (82)	0.0 (0)	82
Citrobacter freundii complex	68.8 (53)	31.2 (24)	77
Acinetobacter baumannii complex	56.5 (35)	43.5 (27)	62
Citrobacter koseri	72.6 (45)	27.4 (17)	62
Raoultella ornithinolytica	90.0 (18)	10.0 (2)	20
Klebsiella species	73.7 (14)	26.3 (5)	19
Acinetobacter species	64.3 (9)	35.7 (5)	14
Acinetobacter ursingii	69.2 (9)	30.8 (4)	13
Providencia rettgeri	76.9 (10)	23.1 (3)	13
Acinetobacter lwoffii	75.0 (9)	25.0 (3)	12
Pantoea agglomerans	83.3 (10)	16.7 (2)	12
Enterobacter species	90.9 (10)	9.1 (1)	11
Other gram-negative species (*n* = 33)	72.2 (65)	27.8 (25)	90
Staphylococcus aureus	79.8 (2,519)	20.2 (638)	3,157
Methicillin resistant	75.1 (438)	24.9 (145)	583
Methicillin susceptible	80.8 (2,081)	19.2 (493)	2,574

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

Note: Vancomycin susceptibility was not available for two *Enterococcus faecium* (community onset) and one *E. faecalis* (hospital onset)

3.3. Onset versus 30-day all-cause mortality

Information on 30-day all-cause mortality was available for 6,160 (65.5%) episodes involving gram-negative species; 1,093 (80.3%) involving *Enterococcus* species and 2,427 (76.9%) involving *S. aureus*.

For gram-negative species, the 30-day all-cause mortality was 11.8% for *Enterobacterales*, 16.5% for *P. aeruginosa* and 11.3% for *Acinetobacter* species. The only gram-negative 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) and *E. cloacae* complex (P = 0.0109) (Table 4). There was a significant difference in 30-day all-cause mortality between children and adults among *Enterobacterales* (5.3% versus 12.6%, P < 0.01), notably *K. pneumoniae* complex (2.0% versus 14.1%, respectively).

There was a significant difference in the 30-day all-cause mortality between *E. faecium* (26.4%) and *E. faecalis* (13.7%) episodes (P < 0.01). However, there was no significant difference in 30-day all-cause mortality between vancomycin-resistant and vancomycin-susceptible *E. faecium* episodes, or between episodes from children and adults.

The 30-day all-cause mortality for *S. aureus* was significantly lower among children (0.5%, 1/210) compared to adults (15.6%, 345/2,217) (P < 0.01). However, there was no significant difference in 30-day all-cause mortality between methicillin-susceptible *S. aureus* (MSSA) (14.3%) and MRSA (14.0%) episodes, or between healthcare-associated MRSA (HA-MRSA) (19.4%) and community-associated MRSA (CA-MRSA) (11.4%) clones.

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), 2019

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Enterococcus species	547	16.5 (90)	546	24.7 (135)	1,093	20.6 (225)
Enterococcus faecalis	364	12.1 (44)	169	17.2 (29)	533	13.7 (73)
Vancomycin resistant	0	0.0 (0)	1	–[†] (0)	1	–[†] (0)
Vancomycin susceptible	364	12.1 (44)	167	16.8 (28)	531	13.6 (72)
Enterococcus faecium	141	23.4 (33)	366	27.6 (101)	507	26.4 (134)
Vancomycin resistant	40	20.0 (8)	173	32.4 (56)	213	30.0 (64)
Vancomycin susceptible	99	25.3 (25)	193	23.3 (45)	292	24.0 (70)
Other enterococcal species (*n* = 7)	42	31.0 (13)	11	45.5 (5)	53	34.0 (18)
Gram-negative species[*]	4,574	10.8 (496)	1,586	16.1 (256)	6,160	12.2 (752)
Escherichia coli	2,733	9.3 (255)	606	16.2 (98)	2,948	10.6 (353)
Klebsiella pneumoniae complex	590	12.4 (73)	255	15.7 (40)	783	13.4 (113)
Pseudomonas aeruginosa	305	15.7 (48)	266	17.3 (46)	533	16.5 (94)
Enterobacter cloacae complex	182	8.2 (15)	143	18.2 (26)	315	12.6 (41)
Proteus mirabilis	158	14.6 (23)	28	10.7 (3)	182	14.0 (26)
Klebsiella oxytoca	121	16.5 (20)	51	15.7 (8)	171	16.3 (28)
Serratia marcescens	72	13.9 (10)	86	16.3 (14)	139	15.2 (24)
Klebsiella aerogenes	54	11.1 (6)	37	13.5 (5)	88	12.1 (11)
Salmonella species (non-typhoidal)	68	5.9 (4)	4	–[†] (0)	69	5.6 (4)
Morganella morganii	44	18.2 (8)	24	16.7 (4)	61	17.6 (12)
Citrobacter freundii complex	38	23.7 (9)	18	22.2 (4)	55	23.2 (13)
Acinetobacter baumannii	24	12.5 (3)	23	8.7 (2)	52	10.6 (5)

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
complex						
Citrobacter koseri	31	16.1 (5)	11	18.2 (2)	48	16.7 (7)
Salmonella species (typhoidal)	41	0.0 (0)	0	n/a	41	0.0 (0)
Raoultella ornithinolytica	14	14.3 (2)	2	–† (0)	27	12.5 (2)
Klebsiella species	10	10.0 (1)	3	–† (0)	16	7.7 (1)
Enterobacter species	10	20.0 (2)	1	–† (0)	11	18.2 (2)
Acinetobacter species	8	–† (2)	3	–† (0)	10	18.2 (2)
Acinetobacter lwoffii	8	–† (1)	2	–† (0)	10	10.0 (1)
Other gram-negative species (*n* = 31)	63	14.3 (9)	23	17.4 (4)	86	15.1 (13)
Staphylococcus aureus	1,928	14.1 (272)	499	14.8 (74)	2,427	14.3 (346)
Methicillin resistant	343	12.8 (44)	114	17.5 (20)	457	14.0 (64)
CA-MRSA	253	9.9 (25)	80	16.3 (13)	333	11.4 (38)
HA-MRSA	66	19.7 (13)	27	18.5 (5)	93	19.4 (18)
Methicillin susceptible	1,585	14.4 (228)	385	14.0 (54)	1,970	14.3 (282)

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

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

† Insufficient numbers (<10) to calculate percentage

Notes:

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

3.4. Patient age and sex

Age and sex were available for all patients with gram-negative, enterococcal or staphylococcal bacteraemia. For gram-negative bacteraemia, the proportion of males was 54.4%. For *Enterococcus* species and SAB, 65.4% and 64.7%, respectively, were male.

Increasing age was a surrogate risk factor for bacteraemia (Figures 1-3); only 13.8% of gram-negative species episodes, 12.0% of *Enterococcus* species episodes and 20.2% 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, 2019

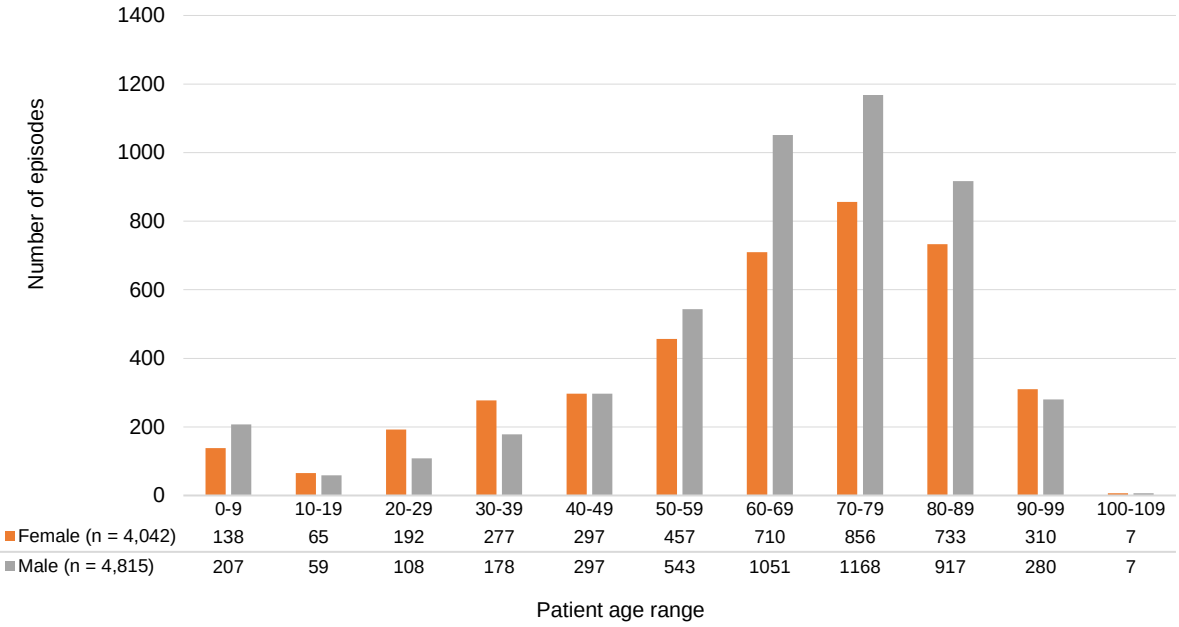


Figure 2: Number of episodes of bacteraemia due to *Enterococcus* species, by patient decade of life and sex, 2019

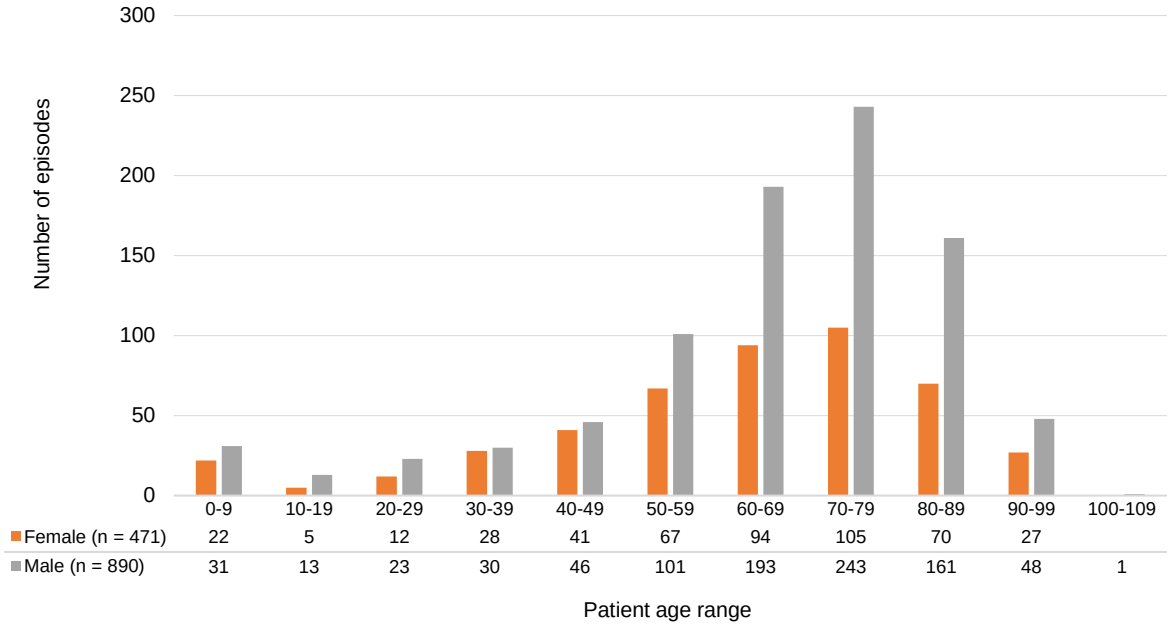
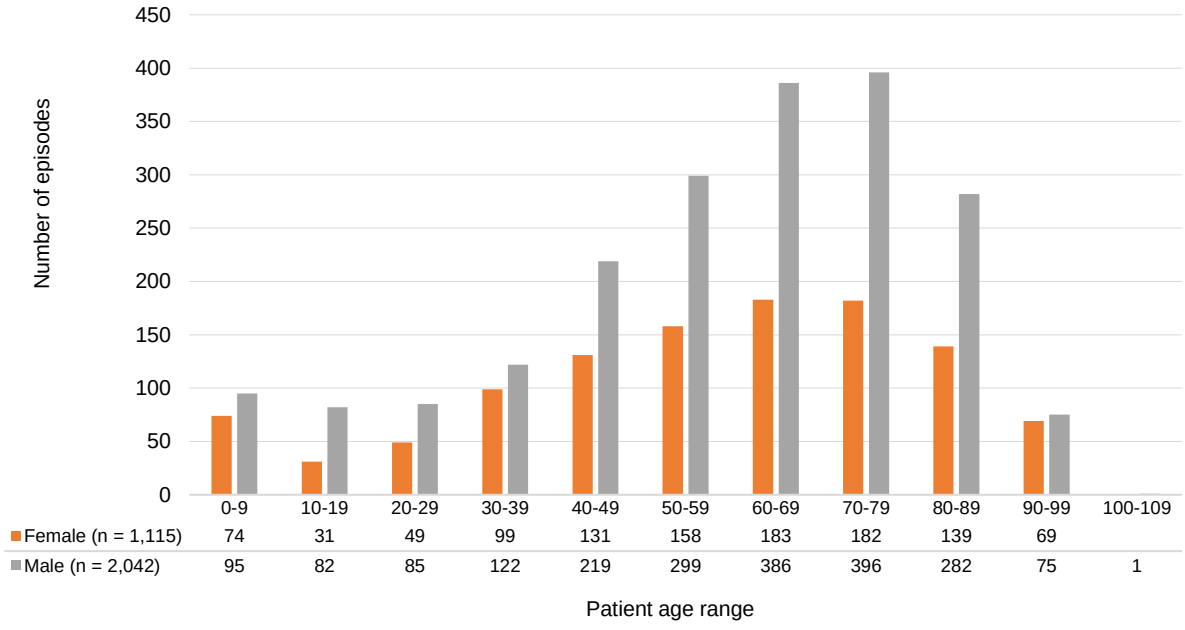


Figure 3: Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient decade of life and sex, 2019



3.5. Principal clinical manifestation

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

Gram-negative bacteria

The principal clinical manifestation was documented for 7,379 (83.3%) patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations were urinary tract infection (42.4%), biliary tract infection (14.6%) and other intra-abdominal infection (10.6%) (Table 5).

Urinary tract infection was the most frequent principal clinical manifestation for both community-onset (50.6%) and hospital-onset (23.3%) episodes caused by *Enterobacterales*. For *P. aeruginosa*, urinary tract infection was most common for community onset (24.8%); for hospital-onset episodes, urinary tract infection (20.5%) and febrile neutropenia (20.1%) were the most common association.

Table 5: Principal clinical manifestation for gram-negative* bacteraemia, by patient sex, 2019

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Gram-negative species*	**3,325**	**4,054**	**7,379**
Enterobacterales	3,066	3,572	6,638
Urinary tract infection	53.1 (1,629)	37.6 (1,342)	44.8 (2,971)
Biliary tract infection (including cholangitis)	13.5 (413)	17.1 (612)	15.4 (1,025)
Intra-abdominal infection other than biliary tract	8.9 (273)	12.7 (452)	10.9 (725)
Febrile neutropenia	7.1 (217)	8.5 (305)	7.9 (522)
No focus (setting not known)	6.5 (199)	8.3 (295)	7.4 (494)
Other clinical syndrome	4.9 (150)	7.6 (272)	6.4 (422)
Device-related infection without metastatic focus	3.6 (111)	3.7 (133)	3.7 (244)
Skin and skin structure infections	1.5 (46)	3.0 (108)	2.3 (154)
Osteomyelitis/septic arthritis	0.5 (15)	1.1 (38)	0.8 (53)
Device-related infection with metastatic focus	0.4 (13)	0.4 (15)	0.4 (28)
Pseudomonas aeruginosa	218	437	655
Urinary tract infection	11.0 (24)	28.8 (126)	22.9 (150)
Febrile neutropenia	21.6 (47)	17.4 (76)	18.8 (123)
Device-related infection without metastatic focus	12.4 (27)	10.8 (47)	11.3 (74)
Other clinical syndrome	11.5 (25)	11.2 (49)	11.3 (74)
No focus (setting not known)	11.5 (25)	9.2 (40)	9.9 (65)
Skin and skin structure infections	11.0 (24)	7.3 (32)	8.5 (56)
Intra-abdominal infection other than biliary tract	8.7 (19)	7.1 (31)	7.6 (50)
Biliary tract infection (including cholangitis)	10.6 (23)	5.7 (25)	7.3 (48)
Osteomyelitis/septic arthritis	1.4 (3)	1.4 (6)	1.4 (9)
Device-related infection with metastatic focus	0.5 (1)	1.1 (5)	0.9 (6)
Acinetobacter species	41	45	86
Device-related infection without metastatic focus	29.3 (12)	28.9 (13)	29.1 (25)
No focus (setting not known)	14.6 (6)	22.2 (10)	18.6 (16)
Other clinical syndrome	19.5 (8)	11.1 (5)	15.1 (13)
Skin and skin structure infections	9.8 (4)	8.9 (4)	9.3 (8)
Urinary tract infection	7.3 (3)	8.9 (4)	8.1 (7)

Febrile neutropenia	9.8 (4)	6.7 (3)	8.1 (7)
Intra-abdominal infection other than biliary tract	2.4 (1)	6.7 (3)	4.7 (4)
Osteomyelitis/septic arthritis	4.9 (2)	2.2 (1)	3.5 (3)
Biliary tract infection (including cholangitis)	2.4 (1)	2.2 (1)	2.3 (2)

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

Enterococcus species

The principal clinical manifestation was known for 1,245 (91.5%) patient episodes of enterococcal bacteraemia. Overall, the most frequent principal clinical manifestations were no focus (setting not known) (16.5%), biliary tract infections (15.9%), and urinary tract (15.4) (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 intra-abdominal infection other than biliary tract (19.4%). Of the community-onset episodes where data were available, the most frequent principal clinical manifestations were biliary tract infection (including cholangitis) and urinary tract infection (both 19.3%).

The principal manifestation was known for 1,183 of the 1,295 (91.4%) *E. faecalis* and *E. faecium* episodes (Table 7). The most common clinical manifestation for *E. faecalis* was urinary tract infection (23.1%), whereas for *E. faecium* it was biliary tract infection (including cholangitis) (20.7%) and intra-abdominal infection other than biliary tract (19.2%). 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, 2019

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance*
No focus (setting not known)	17.5 (74)	16.0 (132)	16.5 (206)	ns
Biliary tract infection (including cholangitis)	15.2 (64)	16.3 (134)	15.9 (198)	ns
Urinary tract infection	11.6 (49)	17.4 (143)	15.4 (192)	*P* < 0.01
Intra-abdominal infection other than biliary tract	14.9 (63)	14.6 (120)	14.7 (183)	ns
Device-related infection without metastatic focus	13.3 (56)	9.2 (76)	10.6 (132)	0.01 < P < 0.05
Febrile neutropenia	10.7 (45)	7.5 (62)	8.6 (107)	ns
Endocarditis, left-sided	4.3 (18)	8.5 (70)	7.1 (88)	*P* < 0.01
Skin and skin structure infections	4.7 (20)	3.9 (32)	4.2 (52)	ns
Other clinical syndrome	5.5 (23)	2.9 (24)	3.8 (47)	0.01 < P < 0.05
Osteomyelitis/septic arthritis	0.9 (4)	1.8 (15)	1.5 (19)	ns
Device-related infection with metastatic focus	0.7 (3)	0.9 (7)	0.8 (10)	ns
Endocarditis, right-sided	0.5 (2)	0.9 (7)	0.7 (9)	ns
Deep abscess(es) excluding those in the CNS	0.2 (1)	0.1 (1)	0.2 (2)	ns
Total	422	823	1,245	

CNS = central nervous system; 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, 2019

Principal clinical manifestation	*E. faecalis* % (*n*)	*E. faecium* % (*n*)	Total % (*n*)	Significance*
No focus (setting not known)	18.2 (115)	14.5 (80)	16.5 (195)	ns
Urinary tract infection	23.1 (146)	8.3 (46)	16.2 (192)	*P* < 0.01
Intra-abdominal infection other than biliary tract	10.3 (65)	19.2 (106)	14.5 (171)	*P* < 0.01
Biliary tract infection (including cholangitis)	8.2 (52)	20.7 (114)	14.0 (166)	*P* < 0.01
Device-related infection without metastatic focus	9.5 (60)	12.5 (69)	10.9 (129)	ns
Febrile neutropenia	2.5 (16)	16.0 (88)	8.8 (104)	*P* < 0.01
Endocarditis, left-sided	13.0 (82)	1.1 (6)	7.4 (88)	*P* < 0.01
Skin and skin structure infections	5.2 (33)	3.4 (19)	4.4 (52)	ns
Other clinical syndrome	5.4 (34)	2.2 (12)	3.9 (46)	*P* < 0.01
Osteomyelitis/septic arthritis	2.5 (16)	0.5 (3)	1.6 (19)	P < 0.01
Device-related infection with metastatic focus	0.8 (5)	0.9 (5)	0.8 (10)	ns
Endocarditis, right-sided	1.3 (8)	0.2 (1)	0.8 (9)	0.01 < *P* < 0.05
Deep abscess(es) excluding those in the CNS	0.0 (0)	0.4 (2)	0.2 (2)	ns
Total	632	551	1,183	

CNS = central nervous system; 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 2,738 (86.7%) episodes of SAB (Table 8). Overall, the most frequent principal clinical manifestation was skin and skin structure infection (21.1%) followed by osteomyelitis/septic arthritis (20.4%), and device-related infection without metastatic focus (17.0%). Just over one-third of the clinical manifestations in children were due to osteomyelitis/septic arthritis.

Of the hospital-onset SABs where data were available, the most common principal clinical manifestation was device-related infection without metastatic focus (36.0%). Of the community-onset SABs where data were available, the most common principal clinical manifestation was osteomyelitis/septic arthritis (23.1%).

Table 8: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient sex, 2019

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Skin and skin structure infections	18.7 (179)	22.4 (399)	21.1 (578)
Osteomyelitis/septic arthritis	20.2 (193)	20.5 (366)	20.4 (559)
Device-related infection without metastatic focus	18.3 (175)	16.3 (290)	17.0 (465)
No focus (setting not known)	13.7 (131)	12.4 (221)	12.9 (352)
Other clinical syndrome	7.6 (73)	8.2 (146)	8.0 (219)
Endocarditis, left-sided	6.3 (60)	7.1 (127)	6.8 (187)
Pneumonia/empyema	4.1 (39)	3.1 (56)	3.5 (95)
Endocarditis, right-sided	2.8 (27)	2.2 (40)	2.4 (67)
CNS infection (meningitis, abscess(es)	3.2 (31)	1.7 (30)	2.2 (61)
Device-related infection with metastatic focus	1.7 (16)	2.1 (37)	1.9 (53)
Deep abscess(es) excluding those in the CNS	1.2 (11)	2.2 (39)	1.8 (50)
Febrile neutropenia	1.8 (17)	1.6 (28)	1.6 (45)
Intra-abdominal infection other than biliary tract	0.3 (3)	0.0 (0)	0.1 (3)
Urinary tract infection	0.0 (0)	0.2 (3)	0.1 (3)
Biliary tract infection (including cholangitis)	0.0 (0)	0.1 (1)	0.0 (1)
Total	955	1,783	2,738

CNS = central nervous system

The most common principal clinical manifestation for methicillin-susceptible *S. aureus* was osteomyelitis/septic arthritis (21.3%), whereas for methicillin-resistant *S. aureus* it was skin and skin structure infection (26.4%) (Table 9).

Table 9: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, 2019

Principal clinical manifestation	Methicillin-resistant % (*n*)	Methicillin-susceptible % (*n*)	Total % (*n*)
Skin and skin structure infections	26.4 (128)	20.0 (450)	21.1 (578)
Osteomyelitis/septic arthritis	16.5 (80)	21.3 (479)	20.4 (559)
Device-related infection without metastatic focus	14.5 (70)	17.5 (395)	17.0 (465)
No focus (setting not known)	13.4 (65)	12.7 (287)	12.9 (352)
Other clinical syndrome	8.9 (43)	7.8 (176)	8.0 (219)
Endocarditis, left-sided	5.6 (27)	7.1 (160)	6.8 (187)
Pneumonia/empyema	4.8 (23)	3.2 (72)	3.5 (95)
Endocarditis, right-sided	1.4 (7)	2.7 (60)	2.4 (67)

CNS infection (meningitis, abscess(es)	0.8 (4)	2.5 (57)	2.2 (61)
Device-related infection with metastatic focus	2.1 (10)	1.9 (43)	1.9 (53)
Deep abscess(es) excluding those in the CNS	3.5 (17)	1.5 (33)	1.8 (50)
Febrile neutropenia	1.7 (8)	1.6 (37)	1.6 (45)
Intra-abdominal infection other than biliary tract	0.2 (1)	0.1 (2)	0.1 (3)
Urinary tract infection	0.2 (1)	0.1 (2)	0.1 (3)
Biliary tract infection (including cholangitis)	0.0 (0)	0.0 (1)	0.0 (1)
Total	484	2,254	2,738

CNS = central nervous system

3.6. Length of hospital stay following bacteraemic episode

Information on length of stay following bacteraemia was available for 8,107 (91.5%) episodes involving gram-negative species, 1,242 (91.3%) episodes involving *Enterococcus* species and 2,846 (90.1%) 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, 22.8% of patients remained in hospital for more than 30 days after enterococcal bacteraemia (Table 11) and 24.2% after staphylococcal bacteraemia (Table 12).

Table 10: Length of stay following gram-negative bacteraemia, by species and place of onset, 2019

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Gram-negative species*	45.6 (3,696)	29.7 (2,404)	15.0 (1,212)	9.8 (795)	8,107
Acinetobacter species	32.7 (32)	26.5 (26)	20.4 (20)	20.4 (20)	98
Community onset	43.5 (27)	33.9 (21)	16.1 (10)	6.5 (4)	62
Hospital onset	13.9 (5)	13.9 (5)	27.8 (10)	44.4 (16)	36
Enterobacterales	47.1 (3,443)	29.4 (2,148)	14.4 (1,051)	9.1 (666)	7,308
Escherichia coli	51.2 (2,301)	28.7 (1,290)	13.2 (594)	6.9 (308)	4,493
Community onset	57.0 (2,135)	28.5 (1,068)	10.3 (386)	4.2 (156)	3,745
Hospital onset	22.2 (166)	29.7 (222)	27.8 (208)	20.3 (152)	748
Klebsiella pneumoniae complex	40.0 (437)	32.1 (350)	15.7 (171)	12.3 (134)	1,092
Community onset	48.5 (379)	33.4 (261)	10.7 (84)	7.4 (58)	782
Hospital onset	18.7 (58)	28.7 (89)	28.1 (87)	24.5 (76)	310
Enterobacter cloacae complex	30.8 (123)	33.3 (133)	18.8 (75)	17.3 (69)	400
Community onset	40.2 (92)	36.7 (84)	14.4 (33)	8.7 (20)	229
Hospital onset	18.1 (31)	28.7 (49)	24.6 (42)	28.7 (49)	171
Other *Enterobacterales* (*n* = 41)	44.0 (582)	28.3 (375)	15.9 (211)	11.7 (155)	1,323
Pseudomonas aeruginosa	31.5 (221)	32.8 (230)	20.1 (141)	15.5 (109)	701
Community onset	42.7 (166)	34.2 (133)	15.7 (61)	7.5 (29)	389
Hospital onset	17.6 (55)	31.1 (97)	25.6 (80)	25.6 (80)	312

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

Table 11: Length of stay following *Enterococcus* species bacteraemia, by vancomycin resistance and place of onset, 2019

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 % days (*n*)	15–30 % days (*n*)	>30 days % (*n*)	
All species	24.2 (301)	27.1 (336)	26.0 (323)	22.7 (282)	1,242
E. faecalis	25.6 (160)	26.2 (164)	26.1 (163)	22.1 (138)	625
Vancomycin resistant	–* (0)	–* (0)	–* (0)	–* (1)	1
Vancomycin susceptible	25.6 (160)	26.3 (164)	26.1 (163)	22.0 (137)	624
E. faecium	21.4 (118)	26.1 (144)	27.2 (150)	25.4 (140)	552
Vancomycin resistant	19.9 (46)	26.4 (61)	28.6 (66)	25.1 (58)	231
Vancomycin susceptible	22.4 (72)	25.9 (83)	26.2 (84)	25.5 (82)	321
Other *Enterococcus* species (*n* = 7)	34.9 (22)	44.4 (28)	15.9 (10)	4.8 (3)	63
Community onset					
E. faecalis	28.9 (125)	27.5 (119)	23.6 (102)	19.9 (86)	432
Vancomycin resistant	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0
Vancomycin susceptible	28.9 (125)	27.5 (119)	23.8 (103)	19.7 (85)	432
E. faecium	33.1 (52)	27.4 (43)	21.7 (34)	17.8 (28)	157
Vancomycin resistant	26.1 (12)	30.4 (14)	28.3 (13)	15.2 (7)	46
Vancomycin susceptible	36.0 (40)	26.1 (29)	18.9 (21)	18.9 (21)	111
Hospital onset					
E. faecalis	18.1 (35)	23.3 (45)	31.1 (60)	26.9 (52)	193
Vancomycin resistant	–* (0)	–* (0)	–* (0)	–* (0)	1
Vancomycin susceptible	18.2 (35)	23.4 (45)	31.3 (60)	27.1 (52)	192
E. faecium	16.7 (66)	25.6 (101)	29.4 (116)	28.4 (112)	395
Vancomycin resistant*	18.4 (34)	25.4 (47)	28.6 (53)	27.6 (51)	185
Vancomycin susceptible*	15.2 (32)	25.7 (54)	30.0 (63)	29.0 (61)	210

* Insufficient numbers (<10) to calculate percentage

Note: vancomycin susceptibility not available for one *E. faecalis* (hospital onset) and one *E. faecium* (community onset)

Table 12: Length of stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, 2019

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Staphylococcus aureus	18.2 (518)	26.3 (749)	31.2 (889)	24.2 (690)	2,846
Methicillin resistant	17.1 (91)	22.7 (121)	34.0 (181)	26.3 (140)	533
Community onset	17.7 (72)	24.9 (101)	36.2 (147)	21.2 (86)	406
Hospital onset	15.0 (19)	15.7 (20)	26.8 (34)	42.5 (54)	127
Methicillin susceptible	18.5 (427)	27.2 (628)	30.6 (708)	23.8 (550)	2,313
Community onset	19.4 (362)	27.9 (520)	30.1 (562)	22.6 (422)	1,866
Hospital onset	14.5 (65)	24.2 (108)	32.7 (146)	28.6 (128)	447

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

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

Supplementary data on percentages susceptible, susceptible – increased exposure (EUCAST), intermediate (CLSI), and resistant for each antimicrobial and all species, and the antimicrobial profiles by state and territory can be found in the 2019 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), 2019

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Acinetobacter baumannii complex					
Piperacillin–tazobactam	59	5.1 (3)	8.5 (5)	–*	–*
Ceftazidime	58	13.8 (8)	1.7 (1)	–*	–*
Cefepime	58	3.4 (2)	3.4 (2)	–*	–*
Gentamicin	61	1.6 (1)	6.6 (4)	–†	8.2 (5)
Tobramycin	61	1.6 (1)	3.3 (2)	–†	4.9 (3)
Amikacin	59	0.0 (0)	0.0 (0)	–†	1.7 (1)
Ciprofloxacin	59	0.0 (0)	3.4 (2)	96.6 (57)	3.4 (2)
Meropenem	61	0.0 (0)	4.9 (3)	0.0 (0)	4.9 (3)
Enterobacter cloacae complex					
Piperacillin–tazobactam	425	6.6 (28)	14.8 (63)	3.5 (15)	21.4 (91)
Ceftriaxone	427	0.7 (3)	23.4 (100)	0.7 (3)	23.4 (100)
Ceftazidime	427	0.2 (1)	21.3 (91)	2.6 (11)	21.5 (92)
Cefepime	427	3.3 (14)§	0.0 (0)	8.7 (37)	2.3 (10)
Gentamicin	427	0.5 (2)	4.9 (21)	–†	6.1 (26)
Tobramycin	427	2.8 (12)	3.5 (15)	–†	6.6 (28)
Amikacin	427	0.0 (0)	0.2 (1)	–†	0.7 (3)
Ciprofloxacin	427	1.2 (5)	5.9 (25)	1.2 (5)	5.9 (25)
Meropenem	427	0.5 (2)	2.1 (9)	0.0 (0)	2.1 (9)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Enterococcus faecalis					
Ampicillin	698	–[†]	0.0 (0)	0.1 (1)	0.0 (0)
Benzylpenicillin	643	–[†]	0.8 (5)	–*	–*
Ciprofloxacin[#]	429	3.3 (14)	8.4 (36)	–*	6.1 (26)**
Daptomycin	679	22.4 (152)	0.1 (1)	–*	–*
Linezolid	698	0.6 (4)	0.0 (0)	–[†]	0.0 (0)
Teicoplanin	698	0.0 (0)	0.0 (0)	–[†]	0.4 (3)
Tetracycline/doxycycline[‡]	481	0.0 (0)	70.7 (340)	–*	–*
Vancomycin	698	0.1 (1)	0.0 (0)	–[†]	0.1 (1)
Enterococcus faecium					
Ampicillin	594	–[†]	91.2 (542)	0.2 (1)	91.2 (542)
Benzylpenicillin	546	–[†]	89.9 (491)	–*	–*
Ciprofloxacin[#]	386	3.1 (12)	89.4 (345)	–*	85.9 (262)**
Linezolid	594	0.3 (2)	0.2 (1)	–[†]	0.2 (1)
Teicoplanin	594	2.0 (12)	16.5 (98)	–[†]	20.2 (120)
Tetracycline/doxycycline[‡]	464	0.2 (1)	64.7 (300)	–*	–*
Vancomycin	594	0.5 (3)	41.1 (244)	–[†]	41.6 (247)
Escherichia coli					
Ampicillin	4,881	1.9 (93)	54.4 (2,656)	–[†]	56.3 (2,749)
Amoxicillin–clavulanic acid	4,382	14.8 (649)	7.8 (342)	–[§§]	–[§§]
Piperacillin–tazobactam	4,867	2.6 (125)	3.2 (154)	1.6 (80)	5.7 (279)
Ceftriaxone	4,885	0.1 (5)	13.3 (648)	0.1 (5)	13.3 (648)
Ceftazidime	4,885	0.9 (42)	6.2 (304)	5.9 (289)	7.1 (346)
Cefepime	4,884	2.1 (105)[§]	0.0 (0)	6.6 (322)	4.1 (202)
Gentamicin	4,881	0.2 (12)	9.0 (439)	–[†]	9.5 (462)
Tobramycin	4,885	6.5 (319)	3.3 (162)	–[†]	10.4 (506)
Amikacin	4,884	0.1 (4)	0.1 (3)	–[†]	0.9 (46)
Ciprofloxacin	4,882	3.5 (172)	16.0 (779)	3.5 (172)	16.0 (779)
Meropenem	4,882	0.1 (4)	0.1 (6)	0.0 (2)	0.1 (4)
Klebsiella (*Enterobacter*) *aerogenes*					
Piperacillin–tazobactam	127	6.3 (8)	28.3 (36)	7.1 (9)	34.6 (44)
Ceftriaxone	127	0.8 (1)	34.6 (44)	0.8 (1)	34.6 (44)
Ceftazidime	127	0.8 (1)	33.9 (43)	5.5 (7)	34.6 (44)
Cefepime	127	0.0 (0)[§]	0.0 (0)	0.8 (1)	0.8 (1)
Gentamicin	126	0.0 (0)	0.8 (1)	–[†]	0.8 (1)
Tobramycin	127	0.0 (0)	0.8 (1)	–[†]	0.8 (1)
Amikacin	127	0.0 (0)	0.0 (0)	–[†]	0.0 (0)
Ciprofloxacin	126	0.0 (0)	1.6 (2)	0.0 (0)	1.6 (2)
Meropenem	127	0.0 (0)	1.6 (2)	0.8 (1)	0.8 (1)
Klebsiella oxytoca					
Amoxicillin–clavulanic acid	215	3.3 (7)	6.0 (13)	–[§§]	–[§§]
Piperacillin–tazobactam	239	1.3 (3)	7.9 (19)	2.1 (5)	9.2 (22)
Ceftriaxone	239	1.3 (3)	6.3 (15)	1.3 (3)	6.3 (15)
Ceftazidime	239	0.0 (0)	1.3 (3)	1.7 (4)	1.3 (3)
Cefepime	239	0.4 (1)[§]	0.0 (0)	1.3 (3)	0.0 (0)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Gentamicin	239	0.0 (0)	0.4 (1)	–[†]	0.4 (1)
Tobramycin	239	0.0 (0)	0.4 (1)	–[†]	0.4 (1)
Amikacin	239	0.0 (0)	0.0 (0)	–[†]	0.0 (0)
Ciprofloxacin	239	0.0 (0)	1.7 (4)	0.0 (0)	1.7 (4)
Meropenem	239	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Klebsiella pneumoniae complex					
Amoxicillin–clavulanic acid	1,066	5.2 (55)	6.7 (71)	–[§§]	–[§§]
Piperacillin–tazobactam	1,189	3.8 (45)	4.7 (56)	6.8 (81)	8.5 (101)
Ceftriaxone	1,190	0.3 (3)	8.4 (100)	0.3 (3)	8.4 (100)
Ceftazidime	1,190	1.1 (13)	6.1 (72)	2.6 (31)	7.1 (85)
Cefepime	1,190	0.8 (10)[§]	0.0 (0)	3.7 (44)	3.3 (39)
Gentamicin	1,190	0.1 (1)	5.1 (61)	–[†]	5.4 (64)
Tobramycin	1,190	3.3 (39)	3.7 (44)	–[†]	7.3 (87)
Amikacin	1,190	0.0 (0)	0.4 (5)	–[†]	1.2 (14)
Ciprofloxacin	1,189	1.3 (15)	10.2 (121)	1.3 (15)	10.2 (121)
Meropenem	1,190	0.3 (3)	0.8 (10)	0.1 (1)	0.8 (9)
Proteus mirabilis					
Ampicillin	265	0.0 (0)	14.7 (39)	–[†]	14.7 (39)
Amoxicillin–clavulanic acid	238	3.4 (8)	2.1 (5)	–[§§]	–[§§]
Piperacillin–tazobactam	262	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Ceftriaxone	265	0.0 (0)	1.5 (4)	0.0 (0)	1.5 (4)
Ceftazidime	264	0.4 (1)	0.0 (0)	0.4 (1)	0.4 (1)
Cefepime	265	1.1 (3)[§]	0.0 (0)	1.1 (3)	0.0 (0)
Gentamicin	265	0.8 (2)	1.1 (3)	–[†]	11.7 (31)
Tobramycin	265	1.9 (5)	0.8 (2)	–[†]	5.3 (14)
Amikacin	265	0.0 (0)	0.0 (0)	–[†]	1.5 (4)
Ciprofloxacin	265	0.4 (1)	1.9 (5)	0.4 (1)	1.9 (5)
Meropenem	265	0.4 (1)	0.4 (1)	0.4 (1)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin–tazobactam	750	5.6 (42)	6.9 (52)	87.5 (656)	12.5 (94)
Ceftazidime	753	3.7 (28)	5.3 (40)	91.0 (685)	9.0 (68)
Cefepime	755	2.4 (18)	2.4 (18)	94.2 (711)	5.8 (44)
Gentamicin	753	1.5 (11)	0.9 (7)	–*	–*
Tobramycin	755	0.1 (1)	0.5 (4)	–[†]	0.9 (7)
Amikacin	755	0.4 (3)	0.4 (3)	–[†]	0.8 (6)
Ciprofloxacin	755	5.2 (39)	4.1 (31)	90.7 (685)	9.3 (70)
Meropenem	752	3.7 (28)	3.5 (26)	4.8 (36)	2.4 (18)
Salmonella species (non-typhoidal)					
Ampicillin	127	0.0 (0)	4.7 (6)	–[†]	4.7 (6)
Amoxicillin–clavulanic acid	124	1.6 (2)	0.8 (1)	–[§§]	–[§§]
Piperacillin–tazobactam	126	0.8 (1)	0.0 (0)	0.0 (0)	0.8 (1)
Ceftriaxone	127	0.0 (0)	0.8 (1)	0.0 (0)	0.8 (1)
Ceftazidime	127	0.0 (0)	0.8 (1)	0.0 (0)	0.8 (1)
Cefepime	127	0.0 (0)[§]	0.0 (0)	0.0 (0)	0.0 (0)
Ciprofloxacin	123	–[##]	4.1 (5)	–[†]	–[##]

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Meropenem	127	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	183	0.5 (1)	0.5 (1)	1.1 (2)	1.1 (2)
Ceftriaxone	213	0.9 (2)	3.8 (8)	0.9 (2)	3.8 (8)
Ceftazidime	213	0.0 (0)	2.3 (5)	0.9 (2)	2.3 (5)
Cefepime	213	0.9 (2)§	0.0 (0)	0.9 (2)	1.4 (3)
Gentamicin	213	1.4 (3)	1.4 (3)	–†	3.8 (8)
Tobramycin	213	10.8 (23)	2.3 (5)	–†	29.6 (63)
Amikacin	213	0.0 (0)	0.5 (1)	–†	1.9 (4)
Ciprofloxacin	213	0.5 (1)	3.8 (8)	0.5 (1)	3.8 (8)
Meropenem	213	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Staphylococcus aureus					
Benzylpenicillin	3,149	–†	79.7 (2,511)	–†	79.7 (2,511)
Ciprofloxacin	3,151	0.9 (28)	8.6 (271)	90.5 (2,852)	9.5 (299)
Clindamycin (constitutive)	3,129	0.0 (1)	3.7 (116)	0.3 (9)	3.7 (117)
Clindamycin (inducible + constitutive resistance)	3,129	0.0 (0)	13.8 (433)	0.3 (9)	14.7 (459)
Daptomycin	3,154	0.0 (1)***	–†	–†	0.0 (1)
Erythromycin	3,142	27.5 (865)	16.7 (526)	1.1 (34)	17.6 (554)
Gentamicin	3,128	1.0 (31)	2.0 (63)	–†	4.0 (125)
Linezolid	3,154	0.0 (0)	0.0 (0)	–†	0.0 (0)
Oxacillin (methicillin)†‡	3,129	–†	18.5 (583)	–†	18.5 (583)
Rifampicin	3,129	0.1 (3)	0.4 (13)	–§§§	0.5 (17)
Trimethoprim–sulfamethoxazole	3,128	–†	3.4 (106)	0.3 (8)	3.1 (98)
Teicoplanin	3,154	0.0 (0)	0.0 (0)	–†	0.1 (2)
Tetracycline/doxycycline‡	3,145	0.2 (6)	5.2 (163)	0.6 (18)	5.7 (178)
Vancomycin	3,154	0.0 (0)	0.0 (0)	–†	0.0 (0)

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

* No guidelines for indicated species
† No category defined
§ Includes sensitive dose dependent category for CLSI
# The ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible and resistant categories (Phoenix card, EUCAST) for *Enterococcus* species
** The ciprofloxacin ECOFF (4 mg/L, *E. faecalis*; 8 mg/L, *E. faecium*) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only
‡ Doxycycline concentration range (Phoenix panel) restricts ability to accurately identify intermediate and resistant category
§§ 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 ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species
*** Non-susceptible; resistance not defined
†‡ Resistance as determined by cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix)
§§§ The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant

Figure 4. Percentage of *Escherichia coli* from patients with bacteraemia with resistance as defined by EUCAST to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, 2019

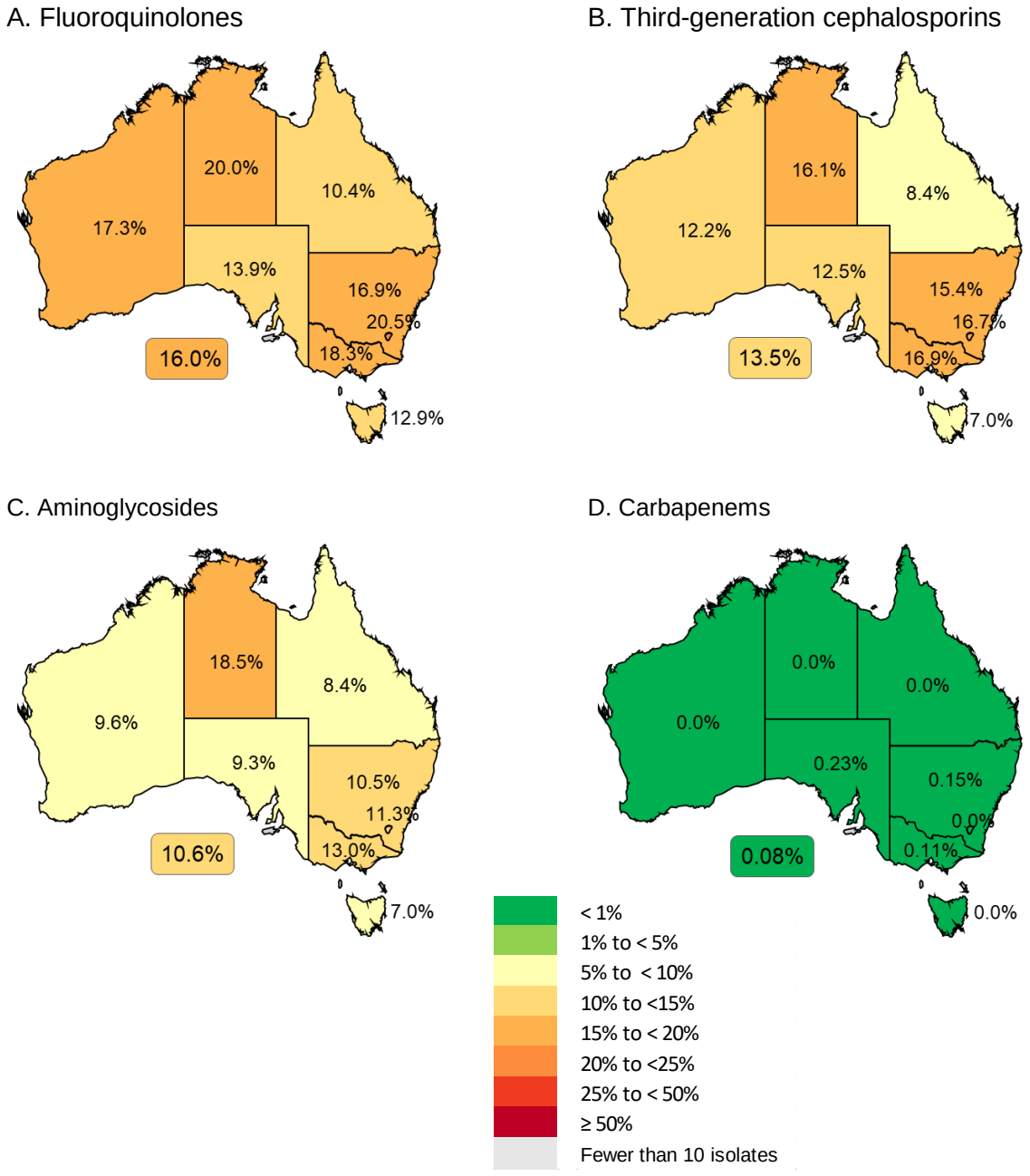


Figure 5. Percentage of *Klebsiella pneumoniae* complex from patients with bacteraemia with resistance as defined by EUCAST to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, 2019

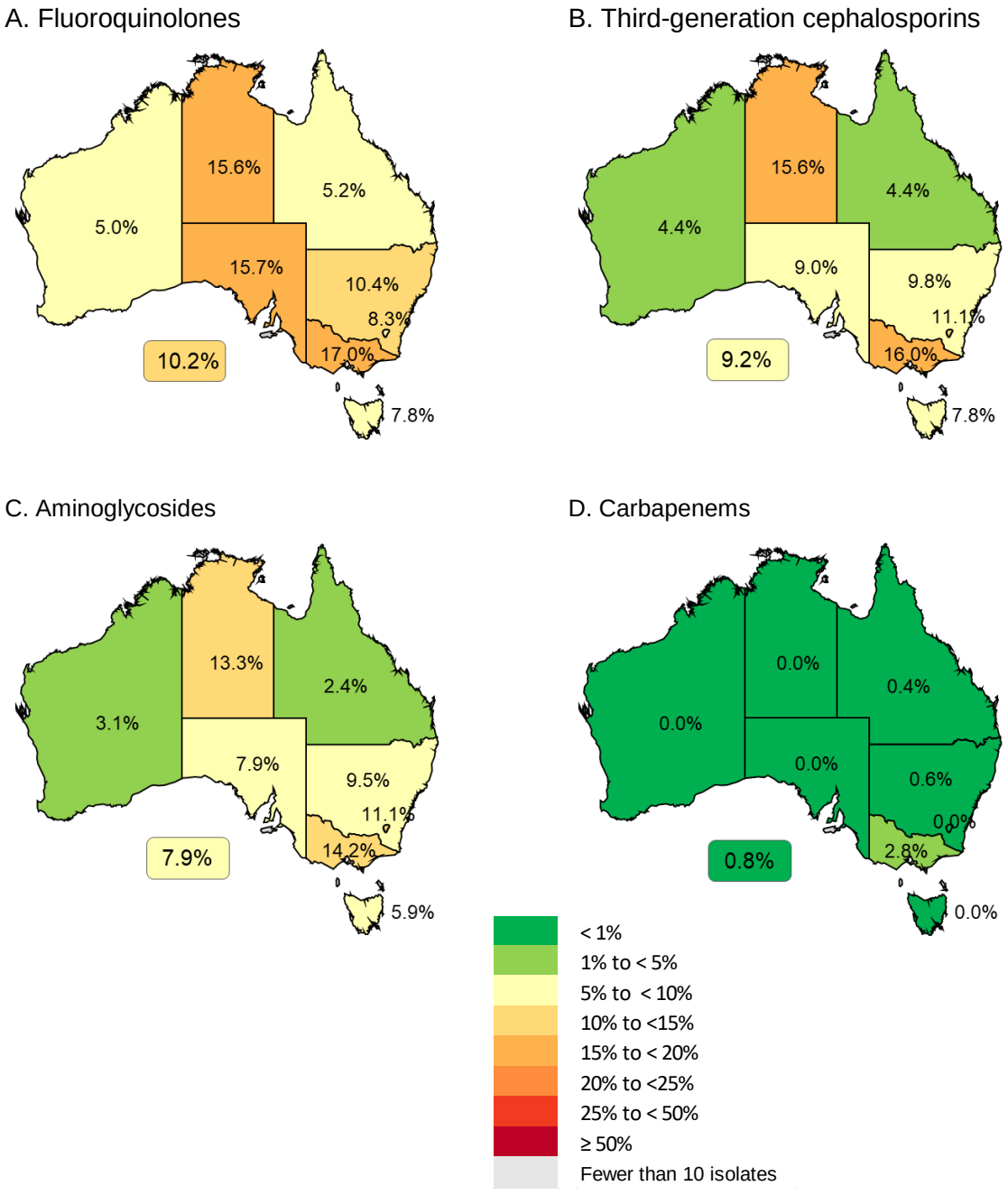


Figure 6. Percentage of *Pseudomonas aeruginosa* from patients with bacteraemia with resistance as defined by EUCAST to piperacillin–tazobactam (A), fluoroquinolones (B), ceftazidime (C) and carbapenems (D), Australia, 2019

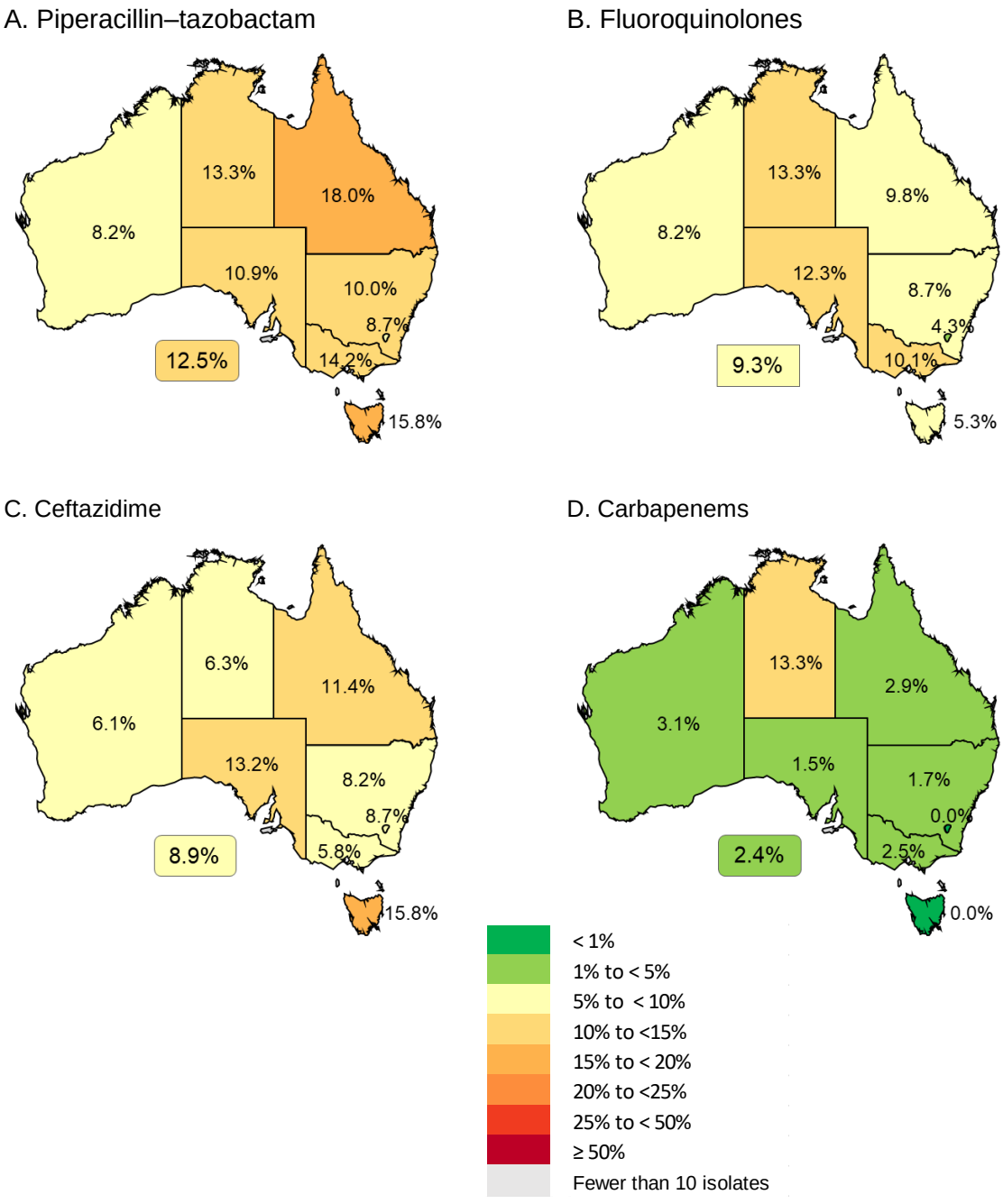


Figure 7. Percentage of *Staphylococcus aureus* from patients with bacteraemia with resistance as defined by EUCAST to methicillin, Australia, 2019

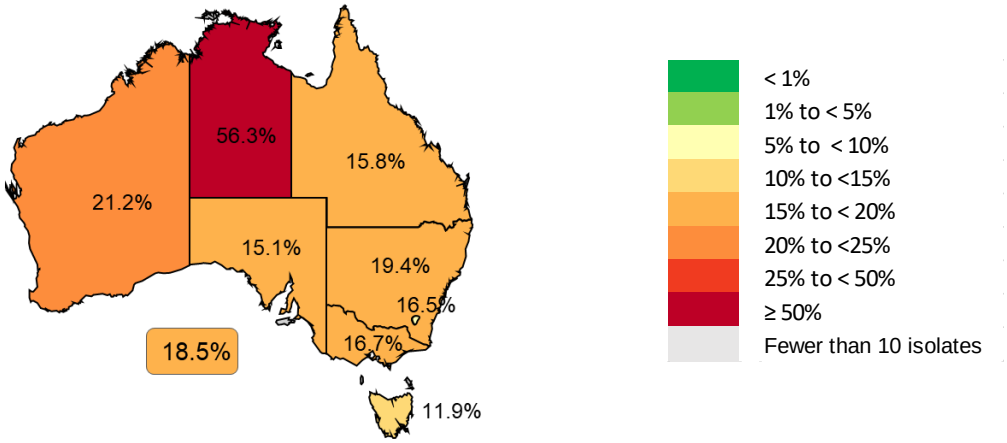
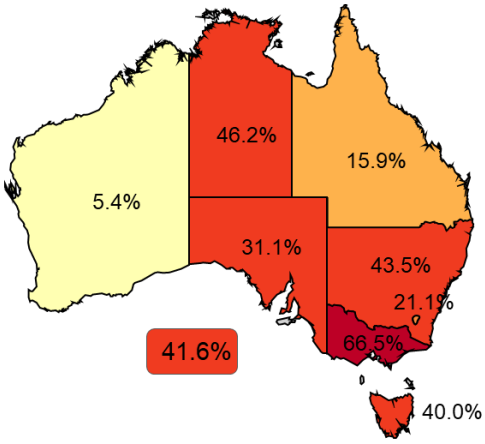
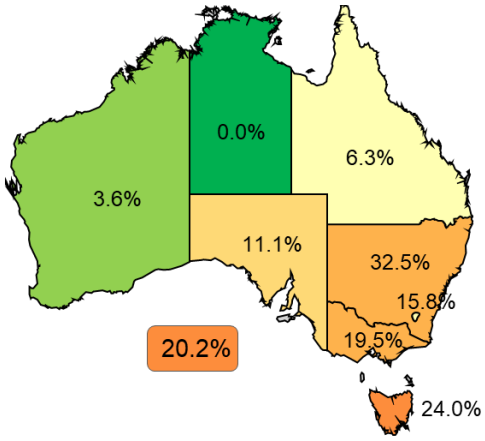


Figure 8. Percentage of *Enterococcus faecium* from patients with bacteraemia with resistance as defined by EUCAST to vancomycin (A) and teicoplanin (B), and *Enterococcus faecalis* with resistance to high-level gentamicin (C), Australia, 2019

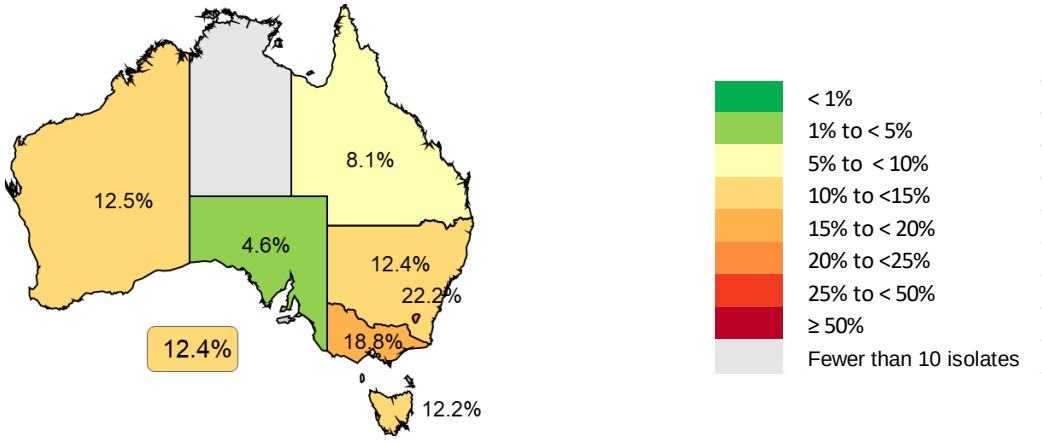
A. Vancomycin



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, 2019

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Acinetobacter baumannii complex					
Piperacillin–tazobactam	59	0.0, –*	5.9, –*	12.0, –*	12.0, –*
Ceftriaxone	57	71.9, –*	3.1, –*	92.0, –*	0.0, –*
Ceftazidime	58	8.8, –*	2.9, –*	20.8, –*	0.0, –*
Cefepime	58	0.0, –*	6.1, –*	8.0, –*	4.0, –*
Gentamicin	61	2.9, –†	8.6, 11.4	0.0, –†	3.8, 3.8
Tobramycin	61	0.0, –†	5.7, 5.7	3.8, –†	0.0, 3.8
Amikacin	59	0.0, –†	0.0, 2.9	0.0, –†	0.0, 0.0
Ciprofloxacin	59	0.0, 94.1	5.9, 5.9	0.0, 100.0	0.0, 0.0
Meropenem	61	0.0, 0.0	5.7, 5.7	0.0, 0.0	3.8, 3.8
Enterobacter cloacae complex					
Piperacillin–tazobactam	425	7.8, 1.6	8.6, 16.5	4.9, 6.0	23.1, 28.0
Ceftriaxone	427	0.8, 0.8	15.9, 15.9	0.5, 0.5	33.5, 33.5
Ceftazidime	427	0.0, 1.6	15.1, 15.1	0.5, 3.8	29.7, 30.2
Cefepime	427	3.7§, 4.9	2.0, 3.7	2.7§, 13.7	0.0, 0.5
Gentamicin	427	0.0, –†	3.7, 4.1	1.1, –†	6.6, 8.8
Tobramycin	427	1.6, –†	2.9, 4.5	4.4, –†	4.4, 9.3
Amikacin	427	0.0, –†	0.0, 0.4	0.0, –†	0.5, 1.1
Ciprofloxacin	427	1.2, 1.2	4.5, 4.5	1.1, 1.1	7.7, 7.7
Meropenem	427	0.4, 0.0	2.9, 2.9	0.5, 0.0	1.1, 1.1
Enterococcus faecalis					
Ampicillin	698	–†, 0.0	0.0, 0.0	–†, 0.5	0.0, 0.0
Benzylpenicillin	643	–†, –*	0.9, –*	–†, –*	0.5, –*
Ciprofloxacin#	429	3.3, –*	8.6, 6.6**	3.2, –*	8.0, 5.0**
Daptomycin	679	22.2, –*	0.2, –*	22.9, –*	0.0, –*
Linezolid	698	0.4, –†	0.0, 0.0	0.9, –†	0.0, 0.0
Teicoplanin	698	0.0, –†	0.0, 0.4	0.0, –†	0.0, 0.5
Tetracycline/doxycycline‡	481	0.0, –*	69.7, –*	0.0, –*	73.0, –*
Vancomycin	698	0.0, –†	0.0, 0.0	0.5, –†	0.0, 0.5
Enterococcus faecium					
Ampicillin	594	–†, 0.0	83.1, 83.1	–†, 0.2	94.7, 94.7
Benzylpenicillin	546	–†, –*	81.2, –*	–†, –*	93.7, –*
Ciprofloxacin#	386	5.7, –*	82.0, 78.3**	1.9, –*	92.8, 89.9**
Linezolid	594	0.0, –†	0.0, 0.0	0.5, –†	0.2, 0.2
Teicoplanin	594	0.0, –†	10.7, 11.8	2.9, –†	19.0, 23.8
Tetracycline/doxycycline‡	464	0.0, –*	62.1, –*	0.3, –*	65.7, –*
Vancomycin	594	0.6, –†	28.7, 29.2	0.7, –†	46.4, 46.9
Escherichia coli					
Ampicillin	4,881	1.9, –†	53.1, 55.0	2.0, –†	61.0, 63.0
Amoxicillin–clavulanic acid	4,382	14.8, –§§	7.2, –§§	0.0, –§§	2.6, –§§

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Piperacillin–tazobactam	4,867	2.4, 1.6	2.4, 4.9	3.2, 1.7	6.9, 10.1
Ceftriaxone	4,885	0.1, 0.1	11.9, 11.9	0.1, 0.1	20.2, 20.2
Ceftazidime	4,885	0.8, 5.5	5.2, 6.0	1.0, 7.8	11.6, 12.6
Cefepime	4,884	1.8[§], 6.1	2.6, 3.4	3.8[§], 9.2	6.2, 7.9
Gentamicin	4,881	0.2, –[†]	8.8, 9.2	0.5, –[†]	10.1, 10.8
Tobramycin	4,885	6.4, –[†]	3.0, 10.0	7.0, –[†]	4.7, 11.9
Amikacin	4,884	0.0, –[†]	0.0, 0.9	0.2, –[†]	0.2, 1.2
Ciprofloxacin	4,882	3.4, 3.4	14.9, 14.9	4.2, 4.2	21.3, 21.3
Meropenem	4,882	0.0, 0.1	0.1, 0.0	0.2, 0.0	0.4, 0.4
Klebsiella (*Enterobacter*) *aerogenes*					
Piperacillin–tazobactam	127	5.1, 11.4	17.7, 22.8	8.3, 0.0	45.8, 54.2
Ceftriaxone	127	1.3, 1.3	22.8, 22.8	0.0, 0.0	54.2, 54.2
Ceftazidime	127	1.3, 8.9	21.5, 22.8	0.0, 0.0	54.2, 54.2
Cefepime	127	0.0[§], 0.0	1.3, 1.3	0.0[§], 2.1	0.0, 0.0
Gentamicin	126	0.0, –[†]	0.0, 0.0	0.0, –[†]	2.1, 2.1
Tobramycin	127	0.0, –[†]	0.0, 0.0	0.0, –[†]	2.1, 2.1
Amikacin	127	0.0, –[†]	0.0, 0.0	0.0, –[†]	0.0, 0.0
Ciprofloxacin	126	0.0, 0.0	0.0, 0.0	0.0, 0.0	4.2, 4.2
Meropenem	127	0.0, 1.3	1.3, 0.0	0.0, 0.0	2.1, 2.1
Klebsiella oxytoca					
Amoxicilli–-clavulanic acid	215	1.9, –[§§]	1.9, –[§§]	0.0, –[§§]	0.6, –[§§]
Piperacillin–tazobactam	239	1.2, 0.6	2.3, 3.5	1.5, 6.1	22.7, 24.2
Ceftriaxone	239	1.2, 1.2	1.7, 1.7	1.5, 1.5	18.2, 18.2
Ceftazidime	239	0.0, 0.6	0.0, 0.0	0.0, 4.5	4.5, 4.5
Cefepime	239	0.0[§], 0.0	0.0, 0.0	1.5[§], 4.5	0.0, 0.0
Gentamicin	239	0.0, –[†]	0.0, 0.0	0.0, –[†]	1.5, 1.5
Tobramycin	239	0.0, –[†]	0.0, 0.0	0.0, –[†]	1.5, 1.5
Amikacin	239	0.0, –[†]	0.0, 0.0	0.0, –[†]	0.0, 0.0
Ciprofloxacin	239	0.0, 0.0	0.6, 0.6	0.0, 0.0	4.5, 4.5
Meropenem	239	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex					
Amoxicillin–clavulanic acid	1,066	3.9, –[§§]	4.8, –[§§]	0.0, –[§§]	1.9, –[§§]
Piperacillin–tazobactam	1,189	2.8, 4.6	3.2, 6.0	6.5, 12.8	8.7, 15.3
Ceftriaxone	1,190	0.1, 0.1	6.3, 6.3	0.6, 0.6	14.0, 14.0
Ceftazidime	1,190	0.9, 1.2	5.2, 6.1	1.6, 6.5	8.4, 10.0
Cefepime	1,190	0.7[§], 2.4	2.1, 2.4	1.2[§], 7.2	5.0, 5.6
Gentamicin	1,190	0.1, –[†]	4.0, 4.4	0.0, –[†]	8.1, 8.1
Tobramycin	1,190	2.8, –[†]	2.4, 5.4	4.7, –[†]	7.2, 12.5
Amikacin	1,190	0.0, –[†]	0.3, 0.8	0.0, –[†]	0.6, 2.2
Ciprofloxacin	1,189	1.0, 1.0	8.3, 8.3	1.9, 1.9	15.3, 15.3
Meropenem	1,190	0.3, 0.1	0.3, 0.2	0.0, 0.0	2.2, 2.2
Proteus mirabilis					
Ampicillin	265	0.0, –[†]	14.8, 14.8	0.0, –[†]	14.3, 14.3
Amoxicillin–clavulanic acid	238	2.5, –[§§]	2.0, –[§§]	8.6, –[§§]	2.9, –[§§]
Piperacillin–tazobactam	262	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Ceftriaxone	265	0.0, 0.0	1.8, 1.8	0.0, 0.0	0.0, 0.0
Ceftazidime	264	0.5, 0.5	0.0, 0.5	0.0, 0.0	0.0, 0.0
Cefepime	265	0.9[§], 0.9	0.0, 0.0	2.4[§], 2.4	0.0, 0.0
Gentamicin	265	0.4, –[†]	0.9, 11.2	2.4, –[†]	2.4, 14.3
Tobramycin	265	1.8, –[†]	0.4, 5.4	2.4, –[†]	2.4, 4.8
Amikacin	265	0.0, –[†]	0.0, 1.3	0.0, –[†]	0.0, 2.4
Ciprofloxacin	265	0.4, 0.4	1.8, 1.8	0.0, 0.0	2.4, 2.4
Meropenem	265	0.4, 0.4	0.4, 0.0	0.0, 0.0	0.0, 0.0
Pseudomonas aeruginosa					
Piperacillin–tazobactam	750	5.2, 88.9	5.9, 11.1	6.1, 85.7	8.2, 14.3
Ceftazidime	753	3.3, 92.9	3.8, 7.1	4.2, 88.5	7.3, 11.5
Cefepime	755	1.2, 95.8	3.1, 4.2	3.9, 92.1	3.9, 7.9
Gentamicin	753	2.1, –*	1.2, –*	0.6, –*	0.6, –*
Tobramycin	755	0.0, –[†]	0.9, 1.2	0.3, –[†]	0.0, 0.6
Amikacin	755	0.7, –[†]	0.5, 1.2	0.0, –[†]	0.3, 0.3
Ciprofloxacin	755	5.0, 90.8	4.2, 9.2	5.4, 90.6	3.9, 9.4
Meropenem	752	2.8, 3.6	2.6, 1.9	4.8, 6.4	4.5, 3.0
Salmonella species (non-typhoidal)					
Ampicillin	127	0.0, –[†]	4.1, 4.1	n/a	n/a
Amoxicillin–clavulanic acid	124	1.7, –[§§]	0.0, –[§§]	n/a	n/a
Piperacillin–tazobactam	126	0.0, 0.0	0.0, 0.0	n/a	n/a
Ceftriaxone	127	0.0, 0.0	0.0, 0.0	n/a	n/a
Ceftazidime	127	0.0, 0.0	0.0, 0.0	n/a	n/a
Cefepime	127	0.0[#], 0.0	0.0, 0.0	n/a	n/a
Ciprofloxacin	123	–[##], –[†]	4.2, –[##]	n/a	n/a
Meropenem	127	0.0, 0.0	0.0, 0.0	n/a	n/a
Serratia marcescens					
Piperacillin–tazobactam	183	0.0, 1.1	0.0, 0.0	1.0, 1.0	1.0, 2.1
Ceftriaxone	213	1.0, 1.0	2.9, 2.9	0.9, 0.9	4.5, 4.5
Ceftazidime	213	0.0, 0.0	2.0, 2.0	0.0, 1.8	2.7, 2.7
Cefepime	213	2.0[§], 0.0	0.0, 2.0	0.0[§], 1.8	0.9, 0.9
Gentamicin	213	1.0, –[†]	2.0, 2.9	1.8, –[†]	0.9, 4.5
Tobramycin	213	5.9, –[†]	2.0, 20.6	15.3, –[†]	2.7, 37.8
Amikacin	213	0.0, –[†]	0.0, 1.0	0.0, –[†]	0.9, 2.7
Ciprofloxacin	213	0.0, 0.0	5.9, 5.9	0.9, 0.9	1.8, 1.8
Meropenem	213	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Staphylococcus aureus					
Benzylpenicillin	3,149	–[†], –[†]	79.2 79.2	–[†], –[†]	82.0, 82.0
Ciprofloxacin	3,151	1.0, 91.2	7.8, 8.8	0.6, 87.6	11.8, 12.4
Clindamycin (constitutive)	3,129	0.0, 0.3	3.4, 3.4	0.0, 0.2	4.9, 4.9
Clindamycin (inducible + constitutive resistance)	3,129	0.0, 0.3	13.3 14.2	0.0, 0.2	16.1, 16.7
Daptomycin	3,155	0.0***, –[†]	–[†], 0.0	0.0***, –[†]	–[†], 0.0
Erythromycin	3,142	26.9, 1.2	16.2, 17.1	30.1, 0.6	19.1, 19.8
Gentamicin	3,128	0.8, –[†]	1.8, 3.7	1.6, –[†]	2.8, 5.0

Species and antimicrobial	Number	Community onset		Hospital onset	
		% intermediate	% resistant	% susceptible, increased exposure	% resistant
Linezolid	3,154	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Oxacillin (methicillin)†‡	3,129	–†, –†	17.4, 17.4	–†, –†	22.7, 22.7
Rifampicin	3,129	0.1, –§§§	0.5, 0.7	0.0, –§§§	0.0, 0.0
Trimethoprim–sulfamethoxazole	3,128	–†, 0.2	3.4, 3.1	–†, 0.3	3.5, 3.1
Teicoplanin	3,154	0.0, –†	0.0, 0.1	0.0, –†	0.0, 0.0
Tetracycline/doxycycline	3,145	0.2, 0.6	4.7***,5.2	0.2, 0.3	7.2***, 7.5
Vancomycin	3,155	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0

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

* No guidelines for indicated species
† No category defined
§ Includes sensitive dose dependent category for CLSI
# The ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible and resistant categories (Phoenix card, EUCAST) for *Enterococcus* species
** The ciprofloxacin ECOFF (4 mg/L, *E. faecalis*; 8 mg/L, *E. faecium*) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only
‡ Doxycycline concentration range (Phoenix panel) restricts ability to accurately identify intermediate and resistant category
§§ 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 ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species
*** Non-susceptible; resistance not defined
†‡ Resistance as determined by cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix)
§§§ The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant

3.8. Multidrug resistance

The most problematic pathogens are those with multiple acquired resistances. The definitions defined by Magiorakos et al.[29] 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 22. 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, 2019

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)				
		0	1	2	%	3	4	5	6	%
NSW	72	48	6	13	93.1	2	1	2	0	6.9
Vic	93	56	9	17	88.2	1	5	2	3	11.8
Qld	94	61	13	13	92.6	1	4	2	0	7.4
SA	20	15	2	3	–*	0	0	0	0	–*
WA	47	33	8	5	97.9	0	1	0	0	2.1
Tas	12	8	1	2	–*	1	0	0	0	–*
NT	14	10	2	2	–*	0	0	0	0	–*
ACT	6	3	0	2	–*	0	1	0	0	–*
Total	**358**	**234**	**41**	**57**	**92.7**	**5**	**12**	**6**	**3**	**7.3**

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

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

Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin or amikacin), 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* = 8), *E. kobei* (*n* = 2), and *E hormaechei* (*n* = 1).

Table 16: Multiple acquired resistance in *Enterococcus faecalis*, by state and territory, 2019

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)			
		0	1	2	%	3	4	5	%
NSW	148	119	25	4	100	0	0	0	0.0
Vic	97	72	13	12	100	0	0	0	0.0
Qld	33	28	4	1	100	0	0	0	0.0
SA	46	43	3	0	100	0	0	0	0.0
WA	78	67	7	4	100	0	0	0	0.0
Tas	17	17	0	0	–*	0	0	0	–*
NT	7	7	0	0	–*	0	0	0	–*
ACT	0†	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**426**	**353**	**52**	**21**	**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 (<30) to calculate
† 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, 2019

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)			
		0	1	2	%	3	4	5	%
NSW	171	11	12	50	42.7	59	39	0	57.3
Vic	90	5	2	23	33.3	31	29	0	66.7
Qld	10	1	0	6	–*	3	0	0	–*
SA	31	3	15	10	90.3	3	0	0	9.7
WA	54	4	2	37	79.6	8	3	0	20.4
Tas	11	2	0	1	–*	4	4	0	–*
NT	13	4	0	1	–*	2	6	0	–*
ACT	0†	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**380**	**30**	**31**	**128**	**49.7**	**110**	**81**	**0**	**50.3**

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

* Not applicable, insufficient numbers (<30) to calculate
† 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, 2019

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	1,043	422	173	157	72.1	88	71	64	43	19	5	1	0	27.9
Vic	916	360	145	146	71.1	62	66	79	28	18	10	1	1	28.9
Qld	809	335	153	158	79.9	50	43	39	21	6	2	2	0	20.1
SA	267	123	40	44	77.5	14	16	17	7	5	1	0	0	22.5
WA	734	273	145	128	74.4	50	42	51	30	7	7	1	0	25.6
Tas	200	89	45	31	82.5	10	8	8	6	3	0	0	0	17.5
NT	205	47	30	54	63.9	23	16	16	15	4	0	0	0	36.1
ACT	184	71	31	26	69.6	15	12	16	9	2	1	1	0	30.4
Total	**4,358**	**1,720**	**762**	**744**	**74.0**	**312**	**274**	**290**	**159**	**64**	**26**	**6**	**1**	**26.0**

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* complex, by state and territory, 2019

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)							
		0	1	2	%	3	4	5	6	7	8	9	%
NSW	264	193	24	11	86.4	6	8	9	6	4	2	1	13.6
Vic	212	150	11	10	80.7	5	5	15	7	2	4	3	19.3
Qld	249	192	23	16	92.8	5	6	4	2	1	0	0	7.2
SA	49	40	3	2	91.8	0	1	1	1	0	1	0	8.2
WA	159	124	19	7	94.3	3	4	0	1	1	0	0	5.7
Tas	51	43	1	2	90.2	2	0	1	0	1	1	0	9.8
NT	45	30	6	2	84.4	0	1	1	3	2	0	0	15.6
ACT	35	22	4	3	82.9	2	3	0	0	1	0	0	17.1
Total	**1,064**	**794**	**91**	**53**	**88.2**	**23**	**28**	**31**	**20**	**12**	**8**	**4**	**11.8**

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

Notes:

1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), non-extended cephalosporins (cefazolin), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins + β-lactamase inhibitor (amoxicillin-clavulanic acid, CLSI).
2. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 46), and *K. quasipneumoniae*(*n* = 4)

Table 20: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, 2019

State or territory	Total	Number of categories (non- multidrug resistant)				Number of categories (multi-drug resistant)			
		0	1	2	%	3	4	5	%
NSW	238	195	24	14	97.9	2	1	2	2.1
Vic	119	97	10	8	96.6	3	1	0	3.4
Qld	171	130	20	14	95.9	5	0	2	4.1
SA	64	51	6	3	93.8	4	0	0	6.3
WA	97	87	4	1	94.8	3	2	0	5.2
Tas	19	13	3	3	–*	0	0	0	–*
NT	15	12	1	0	–*	1	1	0	–*
ACT	23	21	0	1	–*	1	0	0	–*
Total	**746**	**606**	**68**	**44**	**96.2**	**19**	**5**	**4**	**3.8**

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

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

Note: Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin 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, 2019

State or territory	Total	Number of antimicrobial categories*													
		0	1	2	%<2	3	4	5	6	7	8	9	10	11	%≥2
NSW	175	55	33	21	62.3	30	8	22	5	1	0	0	0	0	37.7
Vic	88	19	25	15	67.0	13	9	6	1	0	0	0	0	0	33.0
Qld	102	58	15	11	82.4	4	4	5	5	0	0	0	0	0	17.6
SA	34	15	3	8	76.5	4	1	3	0	0	0	0	0	0	23.5
WA	105	55	18	25	93.3	6	0	1	0	0	0	0	0	0	6.7
Tas	16	6	1	1	50.0	7	0	1	0	0	0	0	0	0	50.0
NT	35	19	8	7	97.1	1	0	0	0	0	0	0	0	0	2.9
ACT	19	2	8	3	68.4	3	0	1	2	0	0	0	0	0	31.6
Total	574	**229**	**111**	**91**	**75.1**	**68**	**22**	**39**	**13**	**1**	**0**	**0**	**0**	**0**	**24.9**

* 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, 2019

State or territory	Total	Number of antimicrobial categories*													
		0	1	2	%<2	3	4	5	6	7	8	9	10	11	%≥2
NSW	718	557	69	69	96.8	14	6	2	1	0	0	0	0	0	3.2
Vic	436	349	34	32	95.2	16	2	2	1	0	0	0	0	0	4.8
Qld	545	424	49	56	97.1	15	1	0	0	0	0	0	0	0	2.9
SA	202	161	26	13	99.0	2	0	0	0	0	0	0	0	0	1.0
WA	390	298	34	46	96.9	10	1	1	0	0	0	0	0	0	3.1
Tas	118	102	5	7	96.6	3	1	0	0	0	0	0	0	0	3.4
NT	28	22	2	0	85.7	4	0	0	0	0	0	0	0	0	14.3
ACT	99	76	12	8	97.0	3	0	0	0	0	0	0	0	0	3.0
Total	**2,536**	**1,989**	**231**	**231**	**96.6**	**67**	**11**	**5**	**2**	**0**	**0**	**0**	**0**	**0**	**3.4**

* 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 (58.2%) 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*, 13.4% were resistant to at least one antimicrobial group (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 24). For *P. aeruginosa*, 18.6% 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 = 4,358), Australia, 2019

Resistance pattern	Number	% of total*
Fully susceptible	**1,823**	**41.8**
Single resistance	1,640	37.6
Aminopenicillins	1,562	35.8
Fluoroquinolones	72	1.7
Aminoglycosides	6	0.1
Resistance to two antimicrobial groups	355	8.1
Aminopenicillins + third-generation cephalosporins	126	2.9
Aminopenicillins + fluoroquinolones	132	3.0
Aminopenicillins + aminoglycosides	96	2.2
Fluoroquinolones + aminoglycosides	1	0.0
Resistance to three antimicrobial groups	344	7.9
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	194	4.5
Aminopenicillins + fluoroquinolones + aminoglycosides	94	2.2
Aminopenicillins + third-generation cephalospoins + aminoglycosides	56	1.3
Resistance to four antimicrobial groups	195	4.5
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	194	4.5
Aminopenicillins + third-generation cephalosporins + aminoglycosides + carbapenems	1	0.0
Resistance to five antimicrobial groups	1	0.0
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	1	0.0

* 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 = 1,013), Australia, 2019

Resistance pattern	Number	% of total
Fully susceptible	**921**	**86.6**
Single resistance	59	5.5
Fluoroquinolones	38	3.6
Third-generation cephalosporins	14	1.3
Aminoglycosides	7	0.7
Resistance to two antimicrobial groups	29	2.7
Third-generation cephalosporins + aminoglycosides	15	1.4
Third-generation cephalosporins + fluoroquinolones	10	0.9
Fluoroquinolones + aminoglycosides	4	0.4
Resistance to three antimicrobial groups	48	4.5
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	46	4.3
Third-generation cephalosporins + aminoglycosides + carbapenem	2	0.2
Resistance to four antimicrobial groups	7	0.7
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	7	0.7

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

Note: *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 46), and *K. quasipneumoniae* (*n* = 4).

Table 25: Resistance combinations among *Pseudomonas aeruginosa* tested against piperacillin-tazobactam, ceftazidime, fluoroquinolones, aminoglycosides and carbapenems (n = 746), Australia, 2019

Resistance pattern	Number	% of total
Fully susceptible	**607**	**81.4**
Single resistance	69	9.2
Fluoroquinolones	35	4.7
Piperacillin–tazobactam	26	3.5
Ceftazidime	4	0.5
Aminoglycosides	3	0.4
Carbapemems	1	0.1
Resistance to two antimicrobial groups	43	5.8
Piperacillin–tazobactam + ceftazidime	32	4.3
Piperacillin–tazobactam + fluoroquinolones	6	0.8
Piperacillin–tazobactam + carbapenems	2	0.3
Ceftazidime + carbapenems	1	0.1
Ceftazidime + aminoglycosides	1	0.1
Fluoroquinolones + aminoglycosides	1	0.1
Resistance to three antimicrobial groups	18	2.4
Piperacillin–tazobactam + ceftazidime + fluoroquinolones	14	1.9
Piperacillin–tazobactam + ceftazidime + carbapenems	2	0.3
Piperacillin–tazobactam + fluoroquinolones + carbapenems	2	0.3
Resistance to four antimicrobial groups	5	0.7
Piperacillin–tazobactam + ceftazidime + fluoroquinolones + carbapenems	4	0.5
Ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	1	0.1
Resistance to five antimicrobial groups	4	0.5
Piperacillin–tazobactam + ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	4	0.5

* 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 = 3,128), Australia, 2019

Resistance pattern	N	% of total
Fully susceptible	**2,443**	**78.6**
Single resistance	2,443	78.6
Methicillin	356	11.4
Fluoroquinolones	83	2.7
Rifampicin	10	0.3
Resistance to two antimicrobial groups	449	14.4
Methicillin + fluoroquinolones	211	6.8
Methicillin + rifampicin	5	0.2
Resistance to three antimicrobial groups	216	6.9
Methicillin + fluoroquinolones + rifampicin	2	0.1

* 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, 2019

Species	Category	Total		Community onset		Hospital onset	
		Number	Deaths, % (n)	Number	Deaths,% (n)	Number	Deaths, % (n)
Escherichia coli	Total	2,924	10.1 (296)	2,412	9.1 (219)	512	15.0 (77)
	Non-MDR (≤2)	2,137	9.8 (209)	1,803	9.0 (162)	334	14.1 (47)
	MDR (>2)	787	11.1 (87)	609	9.4 (57)	178	16.9 (30)
Enterobacter cloacae complex	Total	271	13.3 (36)	149	8.7 (13)	122	18.9 (23)
	Non-MDR (≤2)	246	11.4 (28)	139	7.2 (10)	107	16.8 (18)
	MDR (>2)	25	32.0 (8)	10	30.0 (3)	15	33.3 (5)
Enterococcus faecalis	Total	312	14.7 (46)	220	12.3 (27)	92	20.7 (19)
	Non-MDR (≤2)	312	14.7 (46)	220	12.3 (27)	92	20.7 (19)
	MDR (>2)	0	n/a	0	n/a	0	n/a
Enterococcus faecium	Total	309	24.9 (77)	88	20.5 (18)	221	26.7 (59)
	Non-MDR (≤2)	161	21.1 (34)	50	14.0 (7)	111	24.3 (27)
	MDR (>2)	148	29.1 (43)	38	28.9 (11)	110	29.1 (32)
Klebsiella pneumoniae complex	Total	740	13.2 (98)	509	12.6 (64)	231	14.7 (34)
	Non-MDR (≤2)	647	12.5 (81)	464	12.5 (58)	183	12.6 (23)
	MDR (>2)	93	18.3 (17)	45	13.3 (6)	48	22.9 (11)
Staphylococcus aureus	Total	2,384	14.3 (340)	1,891	14.1 (267)	493	17.6 (73)
	Non-MDR (≤2)	1,871	14.3 (267)	1,505	14.4 (216)	366	16.8 (51)
	MDR (>2)	513	14.2 (73)	386	13.2 (51)	127	20.5 (22)
Pseudomonas aeruginosa	Total	559	16.3 (91)	298	15.4 (46)	261	17.2 (45)
	Non-MDR (≤2)	536	16.2 (87)	288	15.3 (44)	248	17.3 (43)
	MDR (>2)	19	21.1 (4)	10	20.0 (2)	13	15.4 (2)

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

Notes:

1. Antimicrobial categories (agents) for each species are listed under Tables 15 to 22. For *Staphylococcus aureus,* anti-staphylococcal β-lactams (cefoxitin) is also included
2. *Enterobacter cloacae* complex includes *E. asburiae* (*n* = 4), and *E. kobei* (*n* = 1)
3. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 40), and *K. quasipneumoniae* (*n* = 4).

3.9. PCR and whole genome sequencing

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

All referred *Enterobacterales* with meropenem MIC > 0.25 mg/L; and all referred *P. aeruginosa*, *Acinetobacter* species and *Salmonella* species were sequenced. The remaining isolates were initially screened for dominant ESBL, plasmid-borne AmpC, carbapenemase, ribosomal methytransferases and *mcr* genes. Based on phenotypic analysis and PCR results, isolate subsets (*E. coli* and *K. pneumoniae*) were selected for whole genome sequencing and analysed for antimicrobial resistance determinants, as outlined in Appendix B.

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.[30-32] 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.[33]

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 paucity of available oral options for treatment can result in unnecessary hospitalisation and, in the setting of sepsis, increased mortality risk.

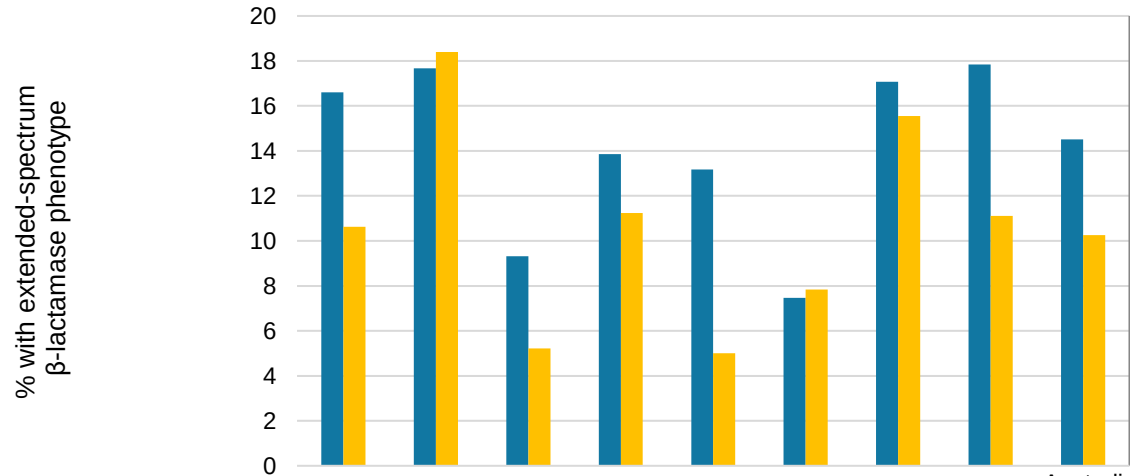
Most ESBL-producing isolates will be detected using the CLSI/EUCAST ceftriaxone ‘susceptible’ breakpoint of 1 mg/L. The CLSI ‘susceptible’ breakpoint of 4 mg/L for ceftazidime is less reliable for ESBL detection. Isolates with either ceftriaxone or ceftazidime minimum inhibitory concentrations (MICs) 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.[34] 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 bla_{SHV} with G→A substitution at position 700 and/or 703, encoding ESBL variants, $bla_{CTX\text{-}M}$ groups 1 and 9, and plasmid-borne *ampC* ($bla_{CMY\text{-}2\text{-}like}$, bla_{DHA}, $bla_{ACT/MIR}$) genes using molecular methods outlined in Appendix B.

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.

Figure 9. Percentage of *Escherichia coli* and *Klebsiella pneumoniae* with extended-spectrum β-lactamase phenotype, by state and territory, and nationally, 2019



	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
E. coli, %	16.6	17.7	9.3	13.9	13.2	7.5	17.1	17.8	14.5
K. pneumoniae, %	10.6	18.4	5.2	11.2	5.0	7.8	15.6	11.1	10.3
E. coli (n = 4,884)	229	163	76	61	97	15	35	33	709
K. pneumoniae complex (n = 1,190)	37	39	13	10	8	4	7	4	122

* Ceftriaxone or ceftazidime MIC > 1 mg/L

Table 28: Numbers of isolates with extended-spectrum β-lactamase phenotype and genotype, by state and territory, 2019

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,379	922	816	440	736	201	205	185	4,884
ESBL phenotype	229	163	76	61	97	15	35	33	709
Confirmed									
Any ESBL/number tested, n (%)	144/213 (67.6)	132/163 (81.0)	43/70 (61.4)	44/58 (75.9)	72/88 (81.8)	9/15 (60.0)	30/34 (88.2)	30/33 (90.9)	504/674 (74.8)
CTX-M types	143	129	43	44	72	8	30	28	497
Plasmid-borne AmpC	31	18	11	6	12	5	4	4	91
SHV (ESBL-types)	1	4	0	0	0	1	0	3	9
Klebsiella pneumoniae complex	348	212	249	89	160	51	45	36	1,190
ESBL phenotype	37	39	13	10	8	4	7	4	122
Confirmed									
Any ESBL/number tested, n (%)	23/34 (67.6)	29/38 (76.3)	4/13 (30.8)	4/10 (40.0)	5/8 (62.5)	3/4 (75.0)	5/7 (71.4)	4/4 (100)	77/118 (65.3)
CTX-M types	20	27	4	4	5	3	5	4	72
Plasmid-borne AmpC	2	3	4	4	1	1	1	0	16
SHV (ESBL-types)	3	2	0	0	1	0	1	0	7
Klebsiella oxytoca	59	55	35	26	32	17	4	11	239
ESBL phenotype	5	8	2	1	2	1	0	0	19
Confirmed									
Any ESBL/number tested	2/5	3/8	1/2	0/1	0/0	0/1	0/0	0/0	6/17 (35.3)*
CTX-M types	1	1	0	0	0	0	0	0	2
SHV (ESBL-types)	1	2	1	0	0	0	0	0	4
Proteus mirabilis	78	45	38	36	39	14	2	12	264
ESBL phenotype	2	1	1	0	1	0	0	0	5
Confirmed									
Any ESBL/number tested	1/2	1/1	1/1	0/0	0/1	0/0	0/0	0/0	3/5
CTX-M types	1	1	1	0	0	0	0	0	3
Plasmid-borne AmpC	1	0	0	0	0	0	0	0	1
Salmonella species†	52	48	52	4	34	6	4	8	208
ESBL phenotype	2	1	0	0	0	0	0	0	3
Confirmed									
Any ESBL/number tested	1/2	1/1	0/0	0/0	0/0	0/0	0/0	0/0	2/3
CTX-M types	1	1	0	0	0	0	0	0	2
Plasmid-borne AmpC	1	0	0	0	0	0	0	0	1

ESBL = extended-spectrum β-lactamase (SHV-ESBL, CTX-M groups 1 and 9, VEB); n/a = not applicable
* See text for an explanation of the low proportion of ESBL
† Non-typhoidal (n = 127), typhoidal (n = 81)

Note: Isolates may possess more than one type of ESBL gene

Based on the tests performed in this study, ESBLs were more common among *E. coli* (10.3% confirmed) and *K. pneumoniae* complex (6.5% confirmed) than among other species. For *Enterobacter* species with cefepime MIC greater than 1 mg/L, 13 of 42 *E. cloacae* complex (31.0%; 3.0% overall) contained an ESBL. Of identified ESBLs, *E. cloacae* contained the following types: SHV only (*n* = 7), CTX-M group 1 only (*n* = 2), CTX-M group 9 only (*n* = 2), CTX-M group 9 and SHV (*n* = 2). Eight of 13 *E. cloacae* complex with confirmed ESBLs also contained $bla_{\text{IMP-4}}$ carbapenemase.

The majority (53%, 8/15) 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.[35] This pattern is not typical of other types of gram-negative β-lactamases.

bla$_{CTX-M}$-types continue to be the prominent ESBL gene in *E. coli*. Of 504 confirmed ESBLs, 497 (98.6%) had *bla*$_{CTX-M}$ genes detected by PCR, either *bla*$_{CTX-M}$ group 1 (*n* = 246), *bla*$_{CTX-M}$ group 9 (*n* = 249), or both *bla*$_{CTX-M}$ group 1 + group 9 (*n* = 2). Among *K. pneumoniae* complex with confirmed ESBLs, 72 of 77 (93.5%) contained CTX-M types: *bla*$_{CTX-M}$ group 1 (*n* = 62), *bla*$_{CTX-M}$ group 9 (*n* = 9), or both *bla*$_{CTX-M}$ group 1 + group 9 (*n* = 1).

ESBL phenotypes were significantly more likely to be found among hospital-onset than community-onset episodes of *E. coli* bacteraemia (180/812 [22.2%] vs 530/4,072 [13.0%]; P < 0.01), and *K. pneumoniae* complex bacteraemia (56/321 [17.4%] vs 66/869 [7.6%]; P < 0.01).

Whole genome sequencing analysis was performed on a subset of 200 *E. coli.* This subset included 187 with an ESBL phenotype and 13 non-ESBL phenotype (Table 29). *bla*$_{CTX-M}$ genes were detected in 80.7% (151/187) of the *E. coli* subset with an ESBL phenotype. In the *bla*$_{CTX-M-1}$ group, *bla*$_{CTX-M-15}$ accounted for 90.1% (73/81). In the *bla*$_{CTX-M-9}$ group, *bla*$_{CTX-M-27}$ and *bla*$_{CTX-M-14}$ were the major genotypes, accounting for 73.5% (50/68) and 23.5% (16/68), respectively.

In the *bla*$_{CTX-M}$-positive isolates, TEM-type and SHV-type ESBLs were not detected. Among 36 *bla*$_{CTX-M}$-negative isolates with an ESBL phenotype, 14 harboured pAmpC (*bla*$_{DHA-1}$ [9], *bla*$_{CMY-2}$ [3], *bla*$_{DHA-6}$ [1], *bla*$_{CMY-2}$ + *bla*$_{DHA}$ +*bla*$_{MOR-2}$ [1], three harboured *bla*$_{SHV-ESBL}$ (*bla*$_{SHV-12}$ [1], *bla*$_{SHV-12}$ and *bla*$_{IMP-4}$ [1], *bla*$_{SHV-2a}$ [1]). Beta-lactam resistance mechanisms were not detected in the remaining 19 isolates.

Table 29: *Escherichia coli*, CTX-M variants, ESBL phenotype, sequence type, 2019

		Phenotype		Sequence type							
CTX-M variant	Number	ESBL	Non-ESBL	131	38	69	1193	–*	648	73	Other types (*n* = 40)
-	47	36	11	2	5	4	5	5	0	2	24
CTX-M-1 group	82	81	1	41	4	8	1	1	4	1	22
CTX-M-15	74	73	1	41	3	5	1	1	3	1	19
CTX-M-55	4	4	0	0	1	1	0	0	0	0	2
Others†	4	4	0	0	0	2	0	0	1	0	1
CTX-M-9 group	69	68	1	37	12	1	7	1	1	2	8
CTX-M-27	51	50	1	34	2	1	7	0	0	2	5
CTX-M-14	16	16	0	2	10	0	0	1	1	0	2
Others§	2	2	0	1	0	0	0	0	0	0	1
CTX-M-1 and CTX-M-9 group	2	2	0	1	0	0	1	0	0	0	0
CTX-M-15 and CTX-M-27	1	1	0	1	0	0	0	0	0	0	0
CTX-M-64#	1	1	0	0	0	0	1	0	0	0	0
	200	**187**	**13**	**81**	**20**	**14**	**14**	**7**	**5**	**5**	**54**

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

* not available
† CTX-M-3 (*n* = 1), CTX-M-182 (*n* = 1), CTX-M-1+TEM-207 (*n* = 1), CTX-M-15+CTX-M-231 (*n* = 1)
§ CTX-M-65 (*n* = 1), CTX-M-14+CTX-M-27 (*n* = 1)
# hybrid of CTX-M-1 and CTX-M-9 group enzymes.

Over half (50.6%, 79/156) of the ESBL-producing *E. coli* subset with confirmed ESBL types belong to sequence type 131 (ST131) (Table 30).

The fluoroquinolone-resistant subclade, H30R, was the most prevalent subclade of ST131 (67%, 53/79). The H30Rx (subclade C2) encompasses almost all ST131 carrying *bla*$_{CTX-M-15}$, a finding reported globally.[36-38] Two-thirds (67%, 34/51) of isolates with *bla*$_{CTX-M-27}$ were ST131; 18/34 belonged to H41 subclade A, and 12/34 belonged to H30R subclade C1-M27.

All ST1193 isolates were ciprofloxacin resistant, and half (7/14) harboured *bla*$_{CTX-M-27}$. This sequence type is of importance as it has recently been identified as an emerging multidrug-resistant type.[32, 39, 40]

Table 30: ESBL-producing *Escherichia coli*, ST131, *fimH* allele, H30Rx, 2019

		ST131					
			H30				
ESBL type	Number	All	H30Rx	H30R	H41	Others	Non-ST131
CTX-M-15	74	41	36	2	3	0	33
CTX-M-27	51	34	0	12	18	4	17
CTX-M-14	16	2	0	0	0	0	14
CTX-M-55	4	0	0	0	0	0	4
CTX-M-14 + CTX-M-27	1	1	0	0	0	1	0
CTX-M-15 + CTX-M-27	1	1	1	0	0	0	0
CTX-M-15 + CTX-M-231	1	0	0	0	0	0	1
SHV-ESBL*	3	0	0	0	0	0	3
Other types (n = 5)†	5	0	0	0	0	0	5
	156	**79**	**37**	**16**	**21**	**5**	**77**

* *bla*$_{SHV-12}$ (*n* = 2), *bla*$_{SHV-2A}$ (*n* = 1)
† *bla*$_{CTX-M-1}$+*bla*$_{TEM-207}$ (*n* = 1), *bla*$_{CTX-M-3}$ (*n* = 1), *bla*$_{CTX-M-64}$ (*n* = 1), *bla*$_{CTX-M-65}$ (*n* = 1), *bla*$_{CTX-M-182}$ (*n* = 1)

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.

Testing included screening all referred isolates for plasmid-borne *ampC* (CMY-2-like, DHA) genes using molecular methods outlined in Appendix B.

The proportions of *E. coli* and *K. pneumoniae* complex with elevated cefoxitin MICs remain low. Only 57% (91/159) of *E. coli* and 23% (16/70) of *K. pneumoniae* complex with cefoxitin MIC ≥32 mg/L that were available for molecular confirmation were confirmed to contain plasmid-borne *ampC* genes (Table 31).

A *bla*$_{DHA}$ gene was found in 56% (51/91) of *E. coli* and 81% (13/16) of *K. pneumoniae* complex with plasmid-borne *ampC* genes.

Carbapenemase genes were detected in nine of 54 cefoxitin-resistant (MIC ≥ 32 mg/L) *K. pneumoniae* complex (*bla*$_{IMP-4}$, *n* = 6; *bla*$_{NDM-4}$, *n* = 2; *bla*$_{OXA-181}$, *n* = 1), and two of 68 *E. coli* (*bla*$_{IMP-4}$, *bla*$_{NDM-5}$) that did not have plasmid-borne *ampC* genes. Five *E. coli* with a cefoxitin MIC of

<32 mg/L also contained or *bla*$_{DHA}$ (*n* = 3) or *bla*$_{CMY}$ (*n* = 2). No plasmid-borne *ampC* genes were found in *K. pneumoniae* complex with cefoxitin MIC < 32 mg/L.

Table 31: Numbers of isolates with presumptive plasmid-borne AmpC β-lactamase production, by state and territory, 2019

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,379	922	816	440	736	201	205	186	4,885
Cefoxitin MIC ≥32 mg/L (%)	59 (4.3)	27 (2.9)	20 (2.5)	11 (2.5)	23 (3.1)	8 (4.0)	8 (3.9)	9 (4.8)	165 (3.4)
Confirmed/number tested*	31/56	19/27	11/20	6/9	12/22	5/8	4/8	3/9	91/159
bla$_{CMY-2-like}$	11	9	6	0	7	3	1	0	37
bla$_{DHA}$	18	10	5	5	5	2	3	3	51
bla$_{CMY-2-like+DHA}$	2	0	0	1	0	0	0	0	3
Klebsiella pneumoniae complex	348	212	249	89	160	51	45	36	1,190
Cefoxitin MIC ≥32 mg/L (%)	20 (5.7)	17 (8.0)	17 (6.8)	5 (5.6)	5 (3.1)	2 (3.9)	3 (6.7)	1 (2.8)	70 (5.9)
Confirmed/number tested	2/20	3/17	4/17	4/5	1/5	1/2	1/3	0/1	16/70
bla$_{DHA}$	1	3	3	3	1	1	1	0	13
bla$_{CMY-2-like}$	1	0	1	1	0	0	0	0	3

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

Note: Isolates were screened for *bla*$_{CMY-2-like}$, *bla*$_{DHA}$ and *bla*$_{ACT/MIR}$ genes only

Carbapenemases

All referred isolates were examined for presence of carbapenemase genes. This included *Enterobacterales* with meropenem MIC > 0.25 mg/L (*n* = 94), and *Acinetobacter* species (*n* = 3) or *P. aeruginosa* (*n* = 26) with meropenem MIC ≥ 8 mg/L. Among meropenem resistant (MIC > 8 mg/L) isolates that were available, carbapenemase genes were found in 90% (18/20) of *Enterobacterales*, 11% (2/18) *P. aeruginosa*, and all *Acinetobacter* species (3/3) (Table 32). Four of the six *Enterobacterales* with class D enzymes (*bla*$_{OXA-181}$) had meropenem MIC ≤2 mg/L.

Table 32: Numbers of isolates with carbapenemase genes, organism group, meropenem MIC, 2019

	***Acinetobacter* (*n* = 98)**			***Enterobacterales* (*n* = 7,936)**			***Pseudomonas* (*n* = 752)**		
	Meropenem MIC (mg/L)			Meropenem MIC (mg/L)			Meropenem MIC (mg/L)		
	≤2	4-8	>8	≤2	4-8	>8	≤2	4-8	>8
Number	95	0	3	7,908	5	23	698	36	18
Carbapenemase									
Confirmed/number tested	0/1	–	3/3	5/1,562	1/5	18/20	0/3	0/8	2/18
Class A*	–	–	0	0	0	0	0	0	1
Class B*	–	–	0	1	0	17	0	0	1
Class D*	–	–	3	4	1	1	0	0	0

* Carbapenemase molecular class: class A (GES); class B (metallo-β-lactamases - IMP, NDM); class D (oxacillinases – OXA-23, OXA-58, OXA-181)

Twenty-nine (0.27%) isolates from 29 patients were found to harbour a carbapenemase gene (Table 33). The *bla*$_{IMP-4}$ gene was detected in 15 isolates: *E. cloacae* complex [8], *K. pneumoniae* [5], *K. variicola* [1], *E coli* [1]; *bla*$_{NDM-4}$ was detected in two *K. pneumoniae* and *bla*$_{NDM-5}$ in one *E. coli*; *bla*$_{OXA-181}$ was detected in five *K. pneumoniae. bla*$_{IMP-1}$ [1], and *bla*$_{GES-5}$ [1] were detected in *P. aeruginosa*. *bla*$_{OXA-23}$ was detected in three isolates: *A. baumannii* [2] and *P. mirabilis* [1]; and one *A. baumannii* harboured both *bla*$_{OXA-23}$ *bla*$_{OXA-58}$.

Fifteen of 19 *Enterobacterales* with confirmed metallo-β-lactamases also contained at least one plasmid-mediated quinolone resistance genes [*aac(6')-Ib-cr, qnrB* or *qnrA*].

One *K. pneumoniae* with *bla*$_{OXA-181}$ had a meropenem MIC ≤ 0.25 mg/L; all other isolates with confirmed carbapenemases had meropenem MICs ≥ 0.5 mg/L.

Overall prevalence of carbapenemase genes among *Enterobacterales* was 0.30% (24/7,883). This consisted of 15 isolates with *bla*$_{IMP-4}$, five with *bla*$_{OXA-181}$, three with *bla*$_{NDM}$, and one with *bla*$_{OXA-23.}$ Prevalence was 0.26% (2/761) for *P. aeruginosa* and 2.8% (3/108) for *Acinetobacter* species.

Carbapenemase-producing isolates were detected in 14 institutions. However, almost one-quarter were from one institution (27.6%, 8/29). Half (7/14) of the institutions had one carbapenemase-producing strain only.

Isolates with meropenem MIC > 0.25 µg/ml where no carbapenemase gene was detected by sequencing are under investigation in order to identify resistance mechanisms (mainly membrane permeability defects or PBP mutations) associated with decreased susceptibility to carbapenems.

Table 33: Number of carbapenemases and associated resistance genes, by species, and state and territory, 2019

Gene	S/T	Species	ST	MEM MIC (mg/L)	ESBL types*	PMQR genes†	RMT	MCR
bla$_{IMP-4}$ (*n* = 15)	NSW	*E. hormaechei* (*n* = 1)	110	≥ 16	*bla*$_{SHV-12}$	*aac(6')-Ib-cr, qnrB2*	–[§]	*mcr*-9.1
	NSW	*E. hormaechei* (*n* = 1)	113	≥ 16	*bla*$_{SHV-12}$	*qnrB2*	–[§]	*mcr*-9.1
	NSW	*K. pneumoniae* (*n* = 1)	25	≥ 16	–[§]	*qnrB2*, *qnrS1*	–[§]	–[§]
	NSW	*K. pneumoniae* (*n* = 1)	403	≥ 16	*bla*$_{CTX-M-15}$	*qnrB1*	–[§]	–[§]
	NSW	*K. pneumoniae* (*n* = 1)	1731	1	–[§]	*aac(6')-Ib-cr, qnrB2*	–[§]	–[§]
	Vic	*E. cloacae* (*n* = 3)[#]	190	≥ 16	*bla*$_{SHV-12}$	*aac(6')-Ib-cr, qnrB2*	–[§]	*mcr*-9.1
	Vic	*E. cloacae* (*n* = 1) [#]	–[§]	≥ 16	*bla*$_{SHV-12}$, *bla*$_{CTX-M-9}$	*aac(6')-Ib-cr, qnrB2*	–[§]	*mcr*-9.1
	Vic	*E. cloacae* (*n* = 1) [#]	–[§]	≥ 16	*bla*$_{SHV-12}$, *bla*$_{CTX-M-9}$	*aac(6')-Ib-cr, qnrA1, qnrB2*	–[§]	*mcr*-9.1
	Vic	*E. coli* (*n* = 1) [#]	176	≥ 16	*bla*$_{SHV-12}$	*aac(6')-Ib-cr, qnrB2*	–[§]	*mcr*-9.1
	Vic	*K. pneumoniae* (*n* = 1) [#]	1905	≥ 16	*bla*$_{SHV-ESBL}$	*aac(6')-Ib-cr, qnrB2*	–[§]	*mcr*-9.1
	Vic	*K variicola* (*n* = 1)	–[§]	≥ 16	–[§]	*qnrB2*	–[§]	–[§]
	Qld	*K. pneumoniae* (*n* = 1)	985	≥ 16	–[§]	–[§]	–[§]	–[§]
	WA	*E. hormaechei* (*n* = 1)	90	≥ 16	*bla*$_{CTX-M-9}$	–[§]	–[§]	–[§]
bla$_{IMP-1}$ (*n* = 1)	Qld	*P. aeruginosa* (*n* = 1)	235	≥ 16	–[§]	–[§]	–[§]	–[§]
bla$_{NDM-4}$ (*n* = 2)	Vic	*K. pneumoniae* (*n* = 1)	15	≥ 16	*bla*$_{CTX-M-14a}$, *bla*$_{CTX-M-15}$	*aac(6')-Ib-cr, qnrS1*	–[§]	–[§]
	Vic	*K. pneumoniae* (*n* = 1)	147	≥ 16	*bla*$_{CTX-M-15}$	*aac(6')-Ib-cr, qnrS1*	–[§]	–[§]
bla$_{NDM-5}$ (*n* = 1)	NSW	*E. coli* (*n* = 1)	354	16	*bla*$_{CTX-M-27}$	–[§]	–[§]	–[§]
bla$_{OXA-181}$ (*n* = 5)	NSW	*K. pneumoniae* (*n* = 1)	25	0.5	–[§]	*qnrS1*	–[§]	–[§]
	NSW	*K. pneumoniae* (*n* = 1)	25	2	–[§]	*qnrS1*	–[§]	–[§]
	Vic	*K. pneumoniae* (*n* = 1)	16	≥ 16	*bla*$_{CTX-M-15}$	*aac(6')-Ib-cr, qnrS1*	*rmtB1*	–[§]
	Qld	*K. pneumoniae* (*n* = 1)	35	0.5	–[§]	*qnrS1*	–[§]	–[§]
	WA	*K. pneumoniae* (*n* = 1)	1963	≤0.25	*bla*$_{SHV-ESBL}$, *bla*$_{CTX-M-15}$	*qnrB1*, *qnrS1*	–[§]	–[§]
bla$_{GES-5}$ (*n* = 1)	NSW	*P. aeruginosa* (*n* = 1)	–[§]	≥ 16	–[§]	–[§]	–[§]	–[§]
bla$_{OXA-23}$ (*n* = 3)	Qld	*A. baumannii* (n = 1)	2	≥ 16	–[§]	–[§]	*armA*	–[§]
	Qld	*A. baumannii* (n = 1)	25	≥ 16	–[§]	–[§]	–[§]	–[§]
	Qld	*P. mirabilis* (*n* = 1)	–[§]	8	–[§]	–[§]	–[§]	–[§]
bla$_{OXA-23+OXA-58}$ (*n* = 1)	Qld	*A. baumannii* (n = 1)	410	≥ 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 included if intrinsic to species)

§ Not detected

Seven isolates from one institution

Plasmid-mediated colistin determinants

Because colistin is currently only available on Phoenix cards, only 1,105 (12.5%) isolates from four laboratories were tested for colistin susceptibility. Excluding intrinsically resistant species, 4/1,023 (0.4%) had colistin MIC >2 mg/L (*P. aeruginosa*, *n* = 2; *E. coli, n* = 1; and *E. cloacae* complex, *n* = 1).

All referred isolates were screened for the presence of plasmid-mediated colistin determinants, *mcr-1*, *mcr-2, mcr-3, mcr-4,* and *mcr-5*, regardless of the resistance profile.

Of 1,413 referred isolates (excluding species intrinsically resistant to colistin) tested by PCR, *mcr-1.1* was detected in 1/1,146 (0.09%) *E. coli*. The isolate was from a 63 year old male who was hospitalised in Western Australia. The isolate harboured *bla*$_{\text{CTX-M-27}}$, was meropenem susceptible (MIC ≤ 0.25 mg/L), and had a colistin MIC = 4 mg/L (Table 34).

Nine isolates with the *bla*$_{\text{IMP-4}}$ carbapenemase gene (*E. cloacae* complex [*n* = 7], *K. pneumoniae* [*n* = 1], *E. coli* [*n* = 1]) also harboured *mcr-9.1* (Table 21). Four additional *E. cloacae* complex isolates that did not produce a carbapenemase gene had *mcr-9.1* (*n* = 3) or *mcr-10.1* (*n* = 1). *mcr-9* has recently been found among several species of *Enterobacterales*[41] often on an IncHI2 plasmid, but the two downstream genes reported to be involved in induction of *mcr-9* expression by sub-inhibitory concentrations of colistin[42] are not present here, and the isolates had colistin MICs between 0.125 and 0.5 mg/L by broth microdilution. One *E. cloacae* complex isolate, which carried *mcr-10.1*, expressed heterogenous colistin resistance.

Table 34: Characteristics of isolates with plasmid-mediated colistin determinants

	WA (collected April 2019) 19GNB-0655
Species	*Escherichia coli*
Patient age / sex	63 / male
Clinical manifestation	Intra-abdominal infection other than biliary tract
Multilocus sequence type	167
MCR	*mcr-1.1*
Other resistance genes	*bla*$_{\text{CTX-M-27}}$, *|dfrA17|aadA5|, strA, strB, oqxA, oqxB, sul1, sul2, floR, erm*(B), *mph*(A) *tet*(A) variant, *aph(3')-IIa* *gyrA (D87A, S83L), parC (S80I), parE (S458A)*
MIC (mg/L)	
Colistin*	4
Ceftriaxone	≥ 64
Gentamicin	≤ 1
Ciprofloxacin	≥ 4
Meropenem	≤ 0.25
Trimethoprim-sulphamethoxazole	≥ 32

* Confirmed by broth microdilution

Colistin MIC was determined by broth microdilution on all referred isolates with meropenem > 0.25 mg/L (*n* = 93). Four isolates were colistin resistant; the *E. coli* harbouring *mcr-1.1* and three other species (*K. variicola*, *E. coli* and *E. cloacae* complex) which are undergoing further investigation.

Fluoroquinolone resistance

Multiple resistance mechanisms against quinolones have been described. Resistance is most commonly due to mutations in DNA gyrase (*gyrA*, *gyrB*) and topoisomerase IV (*parC*, *parE*). More recently, transmissible plasmid-mediated quinolone resistance (PMQR) has emerged in *Enterobacterales*. PMQR may be due to the presence of *qnr* genes (*qnrA, qnrB, qnrC, qnrD, qnrS, qnrVC); aac(6')-Ib-cr*, coding for a variant aminoglycoside acetyltransferase enzyme; or genes coding for efflux pumps (*qepA*, *oqxAB*).[43]

Salmonella species

In 2019, both CLSI and EUCAST introduced *Salmonella* specific breakpoints for ciprofloxacin. The susceptible breakpoint was lowered from ≤0.25 mg/L to ≤0.06 mg/L. Consequently the ciprofloxacin concentration range available in the Vitek and Phoenix cards used does not go low enough to accurately categorize *Salmonella* susceptibility to this agent, restricting the available concentration range to ≤0.25 – ≥4 mg/L.

Ciprofloxacin resistance in non-typhoidal species was at least 4% (5/123). However, for typhoidal *Samonella* species, it was at least 85% (69/81) (Table 35). The vast majority (94%, 29/31) of serovar Paratyphi were resistant to ciprofloxacin, and resistance among serovar Typhi was at least 80% (40/50).

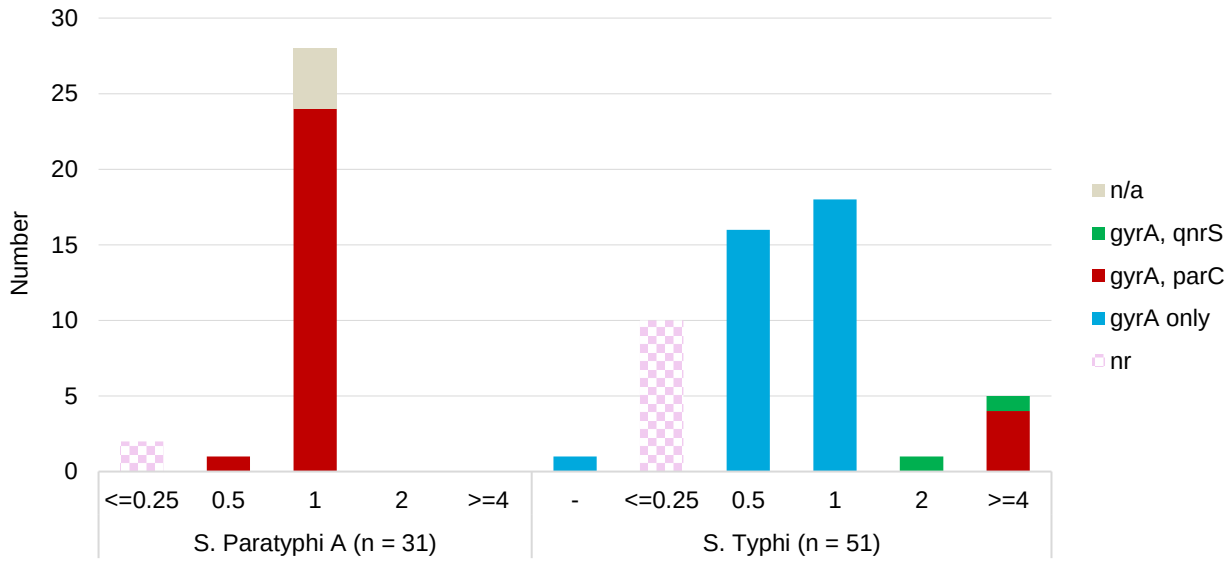
Table 35: *Salmonella* species, ciprofloxacin minimum inhibitory concentrations, 2019

	Ciprofloxacin minimum inhibitory concentration (mg/L)						
Organism	**n/a**	**≤0.25***	**0.5**	**1**	**2**	**≥4**	**Total**
Salmonella species (non-typhoidal)	4	118	0	4	0	1	127
Salmonella species (typhoidal)	1	12	17	46	1	5	82
S. Typhi	1	10	16	18	1	5	51
S. Paratyphi A	0	2	1	28	0	0	31
Total	**5**	**130**	**17**	**50**	**1**	**6**	**209**

n/a = MIC not available
* concentration limit

Whole genome sequencing was performed on all referred *Salmonella* species. A *gyrA* (Ser83) mutation in the quinolone resistance-determining region (QRDR) was detected in all typhoidal isolates referred (Figure 10). This is a common mutation conferring quinolone resistance.[44]

Figure 10: *Salmonella* (typhoidal) species, fluoroquinolone resistance mechanisms*, ciprofloxacin MIC and serovar, 2019



n/a = not available; nr = not referred

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

– Isolate referred, MIC not available

All *S*. Typhi that were resistant to ciprofloxacin harboured a mutation in the QRDR region, in codon 83 of *gyrA*. Ten percent (4/40) of this group also had a second mutation in *gyrA* (codon 87) and one mutation in *parC* (Table 36).

Two *S*. Typhi were extensively resistant. The strains were resistant to third-generation cephalosporins ($bla_{\text{CTX-M-15}}$), chloramphenicol (*catA1*), trimethoprim-sulfamethoxazole (*sul1, sul2, dfrA7*), streptomycin (*strA*, *strB*), ciprofloxacin (*gyrA* (S83F), *qnrS1*). Both isolates carried an IncY replicon (PlasmidFinder). Both isolates were from children (one from Victoria, and one from New South Wales) with recent history of travel to Pakistan.

All serovar Paratyphi A were ciprofloxacin resistant and have reported mutations in both *gyrA* (Ser83) and *parC* (Thr57) (Table 36).[44]

One non-typhoidal isolate had a pAmpC ($bla_{\text{CMY-2}}$) and *gyrA* mutation (ceftriaxone MIC = 32 mg/L, ciprofloxacin MIC ≤ 0.25 mg/L.

Table 36: Fluroquinolone resistance determinants* in ciprofloxacin-resistant *Salmonella* species, 2019

Species	Mutations in QRDR		PMQR genes	Total
	gyrA	*parC*		
Salmonella (non-typhoidal) (*n* = 5)	S83F	–†	–†	2
	S83F	T57S	–†	1
	S83Y	–†	*qnrS1*	1
	–†	T57S	*qnrS1*	1
Salmonella (typhoidal)				
S. Paratyphi A (*n* = 29)	S83F	T57S	–†	16
	S83Y	T57S	–†	9
	n/a	n/a	n/a	4
S. Typhi (*n* = 40)	S83F	–†	–†	27
	S83Y	–†	–†	7
	S83F, D87N	S80I	–†	*4*
	S83F	–†	*qnrS1*	*2*

n/a = isolate not available; PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

* Mutations in either the quinolone resistance-determining region of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[45], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*)

† not detected

Note: Additional *gyrA* and *parE* mutations were found. However, further investigation is required to confirm their contribution to quinolone resistance in *Salmonella* species

1. Two *gyrA* mutations previously reported in S. Typhi (E133G[46] and D538N[47])
2. Four *parE* mutations previously reported as contributing to quinolone resistance in *E. coli* (Table 27 this report, L416F, S458A)[48], *Shigella sonnei* (P571S)[49] or *Vibrio cholerae* (D420N)[50]

Escherichia coli

Nationally, 19.5% (951/4,882) of *E. coli* had a ciprofloxacin MIC > 0.25 mg/L, ranging from 13.2% (108/817) in Queensland to 26.8% in the Northern Territory (55/205). A subset of 200 *E. coli* (4.1% of total, 17.5% of referred) were selected for whole genome sequencing. This included 187 with ESBL phenotype and 140 with ciprofloxacin MIC > 0.25 mg/L (Table 37).

Table 37: *Escherichia coli*, ciprofloxacin susceptibility, ESBL phenotype*, 2019

Subset	Phenotype	Ciprofloxacin MIC (mg/L)			Total	% of total	% of referred
		≤0.25	0.5	>0.5			
Total	ESBL	26.6 (188)	8.6 (61)	64.8 (459)	708	14.5	
	non-ESBL	89.7 (3,742)	2.7 (111)	7.7 (320)	4,173	85.5	
	Total	**80.5 (3,930)**	**3.5 (172)**	**16.0 (779)**	**4,881**		
Referred*	ESBL	181	60	432	673	95.1	
	non-ESBL	66	103	301	470	11.3	
	Total	247	163	733	1,143	23.4	
WGS	ESBL	55	19	113	187	26.4	27.7
	non-ESBL	5	2	6	13	0.3	2.8
	Total	60	21	119	200	4.1	17.5

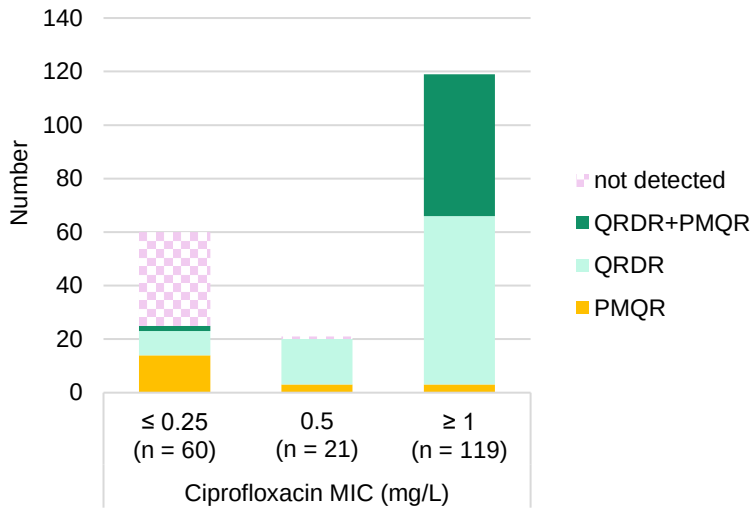
ESBL = ceftriaxone or ceftazidime MIC > 1 mg/L; WGS = whole genome sequencing

* ESBL phenotype or ciprofloxacin MIC > 0.25 mg/L

Over 99% (139/140) of the *E. coli* subset that had a ciprofloxacin MIC > 0.25 mg/L harboured fluoroquinolone resistance determinants (Figure 11).

Almost all (95%, 133/140) of this group harboured a QRDR mutation in codon 83 of *gyrA*. A substantial majority (83%, 99/119) of isolates resistant to ciprofloxacin (MIC ≥ 1 mg/L) also had a second mutation in *gyrA* (codon 87), and 87% (101/119) showed at least one mutation in *parC* (Table 38). PMQR genes (*qnr* variants) alone were more common in ciprofloxacin susceptible isolates.

Figure 11: *Escherichia coli*, fluoroquinolone resistance mechanisms*, ciprofloxacin MIC, 2019



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

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

Just over two-thirds (67.2%, 80/119) of the ciprofloxacin resistant *E. coli* in the subset belonged to either ST131 (*n* = 64) or ST1193 (*n* = 14), both with reported distinguishing *parE* mutations.[51] One-third (33%, 39/119) harboured *aac(6')-Ib-cr*, almost all (97%, 38/39) of which harboured $bla_{\text{CTX-M-15}}$, either alone (*n* = 37) or with $bla_{\text{CTX-M-27}}$ (*n* = 1). The vast majority (87%, 33/38) of the isolates with $bla_{\text{CTX-M-15}}$ belonged to ST131-H30Rx clone.

Table 38: Fluoroquinolone resistance determinants* in *Escherichia coli*, 2019

QRDR mutations				Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*	*PMQR*	≤0.25	0.5	>0.5	Total
–†	–†	–†	–†	34	1	0	35
–†	–†	–†	*qnrB*	8	0	0	8
–†	–†	–†	*qnrS*	5	3	1	9
–†	–†	–†	*aac(6')-Ib-cr, qnrB*	0	0	1	1
–†	–†	–†	*aac(6')-Ib-cr, qnrS*	0	0	1	1
–†	–†	**I529L**	–	1	0	0	1
–†	–†	**I529L**	*qnrB*	1	0	0	1
–†	S57T	–†	*qnrB*	1	0	0	1
–†	S57T	–†	*aac(6')-Ib-cr*	1	0	0	1
D87N	–†	–†	–†	1	0	0	1
S83A	–†	–†	–†	1	0	0	1
S83A	–†	–†	*qnrS*	0	0	1	1
S83L	–†	–†	–†	4	3	4	11
S83L	–†	–†	*qnrB*	0	0	1	1
S83L	–†	–†	*qnrS*	0	0	4	4
S83L	–†	**I529L**	–†	3	13	4	20
S83L	–†	S458A	–†	0	0	1	1
S83L	S80I	–†	–†	0	1	1	2
S83L	S80I	–†	*qnrS*	0	0	1	1
S83L, D87A	S80I	S458A	*oqxAB*	0	0	1	1
S83L, D87N	S80I, E84V	**I529L**	*qepA*	0	0	1	1
S83L, D87N	S80I, E84V	**I529L**	–†	0	0	23	23
S83L, D87N	S80I, E84V	**I529L**	*qnrB*	0	0	2	2
S83L, D87N	S80I, E84V	**I529L**	*aac(6')Ib-cr*	0	0	32	32
S83L, D87N	S80I, E84V	**I529L**	*aac(6')Ib-cr, qnrB*	0	0	1	1
S83L, D87N	S80I	–†	–†	0	0	2	2
S83L, D87N	S80I	E460D	–†	0	0	1	1
S83L, D87N	S80I	**L416F**	–†	0	0	14	14
S83L, D87N	S80I	**L416F**	*qnrB*	0	0	1	1
S83L, D87N	S80I	**L416F**	*aac(6')Ib-cr*	0	0	1	1
S83L, D87N	S80I	S458A	–†	0	0	8	8
S83L, D87N	S80I	S458A	*qnrB*	0	0	3	3
S83L, D87N	S80I	S458A	*qnrS, qepA*	0	0	1	1
S83L, D87N	S80I	S458A	*aac(6')Ib-cr*	0	0	3	3
S83L, D87N	S80I, E84G	–†	–†	0	0	1	1
S83L, D87N	S80I, E84G	I365T	–†	0	0	1	1
S83L, D87Y	S80I	S458A	–†	0	0	2	2
S83L, D87Y	S80I, E84V	**I529L**	–†	0	0	1	1
Total				**60**	**21**	**119**	**200**

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

* Mutations in either the quinolone resistance-determining region of the DNA gyrase and topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[45], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA, oqxAB*) detected by whole genome sequence analysis

† not detected

Notes:

1. Bold formatting highlights ST131 (blue) and **ST1193** (red) isolates
2. Additional *gyrA*, *gyrB*, and *parE* mutations were found:
   gyrA: a novel mutation outside the conventional QRDR of GyrA (R237H) previously found in highly resistant *E. coli* isolates[48]
   gyrB: a mutation (S464Y) associated with high quinolone resistance levels in *P. mirabilis*[52] and *Morganella* spp.[53]
   parE: a novel mutation previously linked to quinolone resistance in *E. coli*[54, 55]

Klebsiella pneumoniae complex

Nationally, 11.4% (136/1,189) of *K. pneumoniae* complex had a ciprofloxacin MIC > 0.25 mg/L, ranging from 6.3% in Western Australia (10/160) to 17.5% in Victoria (37/212). A subset of 56 *K. pneumoniae* (4.7% of total, 28.6% of referred) were selected for whole genome sequencing. This included 51 with ESBL phenotype and 43 with ciprofloxacin MIC > 0.25 mg/L (Table 39).

Table 39: *Klebsiella pneumoniae* complex, ciprofloxacin susceptibility, ESBL phenotype, 2019

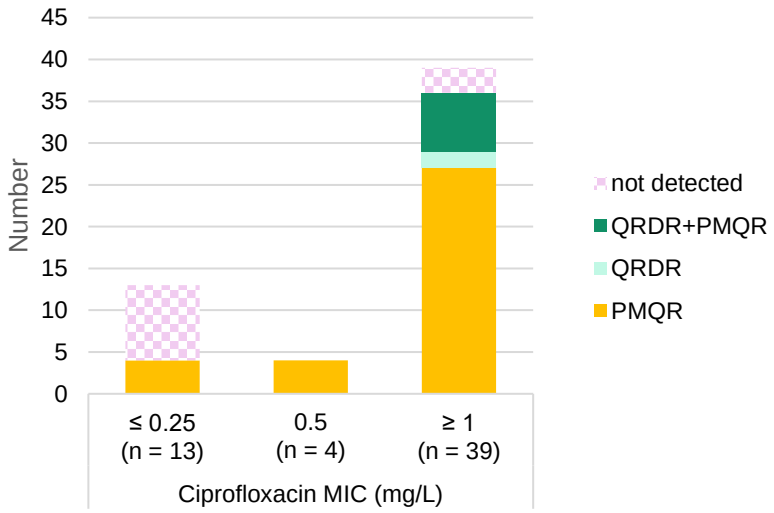
Subset	Phenotype	Ciprofloxacin MIC (mg/L)			Total	% of total	% of referred
		≤0.25	0.5	>0.5			
Total	ESBL	30.3 (37)	4.9 (6)	64.8 (79)	122	10.3	
	non-ESBL	95.2 (1,016)	0.8 (9)	3.9 (42)	1,067	89.7	
	Total	**88.6 (1,053)**	**1.3 (15)**	**10.2 (121)**	**1,189**		
Referred*	ESBL	37	6	75	118	96.7	
	non-ESBL	30	8	40	78	7.3	
	Total	67	14	115	196	16.5	
WGS	ESBL	11	4	36	51	41.8	43.2
	non-ESBL	2	0	3	5	0.5	6.4
	Total	13	4	39	56	4.7	28.6

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

* ESBL phenotype or ciprofloxacin MIC > 0.25 mg/L

Over 93% (40/43) of the *K. pneumoniae* complex subset that had ciprofloxacin MIC > 0.25 mg/L harboured fluoroquinolone resistance determinants (Figure 12). PMQR genes either alone (78%, 31/40), or in combination with QRDR mutations in codon 83 of *gyrA* (18%, 7/40) were prevalent; only 2/40 had *gyrA* mutations alone. No mutations in *parC* were detected (Table 40).

Figure 12: *Klebsiella pneumoniae* complex (*n* = 56), fluoroquinolone resistance mechanisms*, ciprofloxacin MIC, 2019



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

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

Table 40: Fluroquinolone resistance determinants* in *Klebsiella pneumoniae* complex, 2019

QRDR mutations			Ciprofloxacin MIC (mg/L)			
gyrA	parC	PMQR	≤0.25	0.5	>0.5	Total
–†	–†	–†	9	0	3	12
–†	–†	*qnrB*	2	3	2	7
–†	–†	qnrB, qnrS	0	0	2	2
–†	–†	*qnrS*	0	1	6	7
–†	–†	*aac(6')Ib-cr*	1	0	0	1
–†	–†	*aac(6')Ib-cr*, *qnrB*	1	0	15	16
–†	–†	*aac(6')Ib-cr*, *qnrS*	0	0	2	2
S83F	–†	–†	0	0	1	1
S83F	–†	*aac(6')Ib*-cr, q*nrB*	0	0	1	1
S83F, D87A	–†	*aac(6')Ib-cr*, *qnrS*	0	0	1	1
S83F, D87N	–†	*aac(6')Ib-cr*, *qnrS*	0	0	1	1
S83I	–†	*qnrB*, *qnrS*	0	0	1	1
S83I	–†	*aac(6')Ib-cr*, q*nrB*	0	0	1	1
S83Y	–†	–†	0	0	1	1
S83Y	–†	*aac(6')Ib-cr*	0	0	1	1
S83Y	–†	*aac(6')Ib-cr, qnrB*	0	0	1	1
Total			**13**	**4**	**39**	**56**

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

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

† not detected

Note: Mutations in *gyrB* or *parE* were not detected.

Pseudomonas aeruginosa

Thirty-three *P. aeruginosa* with meropenem MIC ≥ 8 mg/L [*n* = 26] , amikacin ≥ 64 mg/L [*n* = 1], colistin ≥ 4 mg/L [*n* = 1] or where MICs were not performed [*n* = 5] were referred for whole genome sequencing.

Only 2/18 (11%) meropenem resistant *P. aeruginosa* harboured a carbapenemase (*bla*$_{GES-5}$ [1], *bla*$_{IMP-1}$ [1]).

No extended-spectrum β-lactamase, 16S rRNA methyltransferase or *mcr* genes were found.

Over 71% (10/14) of the *P. aeruginosa* subset that had a ciprofloxacin MIC > 0.5 mg/L harboured fluoroquinolone resistance determinants. QRDR mutations were found in codon 83 (T83I, *n* = 8) or codon 87 (D87Y, *n* = 1) of *gyrA*. One isolate had two mutations in *gyrA* (T83I, D87L). The recently described *crpP* gene, encoding ciprofloxacin-modifying enzyme CrpP[56], was found in just over half (17/33) of the referred isolates.

3.9.2. Molecular epidemiology of *Enterococcus faecium*

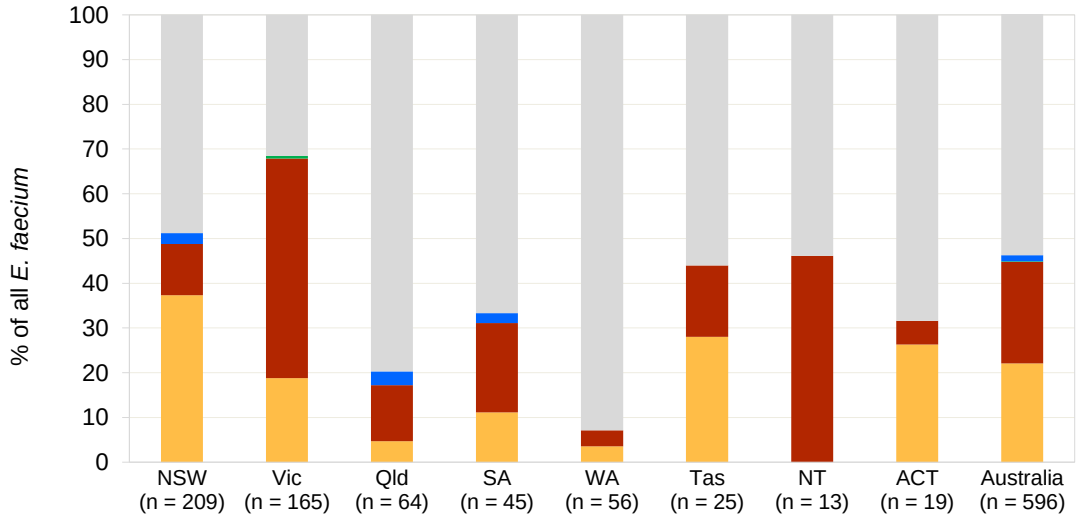
van genes

Results of polymerase chain reaction testing for *vanA* and *vanB* genes were available for 588 (98.7%) of the 596 *E. faecium* isolates. *van* genes were detected in 45.4% (267/588) of *E. faecium*; *vanA* in 131 (22.3%), *vanB* in 135 (23.0%), and *vanA* and *vanB* in one (0.2%) isolates (Figure 13).

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 339 (5.3%) vancomycin-susceptible *E. faecium*; *van* genes were detected: 12 with *vanA* and six with *vanB*. Almost all isolates (17/18, 94%) had vancomycin MIC ≤ 2 mg/L.

Figure 13: Vancomycin genotype of *Enterococcus faecium* isolates, by state and territory, and nationally, 2019



	NSW (n = 209)	Vic (n = 165)	Qld (n = 64)	SA (n = 45)	WA (n = 56)	Tas (n = 25)	NT (n = 13)	ACT (n = 19)	Australia (n = 596)
not vanA or vanB (n = 321)	48.8	31.5	79.7	66.7	92.9	56.0	53.8	68.4	54.0
Not determined (n = 8)	2.4	0.0	3.1	2.2	0.0	0.0	0.0	0.0	1.3
vanA and vanB (n = 1)	0.0	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.2
vanB (n = 135)	11.5	49.1	12.5	20.0	3.6	16.0	46.2	5.3	22.7
vanA (n = 131)	37.3	18.8	4.7	11.1	3.6	28.0	0.0	26.3	22.1

Multilocus sequence type

Of the 596 *E. faecium* isolates reported, 567 (95.1%) were available for typing by whole genome sequencing (Table 41). Based on the MLST, 77 sequence types (STs) were identified. Overall, 72.5% of *E. faecium* could be characterised into six STs: ST1424, formerly known as M-type 3 (n = 133); ST17 (n = 102); ST796 (n = 74); ST80 (n = 52); ST1421, formerly known as M-type 1 (n = 49); and ST78 (n = 22). The *pstS* housekeeping gene is absent in the M-type isolates. M-type 1 was initially identified in 2015. In 2019, there were three M-type single locus variants. There were 48 STs with a single isolate.

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

The distribution of vancomycin-resistant *E. faecium* sequence types throughout Australian states and territories is shown in Figure 14.

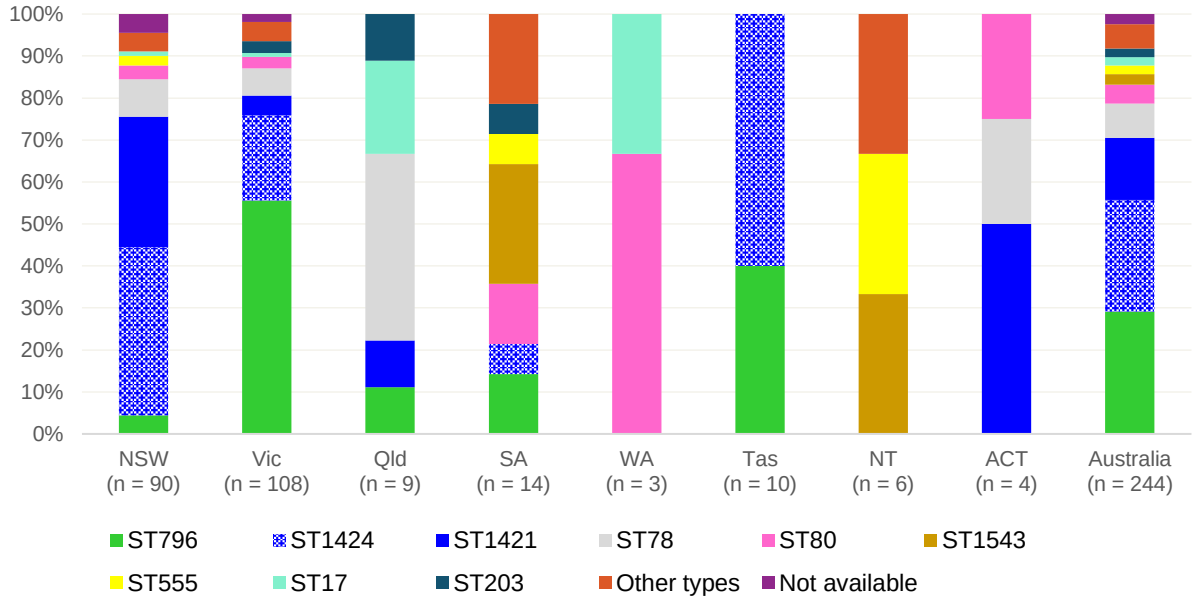
Table 41: *Enterococcus faecium* MLST, by state and territory, 2019

	Percentage, % (*n*)								
MLST	**NSW**	**Vic**	**QLD**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST1424	38.3 (80)	17.6 (29)	4.7 (3)	4.4 (2)	0.0 (0)	64.0 (16)	0.0 (0)	15.8 (3)	22.3 (133)
ST17	7.7 (16)	6.7 (11)	51.6 (33)	31.1 (14)	46.4 (26)	4.0 (1)	7.7 (1)	0.0 (0)	17.1 (102)
ST796	1.9 (4)	37.6 (62)	1.6 (1)	4.4 (2)	1.8 (1)	16.0 (4)	0.0 (0)	0.0 (0)	12.4 (74)
ST80*	8.1 (17)	5.5 (9)	4.7 (3)	11.1 (5)	21.4 (12)	0.0 (0)	7.7 (1)	26.3 (5)	8.7 (52)
ST1421	17.7 (37)	3.6 (6)	3.1 (2)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	21.1 (4)	8.2 (49)
ST78	3.8 (8)	5.5 (9)	6.3 (4)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	5.3 (1)	3.7 (22)
Other types (n = 71)	14.8 (31)	21.2 (35)	21.9 (14)	42.2 (19)	26.8 (15)	16.0 (4)	84.6 (11)	31.6 (6)	22.7 (135)
Total	**193**	**161**	**60**	**42**	**54**	**25**	**13**	**19**	**567**

MLST = multi-locus sequence type; slv = single locus variant

* includes one slv

Figure 14: Distribution of vancomycin-resistant *Enterococcus faecium* sequence types, by state and territory, 2019



MLST and *van* genes

The *vanA* gene alone was detected in 12 STs; ST1424 (*n* = 72), ST1421 (*n* = 37), ST80 (*n* = 6), ST17 (*n* = 3), ST18 (*n* = 2), and one each of ST262, ST1425, ST1283, ST1746, ST202, ST787 and ST412. The *vanB* gene alone was detected in 12 STs: ST796 (*n* = 71), ST78 (*n* = 21), ST1543 (*n* = 7), ST80 (*n* = 5), ST555 (*n* = 5), ST203 (*n* = 5), ST17 (*n* = 4), ST117 (*n* = 3), ST1424 (n = 2), ST252 (n =2), ST1743 (n = 2), and ST992 (*n* = 1) (Table 42). Isolates with both *vanA* and *vanB* genes were found in ST796 (*n* = 1).

Table 42: *Enterococcus faecium* MLST harbouring *vanA* and/or *vanB* genes, 2019

MLST	*vanA*, %* (*n*)	*vanB*, %* (*n*)	*vanA* and *vanB*, %* (*n*)	*vanA* or *vanB* not detected, %* (n)	Total, *n*
ST1424 (M-type 3)	54.1 (72)	1.5 (2)	0.0 (0)	44.4 (59)	133
ST17	2.9 (3)	3.9 (4)	0.0 (0)	93.1 (95)	102
ST796	0.0 (0)	95.9 (71)	1.4 (1)	2.7 (2)	74
ST80†	11.5 (6)	9.6 (5)	0.0 (0)	78.8 (41)	52
ST1421 (M-type 1)	75.5 (37)	0.0 (0)	0.0 (0)	24.5 (12)	49
ST78	0.0 (0)	95.5 (21)	0.0 (0)	4.5 (1)	22
Other types (n = 71)	6.7 (9)	18.5 (25)	0.0 (0)	74.8 (101)	135
Total	**22.4 (127)**	**22.6 (128)**	**0.2 (1)**	**54.9 (311)**	**567**

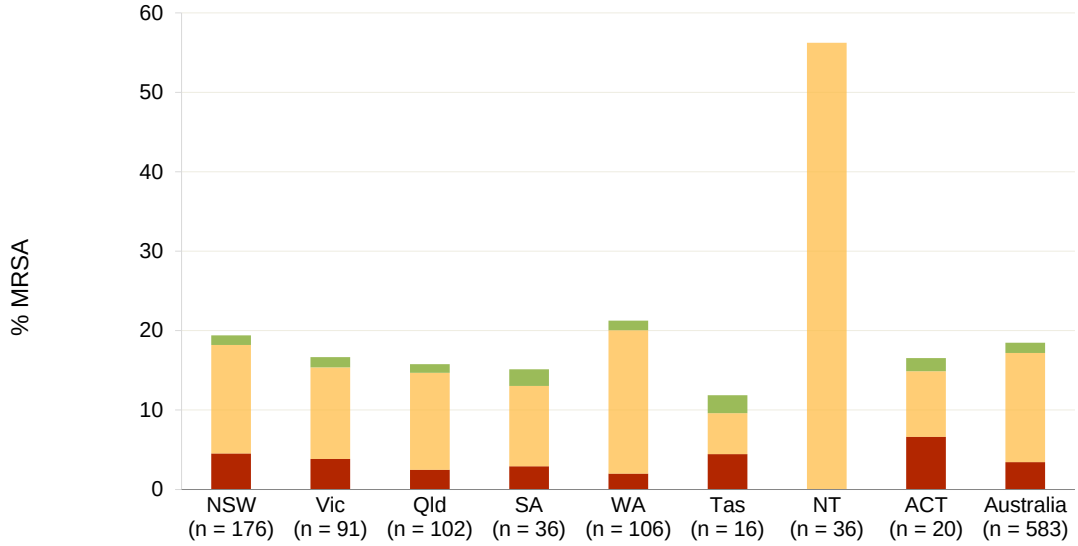
MLST = multi-locus sequence type; slv = single locus variant

* Percentage of total with *van* genes
† includes one slv

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

Of the 583 MRSA reported, 542 (93.0%) 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 15).

Figure 15: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, 2019



	NSW (n = 176)	Vic (n = 91)	Qld (n = 102)	SA (n = 36)	WA (n = 106)	Tas (n = 16)	NT (n = 36)	ACT (n = 20)	Australia (n = 583)
Not available (n = 41)	1.2	1.3	1.1	2.1	1.2	2.2	0.0	1.7	1.3
Community associated (n = 433)	13.7	11.5	12.2	10.1	18.0	5.2	56.3	8.3	13.7
Healthcare associated (n = 109)	4.5	3.8	2.5	2.9	2.0	4.4	0.0	6.6	3.5

MRSA = methicillin-resistant *Staphylococcus aureus*

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

Healthcare-associated MRSA

Based on the MLST and SCC*mec* type, three HA-MRSA clones were identified: ST22-IV (EMRSA-15), ST239-III (Aus 2/3 EMRSA), and ST5-II (NY/Japan) (Tables 43, 44).

PVL-associated genes were not identified in HA-MRSA. Eight PVL positive ST22-IV isolates were identified; three in Victoria, two each in New South Wales and Queensland, and one in 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 and the Northern Territory. ST5-II was only identified in New South Wales (Table 45).

Community-associated MRSA

Based on the MLST and SCC*mec* type, 61 CA-MRSA clones were identified. PVL was detected in 14 CA-MRSA clones. Overall 41.1% of CA MRSA were PVL positive (Tables 43, 44).

The most frequently isolated CA-MRSA clone, ST93-IV (Qld CA-MRSA), was isolated in all states except Tasmania and the Australian Capital Territory (Table 46).

Of the hospital-onset MRSA, 75.6% (102/135) were caused by CA-MRSA.

Table 43: MRSA clones, association, place of onset and PVL carriage, 2019

Clone	Clonal complex	Total, *n*	Community onset, % (*n*)*	Hospital onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)	22	89	69.7 (62)	30.3 (27)	0.0 (0)
ST239-III (Aus2/3 EMRSA)	8	19	73.7 (14)	26.3 (5)	0.0 (0)
ST5-II (NY/Japan)	5	1	0.0 (0)	100.0 (1)	–† (0)
Total HA-MRSA		109	69.7 (76)	30.3 (33)	0.0 (0)
Community-associated					
ST93-IV (Qld CA-MRSA)	93	132	87.1 (115)	12.9 (17)	95.5 (126)
ST5-IV	5	60	78.3 (47)	21.7 (13)	25.0 (15)
ST45-V	45	55	67.3 (37)	32.7 (18)	0.0 (0)
ST1-IV (WA1 MRSA)	1	26	65.4 (17)	34.6 (9)	0.0 (0)
ST30-IV (SWP MRSA)	30	14	92.9 (13)	7.1 (1)	100.0 (14)
ST8-IV	8	11	81.8 (9)	18.2 (2)	36.4 (4)
ST78-IV (WA2 MRSA)	78	11	81.8 (9)	18.2 (2)	0.0 (0)
ST953-IV	97	10	60.0 (6)	40.0 (4)	0.0 (0)
ST22-IV (PVL positive)	22	8	–† (6)	–† (2)	–† (8)
ST97-IV	97	8	–† (5)	–† (3)	–† (0)
ST45-IV	45	7	–† (7)	–† (0)	–† (0)
ST6-IV	5	6	–† (4)	–† (2)	–† (1)
ST872-IV	1	5	–† (4)	–† (1)	–† (0)
ST72-IV	8	5	–† (3)	–† (2)	–† (0)
ST59-IV	Not assigned	5	–† (4)	–† (1)	–† (0)
ST5-V	5	5	–† (5)	–† (0)	–† (0)
Other (*n* = 45)		65	61.5 (40)	38.5 (25)	15.4 (10)
Total CA-MRSA		433	76.4 (331)	23.6 (102)	41.1 (178)
MRSA		**542**	**407**	**135**	

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

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

Table 44: MRSA clones, association, place of onset, 2019

Clone	Clonal complex	Community onset, % (*n*)*	Hospital onset, % (*n*)*	Total, % (*n*)
Healthcare-associated				
ST22-IV (EMRSA-15)	22	15.2 (62)	20.0 (27)	16.4 (89)
ST239-III (Aus2/3 EMRSA)	8	3.4 (14)	3.7 (5)	3.5 (19)
ST5-II (NY/Japan)	5	0.0 (0)	0.7 (1)	0.2 (1)
Total HA-MRSA		18.7 (76)	24.4 (33)	20.1 (109)
Community-associated				
ST93-IV (Qld CA-MRSA)	93	28.3 (115)	12.6 (17)	24.4 (132)
ST5-IV	5	11.5 (47)	9.6 (13)	11.1 (60)
ST45-V	45	9.1 (37)	13.3 (18)	10.1 (55)
ST1-IV (WA1 MRSA)	1	4.2 (17)	6.7 (9)	4.8 (26)
ST30-IV (SWP MRSA)	30	3.2 (13)	0.7 (1)	2.6 (14)
ST8-IV	8	2.2 (9)	1.5 (2)	2.0 (11)
ST78-IV (WA2 MRSA)	78	2.2 (9)	1.5 (2)	2.0 (11)
ST953-IV	97	1.5 (6)	3.0 (4)	1.8 (10)
ST22-IV (PVL positive)	22	1.5 (6)	1.5 (2)	1.5 (8)
ST97-IV	97	1.2 (5)	2.2 (3)	1.5 (8)
ST45-IV	45	1.7 (7)	0.0 (0)	1.3 (7)
ST6-IV	5	1.0 (4)	1.5 (2)	1.1 (6)
ST872-IV	1	1.0 (4)	0.7 (1)	0.9 (5)
ST72-IV	8	0.7 (3)	1.5 (2)	0.9 (5)
ST59-IV	Not assigned	1.0 (4)	0.7 (1)	0.9 (5)
ST5-V	5	1.2 (5)	0.0 (0)	0.9 (5)
Other (*n* = 45)		9.8 (40)	18.5 (25)	12.0 (65)
Total CA-MRSA		81.3 (331)	75.6 (102)	79.9 (433)
MRSA		**75.1 (407)**	**24.9 (135)**	**542**

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

* Percentage of all MRSA

Table 45: Healthcare-associated MRSA clones, by state and territory, 2019

	Percentage, % (*n*)								
Clone	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15)	87.8 (36)	90.5 (19)	50.0 (8)	–* (5)	100.0 (10)	–* (5)	n/a	–* (6)	81.7 (89)
ST239-III (Aus2/3 EMRSA)	9.8 (4)	9.5 (2)	50.0 (8)	–* (2)	0.0 (0)	–* (1)	n/a	–* (2)	17.4 (19)
ST5-II (NY/Japan)	2.4 (1)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	–* (0)	n/a	–* (0)	0.9 (1)
Total	41	21	16	7	10	6	0	8	109

MRSA = methicillin-resistant *Staphylococcus aureus*; n/a = not applicable (no isolates)

* Insufficient numbers (<10) to calculate percentage

Table 46: Major community-associated MRSA clones (> 10 isolates) by state and territory and PVL carriage, 2019

Clone	Percentage, % (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST93-IV (Qld CA-MRSA)	14.5 (18)	19.0 (12)	40.5 (32)	29.2 (7)	45.6 (41)	–* (0)	61.1 (22)	0.0 (0)	30.5 (132)
Number PVL positive	17	12	30	7	40	0	20	0	126
Number PVL negative	1	0	2	0	1	0	2	0	6
ST5-IV	14.5 (18)	9.5 (6)	22.8 (18)	4.2 (1)	10.0 (9)	–* (1)	13.9 (5)	20.0 (2)	13.9 (60)
Number PVL positive	3	1	1	0	5	0	5	0	15
Number PVL negative	15	5	17	1	4	1	0	2	45
ST45-V	29.8 (37)	22.2 (14)	0.0 (0)	12.5 (3)	0.0 (0)	–* (0)	0.0 (0)	10.0 (1)	12.7 (55)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	37	14	0	3	0	0	0	1	55
ST1-IV	4.8 (6)	1.6 (1)	2.5 (2)	16.7 (4)	7.8 (7)	–* (0)	8.3 (3)	30.0 (3)	6.0 (26)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	6	1	2	4	7	0	3	3	26
ST30-IV	6.5 (8)	6.3 (4)	1.3 (1)	0.0 (0)	1.1 (1)	–* (0)	0.0 (0)	0.0 (0)	3.2 (14)
Number PVL positive	8	4	1	0	1	0	0	0	14
Number PVL negative	0	0	0	0	0	0	0	0	0
ST8-IV	3.2 (4)	3.2 (2)	3.8 (3)	4.2 (1)	1.1 (1)	–* (0)	0.0 (0)	0.0 (0)	2.5 (11)
Number PVL positive	1	2	0	1	0	0	0	0	4
Number PVL negative	3	0	3	0	1	0	0	0	7
ST78-IV	0.0 (0)	3.2 (2)	0.0 (0)	0.0 (0)	10.0 (9)	–* (0)	0.0 (0)	0.0 (0)	2.5 (11)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	0	2	0	0	9	0	0	0	11
Other clones (n = 40)	26.6 (33)	34.9 (22)	29.1 (23)	33.3 (8)	24.4 (22)	–* (6)	16.7 (6)	40.0 (4)	28.6 (124)
Number PVL positive	7	3	4	2	1	0	2	0	19
Number PVL negative	26	19	19	6	21	6	4	4	105
Total	**124**	**63**	**79**	**24**	**90**	**7**	**36**	**10**	**433**
PVL positive	36	22	36	10	47	0	27	0	178
PVL negative	88	41	43	14	43	7	9	10	255

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

* Insufficient numbers (<10) to calculate percentage

3.10. Trend analysis (2013–2019)

Trend data were available for *Enterobacterales* for the period 2013 to 2019. *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.

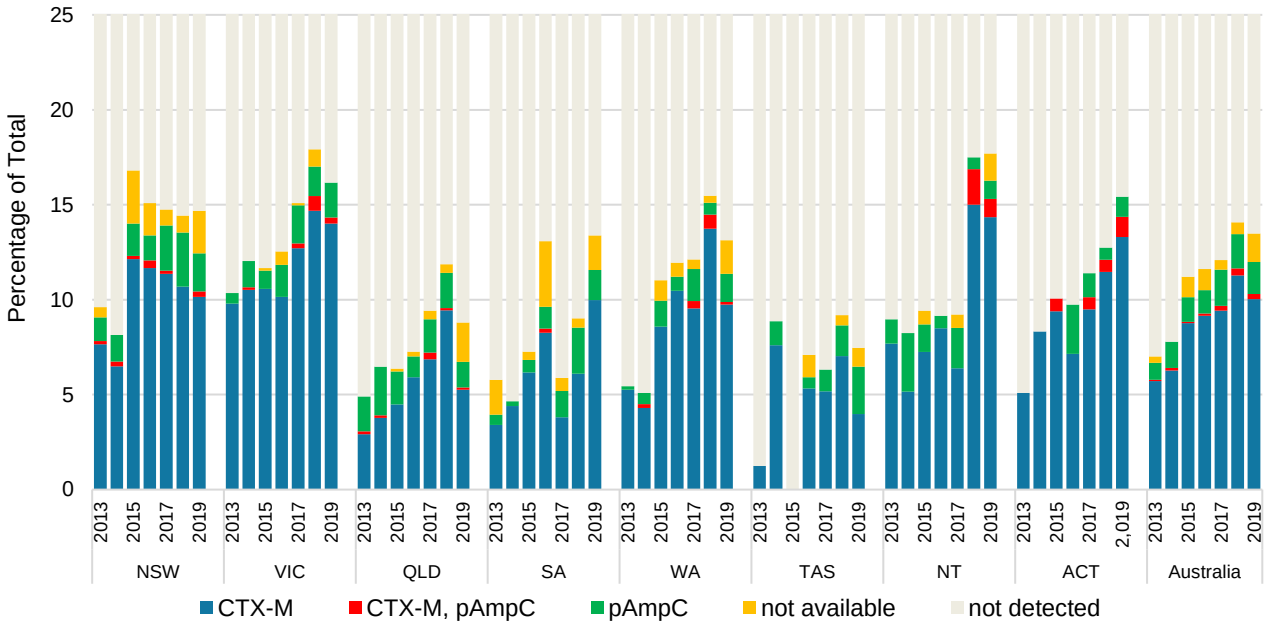
3.10.1. Gram-negative species

Extended-spectrum β-lactamases

Overall, the proportion of *E. coli* with CTX-M-type β-lactamase genes (alone or with pAmpC) declined by 11.6% in 2019 relative to 2018 (10.3% versus 11.6%), most notably in Queensland (5.4% versus 9.6%), Western Australia (9.9% versus 14.5%) and Tasmania (4.0% versus 7.0%). There was an increase in CTX-M types in South Australia (10.0% versus 6.1%). The proportion of plasmid-borne AmpC β-lactamases remained stable (Figure 16).

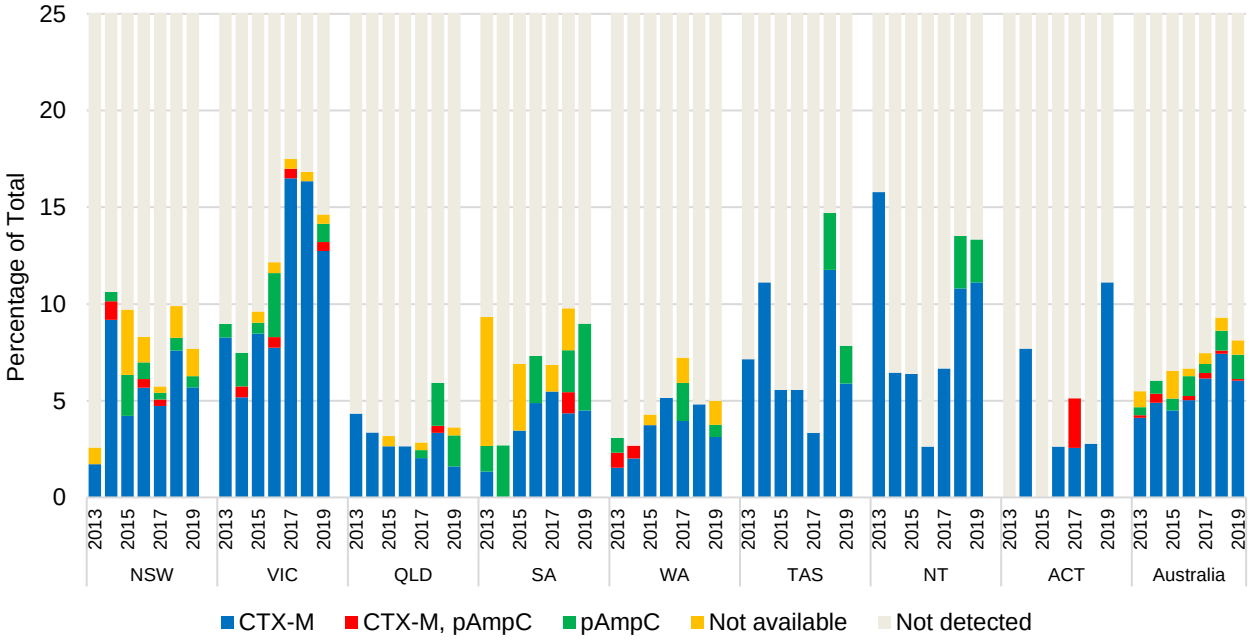
Nationally, the proportion of *K. pneumoniae* complex with CTX-M-type or plasmid-borne AmpC β-lactamase genes in 2019 declined by 14% relative to 2018 (7.4% versus 8.6%). Although regional variations were seen there were no significant changes in any jurisdiction compared to 2018 (Figure 17).

Figure 16. Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Escherichia coli* by state and territory, and nationally, 2013–2019



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

Figure 17. Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Klebsiella pneumoniae* by state and territory, and nationally, 2013–2019



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

Escherichia coli

Relative to 2018, the percentage resistance for *E. coli* in 2019 declined for almost two-thirds (60%, 7/11) of the antimicrobial agents tested. However, compared to 2018, an increase in resistance was seen with ceftazidime (up 7.2%), cefepime (up 11.8%), gentamicin (up 7.3%) and ciprofloxacin (up 4.9%) (Figure 18).

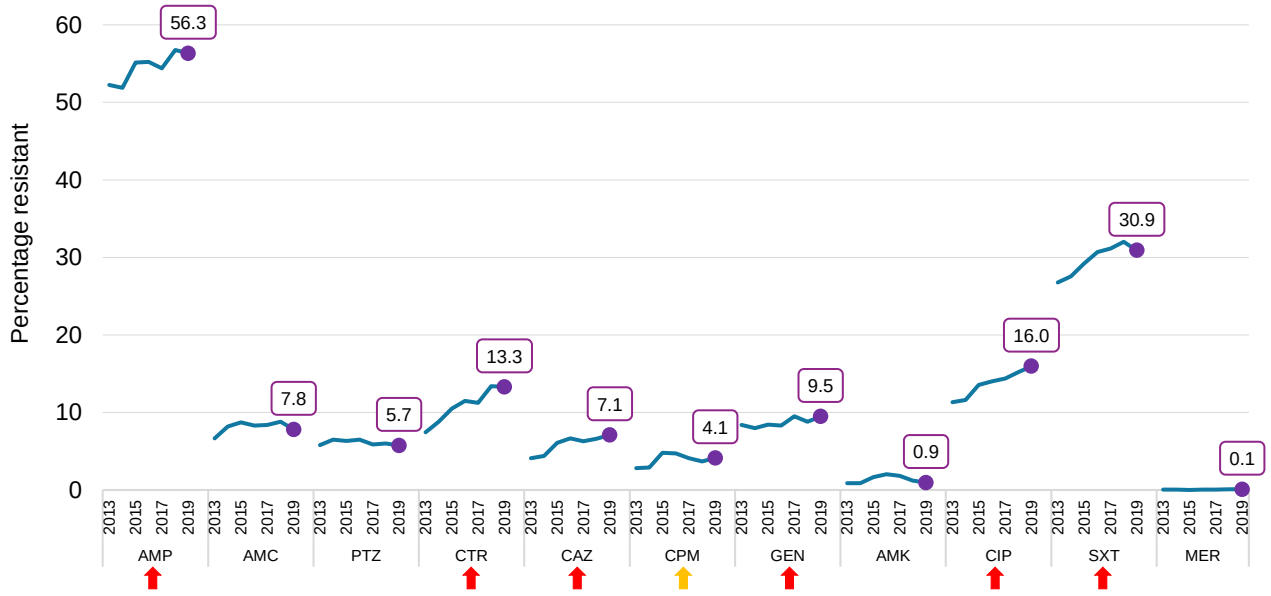
Resistance to key antimicrobial agents showed a steady increase from 2013 to 2019. There was a significant increase in resistance to ampicillin (X^2 for linear trend = 23.83, P < 0.01), ceftriaxone (X^2 for linear trend = 98.18, P < 0.01), ceftazidime (X^2 for linear trend = 40.77, P < 0.01), cefepime (X^2 for linear trend = 5.491, P = 0.0191), gentamicin (X^2 for linear trend = 6.839, P = <0.01), ciprofloxacin (X^2 for linear trend = 53.85, P < 0.01), and trimethoprim–sulfamethoxazole (X^2 for linear trend = 31.63, P < 0.01).

Klebsiella pneumoniae complex

Relative to 2018, the percentage resistance for *K. pneumoniae* complex in 2019 declined for half (50%, 5/10) of the antimicrobial agents tested. A relative increase in resistance was seen with amoxicillin–clavulanic acid (up 22.6%), piperacillin–tazobactam (up 9.9%), ceftazidime (up 1.9%), gentamicin (up 14.4%) and amikacin (up 37.6%) (Figure 19).

There were significant increases in resistance to key antimicrobial agents for *K. pneumoniae* complex over the seven-year period 2013–2019 (Figure 19). Key antimicrobial agents included amoxicillin–clavulanic acid (X^2 for linear trend = 5.290, P = 0.0215), ceftriaxone (X^2 for linear trend = 6.820, P < 0.01), ceftazidime (X^2 for linear trend = 6.608, P = 0.0102), ciprofloxacin (X^2 for linear trend = 12.42, P < 0.01), and trimethoprim–sulfamethoxazole (X^2 for linear trend = 12.78, P < 0.01).

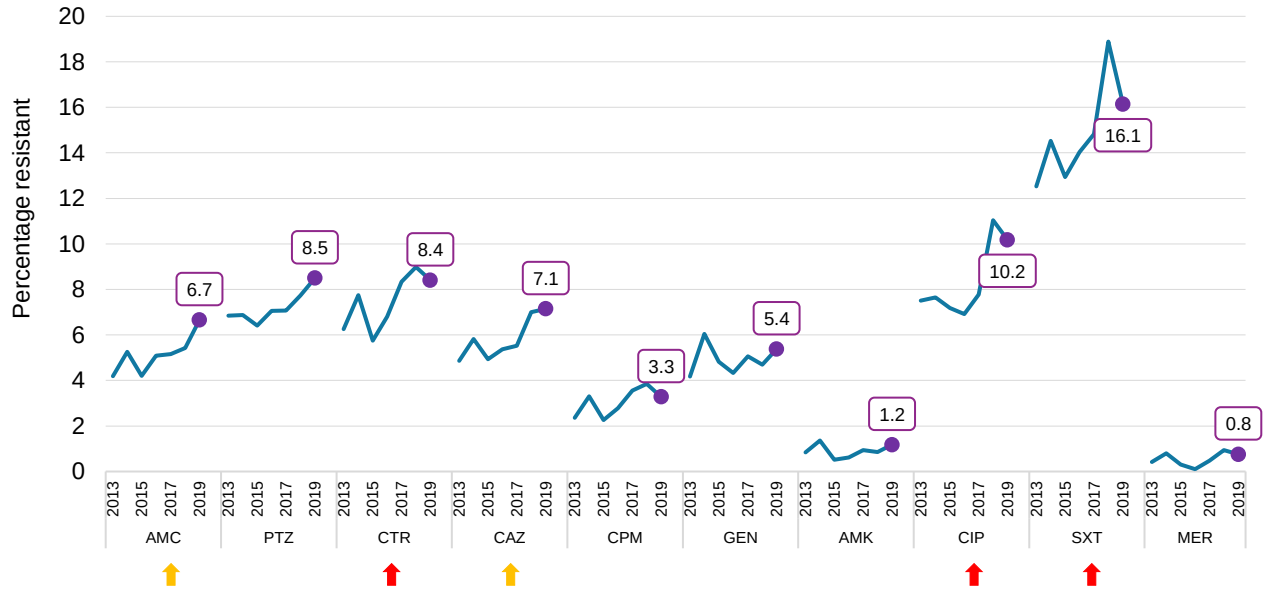
Figure 18. *Escherichia coli* resistance to key antimicrobials (EUCAST), Australia, 2013–2019



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

Notes:
1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the period 2013 to 2019.
3. Orange arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the period 2013 to 2019.

Figure 19. *Klebsiella pneumoniae* complex resistance to key antimicrobials (EUCAST), Australia, 2013–2019



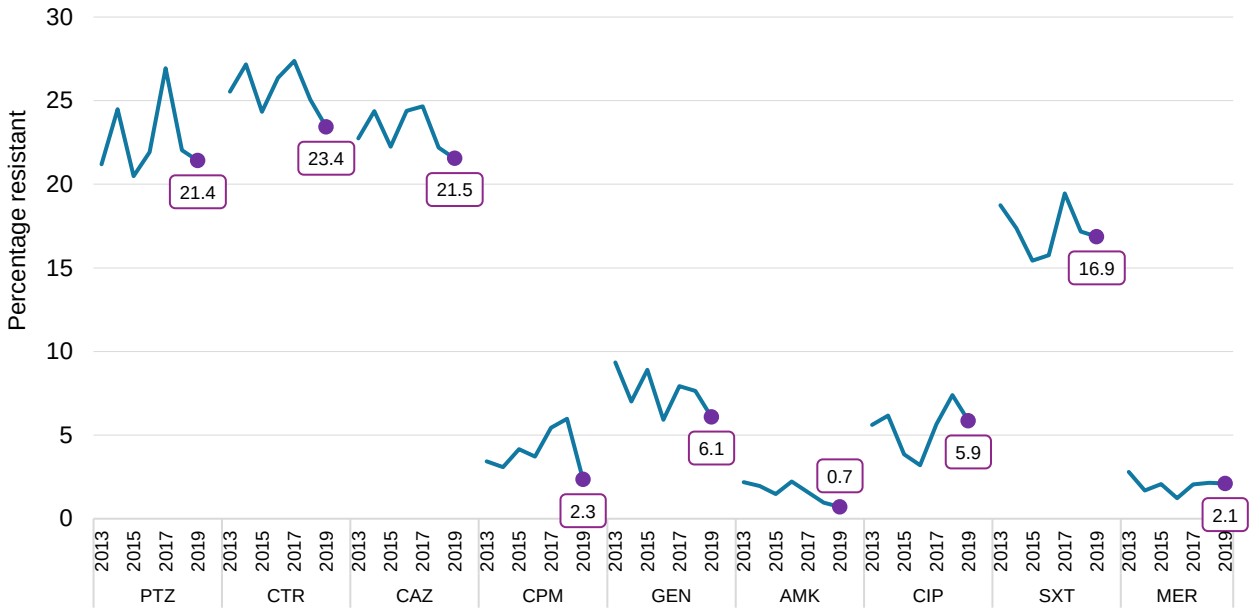
AMC = amoxicillin–clavulanic acid (2:1 ratio); AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; SXT = trimethoprim-sulfamethoxazole

Notes:
1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the period 2013 to 2019
3. Orange arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the period 2013 to 2019.

Enterobacter cloacae complex

Percentage resistance to all key antimicrobials for *E. cloacae* complex in 2019 decreased relative to 2018. There were no significant differences in resistance to key antimicrobials for *E. cloacae* complex over the seven-year period 2013–2019 (Figure 20)

Figure 20. *Enterobacter cloacae* complex resistance to key antimicrobials (EUCAST), Australia, 2013–2019



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

Note: Percentage resistance determined using EUCAST 2020 breakpoints for all years

3.10.2. *Enterococcus* species

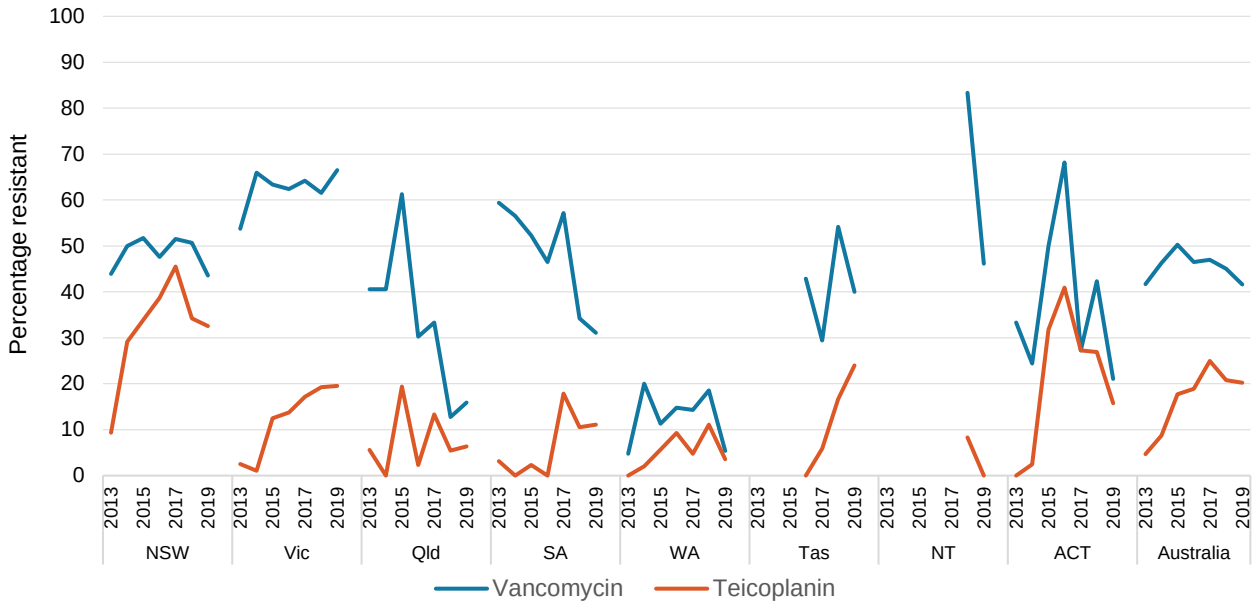
The 2019 program focused on the proportions of *E. faecium* and *E. faecalis* bacteraemia isolates demonstrating resistance to ampicillin, glycopeptides and other anti-enterococcal agents. Important trends for the period 2013–2019 are described below.

Glycopeptide-resistance in *Enterococcus faecium*

The proportion of glycoside-resistant *E. faecium* by state and territory is shown in Figure 21.

In 2019, compared to 2018, vancomycin resistance in *E. faecium* nationally declined (down 7.6%), while teicoplanin resistance remained stable. Regional variations were seen. Most notable was a decline in vancomycin resistance in Western Australia (down 71.1%) and increases in Victoria (up 8.0%) and Queensland (up 24.7%). Notable changes to teicoplanin resistance were seen in Western Australia (down 67.9%), Tasmania (up 44.0%), and the Australian Capital Territory (down 41.4%).

Figure 21. *Enterococcus faecium*, glycopeptide resistance (EUCAST), Australia, 2013–2019

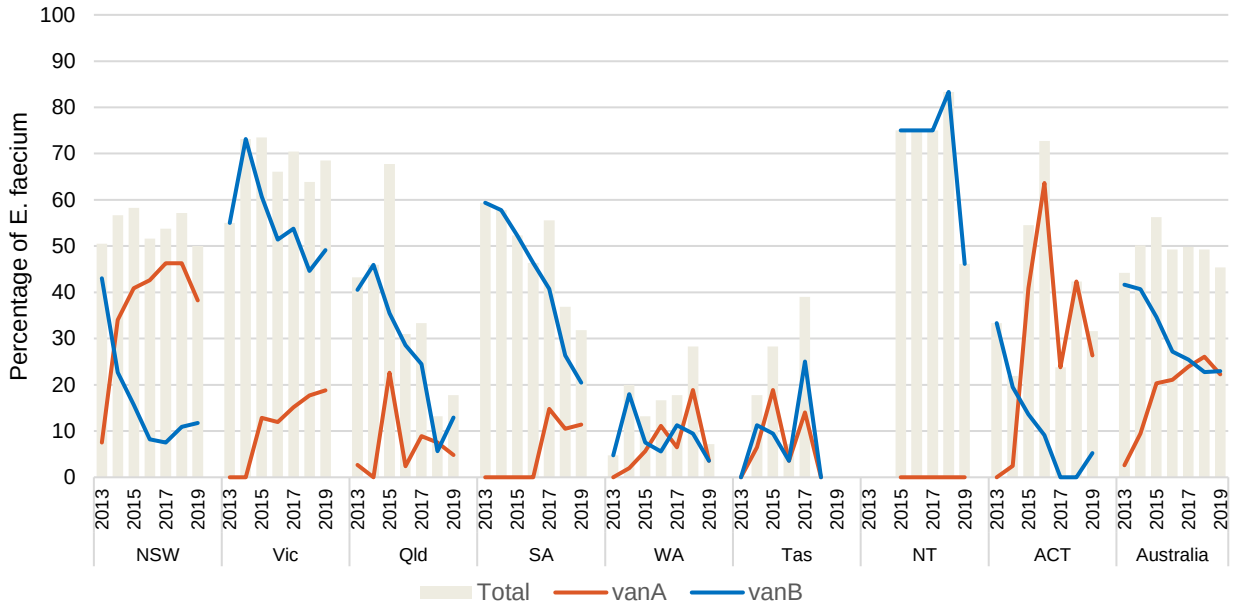


Notes

1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. Insufficient numbers (< 10) to calculate percentage for Tasmania (2013–2015) and the Northern Territory (2013-2017)

Nationally, the proportion of *vanA* and *vanB* genes in *E. faecium* in Australia were similar, with little change since 2018. However, in Victoria the proportion of *vanA* genes continued to increase (Figure 22)

Figure 22. Proportion of *van* genes in *Enterococcus faecium* by state and territory, and nationally, 2013–2019



Notes

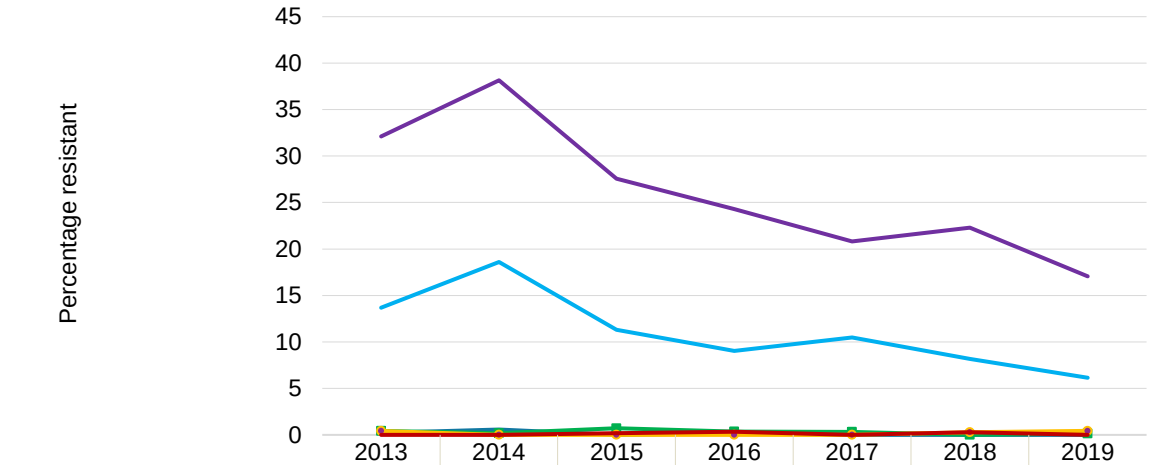
1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. Insufficient numbers (< 10) to calculate percentage for the Northern Territory (2013-2017)

Enterococcus faecalis

Resistance (EUCAST) to key antimicrobial agents for *E. faecalis* over the seven-year period 2013–2019 is shown in Figure 23. Compared to 2018, high-level gentamicin resistance (down 23.5%) and the proportion with ciprofloxacin non-wild-type (down 24.8%) declined in 2019. Resistance to ampicillin, vancomycin, teicoplanin and linezolid remains rare. One vancomycin-resistant (MIC = 16 mg/L, *vanB*) *E. faecalis* was confirmed from New South Wales.

Detailed data on *E. faecalis* resistance by state and territory are available in Appendix E1.

Figure 23. *Enterococcus faecalis*, resistance (EUCAST), Australia, 2013–2019



	2013	2014	2015	2016	2017	2018	2019
Ampicillin	0.2	0.6	0.0	0.2	0.0	0.0	0.0
Vancomycin	0.4	0.2	0.7	0.3	0.3	0.0	0.1
Teicoplanin	0.4	0.0	0.0	0.0	0.0	0.3	0.4
Linezolid	0.0	0.0	0.2	0.3	0.0	0.3	0.0
Gentamicin (high-level)	32.1	38.2	27.6	24.3	20.8	22.3	17.1
Ciprofloxacin (ECOFF)	13.7	18.6	11.3	9.0	10.5	8.2	6.1

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

Notes

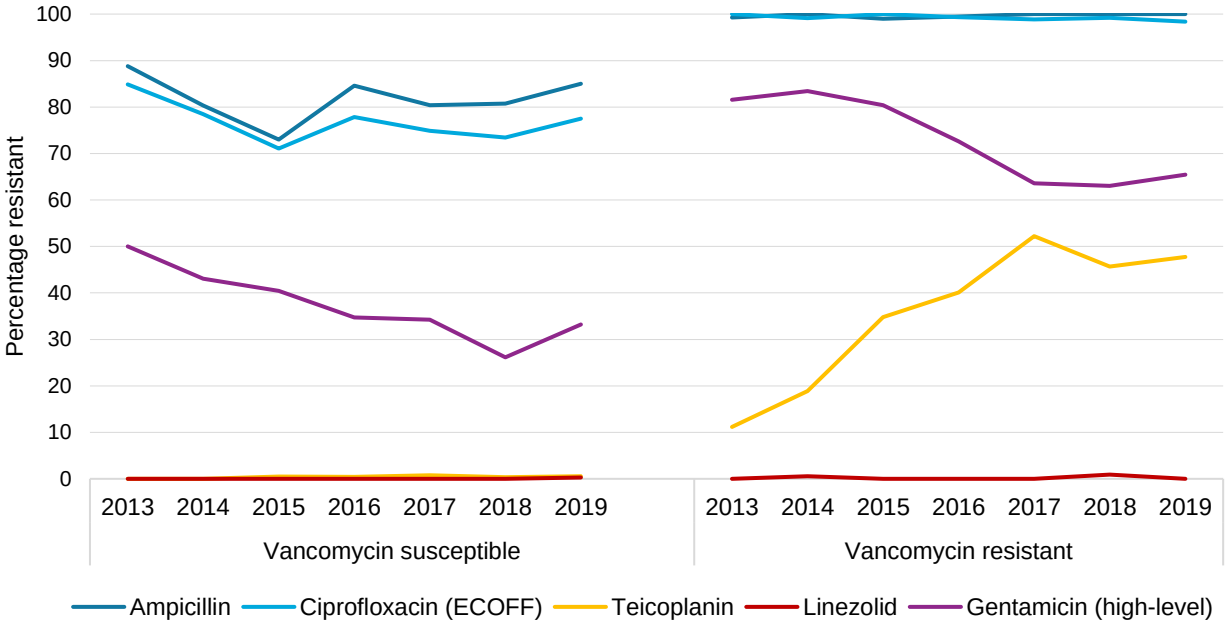
1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. The ciprofloxacin ECOFF (4 mg/L) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only.

Enterococcus faecium

Compared to 2018, high-level gentamicin resistance increased (up 7.9%), mostly among vancomycin-susceptible isolates (Figure 24). Teicoplanin-resistant isolates were detected in all states and territories; One linezolid-resistant *E. faecium* (MIC = 16 mg/L, confirmed by Etest) was confirmed in 2019 from Western Australia. No known resistance mechanism was detected by whole genome sequencing.

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

Figure 24: *Enterococcus faecium,* resistance (EUCAST), by vancomycin susceptibility, Australia, 2013–2019



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

Notes

3. Percentage resistance determined using EUCAST 2020 breakpoints for all years
4. The ciprofloxacin ECOFF (8 mg/L) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only.

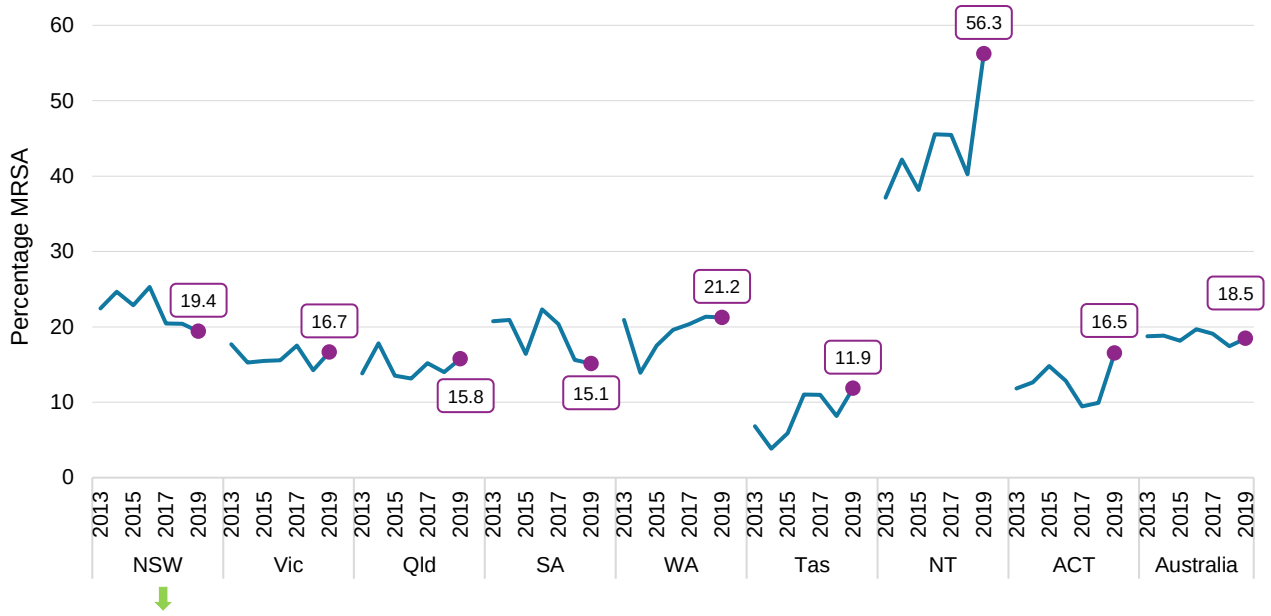
3.10.3. *Staphylococcus aureus*

A primary objective of the 2019 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 2013–2019.

Methicillin-resistant *Staphylococcus aureus*

The proportion of *S. aureus* that was methicillin resistant throughout Australia remained constant over the years 2013–2019, although there were notable variations at state and territory level (Figure 25). Relative to 2018, there were no significant differences in the proportion of MRSA in the states and territories, however there was a ~40% increase in MRSA in Tasmania, Northern Territory and the Australian Capital Territory.

Figure 25: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, 2013–2019

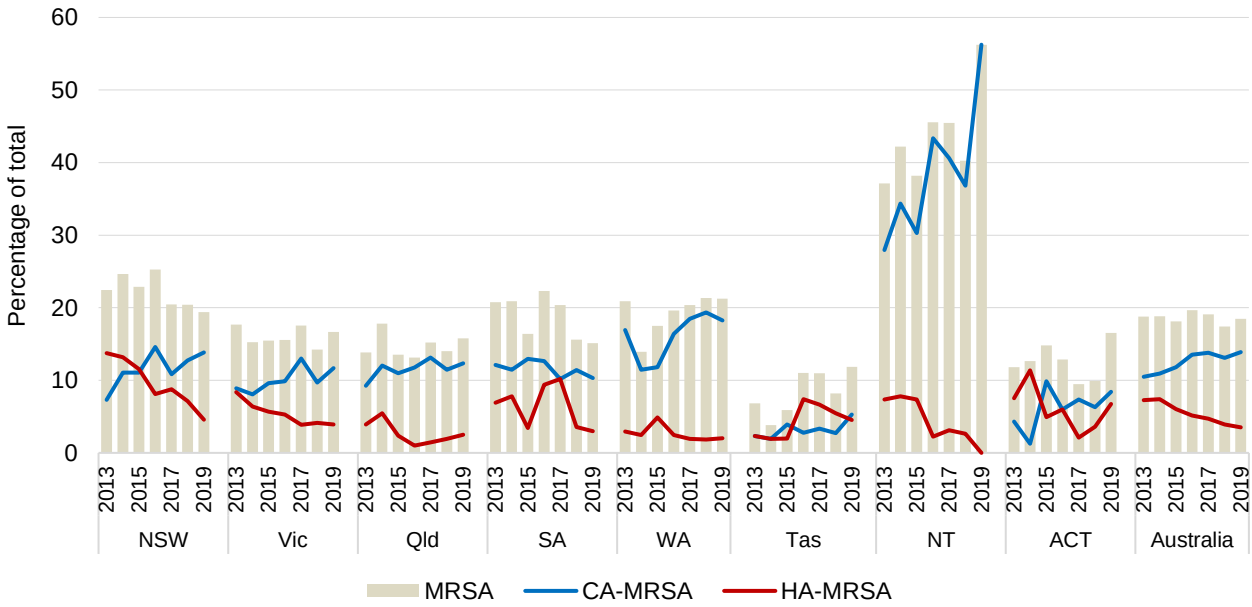


MRSA = methicillin-resistant *Staphylococcus aureus*

Note: Light green arrows indicate antimicrobial agents with significant decrease (0.01 < P < 0.05) over the period 2013 to 2019

There were significant changes in the proportion of CA-MRSA and HA-MRSA over the period 2013–2019. Nationally, there was a significant increase in the proportion of CA-MRSA clones (X^2 for linear trend = 20.71, P < 0.01), notably in New South Wales, Western Australia and the Northern Territory (Figure 26). The proportion of HA-MRSA clones declined nationally (X^2 for linear trend = 68.53, P < 0.01), notably in New South Wales, Victoria, Queensland, and the Northern Territory.

Figure 26: Proportion of methicillin-resistant *Staphylococcus aureus*, by association, state and territory, 2013–2019



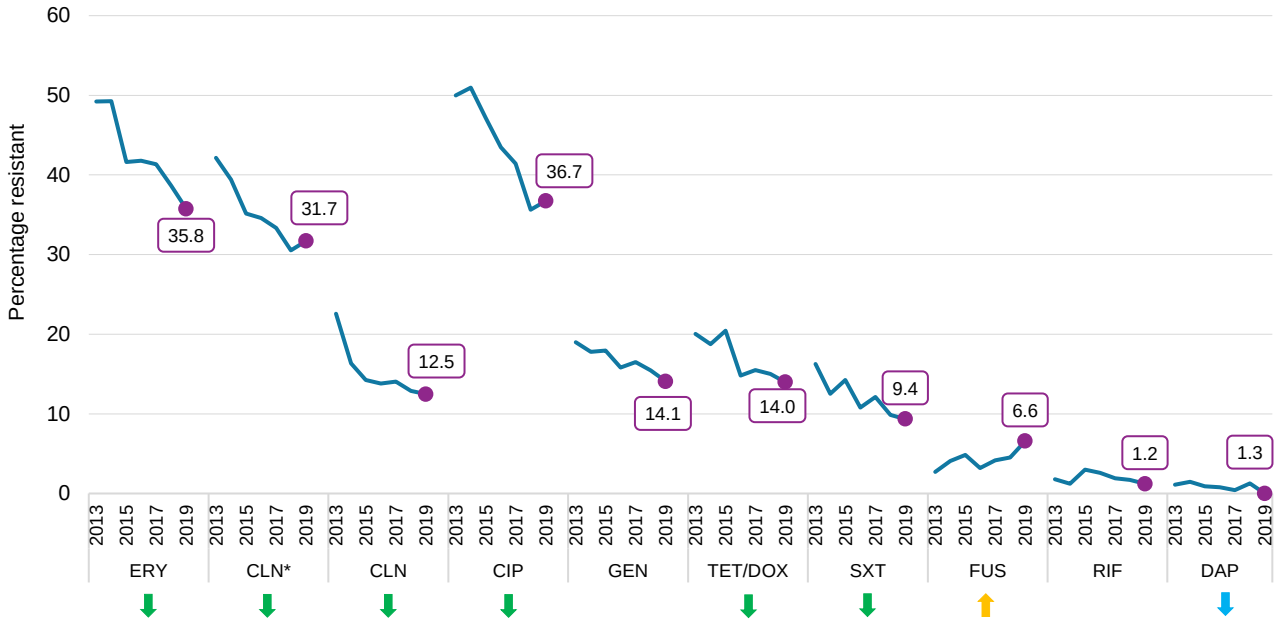
MRSA = methicillin-resistant *Staphylococcus aureus*; CA-MRSA = community-associated MRSA; HA-MRSA = healthcare-associated MRSA

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

Relative to 2018, the percentage resistance to antimicrobial agents tested against MRSA in 2019 remained stable, except for fusidic acid (up 46.1%).

There was a significant decrease in erythromycin (χ^2 for linear trend = 25.91, $P < 0.01$), clindamycin (inducible + constitutive resistance [χ^2 for linear trend = 17.50, $P < 0.01$]), ciprofloxacin (χ^2 for linear trend = 38.92, $P < 0.01$), tetracyclines (χ^2 for linear trend = 10.84, $P = <0.01$) and trimethoprim–sulfamethoxazole (χ^2 for linear trend = 12.12, $P = <0.01$) resistant MRSA, 2013–2019 (Figure 27).

Figure 27: Methicillin-resistant *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, 2013–2019



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

Notes:

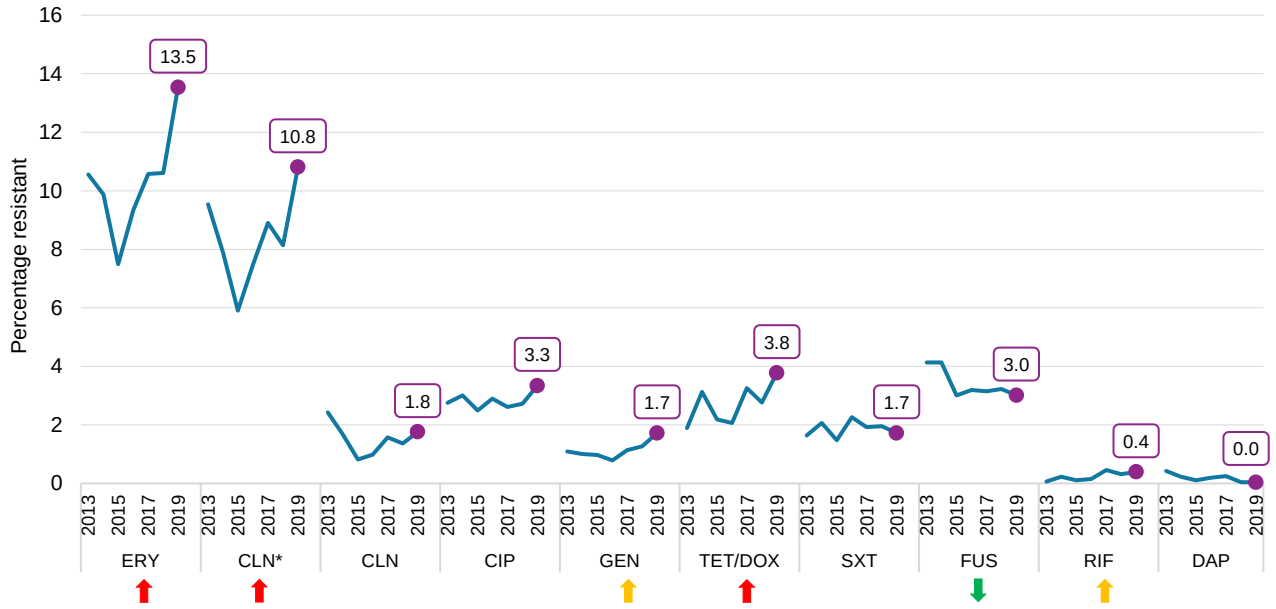
1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. Green arrows indicate antimicrobial agents with significant decrease ($P < 0.01$) over the period 2013 to 2019
3. Light blue arrows indicate antimicrobial agents with significant decrease ($0.01 < P < 0.05$) over the period 2013 to 2019
4. Orange arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the period 2013 to 2019

Methicillin-susceptible *Staphylococcus aureus*

Relative to 2018, the percentage resistance for MSSA in 2019 increased for just over two-thirds (67%, 6/9) of the antimicrobial agents tested. A relative increase in resistance was seen with erythromycin (up 27.6%), clindamycin (inducible + constitutive, up 33.0%), ciprofloxacin (up 22.8%), gentamicin (up 35.5%), tetracyclines (up 36.5%), and rifampicin (up 23.1%) (Figure 28).

However, there was a significant increase in resistance to erythromycin (χ^2 for linear trend = 19.23, $P < 0.01$), clindamycin-resistant (inducible + constitutive resistance) (χ^2 for linear trend = 8.479, $P < 0.01$), and tetracyclines (χ^2 for linear trend = 10.76, $P < 0.01$); and a decrease in fusidic acid resistant (χ^2 for linear trend = 4.930, $P = 0.0264$) MSSA over the period 2013-2019 (Figure 28).

Figure 28: Methicillin-susceptible *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, 2013–2019



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

Notes:

1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the period 2013 to 2019
3. Orange arrows indicate antimicrobial agents with significant increase ($0.01 < P < 0.05$) over the period 2013 to 2019
4. Green arrows indicate antimicrobial agents with significant decrease ($0.01 < P < 0.05$) over the period 2013 to 2019

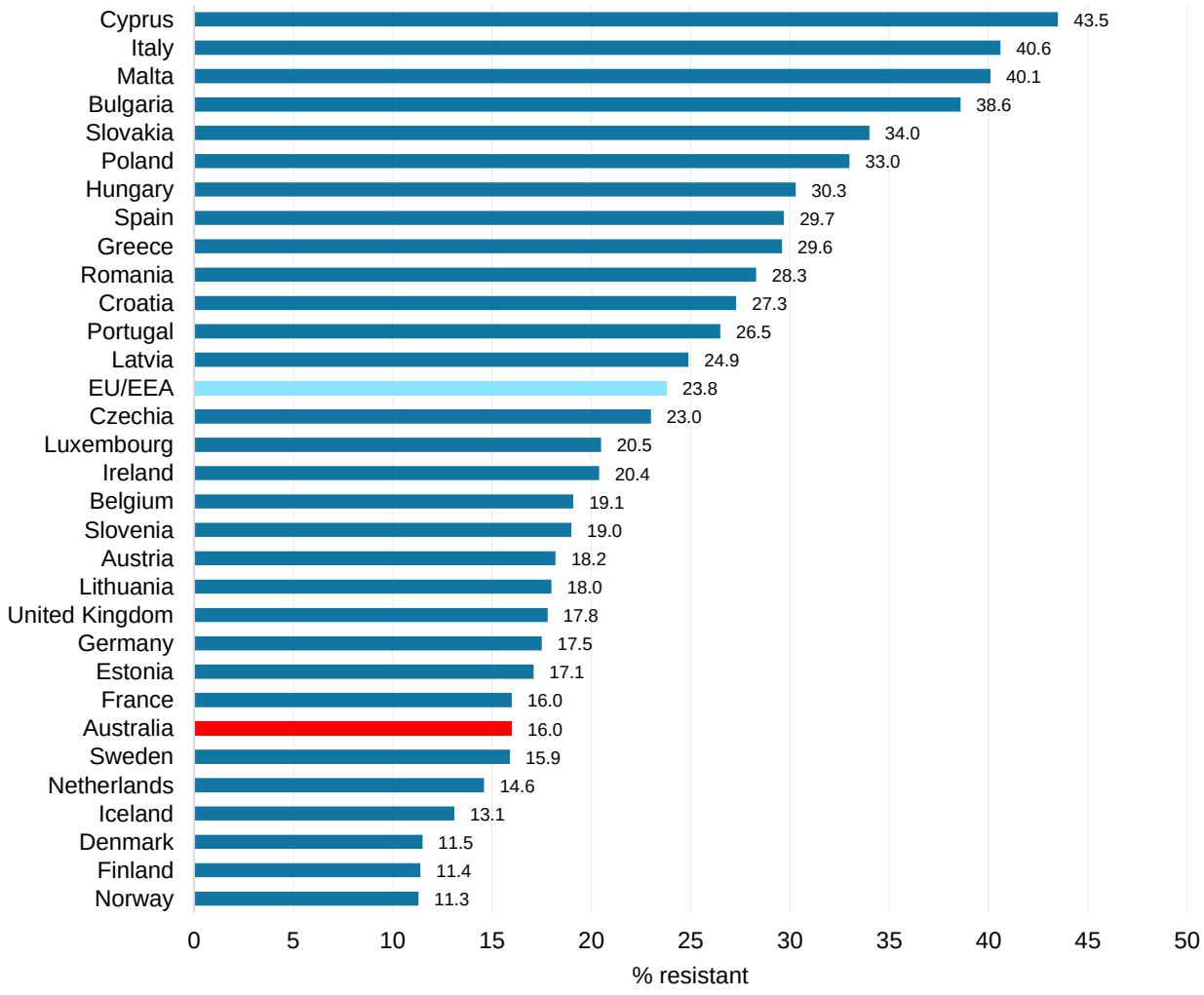
4. International comparisons

Data from AGAR can be compared with data from the European Antimicrobial Resistance Surveillance Network (EARs-Net) program[57], 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 low in Australia compared with most European countries (Figures 29 and 30). 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 31 and 32).

Australia ranks in the top third in rates of resistance to methicillin in *S. aureus* compared to all European countries (Figure 33), and higher than all European countries except Cyprus, Greece and Poland in rates of resistance to vancomycin in *E. faecium* (Figure 34).

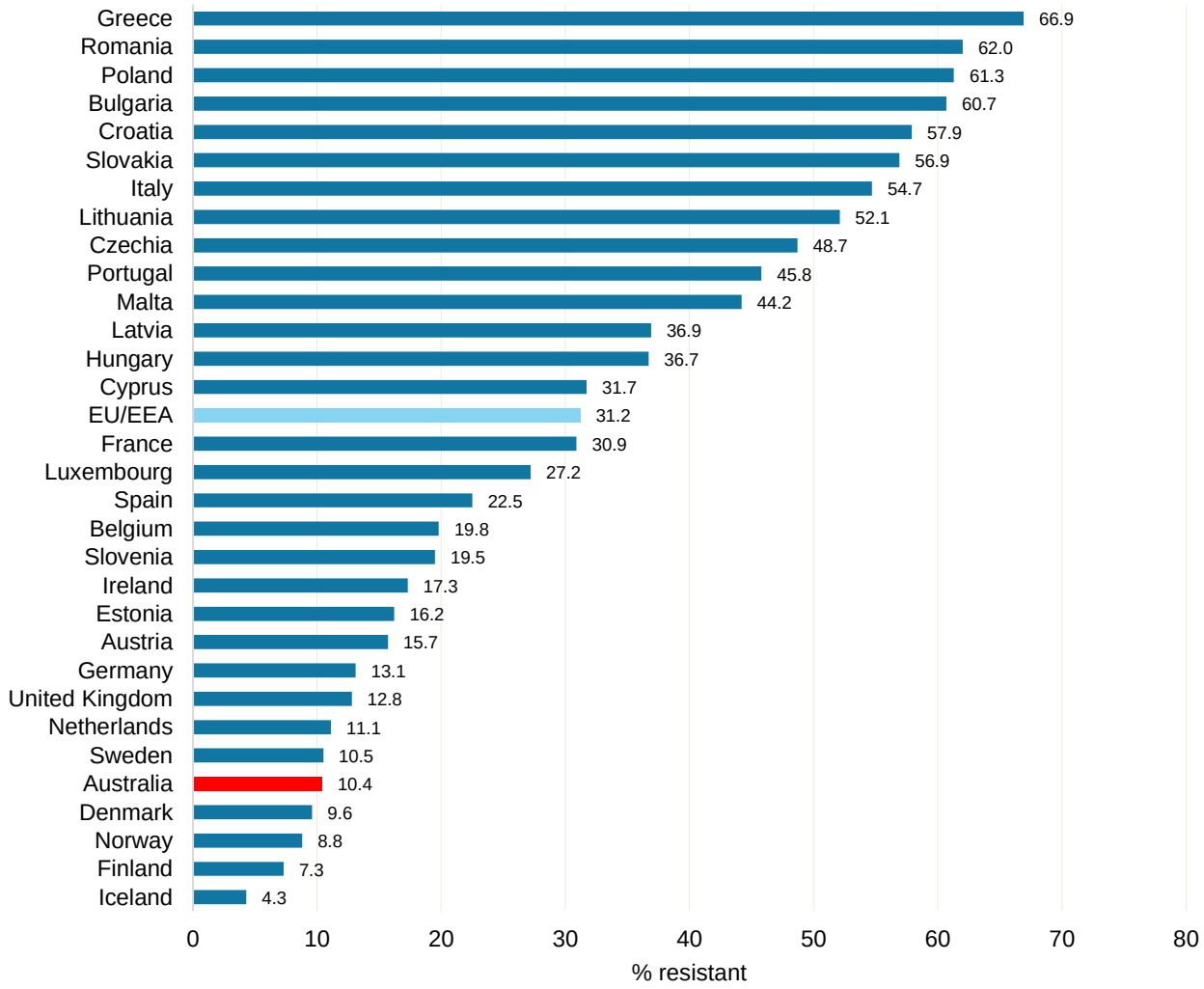
Figure 29: Comparison of *Escherichia coli* rates of resistance to ciprofloxacin in Australia and European countries, blood culture isolates, 2019



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

Source: EARS-Net (Europe)[58]

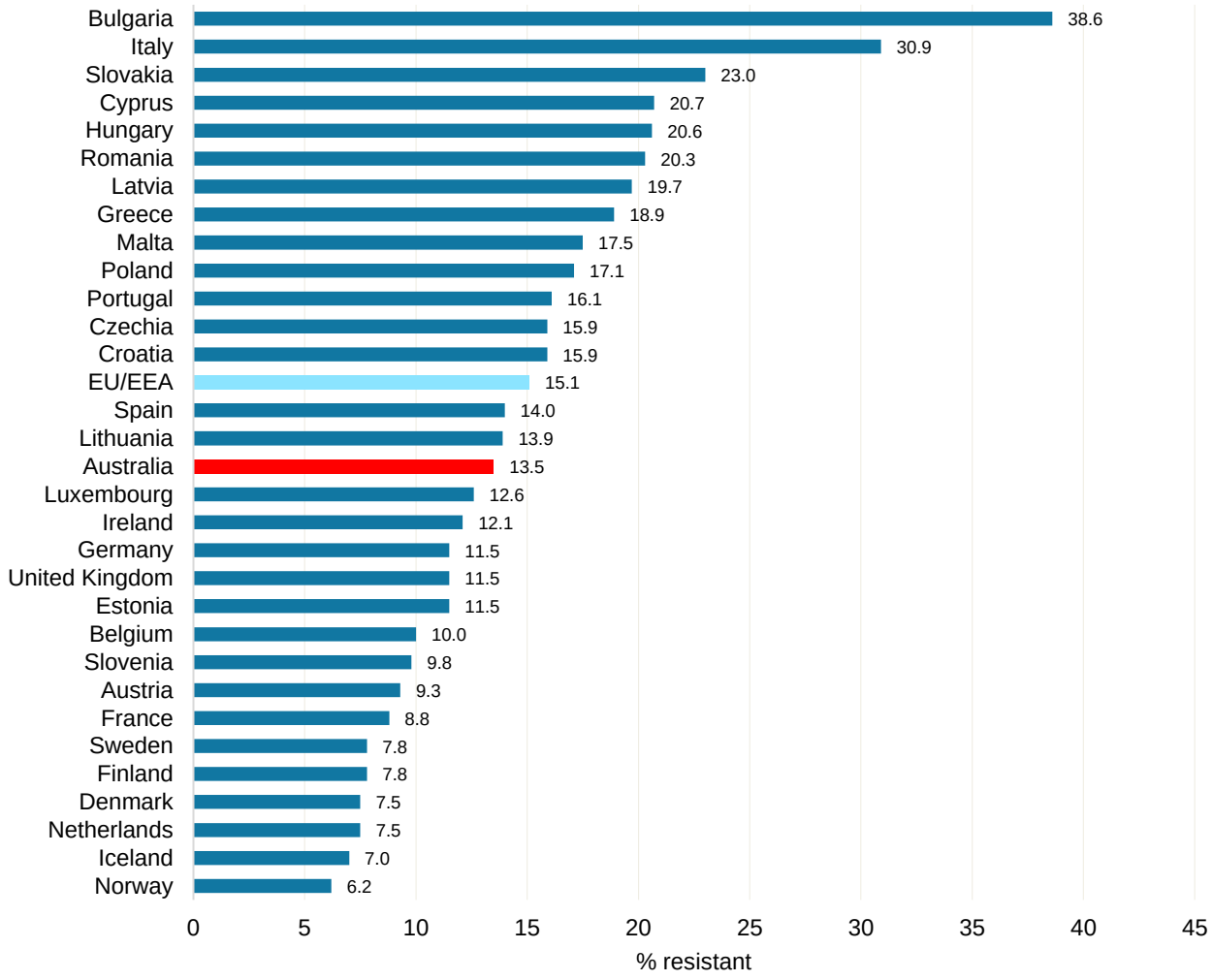
Figure 30: Comparison of *Klebsiella pneumoniae* rates of resistance to ciprofloxacin in Australia and European countries, blood culture isolates, 2019



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

Source: EARS-Net (Europe)[58]

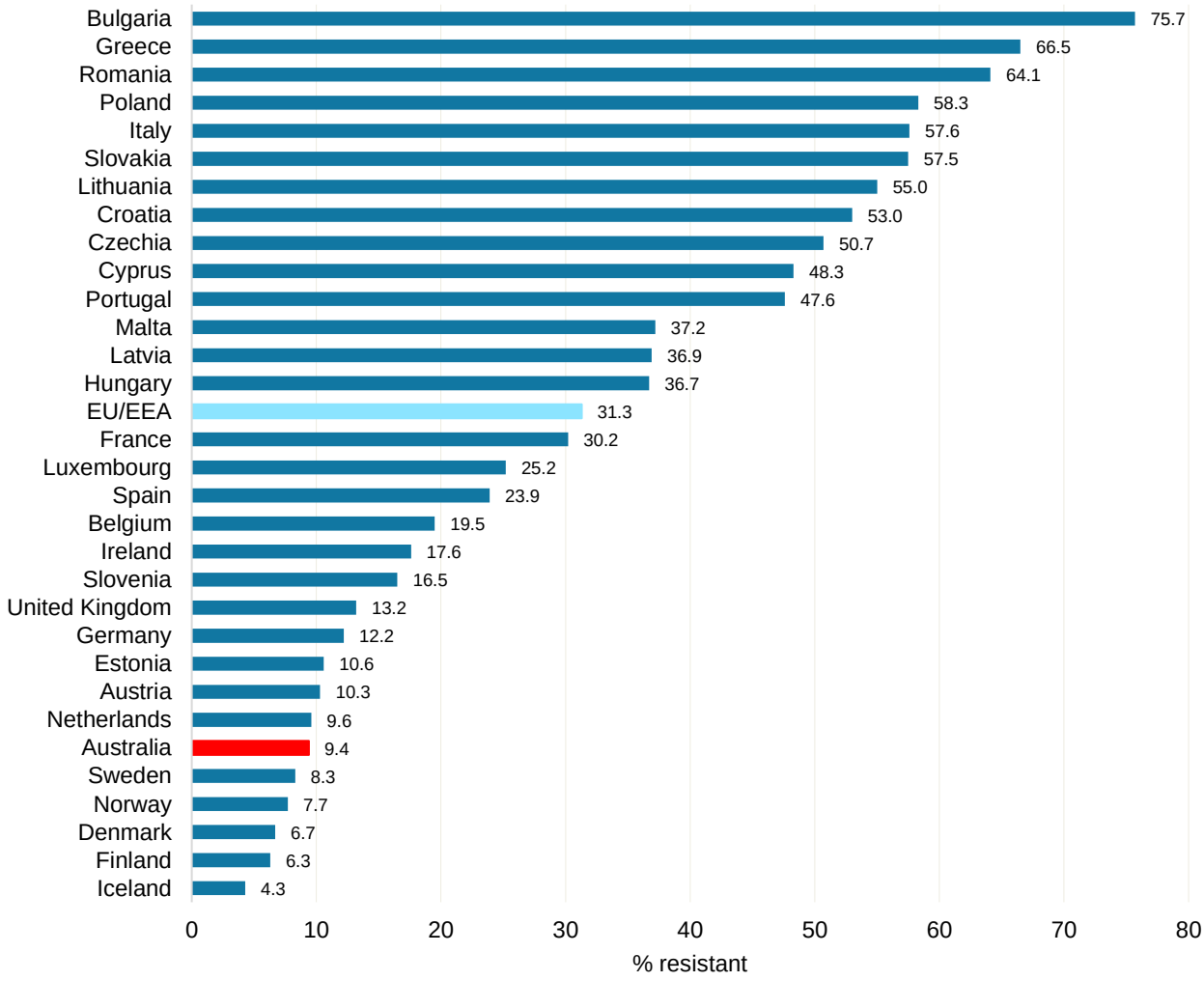
Figure 31: Comparison of *Escherichia coli* rates of resistance to third-generation cephalosporins in Australia and European countries, blood culture isolates, 2019



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

Source: EARS-Net (Europe)[58]

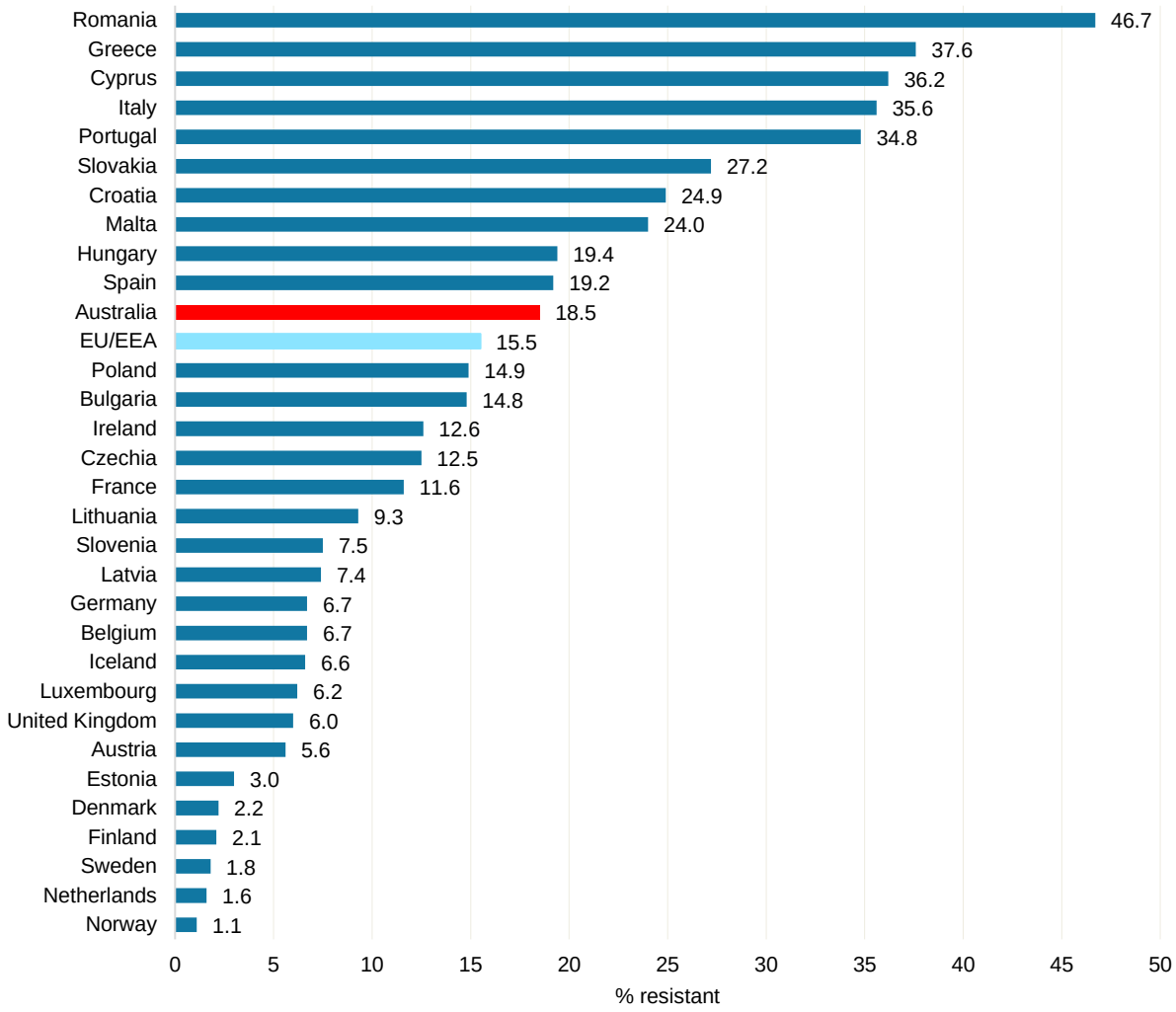
Figure 32: Comparison of *Klebsiella pneumoniae* rates of resistance to third-generation cephalosporins in Australia (2019) and European countries (2018), blood culture isolates



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

Source: EARS-Net (Europe)[58]

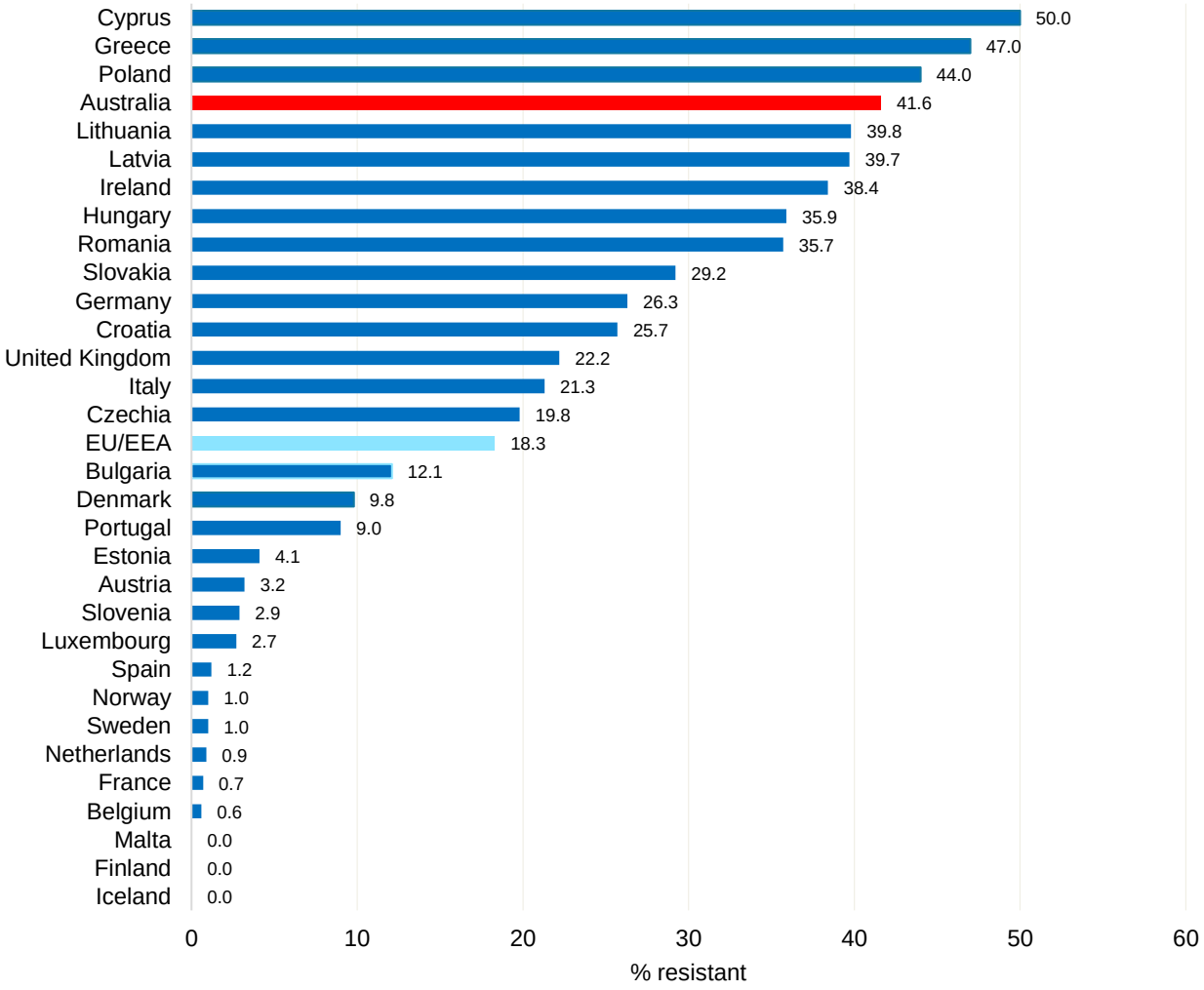
Figure 33: Comparison of *Staphylococcus aureus* rates of resistance to methicillin in Australia and European countries, blood culture isolates, 2019



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

Source: EARS-Net (Europe)[58]

Figure 34: Comparison of *Enterococcus faecium* rates of resistance to vancomycin in Australia (2019) and European countries, blood culture isolates, 2019



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

Source: EARS-Net (Europe)[58]

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 39 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.
- Association with relevant mobile genetic element/s (for example, plasmid/s) is not included in this report
- Analysis of membrane permeability alterations is not included in this report.

In 2019, methods used to screen referred GNSOP isolates for mechanisms of resistance changed as follows:

- Selected isolates underwent whole genome sequencing
- All colistin phenotypes reported were derived by broth microdilution
- In unsequenced strains: gene targets for ESBL and pAmpC genes were limited to the most prevalent variants
- *E. coli* were not screened for ST131-O25b by PCR.

6. Discussion and conclusions

AGAR data show that in 2019 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 skin and skin structure, osteomyelitis/septic arthritis, and device-related infection without metastatic focus. Strategies to reduce blood stream infections should take this information on clinical manifestation (sources of bacteraemia) into account.

AGAR data show a longitudinal trend of increasing *E. coli* resistance to key anti-gram negative antimicrobial agents, such as ceftriaxone and ciprofloxacin. The rate of resistance to amoxicillin–clavulanic acid in *E. coli* (7.8%) is lower than the rate of resistance to ciprofloxacin (16.0%). The steady rise in resistance to fluoroquinolones is more striking in hospital-onset bacteraemia, with a change from 13.7% to 21.3% between 2013 and 2019. In *K. pneumoniae* complex, rates of resistance to amoxicillin–clavulanic acid and ciprofloxacin were lower than for *E. coli,* and were 6.7% and 10.2%, respectively, in 2019.

Emerging fluoroquinolone resistance in Australia is a concern. A little over a decade ago, ciprofloxacin-resistance rates were consistently between 1% and 4%.[23, 59] This was attributed to regulatory controls in human and veterinary prescribing, and national therapeutic guidelines, which sought to restrict unnecessary fluoroquinolone use. This report shows that fluoroquinolones, which have been relied on historically as ‘rear-guard’ oral antimicrobials, can no longer be considered as a broadly reliable antimicrobial choice in empiric management of gram-negative infection. Despite this concerning increase, the percentage of fluoroquinolone-resistant *E. coli* in Australia remains low in comparison to most European countries.[57, 58] Because fluoroquinolone resistance is often linked to cephalosporin resistance caused by ESBLs of the CTX-M type, fluoroquinolone use alone may not be solely responsible for the increase. It is possible that the high use of oral cephalosporins is driving this resistance.

In 2019, 14.5% of *E. coli* and 10.3% of *K. pneumoniae* complex displayed an ESBL phenotype. 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 74.6% 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.[60] If the rate continues to rise, it will potentially affect the application of therapeutic guidelines for empirical treatment of severe infections. Current Australian guidelines recommend third-generation cephalosporins for empirical treatment for many conditions, partly to minimise prescribing of broader-spectrum antimicrobials. 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 20.2% in 2019), however community-onset ceftriaxone resistance has remained steady (11.1% in 2016 and 11.9% in 2019).

To date, carbapenemase-producing *Enterobacterales* (CPE) remain uncommon (<0.1% in *E. coli* and 1.1% in *K. pneumoniae* complex). The overall low rates of CPE bacteraemia are encouraging; however, some organisms harbour them more commonly; 2.5% of *E. cloacae* complex infections harbour a carbapenemase in community-onset infections. Examining previous and current AGAR surveys, most CPEs are endemic in origin.[28, 61] Fifteen of the 24 CPEs had $bla_{\text{IMP-4}}$, reported, predominately from Victoria (8/15, 53.3%) and New South Wales (5/15, 33.3%); one isolate with $bla_{\text{IMP-4}}$ was isolated in Western Australia and one in Queensland. Of note, there were no KPC-types reported in the 2019 survey. The nine non-IMP-4 isolates (9 patients) are thought to be predominantly 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*.[62] 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. One *E. coli* harbouring mobile colistin resistance genes (*mcr-1.1*) was detected from all isolates referred for PCR testing. Whole genome sequencing of isolates with carbapenemase activity detected nine Enterobacterales with the $bla_{\text{IMP-4}}$ carbapenemase gene (*E. cloacae* complex [*n* = 7], *K. pneumoniae* [*n* = 1], *E. coli* [*n* = 1]) also harboured *mcr-9.1*. Four additional *E. cloacae* complex isolates that did not produce a carbapenemase gene had *mcr-9.1* (*n* = 3) or *mcr-10.1* (*n* = 1).

mcr-9 has recently been found among several species of *Enterobacterales*[41] often on an IncHI2 plasmid, but the two downstream genes reported to be involved in induction of *mcr-9* expression by sub-inhibitory concentrations of colistin[42] are not present here, and the isolates had colistin MICs between 0.125 and 0.5 mg/L by broth microdilution. One *E. cloacae* complex isolate which carried *mcr-10.1* expressed heterogenous colistin resistance.

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 2017–2018 was 5.4 days.[63] Thirty-day all-cause mortality due to *E. faecium* in 2019 was high (26.4%); there were no significant differences in 30-day all-cause mortality between community- and hospital-onset cases, or 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* complex and *E. faecium* hospital-onset infections exceeds community-onset infections.

The emergence of ampicillin-resistant clonal complex 17 *E. faecium* bacteraemia is a worldwide phenomenon. In addition to ampicillin 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* (26.4%) and *E. faecalis* (13.7%).

In the 2019 survey, 45.4% 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, 48.8% of vancomycin-resistant *E. faecium* bacteraemias were due to *vanA*; increasing from 6.1% in 2013. Since 2017, vanA genotype has remained around 50% (2018, 52.7%, 2019, 48.2%). This type of vancomycin resistance has emerged rapidly in the past seven years, particularly in New South Wales and the Australian Capital Territory, where it is now the dominant genotype. This in turn has reduced the overall teicoplanin susceptibility of *E. faecium* in Australia.

The percentage of *E. faecium* bacteraemia isolates that are resistant to vancomycin in Australia is significantly higher than that seen in almost all European countries. In 2019, the European Union/European Economic Area (EU/EEA) population-weighted mean percentage was 18.3%; most other countries are below 40%, except for Cyprus (50.1%), Greece (47.0%), and Poland (44.0%).[57, 58]

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

The overall rates of MRSA increased from 17.4% in 2018[64] to 18.5% in the 2019 study. This compares with the 2019 EU/EEA population-weighted mean MRSA percentage of 18.5%, ranging from 1.1% in Norway to 46.7% in Romania.[57, 58]

The rate of community-onset SABs that are methicillin resistant has remained steady. CA-MRSA clones are an increasing source of hospital-onset bacteraemia (particularly 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 *Methicillin-resistant* Staphylococcus aureus *in Australia. MRSA bacteraemia – 2013 to 2018*.[65] This technical paper will be updated as appropriate by AGAR and the Commission to provide further information on the issue.

Although it was not possible to dissect out all the factors affecting all-cause 30-day mortality in the AGAR data, it is notable that multidrug resistance (MDR) plays a contributory role for some species. Higher rates of all-cause mortality with MDR versus non-MDR isolates were seen with *E. coli*, *E. cloacae* complex, *E. faecium* and *P. aeruginosa* in particular. Such a difference was only observed for *S. aureus* in hospital-onset cases,

It should be noted that outbreaks of multidrug-resistant organisms occur in hospitals and other institutional care settings, and substantial transmission occurs before invasive blood stream infections develop. AGAR data may therefore underestimate local or regional spread of multidrug-resistant organisms, and may not assist with early detection of sentinel resistances, such as certain CPEs. AGAR bacteraemia data need to be assessed with other sources of information to provide broader insights into antimicrobial resistance in Australia. The AURA Surveillance System enables these assessments via Australian Passive AMR Surveillance (APAS) and National Alert System for Critical Antimicrobial Resistances (CARAlert) data, which complement AGAR data.

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

Abbreviations

Abbreviation	Term
AGAR	Australian Group on Antimicrobial Resistance
ANCU	*AURA National Coordinating Unit*
APAS	Australian Passive AMR Surveillance
AURA	Antimicrobial Use and Resistance in Australia
CI	confidence interval
CLSI	Clinical and Laboratory Standards Institute
QRDR	Quinolone resistant determining region
ESBL	extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
MIC	minimum inhibitory concentration
PCR	Polymerase chain reaction
PMQR	Plasmid mediated quinolone resistance

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Reference laboratories

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- All isolates with meropenem MIC >0.25 mg/L (*Enterobacterales*) or MIC >4 mg/L (*P. aeruginosa* and *Acinetobacter* species)
- *mcr* positive isolates
- All referred isolates of *P. aeruginosa*
- All referred isolates of *Acinetobacter* species
- All referred *Salmonella* species
- Representatives of bacterial species (mainly *E. coli* and *K. pneumoniae*) by phenotype, genotype and region

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Appendix A. Study design

Thirty-nine institutions participated in the 2019 survey, 33 adult and six children's hospitals. All states and territories were represented. The hospital peer group/type[66] represented were:

Principal referral hospitals (*n* = 25)
Public acute group A hospitals (*n* = 5)
Children's hospitals (*n* = 5)
Combined Women's and children's hospitals (*n* = 1)
Private acute group A hospitals (*n* = 2)
[Regional Western Australia].

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–A3). At Bronze level, participating laboratories provided date of collection, date of birth, sex, postcode and admission date. At Silver level, participating laboratories provided discharge date, device-related infection, principal clinical manifestation, intensive care unit admission, outcome at 30 days and date of death.

Table A1: Level of participation of laboratories that contributed data on gram-negative* bacteraemia, by state and territory, 2019

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	10	2	8
Victoria	7	0	7
Queensland	7	1	6
South Australia†	3	1.5	1.5
January–March		*2*	*0*
April–December		*0*	*2*
Western Australia	7	3	4
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	39	8.5	30.5

* *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
† Two institutions increased participation level from bronze to sliver from April 2019

Table A2: Level of participation of laboratories that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2019

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	10	1	9
Victoria	7	0	7
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	39	6	33

Table A3: Level of participation of laboratories that contributed data on enterococcal bacteraemia, by state and territory, 2019

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	10	1	9
Victoria	7	0	7
Queensland	7	0	7
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	39	5	34

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* = 35) 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, AST-P612, AST-P643, or AST-P656) or Phoenix (NMIC-404, NMIC-422, PMIC-84) cards were used by all participants throughout the survey period.

The CLSI M100-A30[25] and the EUCAST v10.0[26] breakpoints from January 2020 were used in the analysis.

S. aureus were classified as MRSA if cefoxitin screen positive (Vitek) or cefoxitin MIC > 4 mg/L (Phoenix). Cefoxitin screen negative isolates that were oxacillin resistant underwent mecA/nuc PCR. If mecA was detected, the isolate was reported as MRSA. All *S. aureus* with penicillin MIC ≤ 0.12 mg/L and no β-lactamase results provided were tested for penicillinase by disc diffusion. A sharp zone edge around a penicillin 1 unit disc was recorded as a penicillinase producer.[26]

Additional tests were performed on *S. aureus* to confirm unusual resistances or to provide additional information for antimicrobials where issues have been reported with Vitek/Phoenix panels[67-69]

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

Additional tests performed on *Enterococcus* species include:

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

Antimicrobials tested

The antimicrobials tested is shown in Table B1.

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

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v10.0†		
	S	SDD	I	R	S	I	R
Benzylpenicillin							
Enterococcus spp.	≤8		–§	≥16	–#	–#	–#
Staphylococcus aureus	≤0.12		–§	≥0.25	≤0.125	–§	>0.125
Amikacin							
Acinetobacter spp.	≤16		32	≥64	≤8	**–§**	**>8**
Enterobacterales	≤16		32	≥64	≤8	**–§**	**>8**
Pseudomonas spp.	≤16		32	≥64	**≤16**	**–§**	>16
Amoxicillin–clavulanic acid							
Enterobacterales	≤8/4		16/8	≥32/16	≤8**	–§	>8**
Enterococcus spp.	–#		–#	–#	≤4**	8**	>8**
Ampicillin							
Enterobacterales	≤8		16	≥32	≤8	–§	>8
Enterococcus spp.	≤8		–§	≥16	≤4	8	>8
Aztreonam (Phoenix card)							
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	**≤0.001**	**0.002–16**	>16
Cefazolin							
Enterobacterales	≤2		4	≥8	**≤0.001**	**0.002–4**	>4
Cefepime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤2	4–8	–§	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	**≤0.001**	**0.002–8**	>8
Cefalexin	–#		–#	–#	≤16	–§	>16
Cefuroxime (Phoenix card)							
Enterobacterales (parental)	≤8		16	≥32	≤0.001	0.002–8	>8
Enterobacterales (oral)	≤4		8–16	≥32	≤8	–§	>8
Cefoxitin							
Enterobacterales	≤8		16	≥32	–#	–#	–#
Ceftazidime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	**≤0.001**	**0.002–8**	>8
Ceftolozane–tazobactam							
Enterobacterales	≤2/4		4/4	≥8/4	≤2	–§	>2
Pseudomonas spp.	≤4/4		8/4	≥16/4	≤4	–§	>4
Ceftriaxone							
Acinetobacter spp.	≤8		16–32	≥64	–#	–#	–#
Enterobacterales	≤1		2	≥4	≤1	2	>2

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v10.0†		
	S	SDD	I	R	S	I	R
Chloramphenicol (Phoenix card)							
Staphylococcus aureus	≤8		16	≥32	≤8	–§	>8
Ciprofloxacin							
Acinetobacter spp.	≤1		2	≥4	**≤0.001**	**0.002–1**	>1
Enterobacterales	≤0.25		0.5	≥1	≤0.25	0.5	>0.5
Salmonella spp.‡	≤0.06		0.12–0.5	≥1	≤0.06	–§	>0.06
Enterococcus spp.§§	≤1		2	≥4	≤4##	–##	>4##
E. faecalis (ECOFF)##					≤4	–§	>4
E. faecium (ECOFF)##					≤8	–§	>8
Staphylococcus aureus	≤1		2	≥4	**≤0.001**	**0.002–1**	>1
Pseudomonas spp.	≤0.5		1	≥2	**≤0.001**	**0.002–0.5**	>0.5
Clindamycin							
Staphylococcus aureus	≤0.5		1–2	≥4	≤0.25	0.5	>0.5
Colistin (Phoenix card)							
Acinetobacter spp.	**–#**		**≤2**	≥4	≤2	–§	>2
Enterobacterales	**–#**		**≤2**	**≥4**	≤2	–§	>2
Pseudomonas spp.	**–#**		**≤2**	≥4	≤2	–§	>2
Daptomycin							
Enterococcus faecium		≤4	–	≥8	–#	–#	–#
Enterococcus spp. other than *E. faecium*	≤2		4	≥8	–#	–#	–#
Staphylococcus aureus	≤1		–#	–#	≤1	–§	>1
Doxycycline (Phoenix card)							
Enterococcus spp.	≤4		8***	≥16***	–#	–#	–#
Staphylococcus aureus	≤4		8***	≥16***	≤1	2	>2
Ertapenem (Phoenix card)	≤0.5		1	≥2	≤0.5	–§	>0.5
Erythromycin							
Enterococcus spp.	≤0.5		1–4	≥8	–#	–#	–#
Staphylococcus aureus	≤0.5		1–4	≥8	≤1	2	>2
Fosfomycin (Phoenix card)							
Enterobacterales	≤64		128	≥256	≤32	–§	>32
Fusidic acid							
Staphylococcus aureus	–#		–#	–#	≤1	–§	>1
Gentamicin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	>4
Enterobacterales	≤4		8	≥16	≤2	**–§**	**>2**
Pseudomonas spp.	≤4		8	≥16	**–#**	**–#**	**–#**
Staphylococcus aureus	≤4		8	≥16	≤1	–§	>1
Imipenem (Phoenix card)							
Acinetobacter spp.	≤2		4	≥8	≤2	4	>4
Enterobacterales	≤1		2	≥4	≤2	4	>4
Enterococcus spp.	–#		–#	–#	**≤0.001**	**0.002–4**	**>4**
Pseudomonas spp.	≤2		4	≥8	**≤0.001**	**0.002–4**	>4
Linezolid							

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v10.0†		
	S	SDD	I	R	S	I	R
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	–#	–#	–#
Staphylococcus aureus	≤32		64	≥128	–#	–#	–#
Norfloxacin							
Enterobacterales	**≤4**		**8**	**≥16**	≤0.5	**–§**	**>0.5**
Pseudomonas spp.	**≤4**		**8**	**≥16**	–#	–#	–#
Oxacillin							
Staphylococcus aureus	≤2		–§	≥4	–#	–#	–#
Piperacillin–tazobactam							
Acinetobacter spp.	≤16/4		32/4–64/4	≥128/4	–#	–#	–#
Enterobacterales	≤16/4		32/4–64/4	≥128/4	≤8	16	>16
Pseudomonas spp.	≤16/4		32/4–64/4	≥128/4	**≤0.001**	**0.002–16**	>16
Rifampicin							
Enterococcus spp.	≤1		2	≥4	–#	–#	–#
Staphylococcus aureus	≤1		2	≥4	≤0.06§§§	0.12–0.5	>0.5
Teicoplanin							
Enterococcus spp.	≤8		16	≥32	≤2	–§	>2
Staphylococcus aureus	≤8		16	≥32	≤2	–§	>2
Tetracycline							
Acinetobacter spp.	≤4		8	≥16	–#	–#	–#
Enterobacterales	≤4		8	≥16	–#	–#	–#
Enterococcus spp.	≤4		8	≥16	–#	–#	–#
Staphylococcus aureus	≤4		8	≥16	≤1	2	>2
Ticarcillin–clavulanate							
Acinetobacter spp.	≤16/2		32/2–64/2	≥128/2	–#	–#	–#
Enterobacterales	≤16/2		32/2–64/2	≥128/2	≤8	16	>16
Pseudomonas spp.	≤16/2		32/2–64/2	≥128/2	**≤0.001**	**0.002–16**	>16
Tigecycline (Phoenix card)	–#		–#	–#	≤0.5	–§	>0.5
Tobramycin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	>4
Enterobacterales	≤4		8	≥16	≤2	**–§**	**>2**
Pseudomonas spp.	≤4		8	≥16	**≤2**	–§	**>2**
Trimethoprim							
Enterobacterales	≤8		–§	≥16	**≤4**	**–§**	>4
Staphylococcus aureus	≤8		–§	≥16	–#	–#	–#
Trimethoprim–sulfamethoxazole							
Acinetobacter spp.	≤2/38		–§	≥4/76	≤2/38	4/76	>4/76

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v10.0†		
	S	SDD	I	R	S	I	R
Enterobacterales	≤2/38		–§	≥4/76	≤2/38	4/76	>4/76
Staphylococcus aureus	≤2/38		–§	≥4/76	≤2	4	>4
Vancomycin							
Enterococcus spp.	≤4		8–16	≥32	≤4	–§	>4
Staphylococcus aureus	≤2		4–8	≥16	≤2	–§	>2

CLSI = Clinical and Laboratory Standards Institute; ECOFF = epidemiological cut-off value; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate (CLSI) and susceptible, increased exposure (EUCAST); R = resistant; S = susceptible (CLSI) and susceptible, standard dosing regimen (EUCAST); SDD = sensitive dose dependent (CLSI)

Note: Information in **blue** boldface type is new or modified since 2019

* The breakpoints selected to identify resistance are described in *Performance Standards for Antimicrobial Susceptibility Testing: Twenty-seventh informational supplement*, CLSI document M100-S30, January 2020.
† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 10.0, 2020 (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 ciprofloxacin concentration range available on the panels used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species
§§ The ciprofloxacin concentration range on the Phoenix panel restricts the ability to categorise *Enterococcus* spp.
Breakpoints apply to uncomplicated urinary tract infections only. The ciprofloxacin ECOFF was used to distinguish between *E. faecalis* and E. *faecium* with and without acquired resistance mechanisms
*** Doxycycline concentration range (Phoenix panel) restricts ability to accurately identify intermediate and resistant category
†‡ Breakpoints apply to *E. coli* only
§§§ The rifampicin concentration on the cards restricts category interpretation to non-resistant or resistant

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 *Enterobacterales with meropenem MIC >0.25 mg/L; all Acinetobacter species or P. aeruginosa with meropenem MIC* ≥ 8 mg/L; all isolates with amikacin MIC >32 mg/L, and all isolates with colistin MIC > 4 mg/L were referred to a central laboratory (Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research) for PCR screening and/or whole genome sequencing.

All referred isolates, except *P. aeruginosa*, *Acinetobacter* spp., *Salmonella* spp., and *Enterobacterales* with meropenem MIC >0.25 mg/L which underwent WGS, were screened using real-time multiplex polymerase chain reaction (PCR) using published primers to detect ESBLs ($bla_{\text{SHV-ESBL}}$ with G→A substitution at position 700 and/or 703, $bla_{\text{CTX-M}}$ groups 1 and 9, bla_{VEB}), plasmid-borne AmpC ($bla_{\text{CMY-2-like}}$, bla_{DHA}) and carbapenemase bla_{IMP}, bla_{NDM}, bla_{VIM}) genes.[70]

Assays for other extended spectrum β-lactamases targets ($bla_{\text{ACT/MIR}}$, bla_{KPC}, $bla_{\text{OXA-48-like}}$, bla_{GES}, bla_{SME}, bla_{SPM}, bla_{AIM}, bla_{GIM}, bla_{SIM}, $bla_{\text{OXA-23/24/58}}$); aminoglycoside ribosomal methytransferases (*armA*, *rmtA*, *rmtB*, *rmtC*, *rmtD*, *rmtE*, *rmtF*, *rmtG*, *rmtH*); and mobile colistin resistance genes (*mcr-1*, *mcr-2*, *mcr-3*, *mcr-4*, *mcr-5*) were detected using in-house, NATA accredited primers and probes in routine use by the Centre for Infectious Diseases & Microbiology Laboratory Services, ICPMR, at Westmead Hospital.

Whole genome sequencing was performed by the Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, CIDMLS, ICPMR, Westmead Hospital using the Illumina NextSeq 500 platform. Data were analysed using a modification of the Nullarbor bioinformatic pipeline[27], incorporating searching contigs against the NCBI AMRFinder database (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA313047) using ABRicate[71] and AMRFinder[72], followed by a custom AMR-specific pipeline which includes a read-based search using ARIBA[73] against the CARD[74] and NCBI databases. Ambiguities and potential multiple gene copies/variants were checked manually by mapping reads to reference genes from https://www.ncbi.nlm.nih.gov/pathogens/isolates#/refgene/ using Geneious. Reported chromosomal mutations were derived from ARIBA result tables (quinolone mutations) or its mapping-based reassemblies (all other mutations). Additional mutations in *gyr* and *par* genes identified by PointFinder[45] potentially contributing to resistance were also examined manually.

All gram-negative isolates with carbapenemase activity, *E. faecium* and MRSA were subjected to whole genome sequencing using the Illumina NextSeq platform. Data were analysed using the Nullarbor bioinformatic pipeline.[27] The pipeline was used to identify the multi-locus sequence type, *van* gene (*E. faecium*), SCC*mec* type (MRSA) and Panton-Valentine leucocidin (MRSA).

Quality control

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

Data validation

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

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

Appendix C. Susceptibility to antimicrobial agents

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

Table C1: Susceptibility (CLSI and EUCAST) to antimicrobial agents in indicator species of national priority, by state and territory, 2019

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	4	11	27	5	8	1	3	0	59
	%R	n/a	0.0, 0.0	0.0, 3.7	n/a	n/a	n/a	n/a	n/a	0.0, 1.7
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%R	0.0, 0.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	5.0, 10.0	0.0, 0.0	n/a	0.2, 0.7
Escherichia coli	n	1,378	922	817	440	736	201	205	185	4,884
	%R	0.2, 0.9	0.0, 2.2	0.0, 0.4	0.0, 0.2	0.0, 0.5	0.0, 0.5	0.0, 1.5	0.0, 0.5	0.1, 0.9
Klebsiella aerogenes	n	41	32	14	5	19	5	7	4	127
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%R	0.3, 0.9	1.9, 4.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 2.0	0.0, 0.0	0.0, 2.8	0.4, 1.2
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%R	0.0, 5.1	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, 1.5
Pseudomonas aeruginosa	n	242	119	174	65	98	19	15	23	755
	%R	1.2, 1.2	0.0, 0.0	0.0, 0.6	0.0, 0.0	0.0, 0.0	0.0, 10.5	0.0, 0.0	0.0, 0.0	0.4, 0.8
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Serratia marcescens	n	74	32	57	8	26	6	2	8	213
	%R	0.0, 2.7	0.0, 0.0	1.8, 3.5	n/a	0.0, 0.0	n/a	n/a	n/a	0.5, 1.9
Amoxicillin–clavulanic acid										
Escherichia coli	n	1,047	922	817	269	736	201	205	185	4,382
	%I	14.3, –†	13.1, –†	15.2, –†	11.9, –†	15.4, –†	17.9, –†	21.0, –†	16.2, –†	14.8, –†
	%R	9.1, –	8.5, –	6.5, –	5.9,	7.5, –	6.0, –	9.8,	7.0, –	7.8, –†

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		†	†	†	–†	†	†	–†	†	
Klebsiella oxytoca	n	47	55	35	14	32	17	4	11	215
	%I	2.1, –†	3.6, –†	5.7, –†	0.0, –†	0.0, –†	0.0, –†	n/a	18.2, –†	3.3, –†
	%R	2.1, –†	10.9, –†	11.4, –†	0.0, –†	3.1, –†	5.9, –†	n/a	0.0, –†	6.0, –†
Klebsiella pneumoniae complex	n	264	212	249	49	160	51	45	36	1,066
	%I	5.7, –†	7.5, –†	2.4, –†	4.1, –†	3.1, –†	7.8, –†	13.3, –†	2.8, –†	5.2, –†
	%R	8.3, –†	9.9, –†	4.8, –†	4.1, –†	3.8, –†	5.9, –†	4.4, –†	8.3, –†	6.7, –†
Proteus mirabilis	n	66	45	38	22	39	14	2	12	238
	%I	4.5, –†	0.0, –†	0.0, –†	0.0, –†	10.3, –†	7.1, –†	n/a	0.0, –†	3.4, –†
	%R	3.0, –†	0.0, –†	5.3, –†	0.0, –†	0.0, –†	0.0, –†	n/a	8.3, –†	2.1, –†
Salmonella species (non-typhoidal)	n	29	17	39	3	27	5	3	1	124
	%I	3.4, –†	0.0, –†	0.0, –†	n/a	3.7, –†	n/a	n/a	n/a	1.6, –†
	%R	3.4, –†	0.0, –†	0.0, –†	n/a	0.0, –†	n/a	n/a	n/a	0.8, –†
Salmonella species (typhoidal)	n	12	31	13	1	7	1	1	7	73
	%I	8.3, –†	0.0, –†	0.0, –†	n/a	n/a	n/a	n/a	n/a	1.4, –†
	%R	0.0, –†	0.0, –†	0.0, –†	n/a	n/a	n/a	n/a	n/a	0.0, –†
Serratia marcescens	n	62	32	57	3	26	6	2	8	196
	%I	29.0, –†	21.9, –†	17.5, –†	n/a	34.6, –†	n/a	n/a	n/a	26.0, –†
	%R	56.5, –†	59.4, –†	71.9, –†	n/a	34.6, –†	n/a	n/a	n/a	58.2, –†
Ampicillin										
Enterococcus faecalis	n	218	128	124	64	80	41	7	36	698
	%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	209	164	63	45	56	25	13	19	594
	%R	92.8, 92.8	94.5, 94.5	90.5, 90.5	86.7, 86.7	91.1, 91.1	92.0, 92.0	69.2, 69.2	73.7, 73.7	91.2, 91.2
Escherichia coli	n	1,379	918	816	440	736	201	205	186	4,881
	%I	1.6, –§	1.5, –§	1.6, –§	3.0, –§	2.4, –§	4.0, –§	1.5, –§	1.1, –§	1.9, –§
	%R	55.0, 56.6	55.2, 56.8	52.7, 54.3	47.3, 50.2	56.1, 58.6	47.3, 51.2	70.7, 72.2	53.8, 54.8	54.4, 56.3
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%I	78.5, –§	88.9, –§	92.1, –§	91.7, –§	82.1, –§	92.9, –§	n/a	75.0, –§	85.3, –§
	%R	21.5, 21.5	11.1, 11.1	7.9, 7.9	8.3, 8.3	17.9, 17.9	7.1, 7.1	n/a	25.0, 25.0	14.7, 14.7
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%I	0.0, –§	0.0, –§	0.0, –§	n/a	0.0, –§	n/a	n/a	n/a	0.0, –§
	%R	9.4,	0.0,	2.6,	n/a	3.7,	n/a	n/a	n/a	4.7, 4.7

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		9.4	0.0	2.6		3.7				
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%I	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	0.0, –[§]
	%R	5.0, 5.0	9.7, 9.7	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	4.9, 4.9
Benzylpenicillin										
Enterococcus faecalis	n	216	102	123	64	79	17	7	35	643
	%R	0.5, –[#]	1.0, –[#]	0.8, –[#]	0.0, –[#]	1.3, –[#]	0.0, –[#]	0.0, –[#]	2.9, –[#]	0.8, –[#]
Enterococcus faecium	n	206	137	62	44	55	11	13	18	546
	%R	92.7, –[#]	94.2, –[#]	91.9, –[#]	72.7, –[#]	90.9, –[#]	81.8, –[#]	76.9, –[#]	72.2, –[#]	89.9, –[#]
Staphylococcus aureus	n	905	546	647	237	495	135	63	121	3,149
	%R	81.1, 81.1	81.5, 81.5	76.7, 76.7	76.8, 76.8	78.8, 78.8	78.5, 78.5	96.8, 96.8	80.2, 80.2	79.7, 79.7
Cefazolin										
Escherichia coli	n	1,046	922	817	268	736	201	205	185	4,380
	%R	19.1, 26.3	20.3, 25.8	12.1, 20.0	15.7, 19.4	15.5, 23.8	10.9, 17.9	20.5, 30.7	20.0, 26.5	17.0, 24.0
Klebsiella oxytoca	n	47	55	35	14	32	17	4	11	215
	%R	17.0, 51.1	30.9, 58.2	20.0, 60.0	7.1, 42.9	28.1, 62.5	35.3, 64.7	n/a	36.4, 45.5	24.7, 56.3
Klebsiella pneumoniae complex	n	264	212	249	49	160	51	45	35	1,065
	%R	12.1, 15.2	19.8, 20.3	6.8, 8.4	8.2, 8.2	6.3, 6.9	7.8, 9.8	15.6, 17.8	14.3, 17.1	11.4, 13.0
Proteus mirabilis	n	66	45	38	22	39	14	2	12	238
	%R	3.0, 13.6	2.2, 15.6	2.6, 13.2	0.0, 13.6	2.6, 15.4	0.0, 42.9	n/a	0.0, 33.3	2.1, 16.8
Cefepime										
Acinetobacter baumannii	n	6	9	27	5	8	0	3	0	58
	%I	n/a	n/a	3.7, –[#]	n/a	n/a	n/a	n/a	n/a	3.4, –[#]
	%R	n/a	n/a	11.1, –[#]	n/a	n/a	n/a	n/a	n/a	5.2, –[#]
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%SDD/I	5.1, 9.3	4.3, 14.0	1.1, 5.3	3.0, 3.0	2.1, 4.2	5.0, 15.0	0.0, 0.0	n/a	3.3, 8.7
	%R	1.7, 3.4	1.1, 2.2	2.1, 2.1	0.0, 3.0	0.0, 2.1	0.0, 0.0	0.0, 0.0	n/a	1.2, 2.3
Escherichia coli	n	1,379	922	816	440	736	201	205	185	4,884
	%SDD/I	2.5, 6.7	2.7, 8.2	1.0, 5.4	3.0, 3.9	2.0, 7.3	1.0, 2.5	1.5, 9.8	2.7, 7.6	2.1, 6.6
	%R	4.7, 5.7	3.4, 4.6	1.0, 1.2	6.6, 7.7	1.6, 2.6	1.0, 1.5	2.4, 3.4	2.2, 4.3	3.2, 4.1
Klebsiella aerogenes	n	41	32	14	5	19	5	7	4	127
	%SDD/I	0.0, 0.0	0.0, 0.0	0.0, 7.1	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
	%R	2.4, 2.4	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%SDD/I	0.0, 0.0	1.8, 3.6	0.0, 2.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 1.3
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%SDD/I	1.1, 3.2	1.9, 8.5	0.0, 2.0	0.0, 0.0	0.0, 1.9	2.0, 2.0	2.2, 8.9	0.0, 5.6	0.8, 3.7
	%R	4.6, 5.2	4.2, 5.2	0.0, 0.0	5.6, 5.6	0.6, 0.6	2.0, 3.9	0.0, 0.0	5.6, 5.6	2.9, 3.3
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%SDD/I	0.0, 0.0	2.2, 2.2	2.6, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	8.3, 8.3	1.1, 1.1
	%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
Pseudomonas aeruginosa	n	242	119	174	65	98	19	15	23	755
	%I	2.1, 94.6	1.7, 96.6	2.9, 92.5	3.1, 92.3	3.1, 94.9	0.0, 89.5	6.7, 86.7	0.0, 100.0	2.4, 94.2
	%R	3.3, 5.4	1.7, 3.4	4.6, 7.5	4.6, 7.7	2.0, 5.1	10.5, 10.5	6.7, 13.3	0.0, 0.0	3.4, 5.8
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%SDD/I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%SDD/I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	5.0, 5.0	3.2, 3.2	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	2.5, 2.5
Serratia marcescens	n	74	32	57	8	26	6	2	8	213
	%SDD/I	0.0, 0.0	0.0, 0.0	3.5, 1.8	n/a	0.0, 0.0	n/a	n/a	n/a	0.9, 0.9
	%R	0.0, 0.0	0.0, 0.0	1.8, 5.3	n/a	0.0, 0.0	n/a	n/a	n/a	0.5, 1.4
Cefoxitin										
Escherichia coli	n	1,379	922	816	440	736	201	205	186	4,885
	%R/ecoff**	4.3, 6.9	2.9, 6.0	2.5, 4.5	2.5, 5.7	3.1, 5.8	4.0, 6.5	3.9, 5.9	4.8, 9.1	3.4, 6.1
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%R/ecoff**	0.0, 1.7	1.8, 3.6	0.0, 2.9	0.0, 0.0	0.0, 6.3	0.0, 0.0	n/a	0.0, 0.0	0.4, 2.5
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%R/ecoff**	5.7, 6.3	8.0, 9.4	6.8, 6.8	5.6, 6.7	3.1, 5.6	3.9, 3.9	6.7, 6.7	2.8, 5.6	5.9, 6.8
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%R/ecoff**	1.3, 1.3	0.0, 2.2	0.0, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 1.1
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%R/ecoff**	3.1, 3.1	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%R/ecoff**	0.0,	3.2,	0.0,	n/a	n/a	n/a	n/a	n/a	1.2, 1.2

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		0.0	3.2	0.0						
Ceftazidime										
Acinetobacter baumannii complex	n	5	10	27	5	8	0	3	0	58
	%I	n/a	0.0, –[#]	18.5, –[#]	n/a	n/a	n/a	n/a	n/a	13.8, –[#]
	%R	n/a	0.0, –[#]	4.8, –[#]	n/a	n/a	n/a	n/a	n/a	2.0, –[#]
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%I	0.0, 3.4	0.0, 5.4	0.0, 2.1	3.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.2, 2.6
	%R	24.6, 24.6	26.9, 26.9	16.8, 16.8	15.2, 18.2	10.4, 10.4	30.0, 30.0	14.3, 14.3	n/a	21.3, 21.5
Escherichia coli	n	1,379	922	817	440	736	201	205	185	4,885
	%I	1.5, 6.1	0.3, 6.4	0.6, 5.0	0.9, 5.0	0.5, 6.4	0.5, 1.0	0.5, 9.3	1.6, 8.1	0.9, 5.9
	%R	6.9, 8.4	8.7, 9.0	3.1, 3.7	6.4, 7.3	5.4, 6.0	5.5, 6.0	4.9, 5.4	8.1, 9.7	6.2, 7.1
Klebsiella aerogenes	n	41	32	14	5	19	5	7	4	127
	%I	0.0, 7.3	0.0, 3.1	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 5.5
	%R	34.1, 34.1	50.0, 50.0	21.4, 21.4	n/a	36.8, 36.8	n/a	n/a	n/a	33.9, 34.6
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%I	0.0, 1.7	0.0, 1.8	0.0, 2.9	0.0, 0.0	0.0, 3.1	0.0, 0.0	n/a	0.0, 0.0	0.0, 1.7
	%R	1.7, 1.7	3.6, 3.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.3, 1.3
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%I	1.1, 1.1	1.9, 7.5	0.8, 1.6	0.0, 2.2	0.0, 1.3	2.0, 2.0	2.2, 4.4	2.8, 0.0	1.1, 2.6
	%R	7.8, 8.9	8.5, 10.4	2.8, 3.6	9.0, 9.0	1.9, 1.9	3.9, 5.9	8.9, 11.1	8.3, 11.1	6.1, 7.1
Proteus mirabilis	n	78	45	38	36	39	14	2	12	264
	%I	0.0, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.6, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 2.6	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.4
Pseudomonas aeruginosa	n	240	119	174	65	98	19	15	23	753
	%I	4.2, 91.7	2.5, 94.1	4.6, 88.5	6.2, 86.2	1.0, 93.9	5.3, 84.2	0.0, 93.3	4.3, 91.3	3.7, 91.0
	%R	4.2, 8.3	3.4, 5.9	6.9, 11.5	7.7, 13.8	5.1, 6.1	10.5, 15.8	6.7, 6.7	4.3, 8.7	5.3, 9.0
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	3.1, 3.1	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	5.0, 5.0	3.2, 3.2	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	2.5, 2.5

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	n	74	32	57	8	26	6	2	8	213
Serratia marcescens	%I	0.0, 0.0	0.0, 0.0	0.0, 3.5	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.9
	%R	0.0, 0.0	3.1, 3.1	5.3, 5.3	n/a	0.0, 0.0	n/a	n/a	n/a	2.3, 2.3
Ceftriaxone										
	n	5	11	27	2	8	1	3	0	57
Acinetobacter baumannii complex	%I	n/a	72.7, –[#]	77.8, –[#]	n/a	n/a	n/a	n/a	n/a	80.7, –[#]
	%R	n/a	0.0, –[#]	3.7, –[#]	n/a	n/a	n/a	n/a	n/a	1.8, –[#]
	n	118	93	95	33	48	20	14	6	427
Enterobacter cloacae complex	%I	0.8, 0.8	2.2, 2.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.7, 0.7
	%R	26.3, 26.3	32.3, 32.3	17.9, 17.9	18.2, 18.2	10.4, 10.4	30.0, 30.0	14.3, 14.3	n/a	23.4, 23.4
	n	1,379	922	816	440	736	201	205	186	4,885
Escherichia coli	%I	0.1, 0.1	0.1, 0.1	0.0, 0.0	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
	%R	14.9, 14.9	16.7, 16.7	8.2, 8.2	12.3, 12.3	12.2, 12.2	7.0, 7.0	16.1, 16.1	16.1, 16.1	13.3, 13.3
	n	41	32	14	5	19	5	7	4	127
Klebsiella aerogenes	%I	2.4, 2.4	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
	%R	34.1, 34.1	50.0, 50.0	21.4, 21.4	n/a	36.8, 36.8	n/a	n/a	n/a	34.6, 34.6
	n	59	55	35	26	32	17	4	11	239
Klebsiella oxytoca	%I	0.0, 0.0	3.6, 3.6	0.0, 0.0	3.8, 3.8	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.3, 1.3
	%R	8.5, 8.5	9.1, 9.1	5.7, 5.7	0.0, 0.0	6.3, 6.3	5.9, 5.9	n/a	0.0, 0.0	6.3, 6.3
	n	348	212	249	89	160	51	45	36	1,190
Klebsiella pneumoniae complex	%I	0.3, 0.3	0.5, 0.5	0.4, 0.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.3
	%R	9.5, 9.5	15.1, 15.1	3.6, 3.6	7.9, 7.9	3.8, 3.8	5.9, 5.9	13.3, 13.3	11.1, 11.1	8.4, 8.4
	n	79	45	38	36	39	14	2	12	265
Proteus mirabilis	%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	2.5, 2.5	2.2, 2.2	2.6, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.5, 1.5
	n	32	17	39	3	27	5	3	1	127
Salmonella species (non-typhoidal)	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	3.1, 3.1	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
	n	20	31	13	1	7	1	1	7	81
Salmonella species (typhoidal)	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	5.0, 5.0	3.2, 3.2	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	2.5, 2.5
Serratia marcescens	n	74	32	57	8	26	6	2	8	213

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%I	1.4, 1.4	3.1, 3.1	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.9, 0.9
	%R	0.0, 0.0	3.1, 3.1	8.8, 8.8	n/a	0.0, 0.0	n/a	n/a	n/a	3.8, 3.8
Ciprofloxacin										
Acinetobacter baumannii complex	n	6	11	25	5	8	1	3	0	59
	%I‡	n/a	0.0, 100.0	0.0, 92.0	n/a	n/a	n/a	n/a	n/a	0.0, 96.6
	%R	n/a	0.0, 0.0	8.0, 8.0	n/a	n/a	n/a	n/a	n/a	3.4, 3.4
Enterococcus faecalis	n	149	98	33	46	79	17	7	0	429
	%R/ecoff§§	7.4, 4.2	14.3, 13.3	9.1, 6.1	2.2, 0.0	8.9, 6.3	0.0, 0.0	n/a	n/a	8.4, 6.1
Enterococcus faecium	n	172	93	11	31	55	11	13	0	386
	%R/ecoff**	91.9, 88.1	91.4, 90.3	81.8, 81.8	87.1, 0.0	87.3, 87.3	81.8, 72.7	69.2, 69.2	n/a	89.4, 85.9
Staphylococcus aureus	n	907	546	647	237	495	135	63	121	3,151
	%R	13.2, 13.9	10.4, 12.3	4.3, 5.3	8.4, 8.9	4.2, 5.1	6.7, 6.7	0.0, 0.0	13.2, 14.0	8.6, 9.5
Methicillin-resistant *S. aureus*	n	176	91	102	35	105	16	35	20	580
	%R	55.7, 56.3	48.4, 52.7	21.6, 21.6	37.1, 37.1	12.4, 12.4	43.8, 43.8	0.0, 0.0	55.0, 55.0	35.9, 36.7
Methicillin-susceptible *S. aureus*	n	731	455	545	202	390	119	28	101	2,571
	%R	3.0, 3.7	2.9, 4.2	1.1, 2.2	3.5, 4.0	2.1, 3.1	1.7, 1.7	0.0, 0.0	5.0, 5.9	2.5, 3.3
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%I	2.5, 2.5	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	5.0, 5.0	0.0, 0.0	n/a	1.2, 1.2
	%R	5.9, 5.9	8.6, 8.6	7.4, 7.4	0.0, 0.0	4.2, 4.2	0.0, 0.0	0.0, 0.0	n/a	5.9, 5.9
Escherichia coli	n	1,379	919	817	440	736	201	205	185	4,882
	%I	4.2, 4.2	3.2, 3.2	2.8, 2.8	5.9, 5.9	1.9, 1.9	2.0, 2.0	6.8, 6.8	2.2, 2.2	3.5, 3.5
	%R	16.9, 16.9	18.3, 18.3	10.4, 10.4	13.9, 13.9	17.3, 17.3	12.9, 12.9	20.0, 20.0	20.5, 20.5	16.0, 16.0
Klebsiella aerogenes	n	41	31	14	5	19	5	7	4	126
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	6.5, 6.5	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	1.6, 1.6
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%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	3.6, 3.6	2.9, 2.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.7, 1.7
Klebsiella pneumoniae complex	n	347	212	249	89	160	51	45	36	1,189
	%I	1.7, 1.7	0.5, 0.5	1.6, 1.6	1.1, 1.1	1.3, 1.3	0.0, 0.0	0.0, 0.0	2.8, 2.8	1.3, 1.3
	%R	10.4, 10.4	17.0, 17.0	5.2, 5.2	15.7, 15.7	5.0, 5.0	7.8, 7.8	15.6, 15.6	8.3, 8.3	10.2, 10.2
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%I	0.0,	0.0,	2.6,	0.0,	0.0,	0.0,	n/a	0.0,	0.4, 0.4

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	2.6	0.0	0.0	0.0		0.0	
	%R	3.8, 3.8	2.2, 2.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	8.3, 8.3	1.9, 1.9
Pseudomonas aeruginosa	n	242	119	174	65	98	19	15	23	755
	%I	4.1, 91.3	5.9, 89.9	4.6, 90.2	7.7, 87.7	5.1, 91.8	5.3, 94.7	13.3, 86.7	4.3, 95.7	5.2, 90.7
	%R	4.5, 8.7	4.2, 10.1	5.2, 9.8	4.6, 12.3	3.1, 8.2	0.0, 5.3	0.0, 13.3	0.0, 4.3	4.1, 9.3
Salmonella species (non-typhoidal)	n	32	13	39	3	27	5	3	1	123
	%I	–‡, –§	–‡, –§	–‡, –§	n/a	–‡, –§	n/a	n/a	n/a	–‡, –§
	%R	0.0, 0.0	0.0, 0.0	7.7, 7.7	n/a	0.0, 0.0	n/a	n/a	n/a	4.1, 4.1
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%I	–‡, –§	–‡, –§	–‡, –§	n/a	n/a	n/a	n/a	n/a	–‡, –§
	%R	70.0, 85.0	67.7, 80.6	53.8, 76.9	n/a	n/a	n/a	n/a	n/a	64.2, 85.2
Serratia marcescens	n	74	32	57	8	26	6	2	8	213
	%I	1.4, 1.4	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.5, 0.5
	%R	2.7, 2.7	9.4, 9.4	5.3, 5.3	n/a	0.0, 0.0	n/a	n/a	n/a	3.8, 3.8
Clindamycin (inducible + constitutive resistance)										
Staphylococcus aureus	n	907	524	647	237	495	135	63	121	3,129
	%R	14.1, 14.9	14.9, 15.8	13.9, 14.1	7.6, 7.6	14.3, 16.4	12.6, 14.8	19.0, 19.0	15.7, 15.7	13.8, 14.7
Methicillin-resistant *S. aureus*	n	176	88	102	35	105	16	35	20	577
	%R	33.5, 34.7	40.9, 42.0	21.6, 21.6	17.1, 17.1	24.8, 29.5	56.3, 56.3	22.9, 22.9	45.0, 45.0	30.3, 31.7
Methicillin-susceptible *S. aureus*	n	731	436	545	202	390	119	28	101	2,552
	%R	9.4, 10.1	9.6, 10.6	12.5, 12.7	5.9, 5.9	11.5, 12.8	6.7, 9.2	29	9.9, 9.9	10.1, 10.8
Daptomycin										
Enterococcus faecalis	n	217	127	122	63	79	28	7	36	679
	%R	0.0, –#	0.0, –#	0.8, –#	0.0, –#	0.0, –#	0.0, –#	0.0, –#	0.0, –#	0.1, –#
Enterococcus faecium	n	61	0	2	31	2	0	0	0	96
	%R	0.0, –#	n/a	0.0, –#	3.2, –#	0.0, –#	n/a!	n/a	n/a	1.0, –#
Staphylococcus aureus	n	907	546	647	237	498	135	64	121	3,155
	%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
Methicillin-resistant *S. aureus*	n	176	91	102	35	106	16	36	20	582
	%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
Methicillin-susceptible *S. aureus*	n	731	455	545	202	392	119	28	101	2,573
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	<0.0, <0.0
Erythromycin										
Staphylococcus aureus	n	898	546	647	237	495	135	63	121	3,142

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	18.5, 19.4	15.9, 16.8	15.5, 15.6	19.0, 19.0	15.6, 17.6	13.3, 15.6	20.6, 20.6	16.5, 17.4	16.7, 17.6
Methicillin-resistant *S. aureus*	n	175	91	102	35	105	16	35	20	579
	%R	35.4, 37.1	42.9, 44.0	27.5, 27.5	42.9, 42.9	24.8, 29.5	62.5, 62.5	25.7, 25.7	45.0, 45.0	34.2, 35.8
Methicillin-susceptible *S. aureus*	n	723	455	545	202	390	119	28	101	2,563
	%R	14.4, 15.1	10.5, 11.4	13.2, 13.4	14.9, 14.9	13.1, 14.4	6.7, 9.2	14.3, 14.3	10.9, 11.9	12.8, 13.5
Fusidic acid										
Staphylococcus aureus	n	907	525	647	237	496	135	63	121	3,131
	%R	–[#], 2.8	–[#], 5.7	–[#], 5.1	–[#], 1.7	–[#], 2.8	–[#], 1.5	–[#], 3.2	–[#], 4.1	–[#], 3.7
Methicillin-resistant *S. aureus*	n	176	88	102	35	105	16	35	20	577
	%R	–[#], 5.1	–[#], 13.6	–[#], 6.9	–[#], 5.7	–[#], 2.9	–[#], 0.0	–[#], 5.7	–[#], 15.0	–[#], 6.6
Methicillin-susceptible *S. aureus*	n	731	437	545	202	391	119	28	101	2,554
	%R	–[#], 2.2	–[#], 4.1	–[#], 4.8	–[#], 1.0	–[#], 2.8	–[#], 1.7	–[#], 0.0	–[#], 2.0	–[#], 3.0
Gentamicin										
Acinetobacter baumannii complex	n	6	11	27	5	8	1	3	0	61
	%R	n/a	0.0, 0.0	11.1, 11.1	n/a	n/a	n/a	n/a	n/a	6.6, 8.2
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%R	7.6, 7.6	7.5, 10.8	3.2, 3.2	0.0, 0.0	2.1, 2.1	0.0, 10.0	0.0, 0.0	n/a	4.9, 6.1
Escherichia coli	n	1,378	919	816	440	736	201	205	186	4,881
	%R	9.1, 9.5	10.2, 10.8	7.4, 8.0	7.3, 7.7	8.7, 8.8	5.5, 6.0	16.1, 17.1	10.8, 11.3	9.0, 9.5
Klebsiella aerogenes	n	41	31	14	5	19	5	7	4	126
	%R	0.0, 0.0	0.0, 0.0	7.1, 7.1	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%R	0.0, 0.0	0.0, 0.0	2.9, 2.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%R	6.6, 6.9	6.1, 6.6	2.4, 2.4	4.5, 5.6	2.5, 2.5	5.9, 5.9	13.3, 13.3	5.6, 5.6	5.1, 5.4
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%R	0.0, 15.2	0.0, 2.2	0.0, 2.6	2.8, 38.9	0.0, 2.6	0.0, 0.0	n/a	16.7, 16.7	1.1, 11.7
Pseudomonas aeruginosa	n	241	119	174	65	98	19	14	23	753
	%R	1.2, –[#]	0.0, –[#]	1.7, –[#]	0.0, –[#]	1.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.9, –[#]
Serratia marcescens	n	74	32	57	8	26	6	2	8	213
	%R	0.0, 2.7	0.0, 3.1	3.5, 7.0	n/a	0.0, 0.0	n/a	n/a	n/a	1.4, 3.8
Staphylococcus aureus	n	907	525	647	236	495	135	63	120	3,128
	%R	4.0, 6.9	1.5, 4.4	1.2, 3.1	1.3, 2.1	0.6, 1.0	0.7, 0.7	1.6, 7.9	2.5, 2.5	2.0, 4.0
Methicillin-resistant *S. aureus*	n	176	88	102	34	105	16	35	19	575
	%R	17.0,	5.7,	5.9,	8.8,	1.9,	6.3,	0.0,	15.8,	8.7, 14.1

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		29.0	10.2	10.8	11.8	1.9	6.3	0.0	15.8	
Methicillin-susceptible *S. aureus*	n	731	437	545	202	390	119	28	101	2,553
	%R	0.8, 1.6	0.7, 3.2	0.4, 1.7	0.0, 0.5	0.3, 0.8	0.0, 0.0	3.6, 17.9	0.0, 0.0	0.5, 1.7
Linezolid										
Enterococcus faecalis	n	218	128	124	64	80	41	7	36	698
	%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	209	164	63	45	56	25	13	19	594
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
Staphylococcus aureus	n	907	546	647	237	497	135	64	121	3,154
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-resistant *S. aureus*	n	176	91	102	35	106	16	36	20	582
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-susceptible *S. aureus*	n	731	455	545	202	391	119	28	101	2,572
	%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	6	11	27	5	8	1	3	0	61
	%I	n/a	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	11.1, 11.1	n/a	n/a	n/a	n/a	n/a	4.9, 4.9
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%I	0.8, 0.0	1.1, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.5, 0.0
	%R	2.5, 2.5	5.4, 5.4	0.0, 0.0	0.0, 0.0	2.1, 2.1	0.0, 0.0	0.0, 0.0	n/a	2.1, 2.1
Escherichia coli	n	1,379	922	814	440	736	201	205	185	4,882
	%I	0.2, 0.0	0.1, 0.0	0.0, 0.0	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.5	0.1, 0.0
	%R	0.1, 0.1	0.1, 0.1	0.0, 0.0	0.5, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.0	0.1, 0.1
Klebsiella aerogenes	n	41	32	14	5	19	5	7	4	127
	%I	0.0, 2.4	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
	%R	2.4, 0.0	0.0, 0.0	7.1, 7.1	n/a	0.0, 0.0	n/a	n/a	n/a	1.6, 0.8
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%I	0.3, 0.0	0.5, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.6	0.0, 0.0	2.2, 0.0	0.0, 0.0	0.3, 0.1
	%R	0.6, 0.6	2.8, 2.8	0.4, 0.4	0.0, 0.0	0.6, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.8, 0.8

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%I	0.0, 0.0	0.0, 0.0	0.0, 2.6	2.8, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
	%R	0.0, 0.0	0.0, 0.0	2.6, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.0
Pseudomonas aeruginosa	n	241	119	173	65	97	19	15	23	752
	%I	4.1, 6.2	2.5, 3.4	4.6, 5.2	4.6, 6.2	4.1, 4.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.7, 4.8
	%R	3.7, 1.7	3.4, 2.5	3.5, 2.9	3.1, 1.5	3.1, 3.1	0.0, 0.0	13.3, 13.3	0.0, 0.0	3.5, 2.4
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Serratia marcescens	n	74	32	57	8	26	6	2	8	213
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Mupirocin (high-level)										
Staphylococcus aureus	n	902	542	647	237	497	135	62	121	3,143
	%R	0.9, –[#]	0.6, –[#]	3.2, –[#]	0.4, –[#]	0.2, –[#]	0.7, –†[#]	1.6, –[#]	0.0, –[#]	1.1, –[#]
Methicillin-resistant *S. aureus*	n	174	89	102	35	106	16	36	20	578
	%R	1.7, –[#]	0.0, –[#]	2.9, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	2.8, –[#]	0.0, –[#]	1.2, –[#]
Methicillin-susceptible *S. aureus*	n	728	453	545	202	391	119	26	101	2,565
	%R	0.7, –[#]	0.7, –[#]	3.3, –[#]	0.5, –[#]	0.3, –[#]	0.8, –[#]	0.0, –[#]	0.0, –[#]	1.1, –[#]
Nitrofurantoin										
Enterococcus faecalis	n	217	127	123	64	78	41	7	36	693
	%R/ecoff[##]	0.5, 1.8	0.0, 1.6	0.0, 0.0	0.0, 1.6	0.0, 1.3	0.0, 2.4	n/a	0.0, 0.0	0.1, 1.4
Enterococcus faecium	n	188	138	46	44	54	11	13	19	513
	%R	69.7, –[#]	39.9, –[#]	67.4, –[#]	72.7, –[#]	55.6, –[#]	54.5, –[#]	15.4, –[#]	63.2, –[#]	58.3, –[#]
Enterobacter cloacae complex	n	95	92	95	33	48	20	14	6	403
	%R	21.1, –[#]	5.4, –[#]	6.3, –[#]	24.2, –[#]	8.3, –[#]	5.0, –[#]	28.6, –[#]	n/a	11.9, –[#]
Escherichia coli	n	1,379	919	817	439	736	201	205	185	4,881
	%R	0.9, 0.9	0.8, 0.8	0.6, 0.6	0.5, 0.5	0.7, 0.7	3.0, 3.0	1.0, 1.0	1.1, 1.1	0.9, 0.9
Klebsiella (*Enterobacter*) *aerogenes*	n	39	30	14	5	19	5	7	4	123
	%R	30.8, –[#]	50.0, –[#]	35.7, –[#]	n/a	31.6, –[#]	n/a	n/a	n/a	36.6, –[#]

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Klebsiella oxytoca	n	53	52	35	26	32	17	4	11	230
	%R	1.9, –[#]	1.9, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	n/a	0.0, –[#]	0.9, –[#]
Klebsiella pneumoniae complex	n	301	207	249	89	160	51	45	36	1,138
	%R	23.6, –[#]	40.1, –[#]	26.9, –[#]	30.3, –[#]	38.1, –[#]	27.5, –[#]	28.9, –[#]	30.6, –[#]	30.5, –[#]
Proteus mirabilis	n	66	45	38	36	39	14	2	0	240
	%R	89.4, –[#]	97.8, –[#]	97.4, –[#]	88.9, –[#]	97.4, –[#]	100.0, –[#]	n/a	n/a	93.8, –[#]
Salmonella species (non-typhoidal)	n	30	13	39	3	27	5	3	0	120
	%R	16.7, –[#]	7.7, –[#]	2.6, –[#]	n/a	29.6, –[#]	n/a	n/a	n/a	14.2, –[#]
Salmonella species (typhoidal)	n	20	27	13	1	7	1	1	0	70
	%R	5.0, –[#]	3.7, –[#]	7.7, –[#]	n/a	n/a	n/a	n/a	n/a	5.7, –[#]
Serratia marcescens	n	62	32	57	8	26	6	2	8	201
	%R	96.8, –[#]	100.0, –[#]	100.0, –[#]	n/a	100.0, –[#]	n/a	n/a	n/a	99.0, –[#]
Oxacillin/methicillin										
Staphylococcus aureus	n	176	91	102	36	106	16	36	20	583
	%R	19.4, 19.4	16.7, 16.7	15.8, 15.8	15.1, 15.1	21.2, 21.2	11.9, 11.9	56.3, 56.3	16.5, 16.5	18.5, 18.5
Piperacillin–tazobactam										
Acinetobacter baumannii complex	n	6	10	27	5	8	0	3	0	59
	%R	n/a	0.0, –[#]	14.8, –[#]	n/a	n/a	n/a	n/a	n/a	8.5, –[#]
Enterobacter cloacae complex	n	118	93	94	33	47	20	14	6	425
	%R	16.1, 22.9	17.2, 23.7	9.6, 21.3	15.2, 15.2	8.5, 14.9	30.0, 30.0	14.3, 14.3	n/a	14.8, 21.4
Escherichia coli	n	1,375	920	810	439	734	200	205	184	4,867
	%R	4.1, 6.5	2.8, 5.4	2.8, 5.2	2.5, 3.9	2.7, 6.0	2.0, 3.5	2.9, 6.8	3.8, 8.2	3.2, 5.7
Klebsiella (*Enterobacter*) *aerogenes*	n	41	32	14	5	19	5	7	4	127
	%R	29.3, 34.1	43.8, 50.0	14.3, 21.4	n/a	31.6, 36.8	n/a	n/a	n/a	28.3, 34.6
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%R	3.4, 5.1	12.7, 14.5	14.3, 17.1	3.8, 3.8	3.1, 3.1	5.9, 5.9	n/a	18.2, 18.2	7.9, 9.2
Klebsiella pneumoniae complex	n	348	212	249	89	159	51	45	36	1,189
	%R	5.7, 9.5	6.6, 8.5	2.4, 7.6	3.4, 4.5	3.1, 6.3	5.9, 7.8	8.9, 22.2	2.8, 8.3	4.7, 8.5
Proteus mirabilis	n	78	44	37	36	39	14	2	12	262
	%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
Pseudomonas aeruginosa	n	239	120	172	64	98	19	15	23	750
	%R	4.6, 10.0	5.8, 14.2	11.0, 18.0	9.4, 10.9	5.1, 8.2	10.5, 15.8	13.3, 13.3	0.0, 8.7	6.9, 12.5
Salmonella species (non-typhoidal)	n	32	17	38	3	27	5	3	1	126
	%R	0.0, 3.1	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 0.8
Salmonella species	n	20	31	11	1	7	1	1	7	79

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
(typhoidal)	%R	0.0, 5.0	0.0, 3.2	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 2.5
Serratia marcescens	n	70	30	57	8	4	6	0	8	183
	%R	0.0, 0.0	0.0, 0.0	1.8, 3.5	n/a	n/a	n/a	n/a	n/a	0.5, 1.1
Rifampicin										
Staphylococcus aureus	n	907	525	647	236	496	134	63	121	3,129
	%R	0.4, 0.6	0.2, 0.2	0.8, 0.9	0.0, 0.0	0.6, 0.6	0.0, 0.0	0.0, 0.0	0.0, 1.7	0.4, 0.5
Methicillin-resistant *S. aureus*	n	176	88	102	34	105	16	35	20	576
	%R	1.1, 1.1	1.1, 1.1	2.9, 3.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.0, 1.2
Methicillin-susceptible *S. aureus*	n	731	437	545	202	391	118	28	101	2,553
	%R	0.3, 0.4	0.0, 0.0	0.4, 0.4	0.0, 0.0	0.8, 0.8	0.0, 0.0	0.0, 0.0	0.0, 2.0	0.3, 0.4
Teicoplanin										
Enterococcus faecalis	n	218	128	124	64	80	41	7	36	698
	%R	0.0, 0.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 2.8	0.0, 0.4
Enterococcus faecium	n	209	164	63	45	56	25	13	19	594
	%R	23.9, 32.5	18.9, 19.5	6.3, 6.3	11.1, 11.1	3.6, 3.6	12.0, 24.0	0.0, 0.0	15.8, 15.8	16.5, 20.2
Staphylococcus aureus	n	907	546	647	237	497	135	64	121	3,154
	%R	0.0, 0.1	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, 0.0	0.0, 0.1
Tetracycline/doxycycline										
Enterococcus faecalis	n	175	82	75	46	79	17	7	0	481
	%NS***	70.9, –[#]	78.0, –[#]	69.3, –[#]	60.9, –[#]	70.9, –[#]	70.6, –[#]	57.1, –[#]	n/a	70.7, –[#]
Enterococcus faecium	n	188	116	50	31	55	11	13	0	464
	%NS***	56.9, –[#]	79.3, –[#]	90.0, –[#]	3.2, –[#]	78.2, –[#]	45.5, –[#]	61.5, –[#]	n/a	64.9, –[#]
Staphylococcus aureus	n	904	546	647	237	495	135	63	118	3,145
	%NS***	7.4, 8.6	5.5, 5.5	4.0, 4.0	2.5, 4.2	3.8, 3.8	5.9, 5.9	1.6, 1.6	5.1, 5.1	5.2, 5.7
Methicillin-resistant *S. aureus*	n	176	91	102	35	105	16	35	19	579
	%NS***	22.7, 25.0	15.4, 15.4	10.8, 10.8	11.4, 17.1	1.0, 1.0	12.5, 12.5	0.0, 0.0	15.8, 15.8	13.0, 14.0
Methicillin-susceptible *S. aureus*	n	728	455	545	202	390	119	28	99	2,566
	%NS***	3.7, 4.7	3.5, 3.5	2.8, 2.8	1.0, 2.0	4.6, 4.6	5.0, 5.0	3.6, 3.6	3.0, 3.0	3.4, 3.8
Ticarcillin–clavulanic acid										
Acinetobacter baumannii complex	n	5	10	27	1	8	0	3	0	54
	%R	n/a	0.0, –[#]	14.8, –[#]	n/a	n/a	n/a	n/a	n/a	7.4, –[#]
Enterobacter cloacae complex	n	84	93	95	11	48	20	14	6	371
	%R	22.6, 28.6	24.7, 32.3	14.7, 22.1	27.3, 27.3	14.6, 18.8	30.0, 30.0	14.3, 14.3	n/a	20.5, 26.4
Escherichia coli	n	890	921	816	189	736	201	205	184	4,142
	%R	9.7,	6.0,	7.5,	4.2,	8.8,	4.5,	12.2,	13.0,	8.0, 17.4

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		16.2	17.4	17.2	14.3	18.3	15.4	22.9	20.1	
Klebsiella (*Enterobacter*) *aerogenes*	n	27	32	14	4	19	5	7	4	112
	%R	40.7, 55.6	50.0, 59.4	21.4, 35.7	n/a	31.6, 36.8	n/a	n/a	n/a	34.8, 46.4
Klebsiella oxytoca	n	42	55	35	8	32	17	4	11	204
	%R	2.4, 2.4	12.7, 16.4	14.3, 14.3	n/a	3.1, 3.1	5.9, 5.9	n/a	18.2, 18.2	8.3, 9.3
Klebsiella pneumoniae complex	n	236	212	249	31	160	51	45	36	1,020
	%R	9.7, 16.1	9.9, 18.9	5.2, 8.0	3.2, 3.2	3.8, 6.3	7.8, 9.8	13.3, 22.2	8.3, 16.7	7.5, 12.7
Proteus mirabilis	n	53	45	38	11	39	14	2	12	214
	%R	0.0, 0.0	0.0, 0.0	2.6, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.5, 0.5
Pseudomonas aeruginosa	n	157	119	174	30	97	19	15	23	634
	%R	13.4, 49.0	15.1, 58.8	14.4, 61.5	16.7, 63.3	9.3, 50.5	21.1, 68.4	20.0, 53.3	8.7, 39.1	13.7, 55.5
Salmonella species (non-typhoidal)	n	26	17	39	3	27	5	3	1	121
	%R	3.8, 7.7	0.0, 0.0	0.0, 2.6	n/a	0.0, 3.7	n/a	n/a	n/a	0.8, 3.3
Salmonella species (typhoidal)	n	10	31	13	1	7	1	1	7	71
	%R	10.0, 10.0	3.2, 6.5	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	2.8, 4.2
Serratia marcescens	n	46	22	57	1	26	6	2	8	168
	%R	0.0, 0.0	0.0, 0.0	5.3, 8.8	n/a	0.0, 0.0	n/a	n/a	n/a	2.4, 3.6
Tobramycin										
Acinetobacter baumannii complex	n	6	11	27	5	8	1	3	0	61
	%R	n/a	0.0, 0.0	7.4, 11.1	n/a	n/a	n/a	n/a	n/a	3.3, 4.9
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%R	3.4, 6.8	5.4, 12.9	4.2, 5.3	0.0, 0.0	2.1, 2.1	0.0, 5.0	0.0, 0.0	n/a	3.5, 6.6
Escherichia coli	n	1,379	922	817	440	736	201	205	185	4,885
	%R	3.5, 10.2	4.4, 12.9	2.2, 7.8	3.6, 8.9	3.1, 9.5	2.0, 7.0	2.4, 18.5	3.8, 11.4	3.3, 10.4
Klebsiella aerogenes	n	41	32	14	5	19	5	7	4	127
	%R	0.0, 0.0	0.0, 0.0	7.1, 7.1	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%R	0.0, 0.0	0.0, 0.0	2.9, 2.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%R	3.2, 8.3	9.4, 14.2	0.8, 2.0	2.2, 6.7	0.6, 2.5	5.9, 5.9	6.7, 13.3	5.6, 11.1	3.7, 7.3
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%R	1.3, 7.6	0.0, 2.2	0.0, 2.6	2.8, 11.1	0.0, 0.0	0.0, 0.0	n/a	0.0, 16.7	0.8, 5.3
Pseudomonas aeruginosa	n	242	119	174	65	98	19	15	23	755
	%R	0.4, 1.2	0.0, 0.0	1.1, 1.7	0.0, 0.0	1.0, 1.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.9
Serratia marcescens	n	74	32	57	8	26	6	2	8	213

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	1.4, 32.4	3.1, 37.5	3.5, 28.1	n/a	0.0, 23.1	n/a	n/a	n/a	2.3, 29.6
Trimethoprim										
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%R	16.9, 16.9	20.4, 20.4	20.0, 20.0	12.1, 12.1	14.6, 14.6	10.0, 15.0	14.3, 14.3	n/a	17.3, 17.6
Escherichia coli	n	1,379	922	816	439	736	201	205	186	4,884
	%R	32.8, 33.0	34.7, 35.0	32.8, 32.8	30.8, 31.0	35.2, 35.2	23.4, 23.9	54.1, 54.6	34.4, 34.9	33.9, 34.1
Klebsiella aerogenes	n	41	32	14	5	19	5	7	4	127
	%R	0.0, 2.4	3.1, 6.3	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 2.4
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%R	5.1, 5.1	1.8, 1.8	8.6, 8.6	3.8, 3.8	12.5, 12.5	11.8, 11.8	n/a	0.0, 0.0	5.9, 5.9
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%R	16.4, 17.8	24.1, 24.1	14.9, 15.7	19.1, 20.2	15.0, 15.6	11.8, 11.8	22.2, 24.4	30.6, 33.3	17.9, 18.8
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265
	%R	22.8, 22.8	13.3, 13.3	13.2, 13.2	19.4, 19.4	25.6, 25.6	7.1, 7.1	n/a	25.0, 25.0	18.9, 18.9
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%R	0.0, 0.0	0.0, 0.0	2.6, 2.6	n/a	0.0, 0.0	n/a	n/a	n/a	2.4, 2.4
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%R	5.0, 5.0	9.7, 9.7	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	4.9, 4.9
Serratia marcescens	n	74	32	57	8	26	6	2	8	213
	%R	1.4, 2.7	0.0, 3.1	5.3, 5.3	n/a	0.0, 0.0	n/a	n/a	n/a	1.9, 2.8
Trimethoprim–sulfamethoxazole										
Acinetobacter baumannii complex	n	6	11	27	5	8	1	3	0	61
	%R	n/a	9.1, 9.1	18.5, 18.5	n/a	n/a	n/a	n/a	n/a	11.5, 11.5
Enterobacter cloacae complex	n	118	93	95	33	48	20	14	6	427
	%R	17.8, 17.8	18.3, 18.3	21.1, 21.1	9.1, 9.1	12.5, 12.5	10.0, 10.0	14.3, 14.3	n/a	16.9, 16.9
Escherichia coli	n	1,379	917	817	439	736	201	205	186	4,880
	%R	30.1, 30.0	32.2, 32.2	29.7, 29.6	28.2, 28.2	31.9, 31.9	21.4, 21.4	48.8, 48.8	29.6, 29.6	30.9, 30.9
Klebsiella aerogenes	n	41	31	14	5	19	5	7	4	126
	%R	0.0, 0.0	3.2, 3.2	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Klebsiella oxytoca	n	59	55	35	26	32	17	4	11	239
	%R	3.4, 3.4	1.8, 1.8	8.6, 8.6	3.8, 3.8	9.4, 9.4	11.8, 11.8	n/a	0.0, 0.0	5.0, 5.0
Klebsiella pneumoniae complex	n	348	212	249	89	160	51	45	36	1,190
	%R	15.5, 15.5	22.6, 22.6	14.1, 13.3	19.1, 19.1	10.0, 10.0	11.8, 11.8	17.8, 17.8	27.8, 27.8	16.3, 16.1
Proteus mirabilis	n	79	45	38	36	39	14	2	12	265

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	19.0, 19.0	13.3, 13.3	13.2, 13.2	8.3, 8.3	23.1, 23.1	7.1, 7.1	n/a	25.0, 25.0	15.8, 15.8
Salmonella species (non-typhoidal)	n	32	17	39	3	27	5	3	1	127
	%R	0.0, 0.0	0.0, 0.0	2.6, 2.6	n/a	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
Salmonella species (typhoidal)	n	20	31	13	1	7	1	1	7	81
	%R	5.0, 5.0	9.7, 9.7	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	4.9, 4.9
Serratia marcescens	n	74	32	57	8	26	6	2	8	213
	%R	0.0, 0.0	0.0, 0.0	5.3, 5.3	n/a	0.0, 0.0	n/a	n/a	n/a	1.4, 1.4
Staphylococcus aureus	n	905	525	647	237	495	135	63	121	3,128
	%R	3.1, 3.1	3.0, 2.7	3.6, 2.9	2.1, 2.1	4.6, 4.2	0.0, 0.0	9.5, 9.5	4.1, 4.1	3.4, 3.1
Methicillin-resistant *S. aureus*	n	176	88	102	35	105	16	35	20	577
	%R	7.4, 7.4	6.8, 4.5	16.7, 14.7	11.4, 11.4	9.5, 9.5	0.0, 0.0	17.1, 17.1	10.0, 10.0	10.1, 9.4
Methicillin-susceptible *S. aureus*	n	729	437	545	202	390	119	28	101	2,551
	%R	2.1, 2.1	2.3, 2.3	1.1, 0.7	0.5, 0.5	3.3, 2.8	0.0, 0.0	0.0, 0.0	3.0, 3.0	1.9, 1.7
Vancomycin										
Enterococcus faecalis	n	218	128	124	64	80	41	7	36	698
	%R	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, 0.0	0.0, 0.1
Enterococcus faecium	n	209	164	63	45	56	25	13	19	594
	%R	43.5, 43.5	65.2, 66.5	14.3, 15.9	31.1, 31.1	5.4, 5.4	40.0, 40.0	46.2, 46.2	21.1, 21.1	41.1, 41.6
Staphylococcus aureus	n	907	546	647	237	498	135	64	121	3,155
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

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

** ECOFF = 8 mg/L

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

§§ ECOFF = 4 mg/L

\## ECOFF = 32 mg/L

*** The doxycycline concentration range available on the Phoenix card used restricts the ability to accurately identify intermediate and resistant (CLSI) categories for *Staphylococcus aureus* and *Enterococcus* 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, 2019

State or territory		Number of categories (non-multidrug resistant)				Number of categories (multidrug resistant)		
	Total	0	1	2	%	3	4	%
NSW	6	5	1	0	–*	0	0	–*
Vic	11	10	1	0	–*	0	0	–*
Qld	25	20	2	0	–*	1	2	–*
SA	5	3	2	0	–*	0	0	–*
WA	8	8	0	0	–*	0	0	–*
Tas	1	1	0	0	–*	0	0	–*
NT	3	3	0	0	–*	0	0	–*
ACT	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**59**	**50**	**6**	**0**	**94.9**	**1**	**2**	**5.1**

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

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

Notes:
1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin or amikacin), carbapenems (meropenem), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim-sulfamethoxazole).
2. *Acinetobacter baumannii* complex includes *A. pittii* (*n* = 8), *A. nosocomialis* (*n* = 1), and *A. dijkshoorniae* (*n* = 1).

Table D2: Multiple acquired resistance in *Citrobacter koseri,* by state and territory, 2019

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	5	5	0	0	–*	0	0	0	0	0	0	0	–*
Vic	7	7	0	0	–*	0	0	0	0	0	0	0	–*
Qld	16	14	1	0	–*	1	0	0	0	0	0	0	–*
SA	2	2	0	0	–*	0	0	0	0	0	0	0	–*
WA	17	17	0	0	–*	0	0	0	0	0	0	0	–*
Tas	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
NT	1	1	0	0	–*	0	0	0	0	0	0	0	–*
ACT	2	2	0	0	–*	0	0	0	0	0	0	0	–*
Total	**50**	**48**	**1**	**0**	**98.0**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**2.0**

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

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

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

Table D3: Multiple acquired resistance in *Citrobacter freundii* complex, by state and territory, 2019

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	23	18	1	3	–*	1	0	0	0	–*
Vic	11	8	0	3	–*	0	0	0	0	–*
Qld	9	6	1	2	–*	0	0	0	0	–*
SA	6	3	1	1	–*	0	0	1	0	–*
WA	13	11	0	1	–*	1	0	0	0	–*
Tas	1	1	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
ACT	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	**63**	**47**	**3**	**10**	**95.2**	**2**	**0**	**1**	**0**	**4.8**

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

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

Notes:

1. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin or amikacin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime or cefepime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Citrobacter freundii* complex includes *C. braakii* (*n* = 6), and *C. youngae* (*n* = 2).

Table D4: Multiple acquired resistance in *Enterococcus faecium* (vancomycin resistant) by state and territory, 2019

		Number of categories				
State or territory	**Total**	**0**	**1**	**2**	**3**	**4**
NSW	76	0	6	32	38	0
Vic	51	0	1	21	29	0
Qld	2	0	0	2	0	0
SA	8	0	5	3	0	0
WA	3	0	0	1	2	0
Tas	7	0	0	3	4	0
NT	6	0	0	0	6	0
ACT	0	n/a	n/a	n/a	n/a	n/a
Total	**153**	**0**	**12**	**62**	**79**	**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, 2019

		Number of categories				
State or territory	**Total**	**0**	**1**	**2**	**3**	**4**
NSW	95	11	12	44	28	0
Vic	39	5	2	22	10	0
Qld	8	1	0	6	1	0
SA	23	3	15	5	0	0
WA	51	4	2	37	7	1
Tas	4	2	0	1	1	0
NT	7	4	0	1	2	0
ACT	0	n/a	n/a	n/a	n/a	n/a
Total	**227**	**30**	**31**	**116**	**49**	**1**

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, 2019

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	30	19	0	11	100.0	0	0	0	0	0.0
Vic	31	13	1	16	96.8	1	0	0	0	3.2
Qld	14	11	0	2	–*	0	1	0	0	–*
SA	5	4	1	0	–*	0	0	0	0	–*
WA	19	12	0	7	–*	0	0	0	0	–*
Tas	5	5	0	0	–*	0	0	0	0	–*
NT	7	5	0	2	–*	0	0	0	0	–*
ACT	4	2	1	1	–*	0	0	0	0	–*
Total	**115**	**71**	**3**	**39**	**98.3**	**1**	**1**	**0**	**0**	**1.7**

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

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

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

Table D7: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, 2019

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	47	22	19	4	95.7	1	1	0	0	0	0	0	4.3
Vic	55	23	23	1	85.5	2	5	1	0	0	0	0	14.5
Qld	35	12	17	2	88.6	2	1	0	0	0	1	0	11.4
SA	14	8	6	0	–*	0	0	0	0	0	0	0	–*
WA	32	11	16	4	96.9	0	0	1	0	0	0	0	3.1
Tas	17	6	9	1	–*	0	0	1	0	0	0	0	–*
NT	4	2	1	1	–*	0	0	0	0	0	0	0	–*
ACT	11	6	3	2	–*	0	0	0	0	0	0	0	–*
Total	**215**	**90**	**94**	**15**	**92.6**	**5**	**7**	**3**	**0**	**0**	**1**	**0**	**7.4**

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

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

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

Table D8: Multiple acquired resistance in *Morganella morganii*, by state and territory, 2019

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	28	15	10	1	–*	2	0	0	0	0	–*
Vic	9	1	6	0	–*	1	1	0	0	0	–*
Qld	20	11	5	1	–*	1	1	1	0	0	–*
SA	6	4	2	0	–*	0	0	0	0	0	–*
WA	10	6	3	1	–*	0	0	0	0	0	–*
Tas	6	4	1	1	–*	0	0	0	0	0	–*
NT	1	1	0	0	–*	0	0	0	0	0	–*
ACT	3	0	3	0	–*	0	0	0	0	0	–*
Total	**83**	**42**	**30**	**4**	**91.6**	**4**	**2**	**1**	**0**	**0**	**8.4**

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

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

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

Table D9: Multiple acquired resistance in *Proteus mirabilis*, by state and territory, 2019

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	65	44	8	6	89.2	2	4	0	0	0	1	0	0	10.8
Vic	44	32	8	2	95.5	1	0	0	1	0	0	0	0	4.5
Qld	37	30	5	0	94.6	1	0	0	1	0	0	0	0	5.4
SA	22	12	7	3	–*	0	0	0	0	0	0	0	0	–*
WA	39	26	6	4	92.3	2	1	0	0	0	0	0	0	7.7
Tas	14	8	5	0	–*	1	0	0	0	0	0	0	0	–*
NT	2	2	0	0	–*	0	0	0	0	0	0	0	0	–*
ACT	12	8	1	0	–*	1	0	2	0	0	0	0	0	–*
Total	**235**	**162**	**40**	**15**	**92.3**	**8**	**5**	**2**	**2**	**0**	**1**	**0**	**0**	**7.7**

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

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

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

Table D10: Multiple acquired resistance in *Salmonella* species (non-typhoidal), by state and territory, 2019

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	29	26	2	0	96.6	0	0	0	1	0	0	0	3.4
Vic	13	13	0	0	–*	0	0	0	0	0	0	0	–*
Qld	38	34	3	1	100.0	0	0	0	0	0	0	0	0.0
SA	3	3	0	0	–*	0	0	0	0	0	0	0	–*
WA	27	26	1	0	–*	0	0	0	0	0	0	0	–*
Tas	5	4	0	1	–*	0	0	0	0	0	0	0	–*
NT	3	3	0	0	–*	0	0	0	0	0	0	0	–*
ACT	1	0	1	0	–*	0	0	0	0	0	0	0	–*
Total	**119**	**109**	**7**	**2**	**99.2**	**0**	**0**	**0**	**1**	**0**	**0**	**0**	**0.8**

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, 2019

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	12	2	9	0	–*	0	0	0	1	0	0	0	–*
Vic	31	5	22	2	93.5	0	1	0	1	0	0	0	6.5
Qld	11	3	8	0	–*	0	0	0	0	0	0	0	–*
SA	1	0	1	0	–*	0	0	0	0	0	0	0	–*
WA	7	0	7	0	–*	0	0	0	0	0	0	0	–*
Tas	1	0	1	0	–*	0	0	0	0	0	0	0	–*
NT	1	0	1	0	–*	0	0	0	0	0	0	0	–*
ACT	7	0	7	0	–*	0	0	0	0	0	0	0	–*
Total	**71**	**10**	**56**	**2**	**95.8**	**0**	**1**	**0**	**2**	**0**	**0**	**0**	**4.2**

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, 2019

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	54	20	21	13	100.0	0	0	0	0	0	0.0
Vic	30	10	13	7	100.0	0	0	0	0	0	0.0
Qld	57	13	33	6	91.2	0	4	1	0	0	8.8
SA	3	0	1	1	–*	1	0	0	0	0	–*
WA	4	3	1	0	–*	0	0	0	0	0	–*
Tas	3	0	2	1	–*	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	8	3	5	0	–*	0	0	0	0	0	–*
Total	**159**	**49**	**76**	**28**	**96.2**	**1**	**4**	**1**	**0**	**0**	**3.8**

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

* Not applicable (insufficient numbers)

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

Appendix E. *Enterococcus* resistance by species and state or territory, 2013-2019

Table E1: *Enterococcus faecalis*, resistant (EUCAST), by state and territory, 2013–2019

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)
	2019	698	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.0 (0)
Ciprofloxacin†	2013	417	16.4 (18)	11.3 (12)	14.9 (11)	14.8 (4)	9.9 (7)	na	–* (1)	17.4 (4)	13.7 (57)
	2014	457	18.3 (23)	20.0 (24)	15.7 (14)	0.0 (0)	11.1 (7)	na	–* (3)	42.4 (14)	18.6 (85)
	2015	504	9.3 (13)	15.5 (17)	9.6 (8)	8.6 (3)	8.8 (8)	na	30.0 (3)	14.3 (5)	11.3 (57)
	2016	542	7.8 (11)	11.5 (15)	8.2 (7)	4.4 (2)	8.0 (7)	21.4 (3)	–* (0)	12.1 (4)	9.0 (49)
	2017	535	7.3 (13)	13.6 (16)	16.8 (16)	11.1 (3)	5.5 (5)	6.3 (1)	20.0 (2)	na	10.5 (56)
	2018	538	9.0 (15)	12.8 (12)	6.7 (8)	2.5 (1)	4.4 (4)	18.8 (3)	9.1 (1)	na	8.2 (44)
	2019	423	4.2 (6)	13.3 (13)	6.1 (2)	0.0 (0)	6.3 (5)	0.0 (0)	–* (0)	na	6.1 (26)
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)
	2019	510	17.9 (27)	24.7 (24)	13.7 (10)	6.5 (3)	12.8 (10)	12.2 (5)	–* (0)	47.1 (8)	17.1 (87)
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	602	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)

Antimicrobial	Year	Number tested	Percentage resistant, % (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	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)
	2019	698	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.0 (0)
Nitrofurantoin§	2013	468	1.7 (2)	0.9 (1)	2.3 (2)	4.7 (2)	1.4 (1)	9.1 (1)	–* (0)	0.0 (0)	1.9 (9)
	2014	521	3.8 (5)	0.0 ()	2.0 (2)	5.9 (3)	0.0 ()	7.7 (1)	–* (0)	0.0 (0)	2.1 (11)
	2015	558	2.7 (4)	2.8 (3)	2.1 (2)	1.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	2.9 (1)	2.0 (11)
	2016	591	0.0 (0)	0.0 (0)	0.0 (0)	2.0 (1)	1.1 (1)	0.0 (0)	–* (0)	2.5 (1)	0.5 (3)
	2017	595	0.5 (1)	1.7 (2)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.5 (3)
	2018	668	1.9 (4)	0.9 (1)	1.5 (2)	1.8 (1)	2.2 (2)	0.0 (0)	0.0 (0)	0.0 (0)	1.5 (10)
	2019	693	1.8 (4)	1.6 (2)	0.0 (0)	1.6 (1)	1.3 (1)	2.4 (1)	–* (1)	0.0 (0)	1.4 (10)
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)
	2019	698	0.9 (2)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	2.8 (1)	0.4 (3)
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)
	2019	698	0.5 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	0.1 (1)

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

* Insufficient numbers to calculate percentage (< 10 isolates)
† The ciprofloxacin ECOFF (4 mg/L) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only
§ The nitrofurantoin ECOFF (32 mg/L) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only

Notes

1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. The ciprofloxacin concentration range available on the Phoenix panel used restricts the ability to accurately identify susceptible and resistant categories for *Enterococcus* species

Table E2: *Enterococcus faecium*, non-susceptible (EUCAST), by state and territory, 2013–2019

Antimicrobial	Year	Number tested	Percentage non-susceptible (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ampicillin	2013	321	90.7 (97)	92.5 (74)	88.9 (32)	96.9 (31)	97.6 (41)	-* (5)	-* (3)	100.0 (16)	93.1 (299)
	2014	379	89.3 (92)	93.6 (88)	81.1 (30)	89.1 (41)	94.0 (47)	-* (5)	-* (0)	87.8 (36)	89.4 (339)
	2015	400	85.2 (98)	88.3 (106)	83.3 (25)	93.2 (41)	79.2 (42)	-* (4)	-* (7)	95.5 (21)	86.0 (344)
	2016	412	91.9 (113)	89.0 (97)	90.7 (39)	97.7 (42)	92.6 (50)	85.7 (12)	-* (4)	90.9 (20)	91.5 (377)
	2017	481	89.2 (149)	92.5 (124)	95.6 (43)	85.7 (24)	81.0 (51)	88.2 (15)	-* (4)	95.5 (21)	89.6 (431)
	2018	491	89.5 (136)	95.4 (124)	74.5 (41)	84.2 (32)	90.7 (49)	91.7 (22)	91.7 (11)	92.3 (24)	89.4 (439)
	2019	594	92.8 (194)	94.5 (155)	90.5 (57)	86.7 (39)	91.1 (51)	92.0 (23)	69.2 (9)	73.7 (14)	91.2 (542)
Ciprofloxacin†	2013	267	88.5 (77)	93.8 (75)	87.9 (29)	-* (5)	90.5 (38)	na	-* (3)	93.8 (15)	90.6 (242)
	2014	283	84.6 (55)	92.6 (87)	71.4 (20)	-* (0)	94.0 (47)	na	-* (0)	90.2 (37)	86.9 (246)
	2015	310	79.7 (59)	90.0 (108)	82.1 (23)	-* (3)	79.2 (42)	-* (1)	-* (7)	95.5 (21)	85.2 (264)
	2016	334	84.9 (73)	85.3 (93)	89.7 (35)	90.9 (10)	90.7 (49)	91.7 (11)	-* (4)	89.5 (17)	87.4 (292)
	2017	379	81.3 (91)	91.7 (122)	90.0 (36)	75.0 (12)	79.4 (50)	100.0 (10)	-* (4)	na	85.8 (325)
	2018	309	77.6 (66)	93.0 (80)	70.6 (36)	-* (0)	90.7 (49)	94.1 (16)	91.7 (11)	na	83.5 (258)
	2019	305	88.1 (104)	90.3 (84)	81.8 (9)	0.0 (0)	87.3 (48)	72.7 (8)	69.2 (9)	na	85.9 (262)
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)
	2019	427	60.6 (106)	43.3 (39)	17.1 (6)	25.8 (8)	18.5 (10)	64.0 (16)	61.5 (8)	–* (1)	45.4 (194)
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)
	2019	594	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	1.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.2 (1)
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)

Antimicrobial	Year	Number tested	Percentage non-susceptible (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	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)
	2019	594	32.5 (68)	19.5 (32)	6.3 (4)	11.1 (5)	3.6 (2)	24.0 (6)	0.0 (0)	15.8 (3)	20.2 (120)
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)
	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)
	2019	594	43.5 (91)	66.5 (109)	15.9 (10)	31.1 (14)	5.4 (3)	40.0 (10)	46.2 (6)	21.1 (4)	41.6 (247)

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

* Insufficient numbers to calculate percentage (< 10 isolates)
† The ciprofloxacin ECOFF (8 mg/L) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only

Notes

1. Percentage resistance determined using EUCAST 2020 breakpoints for all years
2. The ciprofloxacin concentration range available on the Phoenix panel used restricts the ability to accurately identify susceptible and resistant categories for *Enterococcus* species

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