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ON SAFETY AND QUALITY IN HEALTH CARE

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Antimicrobial Use and Resistance in Australia

AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Sepsis Outcome Programs

2017 report

AGAR

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Overview

This report presents analyses of antimicrobial resistance (AMR) associated with episodes of bacteraemia that were reported by 36 participating public and private laboratories across Australia in 2017.

As part of the Antimicrobial Use and Resistance in Australia (AURA) Surveillance System, the Australian Group on Antimicrobial Resistance (AGAR) reports on sepsis outcome programs in Australia; and contributes data to the AURA Surveillance System, which is coordinated by the Australian Commission on Safety and Quality in Health Care (the Commission). AGAR operates three sepsis outcome programs:

- The Gram-negative Sepsis Outcome Program
- The Australian Enterococcal Sepsis Outcome Program and,
- The Australian Staphylococcal Sepsis Outcome Program.

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

AMR is an important patient safety issue because infections caused by resistant organisms may need to be treated with other antimicrobials, which may have more severe side effects, be more expensive or take longer to work. In some severe cases, resistant organisms may not be able to be treated by currently available antimicrobials. International evidence consistently demonstrates the growing effect that AMR is having on human health, and confirms that resistant pathogens are causing an increasing numbers of infections in health service organisations and in the community.

To protect the public from harm and improve the quality of health service provision, the Commission developed the National Safety and Quality Health Service (NSQHS) Standards in collaboration with the states and territories, clinical experts, patients and carers.

The Preventing and Controlling Healthcare-Associated Infection Standard requires health service organisations to monitor patterns of AMR and antimicrobial use, and use this information to guide antimicrobial stewardship practices and meet infection control requirements. Data from AGAR directly support this standard.

What does the AGAR data tell us?

Nationally, rates of resistance for organisms monitored by AGAR have not changed substantially since 2016. However, some long term increases in resistance are important to consider in the context of infection prevention and control, and antimicrobial prescribing. In 2017, over three-quarters of bacteraemia episodes reported to AGAR had their onset in the community; particularly those caused by *Escherichia coli*, *Enterococcus* species and methicillin-resistant *Staphylococcus aureus* (MRSA).

AGAR's focus on bacteraemia allows examination of laboratory-confirmed, invasive infections and meaningful comparison of rates over time for hospitals, states and territories. AGAR aligns Australian data with the European Antimicrobial Resistance Surveillance Network, enabling benchmarking and better projections of future trends. After five years, early longitudinal data have now been collected and standardised. Over time, these data will become increasingly valuable for understanding trends and changes that have implications for antimicrobial use and infection prevention and control.

In *E. coli*, resistances to common agents used for treatment continue to increase. Resistance to ciprofloxacin and other fluoroquinolones has continued to rise in isolates from community-onset infections. These changes in resistance may mean increasing treatment failures and greater reliance on last-line treatments such as carbapenems. *E. coli* is the most common cause of urinary tract infection and bacteraemia in the community and in otherwise healthy people. Less frequently, it causes bacteraemia from intravascular lines.

The overall rates of vancomycin resistance in *Enterococcus faecium* are declining nationally. However, of the countries highlighted in this report, Australia has the highest rates of resistance to vancomycin in *E. faecium*. *Enterococcus* species such as *E. faecium* cause a range of infections in patients who have had surgery or have invasive devices. They rarely cause disease in healthy people, but may cause infections in vulnerable patients, such as people who are very elderly or immunosuppressed. The most common clinical syndromes associated with enterococcal bacteraemia are biliary and urinary tract infections.

The rate of community-onset MRSA bacteraemia is increasing. In addition, community-associated MRSA clones are an increasing source of hospital-onset bacteraemia. Over the last 15 years, AGAR has shown a rapidly changing picture of MRSA in Australia; findings that are important for informing strategies to prevent and control MRSA in the Australia. *S. aureus* is a common human pathogen that causes a wide range of infections, including minor infections such as boils, impetigo and wound infections; moderate infections such as cellulitis; and serious infections such as bone and joint infections, pneumonia, endocarditis and bacteraemia. *S. aureus* is also a common cause of healthcare-associated infections, especially surgical site infections, intravascular line infections with bacteraemia, and infections of prosthetic devices.

Patterns of resistance vary between states and territories in *E. coli*, MRSA and *E. faecium*. This variation creates the need for local tailoring of antibiotic prescribing.

There are also differences in the patterns of resistance between hospital and community settings. *E. coli* infections more commonly have their onset in the community. Vancomycin-resistant *E. faecium* bacteraemias are more common in the hospital setting than the community. These variations have important implications for the choice of antimicrobial therapy and the development of local treatment guidelines.

Awareness of variations in AMR between states and territories and between community and hospital settings is important for design and implementation of infection prevention and control programs. For example, implementation of strategies to screen and manage patients with a high risk of infection with a resistant organism when they are admitted to hospital, and when they move between hospital and community settings such as aged care homes.

The Commission will continue to support states and territories and the private health sector to act on opportunities to refine the infection prevention and control, antimicrobial stewardship and antibiotic treatment approaches, identified by analyses of the AGAR data, so that patients receive the best possible care.

Key findings and implications for health care

A. Key findings

Gram-negative species

- A total of 7,910 episodes of gram-negative bacteraemia were reported, including Enterobacterales (89.8%), *Pseudomonas aeruginosa* (8.8%) and *Acinetobacter* species (1.4%)
- Three genera – *Escherichia* (61.6%), *Klebsiella* (19.9%) and *Enterobacter* (6.3%), accounted for 87.8% of all Enterobacterales bacteraemias
- The all-cause 30-day mortality for gram-negative bacteraemia was 12.5% (10.1% in *E. coli*, 20.6% in *P. aeruginosa*)
- Urinary tract infection was the most frequent source of sepsis (41.2%)
- Over 11% of *E. coli* isolates causing community-onset bacteraemia (which accounted for 84% of all *E. coli* bacteraemia cases) were ceftriaxone resistant
- There was a significant difference in 30-day all-cause mortality between community (9.4%) and hospital onset (13.2%) *E coli* bacteraemia episodes
- In 2017, extended-spectrum β-lactamase (ESBL) phenotypes were found in 12.6% of *E. coli* and 9.8% of *Klebsiella pneumoniae,* and were more common in hospital onset episodes. The CTX-M type gene was present in 76.1% of *E. coli* with an ESBL phenotype
- Increasing fluoroquinolone non-susceptibility in *E. coli* is a continuing concern and increased in hospital-onset bacteraemia from 16.1% in 2013 to 21.1% in 2017
- Fluoroquinolone resistance is commonly linked to cephalosporin resistance caused by ESBLs of the CTX-M type. O25b-ST131 accounted for 57.3% of *E. coli* ESBL phenotypes that were ciprofloxacin resistant
- The low proportions of carbapenemase-producing Enterobacterales (CPE) bacteraemia are encouraging (0.1% in *E. coli* and 0.7% in *K. pneumoniae*), although the *Enterobacter cloacae* complex hospital-onset figure is higher at 3.6%
- The rate of colistin resistance (when tested for, but excluding species with intrinsic resistance) was 0.9% (7/752). No mobile colistin resistance genes were detected among all referred isolates.

Enterococcus species

- A total of 1,137 episodes of enterococcal bacteraemia were reported; the majority of enterococcal bacteraemia episodes were caused by *Enterococcus faecalis* or *E. faecium* (95.3%)
- The majority of *E. faecalis* bacteraemia were community-onset (71.3%), compared to only 30.1% in *E. faecium*
- The combined 30-day all-cause mortality for *E. faecalis* and *E. faecium* was 20.3%; the 30-day all-cause mortality for *E. faecium* bacteraemia was higher, particularly hospital-onset vancomycin-susceptible (22.4%) and vancomycin-resistant (30.5%) isolates
- There was a significant difference in 30-day all-cause mortality between *E. faecalis* (14.3%) and *E. faecium* (27.7%)
- The most frequent source of sepsis or clinical manifestation for *E. faecalis* was urinary tract infection (30.9%); for *E. faecium*, it was intra-abdominal infection other than that from the biliary tract (21.8%)
- The length of stay following enterococcal bacteraemia was more than 30 days for 21.4% of patients
- Overall, 50.9% of *E. faecium* harboured *vanA* or *vanB* genes or both, with 50% of vancomycin-resistant *E. faecium* bacteraemias due to *vanA*; this type of vancomycin resistance has emerged rapidly in the past six years, particularly in New South Wales, where it is now the dominant genotype

- Of bloodstream infections caused by *E. faecium*, 47.0% were phenotypically vancomycin resistant; 50.9% of *E. faecium* harboured *vanA* and/or *vanB* genes (*vanA* 25.1%, *vanB* 25.3%, both 0.6%)
- There were 64 *E. faecium* multilocus sequence types (STs), of which ST17, ST1421, ST796, ST1424, ST80, ST555, ST203, ST18, and ST78 were the nine most frequently identified
- *vanA* genes were detected in nine STs, and *vanB* genes were detected in 12 STs; two STs harboured *vanA* and *vanB* genes and the clonal diversity varies across Australia
- The percentage of *E. faecium* bacteraemia isolates resistant to vancomycin is now much higher in Australia than in all European countries.

Staphylococcus aureus

- A total of 2,515 *Staphylococcus aureus* bacteraemia episodes were reported, 77% of which were community onset. Almost one in five of all episodes were methicillin resistant (19%)
- The 30-day all-cause mortality was 14.8% with a significant difference between methicillin-resistant *S. aureus* (MRSA) (18.9%) and methicillin-sensitive *S. aureus* (MSSA) (13.9%); and between community-onset (13.8%) and hospital-onset *S. aureus* bacteraemia (18.3%)
- The most common principal clinical manifestations were osteomyelitis/septic arthritis (19.0%) and skin and soft tissue infections (18.6%)
- The length of stay was more than 30 days in 26.1% of patients (26.6% in MRSA, 26.0% in MSSA)
- There is an increasing rate of community-associated methicillin-resistant *S. aureus* (CA-MRSA) bacteraemia, and CA-MRSA dominate 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
- Thirty-nine CA-MRSA clones were identified; the dominant CA-MRSA clone was ST93-IV (Queensland clone)
- 49.7% of CA-MRSA isolates harboured the PVL associated genes
- Trimethoprim-sulfamethoxazole is a more reliable treatment than clindamycin, as clindamycin resistance (constitutive and inducible) is four times as high in all *S. aureus* (15.4%), compared to trimethoprim-sulfamethoxazole (3.8%)
- In MRSA, clindamycin non-susceptibility is 34.9% and trimethoprim-sulfamethoxazole non-susceptibility is 12.0%
- EMRSA-15 (ST22-IV) is the major HA-MRSA, and now outranks the long-established Aus2/3 EMRSA (ST239-III) HA-MRSA clone; however, the majority of EMRSA-15 bacteraemias arise in the community, which is consistent with the prevalence of this clone in Australian aged care facilities
- The Queensland clone of CA-MRSA (ST93-IV), which harbours the PVL associated genes, has become the dominant CA-MRSA type and is now seen throughout Australia; it is now the most common CA-MRSA clone in Queensland, Western Australia and the Northern Territory.

B. Implications for health care

Several themes identified from the analyses of AGAR data, have implications for the delivery of health care services.

Reliability of common therapies for severe and multidrug-resistant infections

AGAR data show a longitudinal trend of increasing *E. coli* non-susceptibility to key anti-gram negative antimicrobial agents such as ceftriaxone and ciprofloxacin. The percentage of invasive *E. coli* that are fluoroquinolone resistant in Australia is comparable to northern European countries. The overall proportion of ceftriaxone and ciprofloxacin non-susceptibility in *E. coli* is now 11.3% and 18.0% respectively; and vancomycin non-susceptibility in *E. faecium* occurs in almost one in two bacteraemias with this organism (47.0%). These agents are commonly used as empiric therapies for certain prescribing conditions; particularly in patients with allergies, in some cases to avoid even broader-spectrum antibiotic prescribing. Fluoroquinolone non-susceptibility in hospital-onset *E. coli* bacteraemia is now 21.1%. Empiric use of fluoroquinolones for *E. coli* without susceptibilities to direct therapy is no longer a reliable strategy in serious hospital onset infections.

It may be necessary to customise empiric therapy recommendations based on local antibiograms, prior individual antibiotic exposure, and colonisation for these organisms, particularly for severe infections.

Approximately one in five *E. coli* blood stream infections reported to AGAR in 2017 were multidrug resistant. More than one in 25 (3.4%) *E. cloacae* complex hospital-onset blood stream infections harboured a carbapenemase. As the number of resistance classes or proportion of resistance genes increase, suitable oral therapies for step down outpatient therapy may become limited. This has the potential to increase dependence on parenteral therapy, either via admission to hospital or hospital in the home intravenous antimicrobial therapy in the future; this will increase length of stay and healthcare costs. It is essential that health services monitor local resistance patterns and their impact on healthcare utilisation.

Geographical variation: tailored prescribing guidelines

Third generation cephalosporin (ceftriaxone) non-susceptibility in *E. coli* varies from 4.5% to 14.1% across Australia. The proportion of MRSA in blood stream infections varies almost five-fold between the Australian Capital Territory (9.5%) and the Northern Territory (44.4%), where 9.2% of all reported MRSA bacteraemias occurred.

There is an almost 10-fold variation in teicoplanin susceptibility in *E. faecium*, which can be explained by the proportions of *vanA/vanB* genes by jurisdiction. Teicoplanin resistance is more common in New South Wales (45.5%) and the Australian Capital Territory (27.3%).

Carbapenem resistance, although low in general, is most apparent in gram-negative bacteraemias in Victoria.

Variations between hospital and community settings: the need for risk assessment

The epidemiology of blood stream infections and associated resistance varies between hospital and community settings. For example, organisms such as *P. aeruginosa* and *E. cloacae* complex are evenly distributed between community- and hospital-onset infections, whilst others such as *E.* coli are more commonly community-onset. Vancomycin resistance in *E. faecium* blood stream infections are more common in the hospital setting than the community (53.0% versus 33.1%). These variations have implications for choice of empiric antimicrobial therapy.

Infection control and prevention strategies: between and within hospital and community settings and states and territories

Infection prevention and control and antimicrobial stewardship are essential to the response to AMR. However, reducing person to person transmission and improving antimicrobial use are only part of a comprehensive response.

A large proportion of gram-negative and enterococcal bacteraemias, and associated resistant infections, are attributed to urinary tract or intra-abdominal infections. Therefore, strategies focused on improving urinary health and/or reducing infective complications of intra-abdominal pathology may assist in reducing both infections and last-line antibiotic use on a population basis. Reductions in urinary source bacteraemias would be of most benefit in reducing community-onset gram-negative and *E. faecalis* infections. Strategies to reduce intra-abdominal infections will be of benefit for both susceptible and non-susceptible *E. faecium* infections.

Community-associated MRSA clones now cause more hospital-onset disease than HA-MRSA clones. This has implications for infection control strategies intended to reduce healthcare-associated bloodstream infections. Extended-spectrum β-lactamases (ESBL) are increasing in the community, but still more prevalent in hospital-onset bacteraemias; for *E. coli* 17.6% were hospital onset versus 11.6% in 2017, and for *K. pneumoniae* 17.4% were hospital onset versus 7% community-onset in 2017).

There are also variations in susceptibility between and within states and territories that have the potential to impact across health services over time, influenced by patient transfers.

Longitudinal trends

The 2017 data reinforce notable changes in resistance patterns over the last decade. For example, the increasing proportion of *E. coli* isolates harbouring an ESBL. Despite infection prevention and control and antimicrobial stewardship initiatives, this proportion increased from 3.0% in 2006 to 12.6% in 2017.[4]

Similarly, there has been a marked increase in the proportion of vancomycin-resistance in *E. faecium* bacteraemias, from 3.7% in 2005 to 47.0% in 2017, for isolates from blood and cerebrospinal fluid specimens combined.[5]

There have been small increases in the proportion of *E. cloacae* complex hospital-onset bacteraemias carrying plasmid borne carbapenemases. In the 2006 AGAR survey[3], the proportion was 0.6% compared to 3.6% in 2017. This means that last-line antimicrobials, such as meropenem, are ineffective in these organisms. This is in contrast to rates of Enterobacterales infections more generally, which have remained low overall (0.31%); for example, *P. aeruginosa* (0.29%) and *Acinetobacter* species (2.7%).

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[3] and other expert guideline development groups to ensure that data, such as the level of ceftriaxone and ciprofloxacin non-susceptibility, are considered
- Work with states and territories and the private laboratory sector to encourage the use of local antibiograms (tables of antimicrobial susceptibilities that are used to inform local empirical and therapeutic antimicrobial recommendations and formulary management)
- Promote prescribing practices that are tailored to local resistance patterns, and regular review of prescribing guidance by local antimicrobial stewardship services; this will support the use of broad-spectrum antibiotics where necessary, while limiting their use in areas where this is not justified due to the lower rate of AMR

- Promote incorporation of concepts of geographical variation in AMR into clinical practice; particularly to support clinicians who regularly work in a range of settings, such as trainees and locums
- Promote the adoption of risk assessment strategies, which include whether the onset of bacteraemia occurred in the community or in a hospital, to assist with minimising the use of broad-spectrum antibiotics for community-onset infections
- Support collaboration and coordination between states and territories, and between hospital and community care settings to explore the drivers of variation and improve local control efforts to help limit progression of AMR
- Maintain and enhance the AURA Surveillance System and ensure that AMR and antimicrobial use data are readily available to inform antimicrobial stewardship and infection prevention and control programs
- Promote effective infection prevention and control measures, such as those included in the *Recommendations for the Control of Carbapenemase-Producing Enterobacterales*: *A guide for acute care health facilities*[6], to limit the transmission of carbapenemase-producing Enterobacterales
- Support development of guidance for surveillance, prevention and control of specific organisms and resistances.

1. Background and objectives

The Antimicrobial Use and Resistance in Australia (AURA) Surveillance System, which is coordinated by the Australian Commission on Safety and Quality in Health Care (the Commission), provides essential information to develop and implement strategies to prevent and contain antimicrobial resistance (AMR) in human health, and improve antimicrobial use across hospital, aged care home and community healthcare settings.

AURA also supports the National Safety and Quality Health Service (NSQHS) Standard Preventing and Controlling Healthcare-Associated Infection[1] and Australia's National Antimicrobial Resistance Strategy (2015–2019).[2] Funding for AURA is provided by the Australian Government Department of Health and state and territory health departments.

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

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

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

Historically, the main focus of the group 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. Using standardised methods, AGAR has collected ongoing data on the prevalence of antimicrobial resistance in Australia over a long period. AGAR now focuses on bloodstream infections and has three major programs: the Gram-negative Sepsis Outcome Program, the Australian Enterococcal Sepsis Outcome Program and the Australian Staphylococcal Sepsis Outcome Program.

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

Table 1: Hospitals that contributed to AGAR, by state and territory, 2017

State or territory	Hospital
New South Wales	Concord Repatriation General Hospital
	John Hunter Hospital
	Nepean Hospital
	Royal North Shore Hospital
	Royal Prince Alfred Hospital
	St Vincent's Hospital, Sydney
	Westmead Hospital
	Wollongong Hospital
Victoria	Alfred Hospital
	Austin Hospital (Austin Health)
	Monash Children's Hospital
	Monash Medical Centre (Monash Health)
	Royal Children's Hospital
	St Vincent's Hospital
Queensland	Cairns Base Hospital
	Gold Coast Hospital
	Lady Cilento 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
	Princess Margaret Hospital for Children
	Royal Perth Hospital#
	Sir Charles Gairdner Hospital
	St John of God Hospital, Murdoch
	Kimberley regional hospitals (Broome, Kununurra, Derby)
Tasmania	Launceston General Hospital
	Royal Hobart Hospital
Northern Territory	Alice Springs Hospital
	Royal Darwin Hospital
Australian Capital Territory	Canberra Hospital

* Microbiology services provided by Pathology Queensland Central Laboratory
† Microbiology services provided by Sullivan Nicolaides Pathology
§ Microbiology services provided by SA Pathology, Royal Adelaide Hospital
# Microbiology services provided by PathWest Laboratory Medicine WA, Fiona Stanley Hospital

1.1. Gram-negative Sepsis Outcome Program

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

Enterobacter, another genus of gram-negative pathogens in which resistance can be of clinical importance, was added in 2004. *E. coli* is the most common cause of community-onset urinary tract infection, whereas *Klebsiella* species are less common but are known to harbour important resistances. *Enterobacter* species are less common in the community, but of high importance because of their intrinsic resistance to first-line antimicrobials in the community.

The three groups of species surveyed are considered valuable sentinels for multidrug resistance and emerging resistance in enteric gram-negative bacilli. In 2013, AGAR began the Enterobacteriaceae Sepsis Outcome Program (EnSOP), which focused on the prospective collection of resistance and demographic data on all isolates from patients with documented bacteraemia. In 2015, *Pseudomonas aeruginosa* and *Acinetobacter* species were added, and the program changed its name to the Gram-negative Sepsis Outcome Program (GNSOP).

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

The objectives of the 2017 surveillance program were to:

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

1.2. Australian Enterococcal Sepsis Outcome Program

Globally, enterococci are thought to account for approximately 10% of all bacteraemias, and in North America and Europe are the fourth and fifth leading causes of sepsis respectively.[7, 8] In the 1970s, healthcare-associated enterococcal infections were primarily due to *E. faecalis*, subsequently there has been a steadily increasing prevalence of nosocomial *E. faecium* infections.[9-11] Worldwide, the increase in nosocomial *E. faecium* infections has primarily been due to the expansion of polyclonal hospital-adapted clonal complex (CC) 17 isolates. While innately resistant to many classes of antibiotics, *E. faecium* CC17 has demonstrated a remarkable capacity to evolve new antimicrobial resistances. In 2009, the Infectious Diseases Society of America highlighted *E. faecium* as one of the key problem bacteria or ESKAPE (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa,* and *Enterobacter* species) pathogens requiring new therapies.[12]

AGAR began surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[13] In 2011, AGAR commenced the Australian Enterococcal Sepsis Outcome Program (AESOP).[14]

In 2017, in order to provide data to support improved antimicrobial prescribing and patient care, AESOP sought to determine the proportion of *E. faecalis* and *E. faecium* bacteraemia isolates demonstrating antimicrobial resistance, with a particular emphasis on:

- Assessing susceptibility to ampicillin
- Assessing susceptibility to glycopeptides
- Monitoring the molecular epidemiology of *E. faecium.*

1.3. Australian Staphylococcal Sepsis Outcome Program

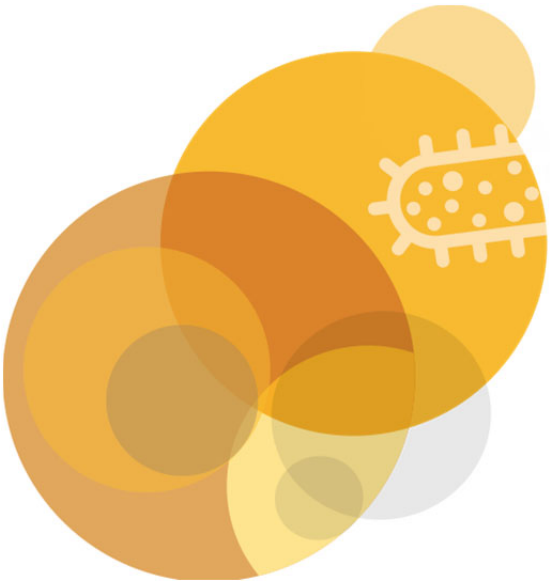
Globally, *Staphylococcus aureus* is one of the most frequent causes of hospital-acquired and community-acquired blood stream infections.[15] Although there are a wide variety of manifestations of serious invasive infection caused by *S. aureus*, in the great majority of cases, the organism can be detected in blood cultures. Therefore, *S. aureus* bacteraemia (SAB) is considered a very useful marker for serious invasive infection.[16]

Despite standardised treatment protocols for SAB, including prolonged antimicrobial therapy and prompt source control, [17] mortality ranged from as low as 2.5% to as high as 40%.[18-20] Mortality rates however, are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[21, 22] 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.[23]

AGAR began surveillance of antimicrobial resistance in *S. aureus* in 1986.[24] In 2013, AGAR commenced the Australian Staphylococcal Sepsis Outcome Program (ASSOP).[25]

The primary objective of ASSOP 2017 was to determine the proportion of SAB isolates demonstrating antimicrobial resistance, with particular emphasis on:

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



2. Summary of methods

Thirty-six institutions, in each state and territory of Australia, were enrolled in the 2017 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 2017 to 31 December 2017. 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 residential postcode 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, mass spectrometry (MALDI- TOF).

For this report, *Enterobacter cloacae* complex comprises *E. cloacae, E. asburiae, E. kobei, E. ludwigii, E. hormaechei* and *E. nimipressuralis*; and *Citrobacter freundii* comprises all species of the *C. freundii* complex (*C. freundii, C. braakii, C. gillenii, C. murliniae, C. rodenticum, C. sedlakii, C. werkmanii* and *C. youngae*). *Klebsiella aerogenes* was previously known as *Enterobacter aerogenes*.

2.3. Susceptibility testing

Susceptibility testing of isolates is described in Appendix B. The analysis used breakpoints from the Clinical and Laboratory Standards Institute (CLSI) M100–A28[26] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v8.1.[27]

2.4. Molecular testing

E. coli, *Klebsiella* spp., *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone MIC >1 mg/L, or cefoxitin MIC >8 mg/L; any other Enterobacterales with cefepime MIC >1 mg/L; all isolates with ciprofloxacin MIC >0.25 mg/L; all isolates with meropenem MIC >0.25 mg/L; and all isolates with amikacin MIC >32 mg/L were referred to a central laboratory molecular confirmation of resistance.

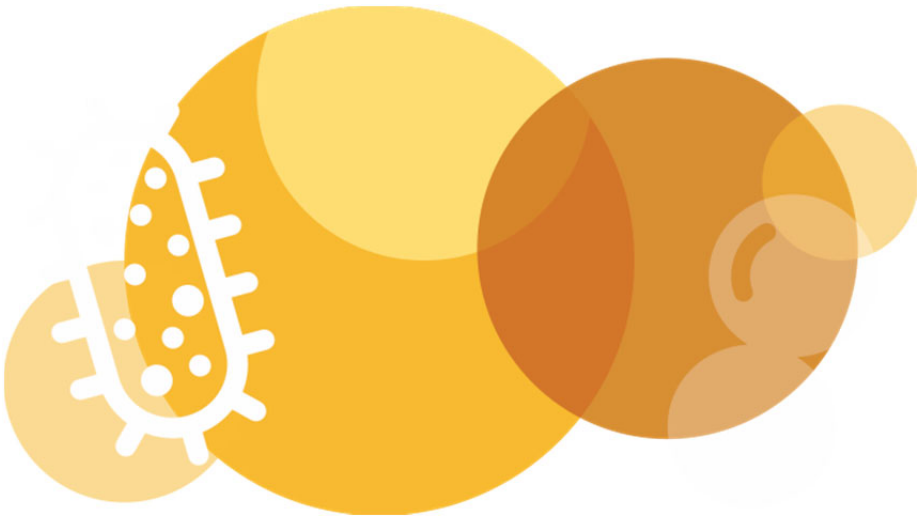
All referred isolates were screened using real-time polymerase chain reaction (PCR) platform (Roche LC-480) and published primers for the presence of bla_{TEM} and bla_{SHV}, CTX-M-type genes (groups 1, 2, 9, 8/25), plasmid-borne AmpC (bla_{CIT}, bla_{DHA}, bla_{EBC}, bla_{ACC}, bla_{FOX}, bla_{MOX}), and carbapenemases genes (bla_{IMP}, bla_{NDM}, bla_{KPC}, $bla_{OXA-48-like}$, bla_{VIM}, bla_{GES}, bla_{SME}, bla_{IMI}).[28-30]

PCRs were also used to detect bla_{IMP} types, known plasmid-mediated quinolone resistance mechanisms (*qnr*, efflux [*qepA*, *oqxAB*] and *aac* (*6')-Ib-cr*), aminoglycoside ribosomal methyltransferases (armA, rmtB, rmtC, rmtF), and mobile colistin resistance genes (mcr-1, mcr-2, mcr-3)[31-36]. All referred *E. coli* were examined for membership of the O25b-ST131 clone.[37] All isolates with demonstrated carbapenemase activity and any amikacin resistant isolates were also screened for OXA-23-like, -24, and -58 carbapenemases.[38]

All gram-negative isolates with carbapenemase activity, *E. faecium* and MRSA were subjected to whole genome sequencing using the Illumina MiSeq platform. Data were analysed using the Nullarbor bioinformatic pipeline.[39] The pipeline was used to identify the multi-locus sequence type and the resistome.

2.5. Statistical analysis

Confidence intervals of proportions, Fisher's exact test for categorical variables, and chi-square test for trend were calculated, if appropriate, using GraphPad Prism version 7.01 for Windows (GraphPad Software, La Jolla, California).



3. Results

3.1. Isolates recovered

A total of 7,910 gram-negative isolates (61 species, 19 genera) were reported from 36 participating hospitals. Enterobacterales accounted for 89.8%, followed by *P. aeruginosa* (8.8%) and *Acinetobacter* species (1.4%). Of the Enterobacterales, three genera – *Escherichia* (61.6%), *Klebsiella* (19.9%) and *Enterobacter* (6.3%) – contributed 87.8% of all isolates.

The top 10 species by rank were *E. coli* (55.2%), *K. pneumoniae* (12.7%), *P. aeruginosa* (8.8%), *E. cloacae* complex (5.5%), *Proteus mirabilis* (3.0%), *K. oxytoca* (2.9%), *Serratia marcescens* (2.1%), *Salmonella* species (non-typhoidal) (1.7%), *K. aerogenes* (1.3%), and *Morganella morganii* (1.1%). These 10 species comprised 94.3% of all isolates (Table 2).

There were 1,137 episodes of enterococcal bacteraemia. *E. faecalis* and *E. faecium* accounted for 95.3% of all enterococcal isolates (Table 2).

Of 2,515 SAB episodes, 478 (19.0%; 95% confidence interval [CI] 17.5-20.6) were methicillin resistant, ranging from 9.5% (95%CI 5.1-17.0) in the Australian Capital Territory to 44.4% (95%CI: 35.0-54.3) in the Northern Territory (Table 2).

Table 2: Number of each species recovered, by state and territory, 2017

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Gram-negative species*	2,168	1,408	1,666	543	1,300	291	243	291	7,910
Escherichia coli	1,179	795	859	289	775	174	141	158	4,370
Klebsiella pneumoniae	269	198	246	57	152	22	30	27	1,001
Pseudomonas aeruginosa	198	89	205	59	86	15	15	30	697
Enterobacter cloacae complex	136	75	107	26	55	17	7	10	433
Proteus mirabilis	65	38	47	22	38	11	5	9	235
Klebsiella oxytoca	58	35	36	22	44	20	2	12	229
Serratia marcescens	50	29	40	11	24	6	2	5	167
Salmonella species (non-typhoidal)	20	15	28	5	39	2	21	4	134
Klebsiella (*Enterobacter*) *aerogenes*	45	25	10	3	13	3	1	5	105
Morganella morganii	30	18	16	2	9	1	4	5	85
Klebsiella variicola	27	2	0	16	7	8	0	12	72
Acinetobacter baumannii complex	9	12	19	6	8	2	8	1	65
Citrobacter freundii	9	19	4	4	10	4	0	6	56
Citrobacter koseri	11	6	11	2	9	2	2	0	43
Salmonella species (typhoidal)	5	12	7	1	4	0	1	1	31
Pantoea agglomerans	2	3	2	5	2	0	0	0	14
Raoultella ornithinolytica	4	5	1	2	2	0	0	0	14
Acinetobacter species	4	3	2	0	3	0	0	0	12
Acinetobacter lwoffii	2	0	0	1	5	0	1	2	11
Other species (*n* = 42)	45	29	26	9	15	4	3	4	136
Enterococcus species	373	263	158	60	165	51	15	52	1,137
Enterococcus faecalis	187	119	102	31	94	31	10	28	602
vancomycin susceptible, per cent	100	98.3	100	100	100	100	100	100	99.7
vancomycin resistant, per cent	0.0	1.7	0.0	0.0	0.0	0.0	0.0	0.0	0.3
Enterococcus faecium	167	134	45	28	63	17	5	22	481
vancomycin resistant, per cent	51.5	64.2	33.3	57.1	14.3	29.4	–†	27.3	47.0
vancomycin susceptible, per cent	48.5	35.8	66.7	42.9	85.7	70.6	–†	72.7	53.0

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Other enterococcal species	19	10	11	1	8	3	0	2	54
Enterococcus casseliflavus	8	4	4	0	3	0	0	0	19
Enterococcus gallinarum	6	2	2	0	1	2	0	1	14
Enterococcus avium	2	3	1	0	2	1	0	0	9
Enterococcus durans	1	0	2	1	1	0	0	0	5
Enterococcus raffinosus	1	1	0	0	1	0	0	1	4
Enterococcus hirae	1	0	1	0	0	0	0	0	2
Enterococcus saccharolyticus	0	0	1	0	0	0	0	0	1
Staphylococcus aureus	679	365	553	167	466	91	99	95	2,515
methicillin resistant, per cent	20.5	17.5	15.0	20.4	20.4	11.0	44.4	9.5	19.0
methicillin susceptible, per cent	79.5	82.5	85.0	79.6	79.6	89.0	55.6	90.5	81.0

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

† Insufficient numbers (<10) to calculate percentage

3.2. Place of onset of bacteraemia

Almost all patients with bacteraemia were admitted to hospital (gram-negative species, 97.9%; *Enterococcus* species, 98.3%; *S. aureus*, 98.2%).

Information on place of onset of bacteraemia was available for 7,910 (100%) gram-negative episodes, 1,137 (100%) *Enterococcus* species episodes and 2,515 (100%) *S. aureus* episodes (Table 3).

For gram-negative species, 76.6% of all episodes were community-onset, although differences were observed with different species. Episodes involving *E. faecalis* and 'other' *Enterococcus* species were predominantly community onset (71.3%, 95%CI: 67.5-74.7 for *E. faecalis*); however, *E. faecium* episodes were predominantly hospital-onset (69.9%; 95%CI: 65.6-73.8). Most SABs were community-onset (77.0%; 95%CI 75.3-78.6).

Table 3: Species recovered, by place of onset, 2017

Organism	Community onset % (*n*)	Hospital onset % (*n*)	Total, 100%
Gram-negative species*	76.6 (6,060)	23.4 (1,850)	7,910
Escherichia coli	83.6 (3,655)	16.4 (715)	4,370
Klebsiella pneumoniae	71.7 (718)	28.3 (283)	1,001
Pseudomonas aeruginosa	58.7 (409)	41.3 (288)	697
Enterobacter cloacae complex	55.0 (238)	45.0 (195)	433
Proteus mirabilis	82.6 (194)	17.4 (41)	235
Klebsiella oxytoca	74.7 (171)	25.3 (58)	229
Serratia marcescens	57.5 (96)	42.5 (71)	167
Salmonella species (non-typhoidal)	90.3 (121)	9.7 (13)	134
Klebsiella (*Enterobacter*) *aerogenes*	56.2 (59)	43.8 (46)	105
Morganella morganii	68.2 (58)	31.8 (27)	85
Klebsiella variicola	70.8 (51)	29.2 (21)	72
Acinetobacter baumannii complex	70.8 (46)	29.2 (19)	65
Citrobacter freundii	71.4 (40)	28.6 (16)	56
Citrobacter koseri	72.1 (31)	27.9 (12)	43
Salmonella species (typhoidal)	100 (31)	0.0 (0)	31
Pantoea agglomerans	92.9 (13)	7.1 (1)	14
Raoultella ornithinolytica	78.6 (11)	21.4 (3)	14

Organism	Community onset % (*n*)	Hospital onset % (*n*)	Total, 100%
Acinetobacter species	75.0 (9)	25.0 (3)	12
Acinetobacter lwoffii	72.7 (8)	27.3 (3)	11
Other gram-negative species (n = 42)	74.3 (101)	25.7 (35)	136
Enterococcus species	54.1 (615)	45.9 (522)	1,137
Enterococcus faecalis	71.3 (429)	28.7 (173)	602
Vancomycin resistant	–† (2)	–† (0)	2
Vancomycin susceptible	71.2 (427)	28.8 (173)	600
Enterococcus faecium	30.1 (145)	69.9 (336)	481
Vancomycin resistant	21.2 (48)	78.8 (178)	226
Vancomycin susceptible	38.0 (97)	62.0 (158)	255
Other *Enterococcus* species (*n* = 54)	75.9 (41)	24.1 (13)	54
Staphylococcus aureus	77.0 (1,936)	23.0 (579)	2,515
Methicillin resistant	69.9 (334)	30.1 (144)	478
Methicillin susceptible	78.6 (1,602)	21.4 (435)	2,037

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

3.3. Onset versus 30-day all-cause mortality

Information on 30-day all-cause mortality was available for 5,373 (67.9%) episodes involving gram-negative species; 951 (83.6%) involving *Enterococcus* species and 1,996 (79.4%) involving *S. aureus*. The only species for which a significant difference was seen in the 30-day all-cause mortality between community-onset and hospital-onset episodes were *E. coli* ($P < 0.01$) and *E. cloacae* complex ($P < 0.01$) (Table 4).

There was a significant difference in the 30-day all-cause mortality between *E. faecium* (27.7%) and *E. faecalis* (14.3%) episodes ($P < 0.0001$). However, there was no significant difference in 30-day all-cause mortality between vancomycin-resistant and vancomycin-susceptible *E. faecium* episodes.

For *S. aureus*, there was a significant difference in 30-day all-cause mortality between methicillin-susceptible *S. aureus* (MSSA) (13.9%) and MRSA (18.9%) episodes ($P = 0.0154$); and between healthcare-associated MRSA (HA-MRSA) (26.5%) and community-associated MRSA (CA-MRSA) (16.0%) clones ($P = 0.0232$).

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), 2017

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Enterococcus species	496	17.7 (88)	455	23.1 (105)	951	20.3 (193)
Enterococcus faecalis	345	14.2 (49)	145	14.5 (21)	490	14.3 (70)
Enterococcus faecium	117	29.9 (35)	298	26.8 (80)	415	27.7 (115)
Vancomycin resistant	39	23.1 (9)	164	30.5 (50)	203	29.1 (58)
Vancomycin susceptible	78	33.3 (26)	134	22.4 (30)	212	26.4 (56)
Other enterococcal species (*n* = 7)	34	11.8 (4)	12	33.3 (4)	46	17.4 (8)
Gram-negative species*	3,952	11.4 (450)	1,421	15.6 (221)	5,373	12.5 (671)
Escherichia coli	2,286	9.4 (214)	546	13.2 (72)	2,832	10.1 (286)
Klebsiella pneumoniae	482	12.4 (60)	224	15.6 (35)	706	13.5 (95)
Pseudomonas aeruginosa	296	19.9 (59)	229	21.4 (49)	525	20.6 (108)
Enterobacter cloacae complex	169	8.3 (14)	145	19.3 (28)	314	13.4 (42)
Klebsiella oxytoca	122	13.9 (17)	42	14.3 (6)	164	14.0 (23)
Proteus mirabilis	132	20.5 (27)	29	20.7 (6)	161	20.5 (33)
Serratia marcescens	72	16.7 (12)	57	15.8 (9)	129	16.3 (21)
Salmonella species (non-typhoidal)	75	2.7 (2)	13	7.7 (1)	88	3.4 (3)
Klebsiella (*Enterobacter*) *aerogenes*	42	9.5 (4)	37	13.5 (5)	79	11.4 (9)
Morganella morganii	42	19.0 (8)	20	0.0 (0)	62	12.9 (8)
Klebsiella variicola	36	16.7 (6)	16	12.5 (2)	52	15.4 (8)
Citrobacter freundii	35	22.9 (8)	13	23.1 (3)	48	22.9 (11)
Acinetobacter baumannii complex	26	19.2 (5)	15	6.7 (1)	41	14.6 (6)
Citrobacter koseri	24	4.2 (1)	8	–† (0)	32	3.1 (1)
Salmonella species (typhoidal)	15	0.0 (0)	0	–† (0)	15	0.0 (0)
Raoultella ornithinolytica	10	30.0 (3)	2	–† (0)	12	25.0 (3)
Other gram-negative species (*n* = 39)	88	11.4 (10)	25	16.0 (4)	113	12.4 (14)
Staphylococcus aureus	1,520	13.8 (209)	476	18.3 (87)	1,996	14.8 (296)
Methicillin resistant	241	16.6 (40)	124	23.4 (29)	365	18.9 (69)
CA-MRSA	180	14.47 (26)	70	20.0 (14)	250	16.0 (40)
HA-MRSA	53	22.6 (12)	49	30.6 (15)	102	26.5 (27)
Methicillin susceptible	1,279	13.2 (169)	352	16.5 (58)	1,631	13.9 (227)

CA-MRSA = community-associated methicillin-resistant *Staphylococcus aureus*; HA-MRSA = healthcare-associated methicillin-resistant *S. aureus*; ns = not significant

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

† Insufficient numbers (<10) to calculate percentage

3.4. Patient age and sex

Age and sex were available for all patients with gram-negative, enterococcal or staphylococcal bacteraemia. For gram-negative bacteraemia, the proportion of males was 52.4%. For *Enterococcus* species and SAB, 64.3% and 66.5%, respectively, were male.

Increasing age was a surrogate risk factor for bacteraemia (Figures 1-3); only 14.1% of gram-negative species episodes, 12.0% of *Enterococcus* species episodes and 21.4% 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, 2017

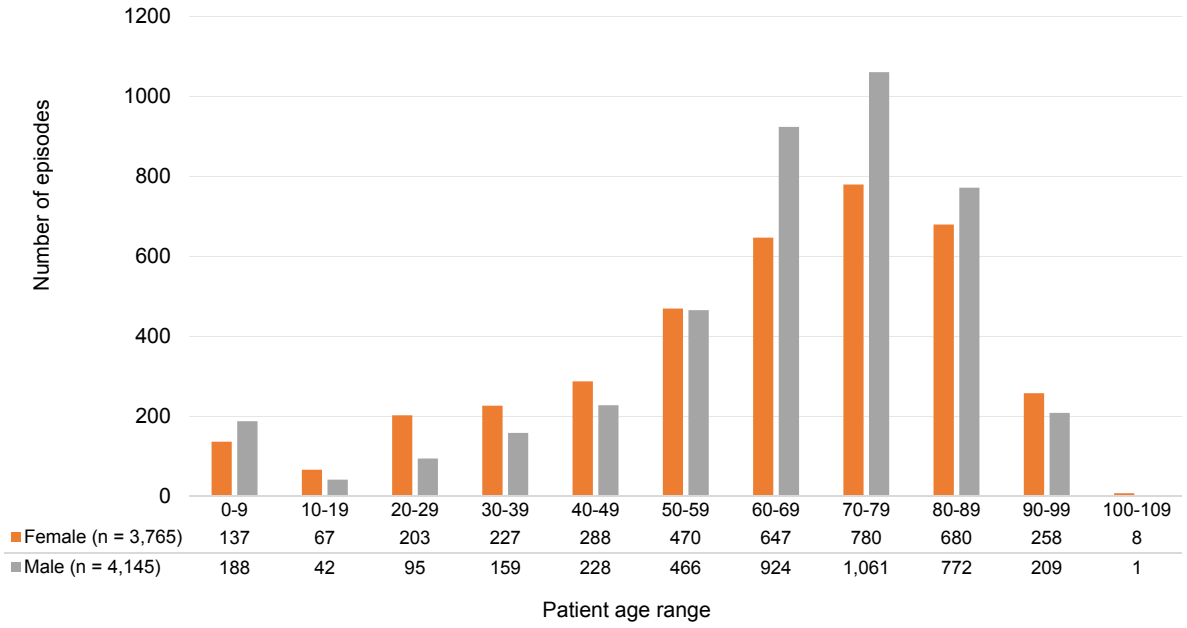


Figure 2: Number of episodes of bacteraemia due to *Enterococcus* species, by patient decade of life and sex, 2017

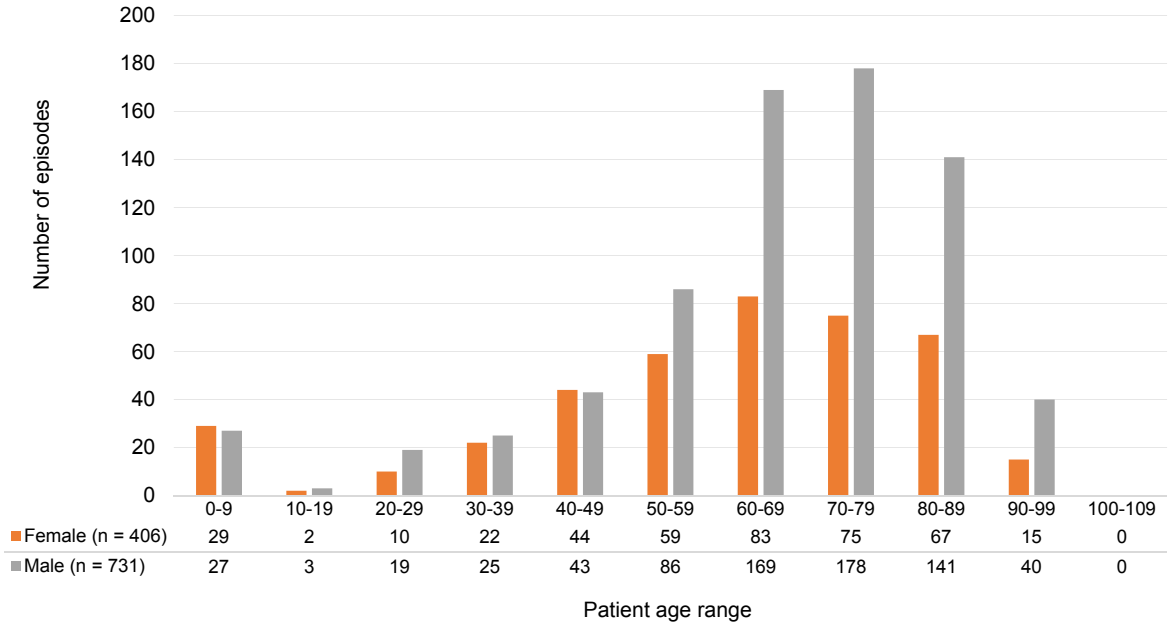
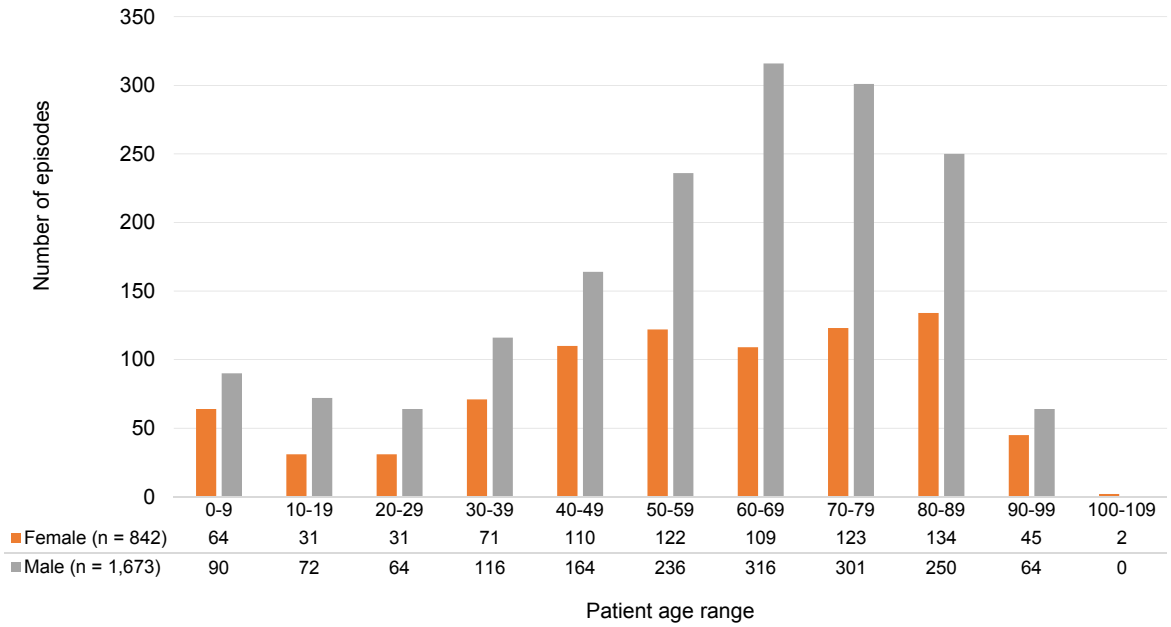


Figure 3: Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient decade of life and sex, 2017



3.5. Principal clinical manifestation

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

Gram-negative bacteria

The principal clinical manifestation was documented for 6,414 (81.1%) patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations were urinary tract infection (41.2%), biliary tract infection (14.7%) and other intra-abdominal infection (10.9%) (Table 5).

Urinary tract infection was the most frequent principal clinical manifestation for both community-onset (47.1%) and hospital-onset (21.9%) episodes.

Table 5: Principal clinical manifestation for gram-negative* bacteraemia, by patient sex, 2017

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance†
Urinary tract infection	46.7 (1,404)	36.3 (1,236)	41.2 (2,640)	$P < 0.01$
Biliary tract infection (including cholangitis)	13.4 (404)	15.9 (540)	14.7 (944)	$P < 0.01$
Intra-abdominal infection other than biliary tract	9.2 (276)	12.4 (422)	10.9 (698)	$P < 0.01$
Febrile neutropenia (when specified)	7.5 (226)	9.4 (320)	8.5 (546)	$P < 0.01$
No focus (setting not known)	7.7 (232)	8.6 (292)	8.2 (524)	ns
Other clinical syndrome	7.0 (212)	7.4 (252)	7.2 (464)	ns
Device-related infection without metastatic focus	4.7 (142)	4.8 (165)	4.8 (307)	ns
Skin and skin structure infections	2.3 (68)	2.8 (95)	2.5 (163)	ns
Osteomyelitis/septic arthritis	0.5 (15)	1.1 (39)	0.8 (54)	$P < 0.01$
Pneumonia/empyema	0.3 (9)	0.7 (23)	0.5 (32)	$0.01 < P < 0.05$
Device-related infection with metastatic focus	0.4 (13)	0.5 (18)	0.5 (31)	ns
Deep abscess(es)) excluding those in the CNS	0.2 (6)	0.1 (3)	0.1 (9)	–
CNS infection (meningitis, abscess(es))	0.1 (2)	0.0 (0)	0.0 (2)	–
Total	3,009	3,405	6,414	

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

Enterococcus species

The principal clinical manifestation was known for 1,067 (93.8%) patient episodes of enterococcal bacteraemia. Overall, the most frequent principal clinical manifestations were urinary tract infection (19.4%), followed by intra-abdominal infection and no focus (setting not known) (both 14.8%) (Table 6). There were no significant gender differences in terms of principle clinical manifestation but overall there were more episodes in males.

Of the hospital-onset episodes where data were available, the most frequent principal clinical manifestation was intra-abdominal infection other than biliary tract (20.9%). Of the community-onset episodes where data were available, the most frequent principal clinical manifestation was urinary tract infection (27.1%).

The principal manifestation was known for 1,015 of the 1,083 (93.7%) *E. faecalis* and *E. faecium* episodes (Table 7). The most common clinical manifestation for *E. faecalis* was urinary tract infection, whereas for *E. faecium* it was intra-abdominal infection (other than biliary tract). 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, 2017

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)	Significance*
Urinary tract infection	14.7 (56)	22.0 (151)	19.4 (207)	$P < 0.01$
Intra-abdominal infection other than biliary tract	17.5 (67)	13.3 (91)	14.8 (158)	ns
No focus (setting not known)	13.9 (53)	15.3 (105)	14.8 (158)	ns
Biliary tract infection (including cholangitis)	15.2 (58)	13.9 (95)	14.3 (153)	ns
Febrile neutropenia (when specified)	8.6 (33)	9.2 (63)	9.0 (96)	ns
Device-related infection without metastatic focus	12.3 (47)	6.3 (43)	8.4 (90)	$P < 0.01$
Endocarditis, left-sided	4.2 (16)	7.3 (50)	6.2 (66)	$0.01 < P < 0.05$
Other clinical syndrome	6.5 (25)	5.0 (34)	5.5 (59)	ns
Skin and skin structure infections	5.2 (20)	3.4 (23)	4.0 (43)	ns
Osteomyelitis/septic arthritis	1.0 (4)	2.2 (15)	1.8 (19)	ns
Device-related infection with metastatic focus	0.3 (1)	1.2 (8)	0.8 (9)	–
Endocarditis, right-sided	0.5 (2)	0.9 (6)	0.7 (8)	–
CNS infection (meningitis, abscess(es))	0.0 (0)	0.1 (1)	0.1 (1)	–
Total	382	685	1,067	

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, 2017

Principal clinical manifestation	Total	*E. faecalis* % (*n*)	*E. faecium* % (*n*)	Significance*
Urinary tract infection	205	30.9 (173)	7.0 (32)	$P < 0.01$
No focus (setting not known)	151	16.1 (90)	13.4 (61)	ns
Intra-abdominal infection other than biliary tract	151	9.3 (52)	21.8 (99)	$P < 0.01$
Biliary tract infection (including cholangitis)	128	8.2 (46)	18.0 (82)	$P < 0.01$
Febrile neutropenia (when specified)	94	3.0 (17)	16.9 (77)	$P < 0.01$
Device-related infection without metastatic focus	86	6.8 (38)	10.5 (48)	$0.01 < P < 0.05$
Endocarditis, left-sided	66	10.5 (59)	1.5 (7)	$P < 0.01$
Other clinical syndrome	57	6.6 (37)	4.4 (20)	ns
Skin and skin structure infections	41	3.9 (22)	4.2 (19)	ns
Osteomyelitis/septic arthritis	19	2.3 (13)	1.3 (6)	ns
Device-related infection with metastatic focus	9	1.1 (6)	0.7 (3)	–
Endocarditis, right-sided	7	1.1 (6)	0.2 (1)	–
CNS infection (meningitis, abscess(es))	1	0.2 (1)	0.0 (0)	–
Total	1,015	560	455	

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 2,205 (87.7%) episodes of SAB (Table 8). Overall, the most frequent principal clinical manifestation was osteomyelitis/septic arthritis (19.0%), followed by skin and skin structure infection (18.6%) and device-related infection without metastatic focus (16.4%).

Of the hospital-onset SABs where data were available, the most common principal clinical manifestation was device-related infection without metastatic focus (27.3%). Of the community-onset SABs where data were available, the most common principal clinical manifestation was osteomyelitis/septic arthritis (19.0%).

Table 8: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient sex, 2017

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	17.1 (125)	19.9 (294)	19.0 (419)
Skin and skin structure infections	17.9 (131)	18.9 (279)	18.6 (410)
Device-related infection without metastatic focus	18.6 (136)	15.3 (225)	16.4 (361)
No focus (setting not known)	14.4 (105)	13.0 (192)	13.5 (297)
Other clinical syndrome	7.4 (54)	8.0 (118)	7.8 (172)
Endocarditis, left-sided	6.6 (48)	7.2 (106)	7.0 (154)
Pneumonia/empyema	4.8 (35)	5.2 (77)	5.1 (112)
Deep abscess(es) excluding those in the CNS	4.4 (32)	4.0 (59)	4.1 (91)
Endocarditis, right-sided	2.9 (21)	2.3 (34)	2.5 (55)
Device-related infection with metastatic focus	2.2 (16)	1.6 (24)	1.8 (40)
CNS infection (meningitis, abscess(es))	1.8 (13)	1.8 (26)	1.8 (39)
Febrile neutropenia (when specified)	1.5 (11)	1.7 (25)	1.6 (36)
Urinary tract infection	0.4 (3)	0.7 (11)	0.6 (14)
Intra-abdominal infection other than biliary tract	0.1 (1)	0.2 (3)	0.2 (4)
Biliary tract infection (including cholangitis)	0.0 (0)	0.1 (1)	<0.1 (1)
Total	731	1,474	2,205

CNS = central nervous system

The most common principal clinical manifestation for methicillin-susceptible *S. aureus* was osteomyelitis/septic arthritis (19.8%), whereas for methicillin-resistant *S. aureus* it was skin and skin structure infection (22.7%) (Table 9).

Table 9: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, 2017

Principal clinical manifestation	Total % (*n*)	Methicillin-susceptible % (*n*)	Methicillin-resistant % (*n*)
Osteomyelitis/septic arthritis	419	19.8 (359)	15.2 (60)
Skin and skin structure	410	17.7 (320)	22.7 (90)
Device-related infection without metastatic focus	361	16.4 (297)	16.2 (64)
No focus (setting not known)	297	13.4 (242)	13.9 (55)
Other clinical syndrome	172	7.5 (136)	9.1 (36)
Endocarditis, left-sided	154	7.0 (127)	6.8 (27)
Pneumonia/empyema	112	5.1 (92)	5.1 (20)
Deep abscess(es) excluding those in the CNS	91	4.1 (75)	4.0 (16)
Endocarditis, right-sided	55	2.7 (49)	1.5 (6)
Device-related infection with metastatic focus	40	1.6 (29)	2.8 (11)
CNS infection (meningitis, abscess(es))	39	2.0 (36)	0.8 (3)

Febrile neutropenia (when specified)	36	1.8 (33)	0.8 (3)
Urinary tract infection	14	0.6 (10)	1.0 (4)
Intra-abdominal infection other than biliary tract	4	0.2 (4)	0.0 (0)
Biliary tract infection (including cholangitis)	1	0.0 (0)	0.3 (1)
Total	2,205	1,809	396

CNS = central nervous system

3.6. Length of hospital stay following bacteraemic episode

Information on length of stay following bacteraemia was available for 6,992 (88.4%) episodes involving gram-negative species, 1,055 (92.8%) episodes involving *Enterococcus* species and 2,291 (91.1%) episodes involving *S. aureus*.

The most common length of stay (44.8%) for patients with a gram-negative bacteraemia was less than seven days (Table 10). Overall, 21.4% of patients remained in hospital for more than 30 days after enterococcal bacteraemia (Table 11) and 26.1% after staphylococcal bacteraemia (Table 12).

Table 10: Length of stay following gram-negative bacteraemia, by species and place of onset, 2017

Species	Percentage length of stay following bacteraemia (*n*)				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Gram-negative species*	44.8 (3,134)	30.7 (2,148)	15.1 (1,059)	9.3 (651)	6,992
Enterobacterales	46.3 (2,899)	30.4 (1,905)	14.5 (911)	8.7 (548)	6,263
Escherichia coli	51.4 (1,963)	29.9 (1,140)	12.3 (468)	6.4 (246)	3,817
Community onset	57.7 (1,823)	29.0 (917)	9.6 (302)	3.8 (120)	3,162
Hospital onset	21.4 (140)	34.0 (223)	25.3 (166)	19.2 (126)	655
Klebsiella pneumoniae	35.6 (320)	32.1 (289)	20.6 (185)	11.7 (105)	899
Community onset	44.0 (282)	32.8 (210)	17.6 (113)	5.6 (36)	641
Hospital onset	14.7 (38)	30.6 (79)	27.9 (72)	26.7 (69)	258
Enterobacter cloacae complex	31.5 (124)	32.0 (126)	21.6 (85)	15.0 (59)	394
Community onset	43.5 (94)	34.3 (74)	14.4 (31)	7.9 (17)	216
Hospital onset	16.9 (30)	29.2 (52)	30.3 (54)	23.6 (42)	178
Other Enterobacterales (*n* = 45)	42.7 (492)	30.4 (350)	15.0 (173)	12.0 (138)	1,153
Pseudomonas aeruginosa	32.3 (205)	32.6 (207)	21.1 (134)	13.9 (88)	634
Community onset	41.2 (150)	34.3 (125)	18.4 (67)	6.0 (22)	364
Hospital onset	20.4 (55)	30.4 (82)	24.8 (67)	24.4 (66)	270
Acinetobacter species	31.6 (30)	37.9 (36)	14.7 (14)	15.8 (15)	95
Community onset	34.3 (24)	41.4 (29)	12.9 (9)	11.4 (8)	70
Hospital onset	24.0 (6)	28.0 (7)	20.0 (5)	28.0 (7)	25

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

Table 11: Length of stay following *Enterococcus* species bacteraemia, by vancomycin resistance and place of onset, 2017

Species	Percentage length of stay following bacteraemia (*n*)				Total
	<7 days % (*n*)	7–14 % days (*n*)	15–30 % days (*n*)	>30 days % (*n*)	
All species	26.3 (277)	27.5 (290)	24.8 (262)	21.4 (226)	1,055
E. faecalis	29.1 (160)	28.6 (157)	21.1 (116)	21.1 (116)	549
E. faecium	22.2 (101)	24.8 (113)	29.9 (136)	23.1 (105)	455
Vancomycin susceptible	26.0 (61)	28.1 (66)	24.3 (57)	21.7 (51)	235
Vancomycin resistant	18.2 (40)	21.4 (47)	35.9 (79)	24.5 (54)	220
Other *Enterococcus* species (*n* = 7)	31.4 (16)	39.2 (20)	19.6 (10)	9.8 (5)	51
Community onset					
E. faecalis	36.3 (140)	29.5 (114)	18.1 (70)	16.1 (62)	386
E. faecium	28.2 (37)	34.4 (45)	25.2 (33)	12.2 (16)	131
Vancomycin susceptible	29.9 (26)	40.2 (35)	20.7 (18)	9.2 (8)	87
Vancomycin resistant	25.0 (11)	22.7 (10)	34.1 (15)	18.2 (8)	44
Hospital onset					
E. faecalis	12.3 (20)	26.4 (43)	28.2 (46)	33.1 (54)	163
E. faecium	19.8 (64)	21.0 (68)	31.8 (103)	27.5 (89)	324
Vancomycin susceptible	23.6 (35)	20.9 (31)	26.4 (39)	29.1 (43)	148
Vancomycin resistant	16.5 (29)	21.0 (37)	36.4 (64)	26.1 (46)	176

Table 12: Length of stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, 2017

Species	Percentage length of stay following bacteraemia (*n*)				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Staphylococcus aureus	18.7 (429)	25.6 (586)	29.6 (677)	26.1 (599)	2,291
Methicillin resistant	21.9 (94)	24.5 (105)	27.0 (116)	26.6 (114)	429
Community onset	24.6 (72)	26.6 (78)	25.3 (74)	23.5 (69)	293
Hospital onset	16.2 (22)	19.9 (27)	30.9 (42)	33.1 (45)	136
Methicillin susceptible	18.0 (335)	25.8 (481)	30.1 (561)	26.0 (485)	1,862
Community onset	19.1 (279)	26.4 (387)	29.8 (436)	24.7 (362)	1,464
Hospital onset	14.1 (56)	23.6 (94)	31.4 (125)	30.9 (123)	398

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

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

Supplementary data on percentages susceptible, intermediate and resistant, for each antimicrobial and all species, and the antimicrobial profiles by state and territory can be found in the 2017 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), 2017

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Acinetobacter baumannii complex					
Piperacillin–tazobactam	55	7.3 (4)	12.7 (7)	–*	–*
Ceftazidime	61	19.7 (12)	4.9 (3)	–*	–*
Cefepime	61	6.6 (4)	8.2 (5)	–*	–*
Gentamicin	63	0.0 (0)	6.3 (4)	–†	6.3 (4)
Tobramycin	63	0.0 (0)	6.3 (4)	–†	6.3 (4)
Amikacin	62	0.0 (0)	3.2 (2)	4.8 (3)	3.2 (2)
Ciprofloxacin	63	0.0 (0)	6.3 (4)	–†	6.3 (4)
Meropenem	63	0.0 (0)	4.8 (3)	0.0 (0)	4.8 (3)
Enterobacter cloacae complex					
Piperacillin–tazobactam	351	5.1 (18)	22.5 (79)	2.8 (10)	27.6 (97)
Ceftriaxone	433	0.2 (1)	27.7 (120)	0.2 (1)	27.7 (120)
Ceftazidime	433	0.5 (2)	24.5 (106)	3.2 (14)	24.9 (108)
Cefepime	433	3.7 (16)§	3.2 (14)	9.0 (39)	5.5 (24)
Gentamicin	433	0.5 (2)	6.9 (30)	0.7 (3)	7.4 (32)
Tobramycin	433	1.8 (8)	5.8 (25)	0.5 (2)	7.6 (33)
Amikacin	433	0.0 (0)	0.2 (1)	1.4 (6)	0.2 (1)
Ciprofloxacin	433	1.2 (5)	1.8 (8)	2.8 (12)	5.8 (25)
Meropenem	431	0.0 (0)	2.3 (10)	0.2 (1)	2.1 (9)
Enterococcus faecalis					
Ampicillin	601	–†	0.0 (0)	0.2 (1)	0.0 (0)
Benzylpenicillin	580	–†	0.3 (2)	–*	–*
Ciprofloxacin	546	3.5 (19)	12.6 (69)	–†	10.3 (56)
Daptomycin	580	0.3 (2)§§	–†	–*	–*
Linezolid	601	1.3 (8)	0.0 (0)	–†	0.0 (0)
Teicoplanin	601	0.0 (0)	0.0 (0)	–†	0.0 (0)
Tetracycline	508	0.0 (0)	75.8 (385)	–*	–*
Vancomycin	601	0.3 (2)	0.0 (0)	–†	0.3 (2)
Enterococcus faecium					
Ampicillin	481	–†	89.6 (431)	0.2 (1)	89.6 (431)
Benzylpenicillin	469	–†	91.3 (428)	–*	–*
Ciprofloxacin	444	2.7 (12)	89.6 (398)	–†	77.3 (343)
Linezolid	481	1.0 (5)	0.0 (0)	–†	0.0 (0)
Teicoplanin	481	3.1 (15)	19.8 (95)	–†	24.8 (120)
Tetracycline	411	0.0 (0)	65.2 (268)	–*	–*

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Vancomycin	481	0.6 (3)	46.4 (223)	–[†]	47.0 (226)
Escherichia coli					
Ampicillin	4,353	1.4 (61)	53.0 (2,306)	–[†]	54.4 (2,367)
Amoxicillin–clavulanic acid	4,354	13.6 (594)	8.4 (365)	–[#]	–[#]
Piperacillin–tazobactam	4,345	3.1 (134)	2.8 (121)	1.4 (59)	5.9 (255)
Ceftriaxone	4,355	0.1 (4)	11.2 (489)	0.1 (4)	11.2 (489)
Ceftazidime	4,355	0.5 (21)	5.8 (252)	4.8 (210)	6.3 (273)
Cefepime	4,354	2.2 (97)	2.8 (123)	4.6 (201)	4.1 (178)
Gentamicin	4,353	0.1 (4)	8.4 (366)	1.0 (43)	8.5 (370)
Tobramycin	4,355	5.7 (247)	3.7 (162)	0.6 (25)	9.4 (409)
Amikacin	4,355	0.1 (5)	0.1 (3)	1.7 (72)	0.2 (8)
Ciprofloxacin	4,353	0.2 (8)	11.9 (520)	3.6 (158)	14.4 (626)
Meropenem	4,353	<0.1 (1)	0.1 (4)	<0.0 (1)	0.1 (3)
Klebsiella (*Enterobacter*) *aerogenes*					
Piperacillin–tazobactam	103	9.7 (10)	33.0 (34)	3.9 (4)	42.7 (44)
Ceftriaxone	104	1.0 (1)	42.3 (44)	1.0 (1)	42.3 (44)
Ceftazidime	104	4.8 (5)	36.5 (38)	3.8 (4)	41.3 (43)
Cefepime	104	0.0 (0)[§]	0.0 (0)	1.9 (2)	0.0 (0)
Gentamicin	104	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Tobramycin	104	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Amikacin	104	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Ciprofloxacin	104	1.0 (1)	0.0 (0)	2.9 (3)	2.9 (3)
Meropenem	103	0.0 (0)	1.0 (1)	1.0 (1)	0.0 (0)
Klebsiella oxytoca					
Amoxicillin–clavulanic acid	229	3.5 (8)	8.3 (19)	–[#]	–[#]
Piperacillin–tazobactam	228	1.3 (3)	9.6 (22)	3.5 (8)	11.0 (25)
Ceftriaxone	229	0.4 (1)	5.2 (12)	0.4 (1)	5.2 (12)
Ceftazidime	229	0.0 (0)	0.0 (0)	0.4 (1)	0.0 (0)
Cefepime	229	0.4 (1)[§]	0.0 (0)	0.9 (2)	0.0 (0)
Gentamicin	229	0.0 (0)	0.4 (1)	0.4 (1)	0.4 (1)
Tobramycin	229	1.7 (4)	0.0 (0)	0.0 (0)	1.7 (4)
Amikacin	229	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Ciprofloxacin	229	0.0 (0)	1.3 (3)	1.7 (4)	1.7 (4)
Meropenem	229	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Klebsiella pneumoniae					
Amoxicillin–clavulanic acid	995	4.1 (41)	5.3 (53)	–[#]	–[#]
Piperacillin–tazobactam	990	3.5 (35)	3.7 (37)	6.8 (67)	7.3 (72)
Ceftriaxone	997	0.0 (0)	8.8 (88)	0.0 (0)	8.8 (88)
Ceftazidime	997	0.6 (6)	5.2 (52)	2.8 (28)	5.8 (58)
Cefepime	997	1.0 (10)[§]	3.0 (30)	3.2 (32)	3.7 (37)
Gentamicin	996	0.5 (5)	4.4 (44)	0.4 (4)	4.9 (49)
Tobramycin	997	2.0 (20)	4.4 (44)	0.4 (4)	6.4 (64)
Amikacin	997	0.1 (1)	0.2 (2)	0.7 (7)	0.3 (3)
Ciprofloxacin	996	0.9 (9)	3.5 (35)	2.9 (29)	8.3 (83)
Meropenem	995	0.0 (0)	0.8 (8)	0.3 (3)	0.5 (5)
Proteus mirabilis					

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Ampicillin	235	0.4 (1)	16.6 (39)	–[†]	17.0 (40)
Amoxicillin–clavulanic acid	235	5.5 (13)	2.6 (6)	–[#]	–[#]
Piperacillin–tazobactam	235	1.3 (3)	0.0 (0)	0.0 (0)	1.3 (3)
Ceftriaxone	235	0.0 (0)	2.1 (5)	0.0 (0)	2.1 (5)
Ceftazidime	234	0.0 (0)	1.3 (3)	1.7 (4)	1.3 (3)
Cefepime	235	0.4 (1)[§]	0.9 (2)	0.0 (0)	1.3 (3)
Gentamicin	235	1.3 (3)	3.4 (8)	1.7 (4)	4.7 (11)
Tobramycin	235	2.1 (5)	1.7 (4)	0.4 (1)	3.8 (9)
Amikacin	235	0.0 (0)	0.4 (1)	1.3 (3)	0.4 (1)
Ciprofloxacin	235	0.4 (1)	3.0 (7)	2.1 (5)	4.7 (11)
Meropenem	235	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin–tazobactam	684	6.7 (46)	6.4 (44)	–[†]	13.2 (90)
Ceftazidime	686	4.4 (30)	5.0 (34)	–[†]	9.3 (64)
Cefepime	689	3.2 (22)	3.3 (23)	–[†]	6.5 (45)
Gentamicin	686	1.9 (13)	2.0 (14)	–[†]	3.9 (27)
Tobramycin	689	0.3 (2)	1.3 (9)	–[†]	1.6 (11)
Amikacin	689	0.7 (5)	0.4 (3)	2.9 (20)	1.2 (8)
Ciprofloxacin	685	2.6 (18)	2.5 (17)	0.0 (0)	9.8 (67)
Meropenem	686	2.3 (16)	5.5 (38)	3.5 (24)	4.4 (30)
Salmonella species (non-typhoidal)					
Ampicillin	131	0.0 (0)	8.4 (11)	–[†]	8.4 (11)
Amoxicillin–clavulanic acid	131	0.8 (1)	0.8 (1)	–[#]	–[#]
Piperacillin–tazobactam	130	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Ceftriaxone	131	0.0 (0)	1.5 (2)	0.0 (0)	1.5 (2)
Ceftazidime	131	0.0 (0)	1.5 (2)	0.0 (0)	1.5 (2)
Cefepime	130	0.0 (0)	0.8 (1)	0.0 (0)	0.8 (1)
Ciprofloxacin	129	0.8 (1)**	3.9 (5)	–**	4.7 (6)
Meropenem	131	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	126	–[‡]	–[‡]	–[‡]	–[‡]
Ceftriaxone	167	0.6 (1)	1.8 (3)	0.6 (1)	1.8 (3)
Ceftazidime	167	0.0 (0)	1.8 (3)	0.6 (1)	1.8 (3)
Cefepime	167	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Gentamicin	167	1.8 (3)	0.6 (1)	3.6 (6)	2.4 (4)
Tobramycin	167	28.1 (47)	3.0 (5)	15.6 (26)	31.1 (52)
Amikacin	166	0.6 (1)	0.0 (0)	4.2 (7)	0.6 (1)
Ciprofloxacin	167	0.0 (0)	0.6 (1)	0.6 (1)	3.0 (5)
Meropenem	167	0.0 (0)	0.6 (1)	0.6 (1)	0.0 (0)
Staphylococcus aureus					
Benzylpenicillin	2,509	–[†]	81.5 (2,045)	–[†]	81.5 (2,045)
Ciprofloxacin	2,505	0.6 (15)	9.4 (236)	–[†]	10.0 (251)
Clindamycin (constitutive)	2,509	0.2 (4)	3.8 (95)	0.2 (4)	3.9 (99)
Clindamycin (inducible + constitutive resistance)	2,218	0.2 (4)	15.2 (338)	0.0 (0)	15.4 (342)

Species and antimicrobial	Number	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Intermediate % (*n*)	Resistant % (*n*)
Daptomycin	2,515	0.3 (7)[§§]	–[†]	–[†]	0.3 (7)
Erythromycin	2,511	2.9 (73)	15.1 (379)	0.1 (2)	16.5 (413)
Gentamicin	2,511	0.6 (16)	2.9 (72)	–[†]	4.1 (102)
Linezolid	2,515	0.0 (0)	0.0 (0)	–[†]	0.0 (0)
Oxacillin	2,508	–[†]	18.4 (461)	–[†]	18.4 (461)
Rifampicin	2,464	0.1 (2)	0.6 (15)	–[##]	0.7 (18)
Trimethoprim-sulfamethoxazole	2,508	–[†]	4.2 (105)	0.4 (9)	3.8 (96)
Teicoplanin	2,511	0.0 (0)	0.0 (0)	–[†]	0.2 (5)
Tetracycline	2,239	0.0 (1)	5.4 (121)	0.4 (9)	5.5 (123)
Vancomycin	2,511	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
# 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.
‡ Not indicated on susceptibility testing cards
§§ Non-susceptible; resistance not defined
The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant.

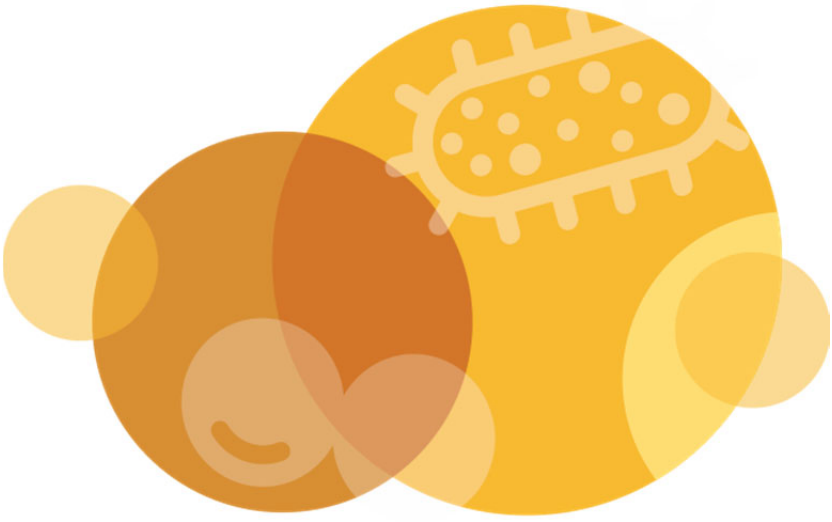
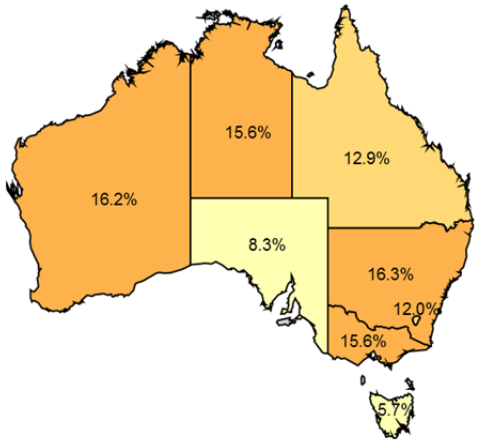
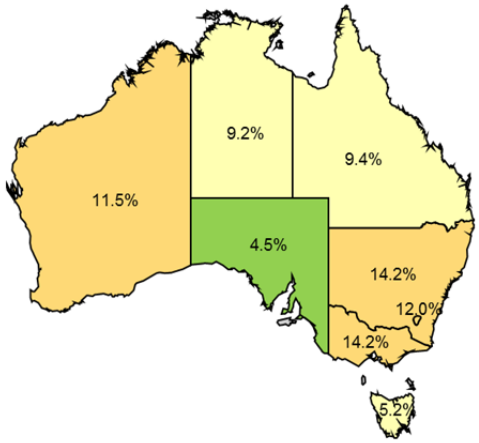


Figure 4. Percentage of *Escherichia coli* from patients with bacteraemia with resistance to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, 2017

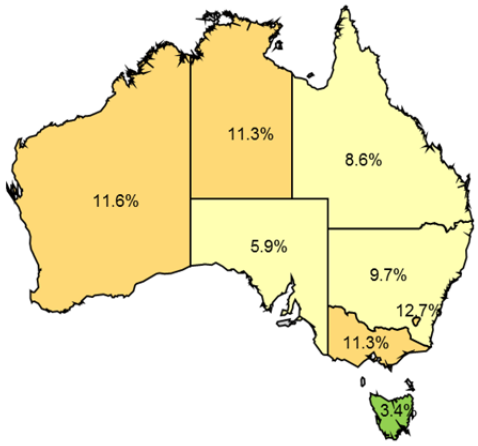
A. Fluoroquinolones



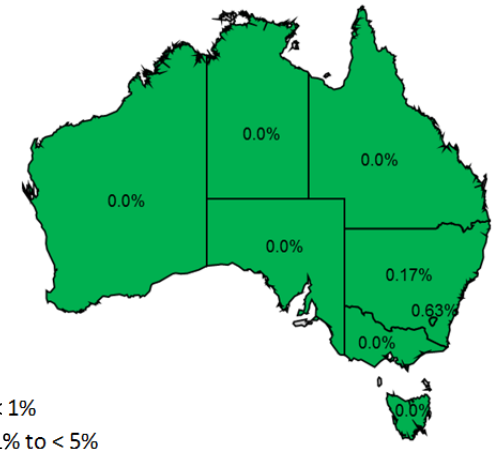
B. Third-generation cephalosporins



C. Aminoglycosides



D. Carbapenems



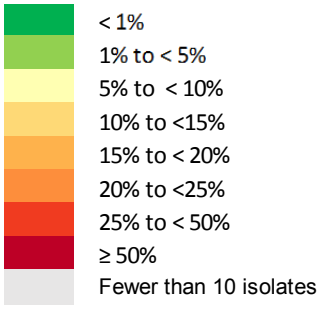
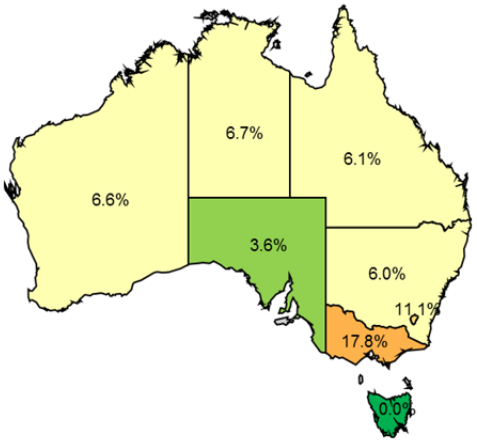
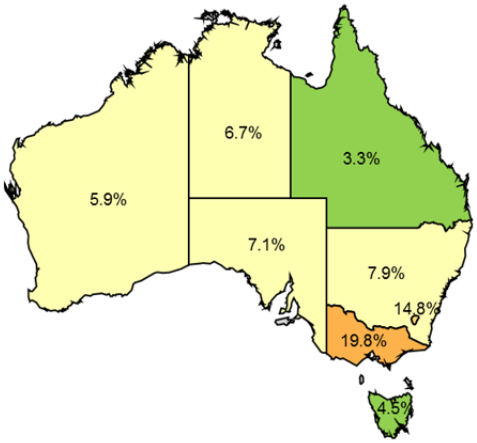


Figure 5. Percentage of *Klebsiella pneumoniae* from patients with bacteraemia with resistance to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, 2017

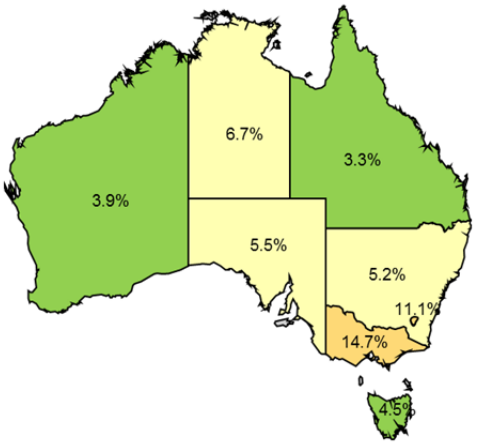
A. Fluoroquinolones



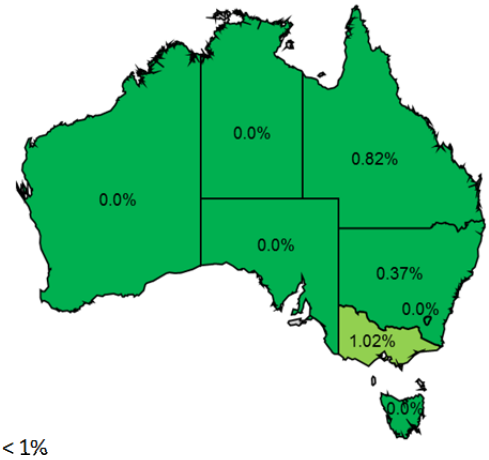
B. Third-generation cephalosporins



C. Aminoglycosides



D. Carbapenems



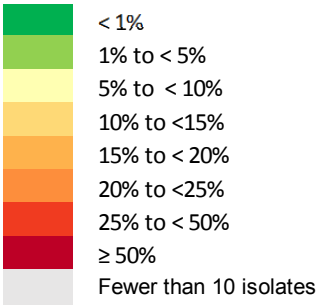
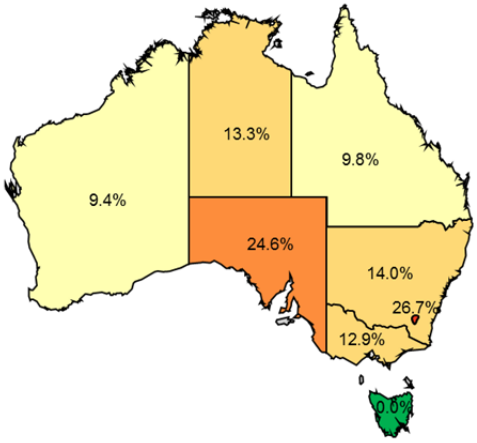
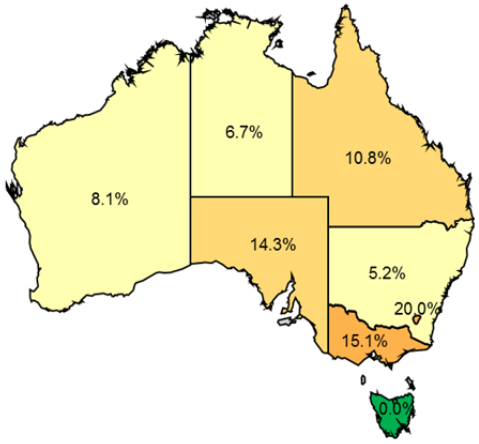


Figure 6. Percentage of *Pseudomonas aeruginosa* from patients with bacteraemia with resistance to piperacillin-tazobactam (A), fluoroquinolones (B), ceftazidime (C) and carbapenems (D), Australia, 2017

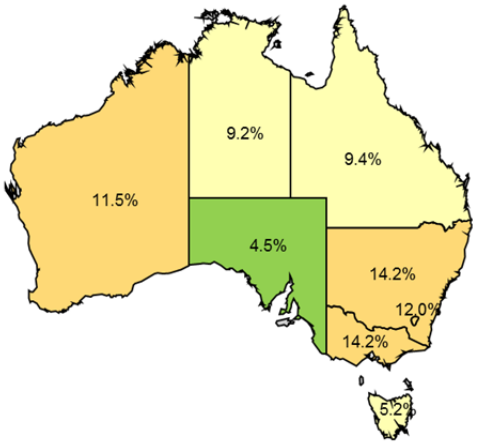
A. Piperacillin-tazobactam



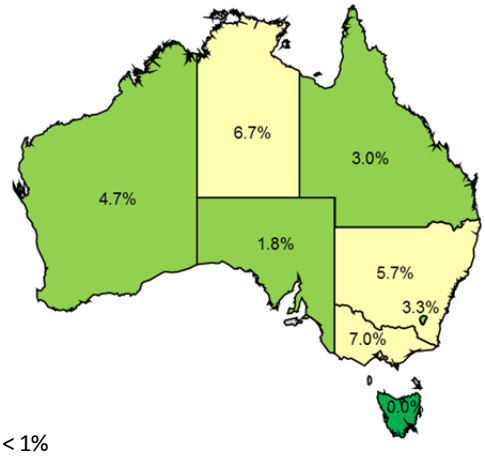
B. Fluoroquinolones



C. Ceftazidime



D. Carbapenems



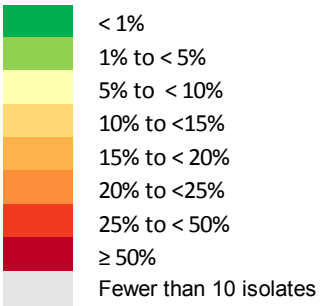


Figure 7. Percentage of *Staphylococcus aureus* from patients with bacteraemia with resistance to methicillin, Australia, 2017

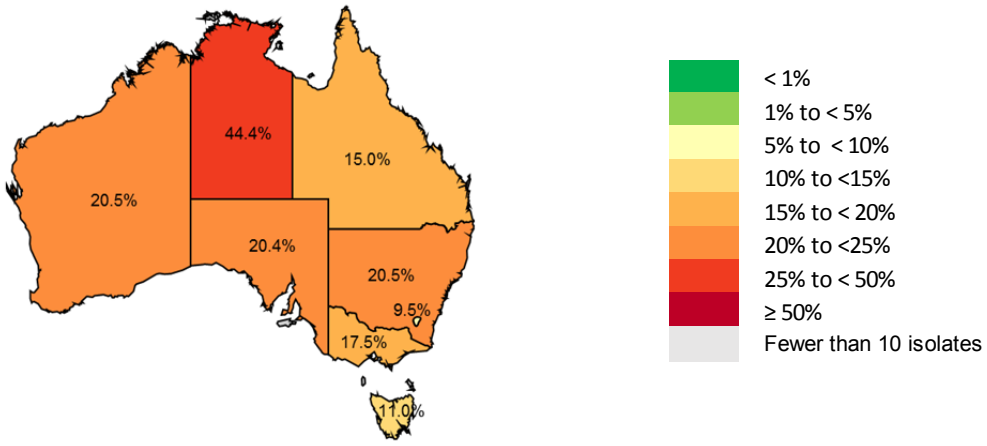
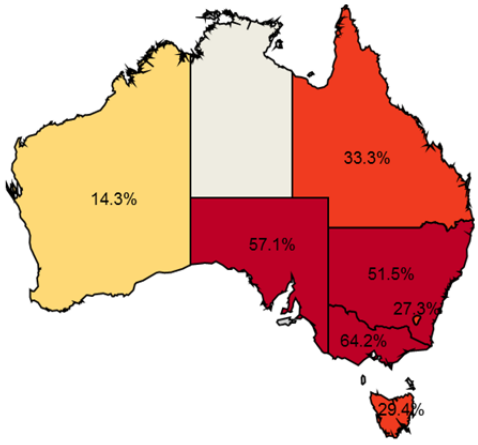
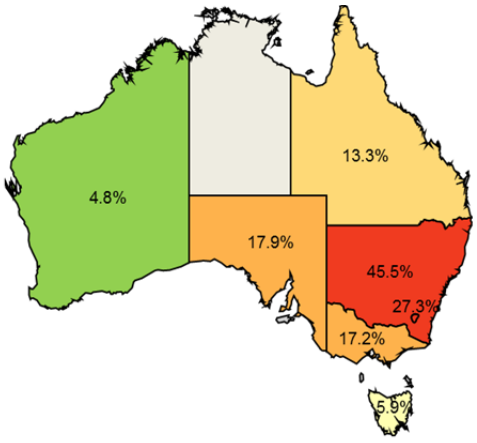


Figure 8. Percentage of *Enterococcus faecium* from patients with bacteraemia with resistance to vancomycin (A) and teicoplanin (B), and *Enterococcus faecalis* with resistance to high-level gentamicin (C), Australia, 2017

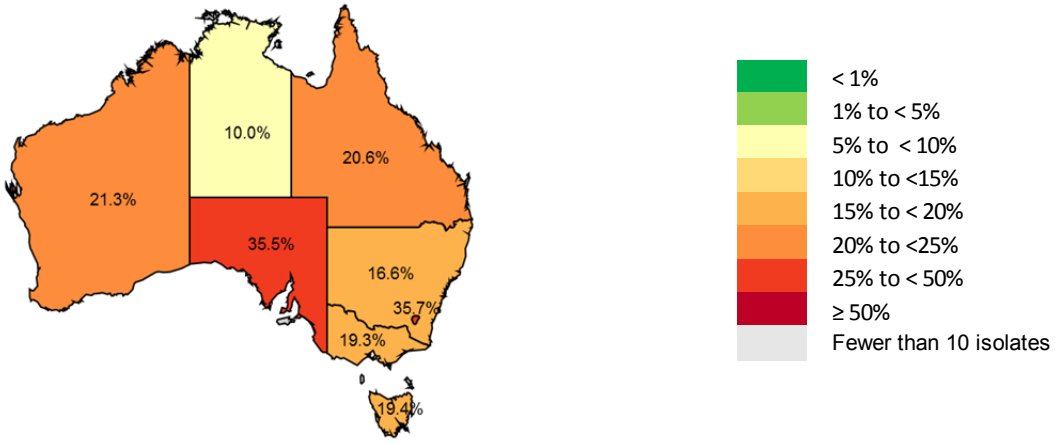
A. Vancomycin



B. Teicoplanin



C. High-level gentamicin



Antimicrobial resistance by place of onset

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

Table 14: Antimicrobial resistances (CLSI, EUCAST), by place of onset, 2017

		Community-onset		Hospital onset	
Species and antimicrobial	**Number**	**% intermediate**	**% resistant**	**% intermediate**	**% resistant**
Acinetobacter baumannii complex					
Piperacillin–tazobactam	55	5.4, –*	8.1, –*	11.1, –*	22.2, –*
Ceftriaxone	57	61.5, –*	12.8, –*	72.2, –*	11.1, –*
Ceftazidime	61	19.0, –*	4.8, –*	21.1, –*	5.3, –*
Cefepime	61	0.0, –*	7.1, –*	0.0, –*	10.5, –*
Gentamicin	63	0.0, –†	6.8, 6.8	0.0, –†	5.3, 5.3
Tobramycin	63	0.0, –†	6.8, 6.8	0.0, –†	5.3, 5.3
Amikacin	62	0.0, 4.5	2.3, 2.3	0.0, 5.6	5.6, 5.6
Ciprofloxacin	63	0.0, –†	4.5, 4.5	0.0, –†	10.5, 10.5
Meropenem	63	0.0, 0.0	4.5, 4.5	0.0, 0.0	5.3, 5.3
Enterobacter cloacae complex					
Piperacillin–tazobactam	351	5.8, 3.1	12.6, 18.3	4.4, 2.5	34.4, 38.8
Ceftriaxone	433	0.0, 0.0	19.3, 19.3	0.5, 0.5	37.9, 37.9
Ceftazidime	433	0.4, 3.8	15.1, 15.5	0.5, 2.6	35.9, 36.4
Cefepime	433	1.7, 5.6§	1.7, 2.9	6.2, 13.3§	5.1, 8.7
Gentamicin	433	0.8, 0.8	5.5, 6.3	0.0, 0.5	8.7, 8.7
Tobramycin	433	2.1, 0.4	4.2, 6.3	1.5, 0.5	7.7, 9.2
Amikacin	433	0.0, 0.4	0.0, 0.0	0.0, 2.6	0.5, 0.5
Ciprofloxacin	433	0.4, 2.5	1.7, 4.2	2.1, 3.1	2.1, 7.7
Meropenem	431	0.0, 0.4	1.3, 0.8	0.0, 0.0	3.6, 3.6
Enterococcus faecalis					
Ampicillin	601	–†, 0.0	0.0, 0.0	–†, 0.0	0.0, 0.0
Benzylpenicillin	580	–†, –*	0.5, –*	–†, –*	0.0, –*
Ciprofloxacin	546	3.8, –†	13.4, 10.9	2.6, –†	10.6, 8.6
Daptomycin	580	0.5#, –*	–†, –*	0.0#, –*	–†, –*
Linezolid	601	1.4, –†	0.0, 0.0	1.2, –†	0.0, 0.0
Teicoplanin	601	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Tetracycline	508	0.0, –*	76.3, –*	0.0, –*	74.7, –*
Vancomycin	601	0.5, –†	0.0, 0.5	0.0, –†	0.0, 0.0
Enterococcus faecium					
Ampicillin	481	–†, 0.0	77.2, 77.2	–†, 0.0	94.9, 94.9
Benzylpenicillin	469	–†, –*	80.6, –*	–†, –*	95.8, –*
Ciprofloxacin	444	6.0, –†	78.9, 64.7	1.3, –†	94.2, 82.6
Linezolid	481	0.0, –†	0.0, 0.0	1.5, –†	0.0, 0.0
Teicoplanin	481	3.4, –†	13.8, 18.6	3.0, –†	22.3, 27.7
Tetracycline	411	0.0, –*	60.8, –*	0.0, –*	67.0, –*
Vancomycin	481	0.7, –†	32.4, 33.1	0.6, –†	52.4, 53.0
Escherichia coli					
Ampicillin	4,353	1.4, –†	51.9, 53.3	1.5, –†	58.5, 60.1
Amoxicillin–clavulanic acid	4,354	13.0, –**	7.6, –**	16.7, –**	12.5, –**
Piperacillin–tazobactam	4,345	2.8, 1.3	2.0, 4.8	4.5, 1.8	6.9, 11.4
Ceftriaxone	4,355	0.1, 0.1	10.4, 10.4	0.3, 0.3	15.5, 15.5

Species and antimicrobial	Number	Community-onset		Hospital onset	
		% intermediate	% resistant	% intermediate	% resistant
Ceftazidime	4,355	0.5, 4.5	5.2, 5.7	0.4, 6.4	8.7, 9.1
Cefepime	4,354	2.2[§], 4.3	2.3, 3.5	2.4[§], 6.3	5.3, 6.9
Gentamicin	4,353	0.1, 1.0	8.0, 8.0	0.3, 1.0	10.6, 10.9
Tobramycin	4,355	5.5, 0.6	3.5, 9.0	6.6, 0.6	4.6, 11.2
Amikacin	4,355	0.1, 1.6	0.0, 0.1	0.1, 2.0	0.3, 0.4
Ciprofloxacin	4,353	0.1, 3.7	11.5, 13.7	0.6, 3.2	14.1, 17.9
Meropenem	4,353	0.0, 0.0	0.1, 0.1	0.1, 0.1	0.3, 0.1
Klebsiella (*Enterobacter*) *aerogenes*					
Piperacillin–tazobactam	103	12.1, 5.2	22.4, 34.5	6.7, 2.2	46.7, 53.3
Ceftriaxone	104	0.0, 0.0	36.2, 36.2	2.2, 2.2	50.0, 50.0
Ceftazidime	104	5.2, 3.4	31.0, 36.2	4.3, 4.3	43.5, 47.8
Cefepime	104	0.0, 0.0	0.0, 0.0	0.0, 4.3[§]	0.0, 0.0
Gentamicin	104	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Tobramycin	104	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Amikacin	104	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Ciprofloxacin	104	0.0, 3.4	0.0, 1.7	2.2, 2.2	0.0, 4.3
Meropenem	103	0.0, 0.0	0.0, 0.0	0.0, 2.2	2.2, 0.0
Klebsiella oxytoca					
Amoxicillin–clavulanic acid	229	2.3, –**	6.4, –**	6.9, –**	13.8, –**
Piperacillin–tazobactam	228	0.6, 2.9	8.2, 8.8	3.5, 5.3	14.0, 17.5
Ceftriaxone	229	0.0, 0.0	4.1, 4.1	1.7, 1.7	8.6, 8.6
Ceftazidime	229	0.0, 0.6	0.0, 0.0	0.0, 0.0	0.0, 0.0
Cefepime	229	0.0[§], 0.6	0.0, 0.0	1.7, 1.7	0.0, 0.0
Gentamicin	229	0.0, 0.0	0.6, 0.6	0.0, 1.7	0.0, 0.0
Tobramycin	229	2.3, 0.0	0.0, 2.3	0.0, 0.0	0.0, 0.0
Amikacin	229	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Ciprofloxacin	229	0.0, 1.2	1.8, 2.3	0.0, 3.4	0.0, 0.0
Meropenem	229	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae					
Amoxicillin–clavulanic acid	995	3.5, –**	3.4, –**	5.7, –**	10.3, –**
Piperacillin–tazobactam	990	2.5, 6.6	2.0, 4.5	6.0, 7.1	8.2, 14.2
Ceftriaxone	997	0.0, 0.0	6.4, 6.4	0.0, 0.0	14.9, 14.9
Ceftazidime	997	0.4, 1.8	3.8, 4.2	1.1, 5.3	8.9, 9.9
Cefepime	997	1.1[§], 2.2	2.1, 2.8	0.7[§], 5.7	5.3, 6.0
Gentamicin	996	0.3, 0.6	3.4, 3.6	1.1, 0.0	7.1, 8.2
Tobramycin	997	1.3, 0.3	3.4, 4.6	3.9, 0.7	7.1, 11.0
Amikacin	997	0.1, 0.6	0.0, 0.1	0.0, 1.1	0.7, 0.7
Ciprofloxacin	996	0.7, 2.9	2.9, 6.6	1.4, 2.8	5.0, 12.8
Meropenem	995	0.0, 0.1	0.4, 0.3	0.0, 0.7	1.8, 1.1
Proteus mirabilis					
Ampicillin	236	0.0, –[†]	16.5, 16.5	2.4, –[†]	17.1, 19.5
Amoxicillin–clavulanic acid	235	6.2, –**	2.1, –**	2.4, –**	4.9, –**
Piperacillin–tazobactam	235	1.0, 0.0	0.0, 1.0	2.4, 0.0	0.0, 2.4
Ceftriaxone	235	0.0, 0.0	1.5, 1.5	0.0, 0.0	4.9, 4.9
Ceftazidime	234	0.0, 2.1	1.0, 1.0	0.0, 0.0	2.4, 2.4
Cefepime	235	0.5[§], 0.0	1.0, 1.5	0.0, 0.0	0.0, 0.0
Gentamicin	235	1.0, 2.1	4.1, 5.2	2.4, 0.0	0.0, 2.4

Species and antimicrobial	Number	Community-onset		Hospital onset	
		% intermediate	% resistant	% intermediate	% resistant
Tobramycin	235	2.1, 0.5	2.1, 4.1	2.4, 0.0	0.0, 2.4
Amikacin	235	0.0, 1.5	0.5, 0.5	0.0, 0.0	0.0, 0.0
Ciprofloxacin	235	0.5, 2.6	3.1, 4.1	0.0, 0.0	2.4, 7.3
Meropenem	235	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Pseudomonas aeruginosa					
Piperacillin–tazobactam	684	4.7, –†	2.5, 7.2	9.5, –†	12.0, 21.6
Ceftazidime	686	3.5, –†	2.2, 5.7	5.7, –†	8.8, 14.5
Cefepime	689	0.0, –†	2.5, 4.0	0.0, –†	4.6, 10.2
Gentamicin	686	2.0, –†	1.5, 3.5	1.8, –†	2.8, 4.6
Tobramycin	689	0.2, –†	0.5, 0.7	0.4, –†	2.5, 2.8
Amikacin	689	1.0, 2.5	0.2, 1.2	0.4, 3.5	0.7, 1.1
Ciprofloxacin	685	3.0, 0.0	2.0, 9.4	2.1, 0.0	3.2, 10.3
Meropenem	686	3.0, 3.5	2.2, 1.7	1.4, 3.5	10.2, 8.1
Salmonella species (non-typhoidal)					
Ampicillin	131	0.0, –†	7.6, 7.6	0.0, –†	15.4, 15.4
Amoxicillin–clavulanic acid	131	0.0, –**	0.8, –**	7.7, –**	0.0, –**
Piperacillin–tazobactam	130	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Ceftriaxone	131	0.0, 0.0	1.7, 1.7	0.0, 0.0	0.0, 0.0
Ceftazidime	131	0.0, 0.0	1.7, 1.7	0.0, 0.0	0.0, 0.0
Cefepime	130	0.0§, 0.0	0.9, 0.9	0.0, 0.0	0.0, 0.0
Ciprofloxacin	129	–‡	4.3, 5.1	–‡	0.0, 0.0
Meropenem	131	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Serratia marcescens					
Ampicillin	156	39.4, –†	28.7, 68.1	43.5, –†	33.9, 77.4
Amoxicillin–clavulanic acid	167	22.9, –†	52.1, –†	26.8, –†	56.3, –†
Piperacillin–tazobactam	126	–§§	–§§	–§§	–§§
Ceftriaxone	167	1.0, 1.0	0.0, 0.0	0.0, 0.0	4.2, 4.2
Ceftazidime	167	0.0, 0.0	0.0, 0.0	0.0, 1.4	4.2, 4.2
Cefepime	167	0.0*, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Gentamicin	167	1.0, 4.2	0.0, 1.0	2.8, 2.8	1.4, 4.2
Tobramycin	167	24.0, 15.6	3.1, 27.1	33.8, 15.5	2.8, 36.6
Amikacin	166	1.0, 5.2	0.0, 1.0	0.0, 2.9	0.0, 0.0
Ciprofloxacin	167	0.0, 0.0	1.0, 1.0	0.0, 1.4	0.0, 5.6
Meropenem	167	0.0, 1.0	1.0, 0.0	0.0, 0.0	0.0, 0.0
Staphylococcus aureus					
Benzylpenicillin	2,509	–†, –†	81.0, 81.0	–†, –†	83.2, 83.2
Ciprofloxacin	2,505	0.6, –†	7.5, 8.1	0.5, –†	15.8, 16.3
Clindamycin (constitutive)	2,509	0.0, 0.1	2.9, 3.1	0.0, 0.3	6.6, 6.9
Clindamycin (inducible + constitutive resistance)***	2,218	0.1, 0.0	14.4, 14.6	0.4, 0.0	17.9, 18.3
Daptomycin	2,515	0.3#, –†	–†, 0.3	0.3#, –†	–†, 0.3
Erythromycin	2,511	2.8, 0.1	14.0, 15.5	3.3, 0.2	18.9, 19.8
Gentamicin	2,511	0.5, –†	1.8, 2.8	1.0, –†	6.6, 8.1
Linezolid	2,515	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Oxacillin	2,508	–†, –†	16.6, 16.6	–†, –†	24.5, 24.5
Rifampicin	2,464	0.1, –##	0.6, 0.7	0.2, –##	0.7, 0.9
Trimethoprim-sulfamethoxazole	2,508	–†, 0.4	3.2, 2.8	–†, 0.3	7.5, 7.1
Teicoplanin	2,511	0.0, –†	0.0, 0.2	0.0, –†	0.0, 0.2

Species and antimicrobial	Number	Community-onset		Hospital onset	
		% intermediate	% resistant	% intermediate	% resistant
Tetracycline	2,239	0.0, 0.3	4.5, 4.5	0.2, 0.6	8.6, 8.8
Vancomycin	2,511	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

Non-susceptible, resistance not defined

** 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.

§§ Not indicated on susceptibility testing cards

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

*** Inducible clindamycin resistance as determined by Vitek or Phoenix

3.8. Multidrug resistance

The most problematic pathogens are those with multiple acquired resistances. For the purpose of this survey, multidrug resistance is defined as acquired resistance to more than three antimicrobial groups. For each species, antimicrobials were excluded from the count if they were affected by intrinsic resistance mechanisms, and/or neither CLSI nor EUCAST breakpoints were available. For this analysis, resistance included intermediate and resistant susceptibility results, if applicable.

Only isolates for which the full range of antimicrobial agents 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. *A. baumannii* complex was not included because there are few breakpoints to permit analysis.

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

Table 15: Multiple acquired resistance in *Enterobacter cloacae* complex, by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)						
		0	1	2	3	%	4	5	6	7	8	9	%
NSW	104	57	7	5	7	73.1	14	2	5	3	2	2	26.9
Vic	65	30	5	1	17	81.5	8	2	1	0	1	0	18.5
Qld	94	54	15	4	10	88.3	2	3	6	0	0	0	11.7
SA	20	10	4	0	1	75.0	2	1	1	1	0	0	25.0
WA	37	27	2	1	3	89.2	3	0	1	0	0	0	10.8
Tas	15	12	0	0	0	80.0	1	0	0	1	1	0	20.0
NT	7	3	2	0	0	71.4	1	0	0	1	0	0	28.6
ACT	9	5	1	0	1	77.8	1	0	0	0	1	0	22.2
Total	351	198	36	11	39	80.9	32	8	14	6	5	2	19.1

MDR = multi-drug resistant
Notes: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem. *Enterobacter cloacae* complex includes *E. asburiae* (n = 6), *E. kobei* (n = 2).and *E hormaechei* (n = 1)

Table 16: Multiple acquired resistance in *Enterococcus faecalis*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)		
		0	1	2	3	%	4	5	%
NSW	184	164	20	0	0	100	0	0	0.0
Vic	118	102	13	3	0	100	0	0	0.0
Qld	94	78	16	0	0	100	0	0	0.0
SA	31	24	7	0	0	100	0	0	0.0
WA	90	85	5	0	0	100	0	0	0.0
Tas	16	15	1	0	0	100	0	0	0.0
NT	10	8	2	0	0	100	0	0	0.0
ACT	0	0	0	0	0	100	0	0	0.0
Total	543	476	64	3	0	100	0	0	0.0

MDR = multi-drug resistant
Notes: Antimicrobials were ampicillin, ciprofloxacin, linezolid, nitrofurantoin and vancomycin

Table 17: Multiple acquired resistance in *Enterococcus faecium*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)	
		0	1	2	3	%	4	%
NSW	165	16	5	60	84	100	0	0.0
Vic	133	8	3	36	86	100	0	0.0
Qld	40	2	2	23	13	100	0	0.0
SA	28	4	0	8	16	100	0	0.0
WA	63	12	1	41	9	100	0	0.0
Tas	10	0	0	6	4	100	0	0.0
NT	5	1	0	1	3	100	0	0.0
ACT	0	0	0	0	0	100	0	0.0
Total	444	43	11	175	215	100	0	0.0

MDR = multi-drug resistant
Notes: Antimicrobials were ampicillin, ciprofloxacin, linezolid, and vancomycin

Table 18: Multiple acquired resistance in *Escherichia coli*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)									
		0	1	2	3	%	4	5	6	7	8	9	10	11	12	13	%
NSW	1,170	439	168	175	106	75.9	75	48	38	41	33	29	15	3	0	0	24.1
Vic	790	299	116	125	65	76.6	50	37	33	26	14	12	9	4	0	0	23.4
Qld	855	342	133	139	63	79.2	60	40	14	25	15	12	8	4	0	0	20.8
SA	286	140	49	36	21	86.0	11	14	4	5	4	1	1	0	0	0	14.0
WA	767	285	112	126	64	76.5	53	31	23	27	26	12	7	1	0	0	23.5
Tas	126	63	22	13	9	84.9	5	8	3	2	0	1	0	0	0	0	15.1
NT	141	49	18	31	15	80.1	11	5	2	5	3	1	1	0	0	0	19.9
ACT	158	69	18	23	18	81.0	5	4	8	4	5	3	1	0	0	0	19.0
Total	4,293	1,686	636	668	361	78.1	270	187	125	135	100	71	42	12	0	0	21.9

MDR = multi-drug resistant
Note: Antimicrobials were ampicillin, amoxicillin–clavulanic acid (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, nitrofurantoin, trimethoprim and meropenem.

Table 19: Multiple acquired resistance in *Klebsiella pneumoniae*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)								
		0	1	2	3	%	4	5	6	7	8	9	10	11	%
NSW	266	189	36	11	7	91.4	4	2	5	3	0	7	2	0	8.6
Vic	195	124	20	5	7	80.0	5	1	6	12	6	7	1	1	20.0
Qld	244	181	29	12	8	94.3	5	2	0	2	2	3	0	0	5.7
SA	54	41	3	4	0	88.9	2	2	0	1	0	1	0	0	11.1
WA	151	112	16	7	3	91.4	3	2	2	0	0	6	0	0	8.6
Tas	16	14	1	0	0	93.8	0	0	0	0	1	0	0	0	6.3
NT	30	20	7	0	0	90.0	0	1	0	0	0	2	0	0	10.0
ACT	27	19	2	1	1	85.2	0	1	0	1	1	0	1	0	14.8
Total	983	700	114	40	26	89.5	19	11	13	19	10	26	4	1	10.5

MDR = multi-drug resistant
Note: Antimicrobials were amoxicillin–clavulanic acid (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem.

Table 20: Multiple acquired resistance in *Staphylococcus aureus* (methicillin resistant), by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)									
		0	1	2	3	%	4	5	6	7	8	9	10	11	12	%
NSW	113	25	32	16	14	77.0	13	13	0	0	0	0	0	0	0	23.0
Vic	64	19	17	13	6	85.9	5	3	1	0	0	0	0	0	0	14.1
Qld	83	44	16	14	4	94.0	0	3	1	1	0	0	0	0	0	6.0
SA	33	7	10	9	3	87.9	1	3	0	0	0	0	0	0	0	12.1
WA	95	43	40	7	2	96.8	2	1	0	0	0	0	0	0	0	3.2
Tas	7	1	3	2	0	85.7	0	1	0	0	0	0	0	0	0	14.3
NT	44	16	22	2	1	93.2	1	2	0	0	0	0	0	0	0	6.8
ACT	9	5	1	2	0	88.9	1	0	0	0	0	0	0	0	0	11.1
Total	448	160	141	65	30	88.4	23	26	2	1	0	0	0	0	0	11.6

MDR = multi-drug resistant
Note: Antimicrobials were ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin (CLSI), rifampicin, trimethoprim-sulfamethoxazole, tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™) and vancomycin.

Table 21: Multiple acquired resistance in *Staphylococcus aureus* (methicillin susceptible), by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)										
		0	1	2	3	%	4	5	6	7	8	9	10	11	12	13	%
NSW	466	78	289	79	17	99.4	2	0	1	0	0	0	0	0	0	0	0.6
Vic	301	54	204	36	7	100	0	0	0	0	0	0	0	0	0	0	0.0
Qld	470	91	302	50	26	99.8	1	0	0	0	0	0	0	0	0	0	0.2
SA	130	20	92	14	3	99.2	1	0	0	0	0	0	0	0	0	0	0.8
WA	370	61	240	61	7	99.7	1	0	0	0	0	0	0	0	0	0	0.3
Tas	37	10	25	2	0	100	0	0	0	0	0	0	0	0	0	0	0.0
NT	55	7	38	7	3	100	0	0	0	0	0	0	0	0	0	0	0.0
ACT	86	23	50	11	2	100	0	0	0	0	0	0	0	0	0	0	0.0
Total	1,915	344	1,240	260	65	99.7	5	0	1	0	0	0	0	0	0	0	0.3

MDR = multi-drug resistant
Note: Antimicrobials were benzylpenicillin, ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin (CLSI), rifampicin, trimethoprim-sulfamethoxazole, tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™) and vancomycin.

Nationally, more than half (55.8%) of all *E. coli* isolates were resistant to at least one of five key antimicrobial groups (aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 22). For *K. pneumoniae*, 12.3% were resistant to at least one antimicrobial group (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 23). Over 20% of *P. aeruginosa* were resistant to at least one antimicrobial group (piperacillin–tazobactam, fluoroquinolones, ceftazidime, aminoglycosides and carbapenems) (Table 24). For *S. aureus*, the most common resistance combination was resistance to methicillin and fluoroquinolones (Table 25).

Table 22: Resistance combinations among *Escherichia coli* tested against aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems (n = 4,352), Australia, 2017

Resistance pattern	Number	% of total*
Fully susceptible	**1,925**	**44.2**
Single resistance	1,600	36.8
Aminopenicillins	1,542	35.4
Fluoroquinolones	52	1.2
Aminoglycosides	6	0.1
Resistance to two antimicrobial groups	352	8.1
Aminopenicillins + fluoroquinolones	144	3.3
Aminopenicillins + third-generation cephalosporins	109	2.5
Aminopenicillins + aminoglycosides	96	2.2
Fluoroquinolones + aminoglycosides	2	0.0
Fluoroquinolones + third-generation cephalosporins	1	0.0
Resistance to three antimicrobial groups	281	6.5
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	152	3.5
Aminopenicillins + fluoroquinolones + aminoglycosides	82	1.9
Aminopenicillins + third-generation cephalosporins + aminoglycosides	46	1.1
Aminopenicillins + third-generation cephalosporins + carbapenems	1	0.0
Resistance to four antimicrobial groups	194	4.5
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	192	4.4
Aminopenicillins + third-generation cephalosporins + aminoglycosides + carbapenems	1	0.0
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + carbapenems	1	0.0

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

Table 23: Resistance combinations among *Klebsiella pneumoniae* tested against fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems (n = 994), Australia, 2017

Resistance pattern	N	% of total
Fully susceptible	**872**	**87.7**
Single resistance	55	5.5
Fluoroquinolones	30	3.0
Third-generation cephalosporins	22	2.2
Aminoglycosides	3	0.3
Resistance to two antimicrobial groups	18	1.8
Third-generation cephalosporins + aminoglycosides	13	1.3
Third-generation cephalosporins + fluoroquinolones	3	0.3
Third-generation cephalosporins + carbapenem	1	0.1
Fluoroquinolone + aminoglycosides	1	0.1
Resistance to three antimicrobial groups	45	4.5
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	45	4.5
Resistance to four antimicrobial groups	4	0.4
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	4	0.4

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

Table 24: Resistance combinations among *Pseudomonas aeruginosa* tested against piperacillin-tazobactam, ceftazidime, fluoroquinolones, aminoglycosides and carbapenems (n = 682), Australia, 2017

Resistance pattern	N	% of total
Fully susceptible	**541**	**79.3**
Single resistance	60	8.8
Fluoroquinolones	30	4.4
Piperacillin-tazobactam	16	2.3
Aminoglycosides	10	1.5
Carbapenems	3	0.4
Ceftazidime	1	0.1
Resistance to two antimicrobial groups	45	6.6
Piperacillin-tazobactam + ceftazidime	32	4.7
Piperacillin-tazobactam + fluoroquinolones	5	0.7
Piperacillin-tazobactam + carbapenems	3	0.4
Fluoroquinolones + aminoglycosides	2	0.3
Other antimicrobial group combinations	3	0.4
Resistance to three antimicrobial groups	20	2.9
Piperacillin-tazobactam + ceftazidime + fluoroquinolones	8	1.2
Piperacillin-tazobactam + ceftazidime + carbapenems	6	0.9
Piperacillin-tazobactam + fluoroquinolones + carbapenems	2	0.3
Other antimicrobial group combinations	4	0.6
Resistance to four antimicrobial groups	13	1.9
Piperacillin-tazobactam + ceftazidime + fluoroquinolones + carbapenems	6	0.9
Piperacillin-tazobactam + fluoroquinolones + aminoglycosides + carbapenems	3	0.4
Piperacillin-tazobactam + ceftazidime + fluoroquinolones + aminoglycosides	3	0.4

Resistance pattern	N	% of total
Ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	1	0.1
Resistance to five antimicrobial groups	**3**	**0.4**
Piperacillin-tazobactam + ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	3	0.4

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

Table 25: Resistance combinations among *Staphylococcus aureus* tested against methicillin, fluoroquinolones and rifampicin (n = 2,458), Australia, 2017

Resistance pattern	N	% of total
Fully susceptible	**1,924**	**78.3**
Single resistance	334	13.6
Methicillin	273	11.1
Fluoroquinolones	52	2.1
Rifampicin	9	0.4
Resistance to two antimicrobial groups	194	7.9
Methicillin + fluoroquinolones	191	7.8
Methicillin + rifampicin	3	0.1
Resistance to three antimicrobial groups	6	0.2
Methicillin + fluoroquinolones + rifampicin	6	0.2

* Only data from isolates tested against all four 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 26.

Table 26: Multidrug resistance, by onset setting and 30-day all-cause mortality, 2017

		Total		Community onset		Hospital onset	
Species	Category*	Number	Deaths (%)	Number	Deaths (%)	Number	Deaths (%)
Escherichia coli	Total	2,736	10.3 (283)	2,218	9.5 (211)	518	13.9 (72)
	Non-MDR (≤3)	2,114	10.0 (212)	1,757	9.4 (166)	357	12.9 (46)
	MDR (>3)	622	11.4 (71)	461	9.8 (45)	161	16.1 (26)
Enterobacter cloacae complex	Total	252	12.3 (31)	133	10.8 (13)	119	15.1 (18)
	Non-MDR (≤3)	203	11.8 (24)	113	10.8 (11)	90	14.4 (13)
	MDR (>3)	49	14.3 (7)	20	11.1 (2)	29	17.2 (5)
Enterococcus faecalis	Total	436	15.1 (66)	312	14.7 (46)	124	16.1 (20)
	Non-MDR (≤3)	436	15.1 (66)	312	14.7 (46)	124	16.1 (20)
	MDR (>3)	0	n/a	0	n/a	0	n/a
Enterococcus faecium	Total	378	27.2 (103)	105	28.6 (30)	273	26.7 (73)
	Non-MDR (≤3)	378	27.2 (103)	105	28.6 (30)	273	26.7 (73)
	MDR (>3)	0	n/a	0	n/a	0	n/a
Klebsiella pneumoniae	Total	680	13.4 (91)	466	13.9 (57)	214	15.9 (34)
	Non-MDR (≤3)	602	13.5 (81)	427	13.9 (52)	175	16.6 (29)
	MDR (>3)	78	12.8 (10)	39	14.7 (5)	39	12.8 (5)
Staphylococcus aureus	Total	1,843	14.4 (265)	1,412	13.2 (187)	431	18.1 (78)
	Non-MDR (≤3)	1,722	13.5 (232)	1,354	12.6 (171)	368	16.6 (61)
	MDR (>3)	121	27.3 (33)	58	27.6 (16)	63	27.0 (17)
Staphylococcus aureus, methicillin resistant	Total	336	18.2 (61)	224	15.6 (35)	112	23.2 (26)
	Non-MDR (≤3)	292	17.1 (50)	209	15.8 (33)	83	20.5 (17)
	MDR (>3)	44	25.0 (11)	15	13.3 (2)	29	31.0 (9)
Staphylococcus aureus, methicillin susceptible	Total	1,510	13.5 (204)	1,190	12.8 (152)	320	16.3 (52)
	Non-MDR (≤3)	1,505	13.4 (202)	1,186	12.7 (151)	319	16.0 (51)
	MDR (>3)	5	–† (2)	4	–† (1)	1	–† (1)
Pseudomonas aeruginosa	Total	511	20.5 (105)	290	25.5 (59)	221	20.8 (46)
	Non-MDR (≤3)	499	19.8 (99)	285	25.0 (57)	214	19.6 (42)
	MDR (>3)	12	50.0 (6)	5	2†	7	4†
	Non-MDR (≤2)	483	19.5 (94)	277	24.2 (54)	206	19.4 (40)
	MDR (>2)	28	39.3 (11)	13	62.5 (5)	15	40.0 (6)

MDR = multi-drug resistant; n/a = not applicable

* For *P. aeruginosa*, resistance to more than two agents was also included.

† Insufficient numbers (<10) to calculate percentage

3.9. Trend analysis (2013–2017)

Trend data were available for Enterobacterales for the period 2013 to 2017. *Acinetobacter* species and *P. aeruginosa* were introduced to the program in 2015.

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

Gram-negative species

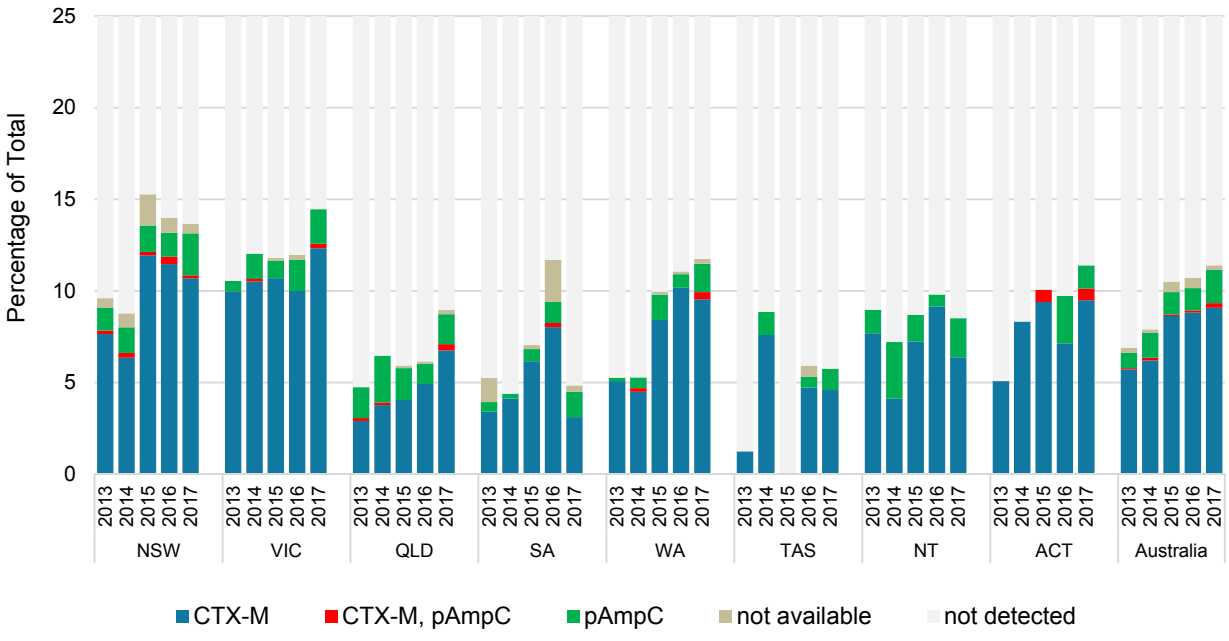
Extended-spectrum β-lactamases

Nationally, there was no significant increase in the proportion of *E. coli* with CTX-M-type (see Section 3.10.1) from 2015 to 2017 (Figure 9). However, there was a significant increase in the proportion of plasmid-borne AmpC β-lactamases (X^2 for linear trend = 11.51, $P < 0.01$), notably from Western Australia. Over the five-year period, both CTX-M types and plasmid-borne AmpC β-lactamases have shown a significant increase nationally, most notable in isolates from Queensland (CTX-M types) and Western Australia.

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

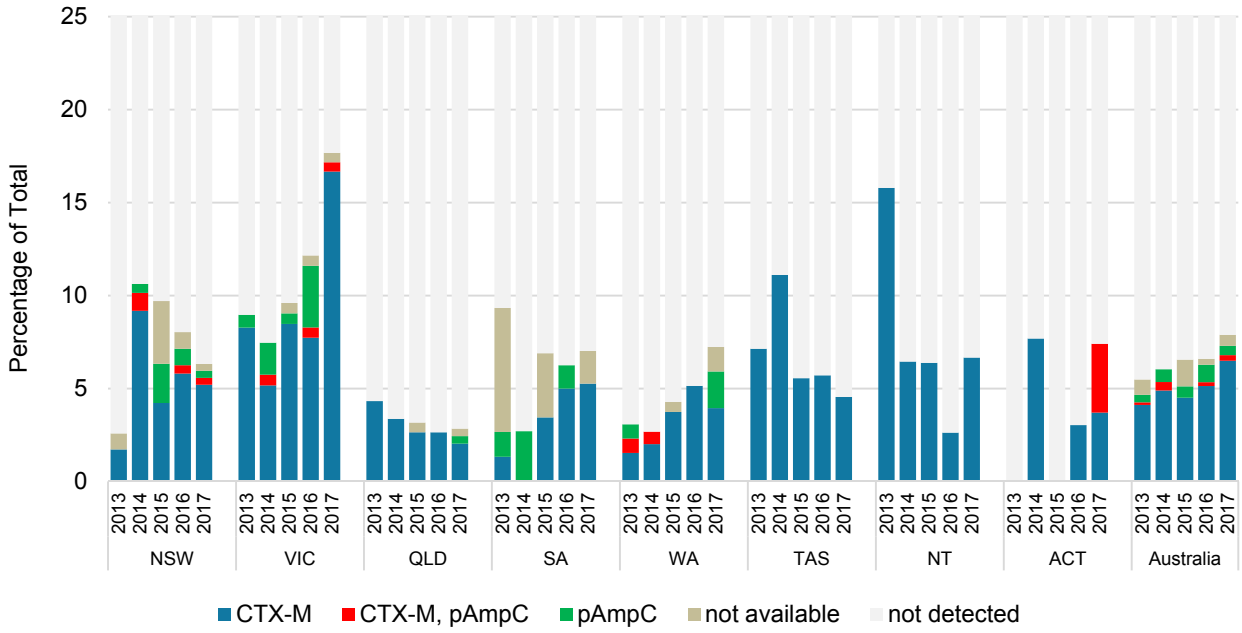
The proportion of *K. pneumoniae* with CTX-M-type or plasmid-borne AmpC β-lactamases increased slowly during the period 2013 to 2017, although regional variations were seen (Figure 10). Most notable was the significant increase in CTX-M types detected from isolates from Victoria (X^2 for linear trend = 9.462, $P < 0.01$).

Figure 9. Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Escherichia coli* by state and territory, and nationally, 2013–2017



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

Figure 10. Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Klebsiella pneumoniae* by state and territory, and nationally, 2013–2017



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

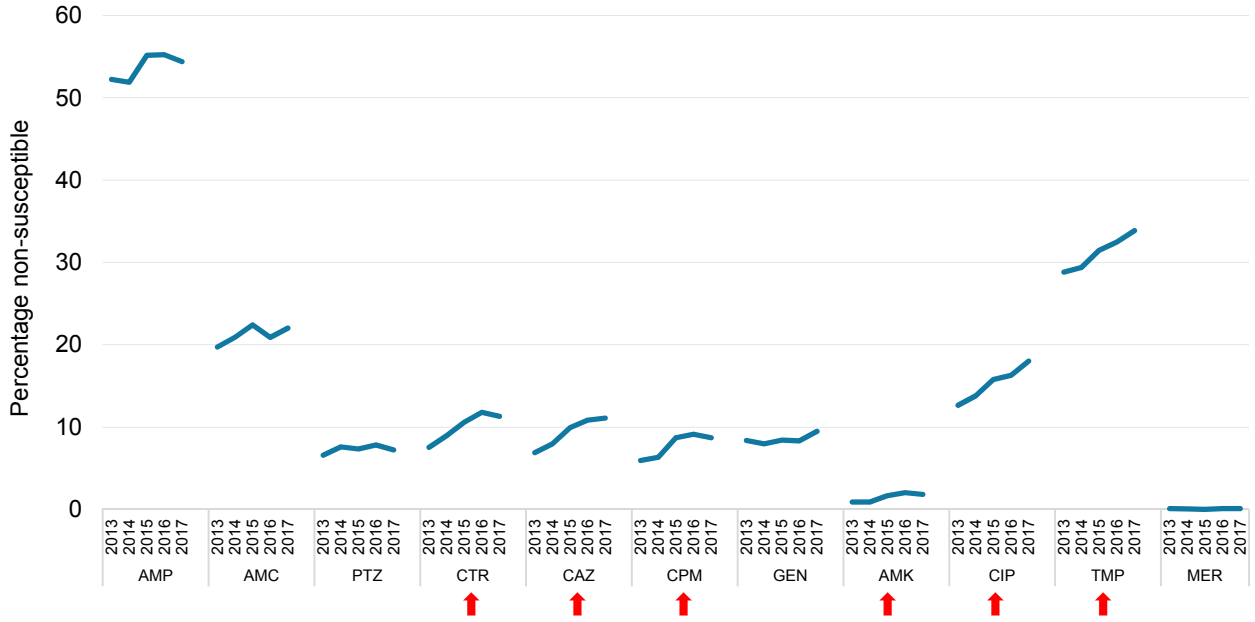
Escherichia coli

Non-susceptibility to key anti-gram negative antimicrobial agents showed a steady increase from 2013 to 2017 (Figure 11). There was a significant increase in non-susceptibility to amikacin (X^2 for linear trend = 20.75, $P < 0.01$), ceftriaxone (X^2 for linear trend = 31.93, $P < 0.01$), ceftazidime (X^2 for linear trend = 41.68, $P < 0.01$), cefepime (X^2 for linear trend = 27.05, $P < 0.01$), ciprofloxacin (X^2 for linear trend = 34.80, $P < 0.01$), and trimethoprim (X^2 for linear trend = 15.18, $P < 0.01$).

Klebsiella pneumoniae

There were no significant changes in non-susceptibility to key antimicrobial agents for *K. pneumoniae* over the five-year period 2013 to 2017 (Figure 12).

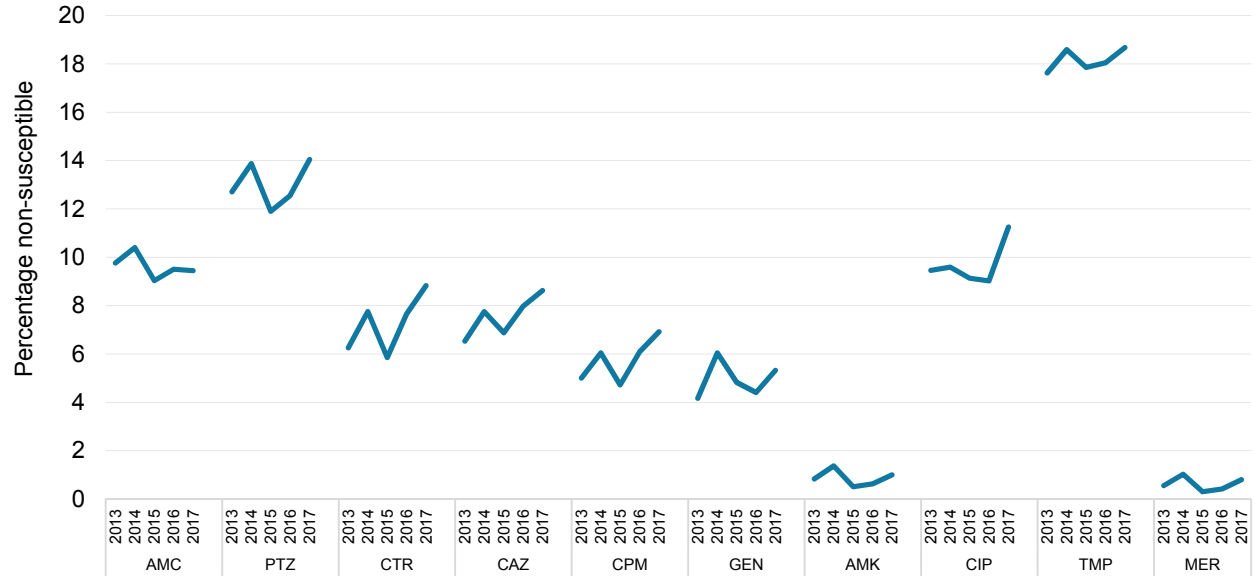
Figure 11. Non-susceptibility of *Escherichia coli* to key antimicrobials (EUCAST), Australia, 2013–2017



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; TMP = trimethoprim

Red arrows indicate antimicrobial agents with significant increase ($P < 0.01$) over the period 2013 to 2017

Figure 12. Non-susceptibility of *Klebsiella pneumoniae* to key antimicrobials (EUCAST), Australia, 2013–2017

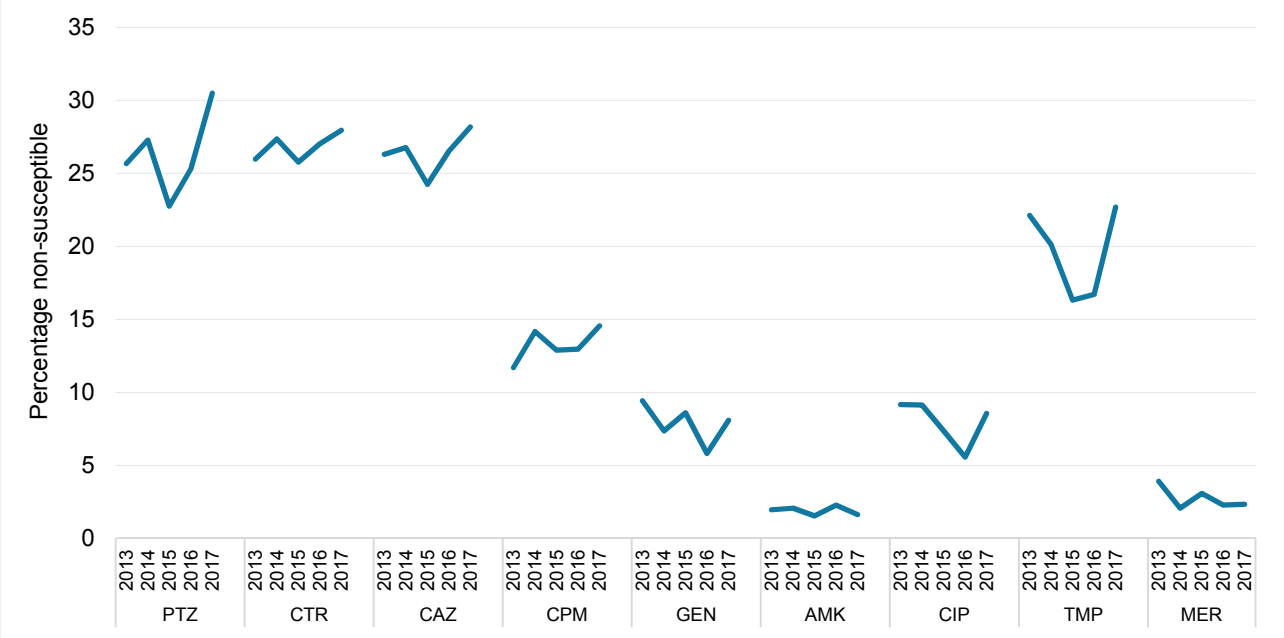


AMC = amoxicillin–clavulanic acid (2:1 ratio); AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; TMP = trimethoprim

Enterobacter cloacae complex

There were no significant differences in non-susceptibility to key antimicrobials for *E. cloacae* over the five-year period 2013 to 2017 (Figure 13)

Figure 13. Non-susceptibility of *Enterobacter cloacae* to key antimicrobials (EUCAST), Australia, 2013–2017



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

Enterococcus species

The 2017 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 2013–2017 are described below.

Vancomycin-resistant *Enterococcus faecium*

The proportion of vancomycin-resistant enterococcus (*E. faecium*) (VRE) by state and territory is shown in Table 27. Although VRE was detected in the Northern Territory, total numbers for each year were less than 10.

Table 27: Vancomycin-resistant *Enterococcus faecium*, by state and territory, 2013–2017

State or Territory	2013		2014		2015		2016		2017		Trend *
	Total	% R (*n*)	Total	% R (*n*)	Total	% R (*n*)	Total	% R (*n*)	Total	% R (*n*)	
NSW	107	43.9 (47)	104	50.0 (52)	116	51.7 (60)	124	47.6 (59)	167	51.5 (86)	
Vic	80	53.8 (43)	94	66.0 (62)	120	63 (76)	109	62.4 (68)	134	64.2 (86)	
Qld	37	40.5 (15)	37	40.5 (15)	31	61.3 (19)	43	30.2 (13)	45	33.3 (15)	
SA	32	59.4 (19)	46	56.5 (26)	44	52.3 (23)	43	46.5 (20)	28	57.1 (16)	
WA	42	4.8 (2)	50	20.0 (10)	53	11.3 (6)	54	14.8 (8)	63	14.3 (9)	
Tas	5	–† (0)	7	–† (1)	8	–† (1)	14	42.9 (6)	17	29.4 (5)	
NT	3	–† (3)	1	–† 0	8	–† 6	4	–† 3	5	–† (3)	
ACT	18	33.3 (6)	41	24.4 (10)	22	50.0 (11)	22	68.2 (15)	22	27.3 (6)	
Australia	**324**	**41.7 (135)**	**380**	**46.3 (176)**	**402**	**50.2 (202)**	**413**	**46.5 (192)**	**481**	**47.0 (226)**	

* sparkline, 2013-2017, with highest point shaded red
† Insufficient numbers to calculate percentage

Enterococcus faecalis

Resistance (EUCAST) to key antimicrobial agents for *E. faecalis* by state and territory is shown in Table 28. The only significant trends over the years 2013 to 2017 was a decrease in ciprofloxacin resistance in New South Wales ($\chi 2$ for linear trend = 13.63, $P = 0.0002$) and South Australia ($\chi 2$ for linear trend = 5.676, $P = 0.0172$); and high-level gentamicin resistance in New South Wales ($\chi 2$ for linear trend = 26.55, $P < 0.0001$) and Victoria ($\chi 2$ for linear trend = 11.86, $P = 0.0006$)

Table 28: *Enterococcus faecalis*, resistant (EUCAST), by state and territory, 2013–2017

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 (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 (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 (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)
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 (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 (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 (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)
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 (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)
	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

Antimicrobial	Year	Number tested	Percentage resistant, % (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
			(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)
Ciprofloxacin	2013	439	24.6 (30)	11.3 (12)	14.9 (11)	37.8 (14)	9.9 (7)	na	24.6 (1)	17.4 (4)	18.0 (79)
	2014	477	23.1 (31)	20.0 (24)	15.7 (14)	37.5 (12)	11.1 (7)	na	23.1 (3)	42.4 (14)	22.0 (105)
	2015	521	14.8 (22)	15.5 (17)	9.6 (8)	25.6 (11)	8.8 (8)	na	14.8 (3)	14.3 (5)	14.2 (74)
	2016	559	14.5 (22)	11.5 (15)	8.2 (7)	15.7 (8)	8.0 (7)	21.4 (3)	0.7 (0)	12.1 (4)	11.8 (66)
	2017	546	10.8 (20)	13.6 (16)	16.8 (16)	22.6 (7)	5.5 (5)	6.2 (1)	20.0 (1)	na	12.3 (67)
Nitrofurantoin	2013	468	0.8 (1)	0.0 (0)	0.0 (0)	2.3 (1)	0.0 (0)	9.1 (1)	0.0 (0)	0.0 (0)	0.6 (3)
	2014	521	0.0 (0)	0.0 (0)	1.0 (1)	2.0 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.4 (2)
	2015	558	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)
	2016	591	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0 (0.0)
	2017	595	0.0 (0)	0.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.2 (1)
Gentamicin (high-level)	2013	408	40.0 (34)	34.0 (36)	27.6 (24)	31.6 (6)	28.2 (20)	18.2 (2)	33.3 (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)	50.0 (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)	28.6 (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)
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)	0.0 (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 (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 (0)	0.3 (2)
	2017	601	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)

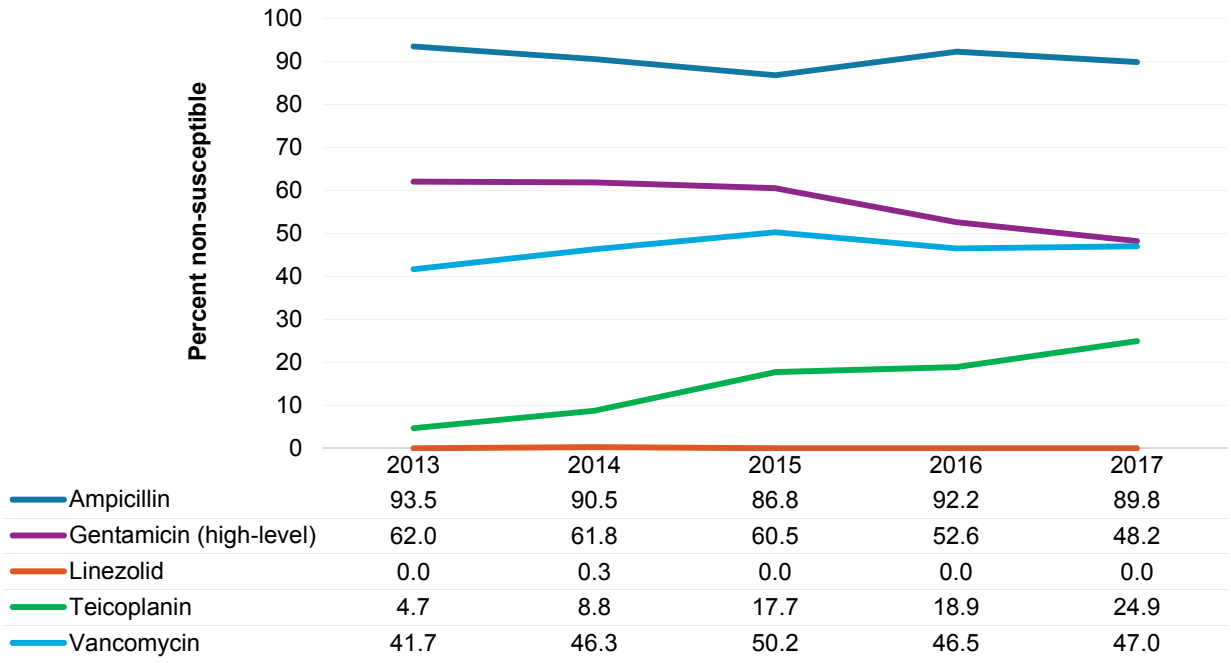
EUCAST = European Committee on Antimicrobial Susceptibility Testing; na = not applicable

Enterococcus faecium

For *E. faecium*, there was a significant decrease in gentamicin (high-level) resistance (χ2 for linear trend = 22.67, $P < 0.0001$) from 2013 to 2017, and a significant increase in teicoplanin resistance (χ2 for linear trend = 74.78, $P < 0.0001$), (Figure 14). No teicoplanin-resistant isolates were detected in the Northern Territory; all other states and territories except Queensland, Western Australia and Tasmania had a significant increase. This was due to the increased prevalence of *E. faecium* carrying *vanA* genes in these regions. No linezolid resistance was confirmed between 2015 and 2017.

Non-susceptibility to the key antimicrobial agents for *E. faecium* is shown in Table 29.

Figure 14: Non-susceptibility of *Enterococcus faecium* to key antimicrobials (EUCAST), Australia, 2013–2017



EUCAST = European Committee on Antimicrobial Susceptibility Testing

Table 29: *Enterococcus faecium*, non-susceptible (EUCAST), by state and territory, 2013–2017

Antimicrobial	Year	Number tested	Percentage non-susceptible (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ampicillin	2013	321	90.7 (97)	93.8 (75)	88.9 (32)	96.9 (31)	97.6 (41)	100 (5)	100 (3)	100 (16)	93.5) (300)
	2014	379	89.3 (92)	93.6 (88)	86.5 (32)	89.1 (41)	94.0 (47)	71.4 (5)	0.0 (0)	92.7 (38)	90.5 (343)
	2015	400	86.1 (99)	90.0 (108)	83.3 (25)	93.2 (41)	79.2 (42)	50.0 (4)	87.5 (7)	95.5 (21)	86.8 (347)
	2016	412	92.7 (114)	89.9 (98)	90.7 (39)	97.7 (42)	92.6 (50)	92.9 (13)	100 (4)	90.9 (20)	92.2 (380)
	2017	481	89.2 (149)	92.5 (124)	95.6 (43)	85.7 (24)	81.0 (51)	88.2 (15)	80.0 (4)	95.5 (21)	89.8 (432)
Vancomycin	2013	324	43.9 (47)	53.8 (43)	40.5 (15)	59.4 (19)	4.8 (2)	0.0 (0)	100 (3)	33.3 (6)	41.7 (135)
	2014	380	50.0 (52)	66.0 (62)	40.5 (15)	56.5 (26)	20.0 (10)	14.3 (1)	0.0 (0)	24.4 (10)	46.3 (176)
	2015	402	51.7 (60)	63.3 (76)	61.3 (19)	52.3 (23)	11.3 (6)	12.5 (1)	75.0 (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)	75.0 (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)	60.0 (3)	27.3 (6)	47.0 (226)
Teicoplanin	2013	321	9.3 (10)	2.5 (2)	5.6 (2)	3.1 (1)	0.0 (0)	0.0 (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 (0)	0.0 (0)	2.4 (1)	8.8 (33)
	2015	401	33.9 (39)	12.5 (15)	19.4 (6)	2.3 (1)	5.7 (3)	0.0 (0)	0.0 (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)	0.0 (0)	40.9 (9)	18.9 (78
	2017	481	45.5 (76)	17.9 (23)	13.3 (6)	17.9 (5)	4.8 (3)	5.9 (1)	0.0 (0)	27.3 (6)	24.9 (120)
Gentamicin (high-level)	2013	271	77.1 (64)	51.3 (41)	77.8 (28)	33.3 (2)	31.0 (13)	60.0 (3)	100 (3)	87.5 (14)	62.0 (168)
	2014	377	70.6 (72)	57.4 (54)	69.4) (25)	67.4 (31)	40.0 (20)	14.3) (1)	0.0 (0)	73.2 (30)	61.8 (233)
	2015	387	65.7	59.2	63.3	81.8	26.4	25.0	75.0	86.4	60.5

Antimicrobial	Year	Number tested	Percentage non-susceptible (*n*)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
			(67)	(71)	(19)	(36)	(14)	(2)	(6)	(19)	(234)
	2016	403	70.1 (82)	39.8 (43)	38.1 (16)	71.4 (30)	24.1 (13)	57.1 (8)	100 (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)	60.0 (3)	68.2 (15)	48.2 (228)
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 (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)	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 (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)	0.0 (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)	0.0 (0)

EUCAST = European Committee on Antimicrobial Susceptibility Testing

Note: Tinted cells indicate a significant trend

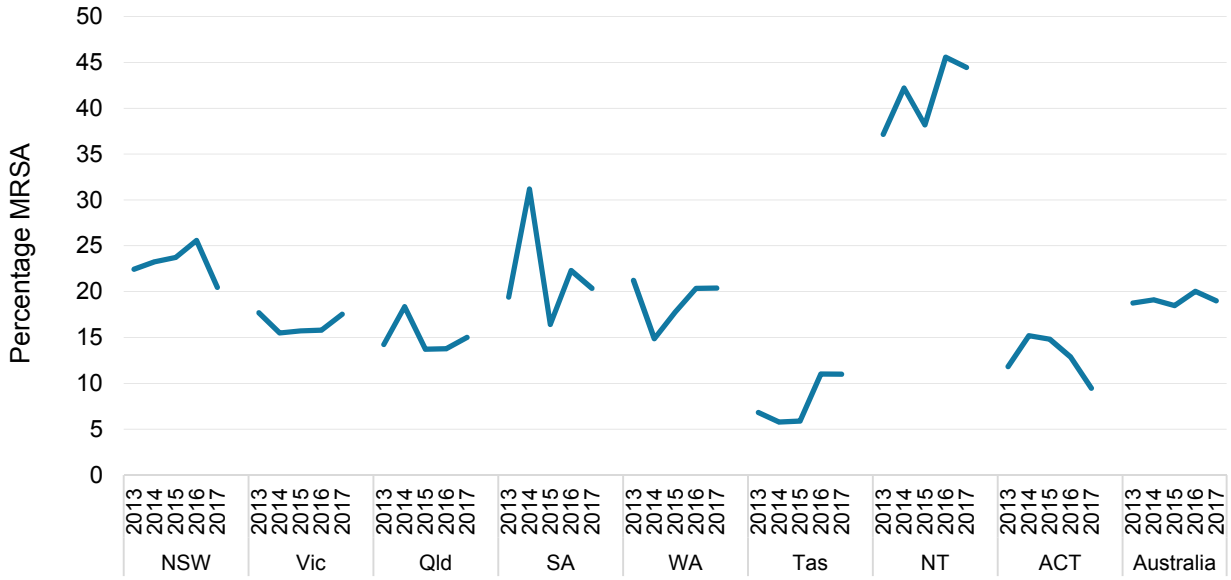
Staphylococcus aureus

A primary objective of the 2017 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 to 2017.

Methicillin-resistant *Staphylococcus aureus*

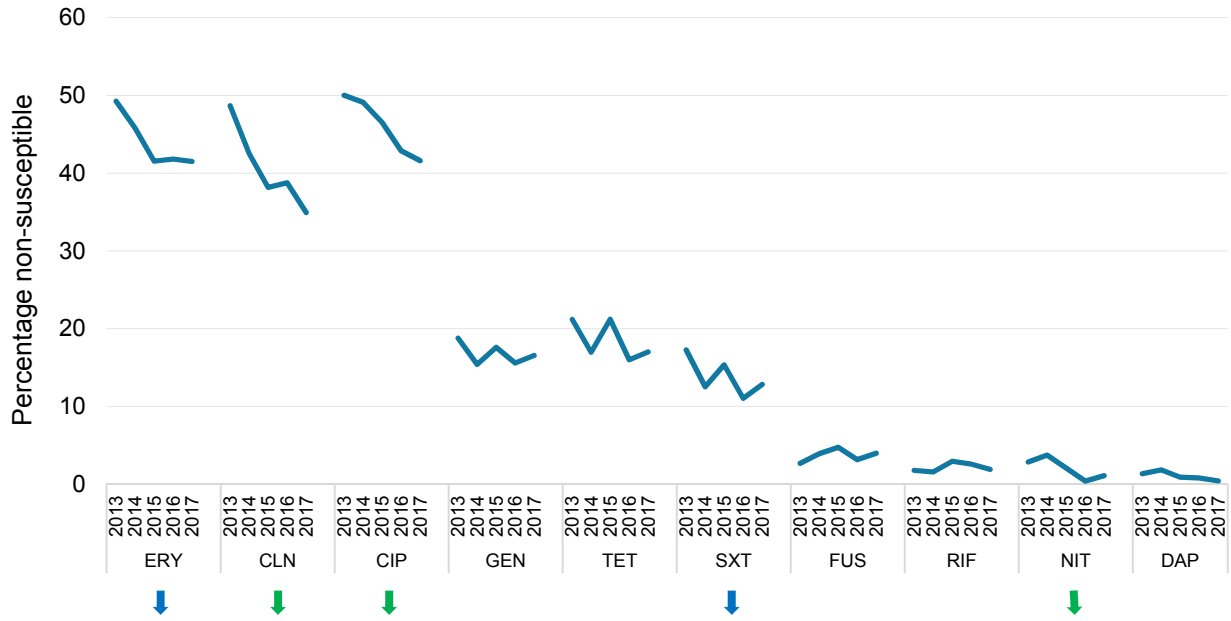
The proportion of *S. aureus* that was methicillin resistant throughout Australia remained constant over the years 2013 to 2017, although there were notable variations at state and territory level (Figure 15).

Figure 15: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, 2013–2017



There was a significant decrease in erythromycin (χ^2 for linear trend = 6.336, P = 0.0118), clindamycin (χ^2 for linear trend = 14.59, P = 0.0001), ciprofloxacin (χ^2 for linear trend = 9.326, P = 0.0023), trimethoprim/sulfamethoxazole (χ^2 for linear trend = 3.981, P = 0.046), and nitrofurantoin (χ^2 for linear trend = 10.47, P = 0.0012) non-susceptible MRSA, from 2013 to 2017 (Figure 16).

Figure 16: Non-susceptibility of methicillin-resistant *Staphylococcus aureus* to key antimicrobials (EUCAST), Australia, 2013–2017



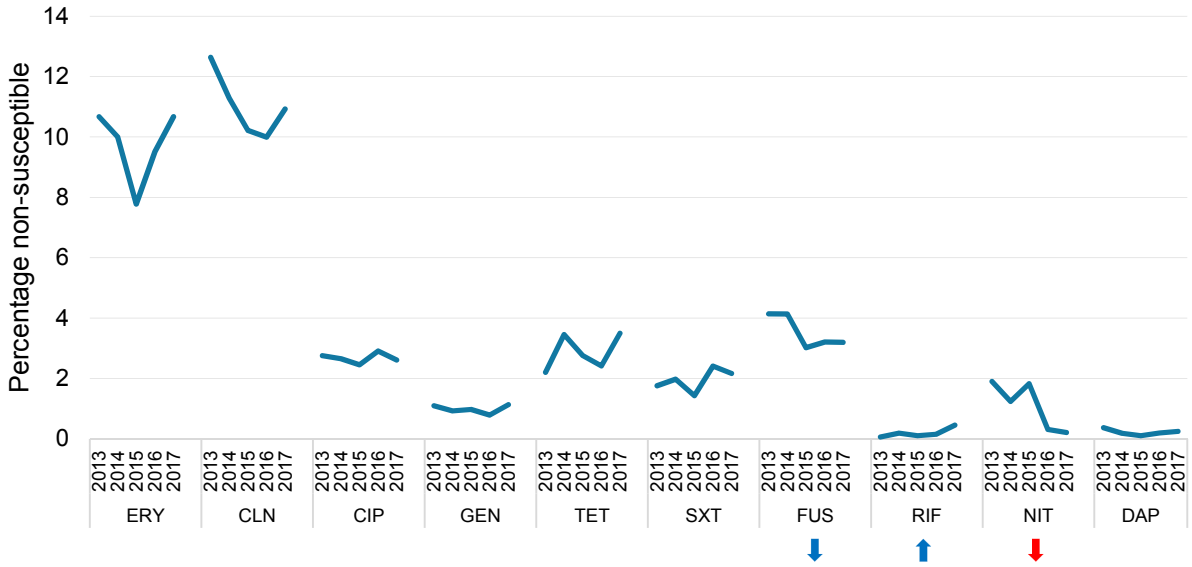
CIP = ciprofloxacin; CLN= clindamycin (inducible and constitutive); DAP = daptomycin; ERY = erythromycin; EUCAST = European Committee on Antimicrobial Susceptibility Testing; FUS = fusidic acid; GEN = gentamicin; NIT = nitrofurantoin [CLSI]; RIF = rifampicin; SXT = trimethoprim/sulfamethoxazole, TET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

Green arrows indicate antimicrobial agents with significant decrease (P < 0.01) over the period 2013 to 2017
Blue arrows indicate antimicrobial agents with significant decrease (0.01 < P < 0.5) over the period 2013 to 2017

Methicillin-susceptible *Staphylococcus aureus*

There was a significant decrease in fusidic acid (χ2 for linear trend = 4.014, *P* = 0.0451) and nitrofurantoin (χ2 for linear trend = 32.45, *P* < 0.0001) non-susceptible MSSA, 2013-2016 (Figure 17). However, there was a significant increase in rifampicin non-susceptibility (χ2 for linear trend = 5.45, *P* = 0.0196).

Figure 17: Non-susceptibility of methicillin-susceptible *Staphylococcus aureus* to key antimicrobials (EUCAST), Australia, 2013–2017



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

Red arrows indicate antimicrobial agents with significant trend (*P* < 0.01); blue arrows indicate antimicrobial agents with significant trend (0.01 < *P* < 0.5), over the period 2013 to 2017

3.10. Molecular studies

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

3.10.1. Gram-negative organisms

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

Extended-spectrum β-lactamases

Resistances conferred by ESBL-containing gram-negative organisms are important internationally, especially in hospital practice. Initially, ESBLs were more common in *Klebsiella* species than in *E. coli*. Recently, two new trends have appeared: the presence of ESBLs in *Enterobacter* species, and the emergence of specific types of ESBLs (CTX-M enzymes) in *E. coli* from the community. The latter is part of a global epidemic. It is unclear what is driving the community expansion of CTX-M ESBLs in Australia, as third-generation cephalosporins are not widely used in that setting; it is thought to be driven by cross-resistance and co-resistance to agents used in community practice. There is also increasing recognition that ESBLs are becoming established in long-term care facilities in Australia.

ESBLs are important because they compromise the efficacy of third-generation cephalosporins, which have been an important therapeutic alternative for infections in patients presenting from the community. ESBL-producing isolates often have co-resistance to other non-β-lactam agents. This can result in delays in the use of effective empirical therapy. The lack of available oral options for treatment can result in unnecessary hospitalisation and, in the setting of sepsis, increased mortality risk.

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

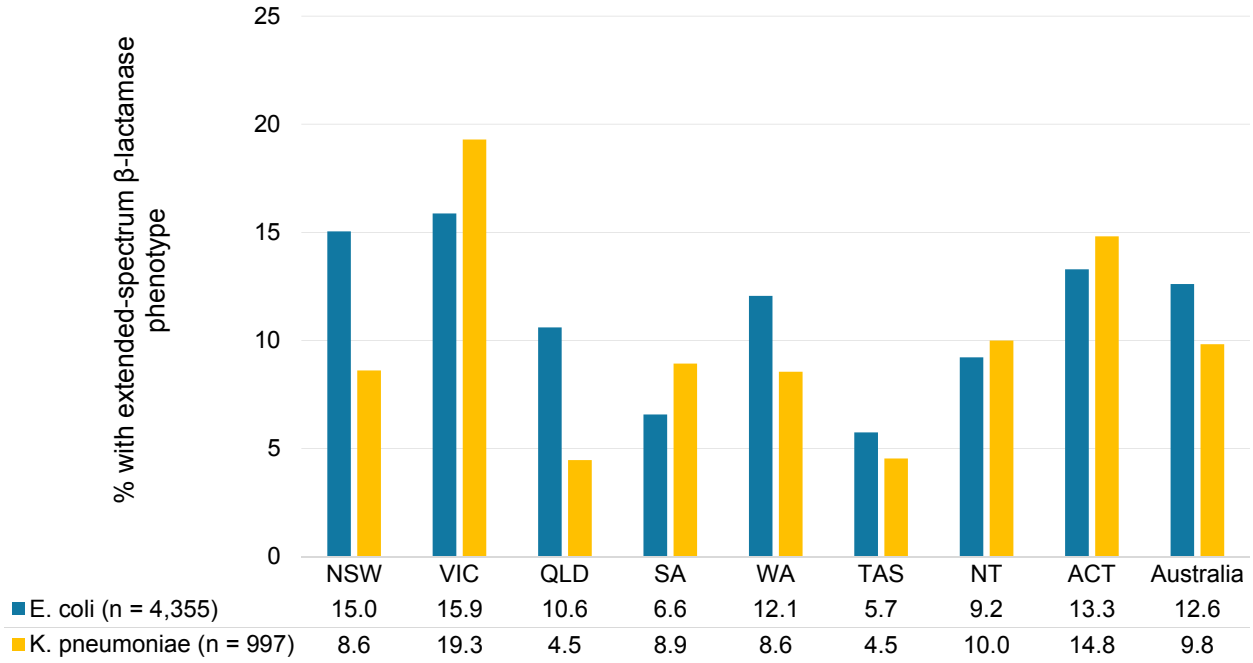
Neither ceftriaxone nor ceftazidime testing will identify ESBL production in *Enterobacter* species because of their intrinsic chromosomal AmpC β-lactamase. In Enterobacter, cefepime MICs of greater than 0.25 mg/L suggest that an isolate of this genus harbours an ESBL.[41] However, because of the susceptibility card range, isolates with a cefepime MIC of greater than 1 mg/L were selected for molecular testing.

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

E. coli and *K. pneumoniae* resistant to ceftriaxone and/or ceftazidime (MIC >1 mg/L), and their variation across states and territories, are shown in Figure 18. The presumptive and confirmed ESBLs by state and territory are shown in Table 30.

ESBL phenotypes were significantly more likely to be found among hospital-onset than community-onset episodes of *E. coli* bacteraemia (126/714 [17.6%] vs 421/3,641 [11.6%]; P < 0.01), *K. pneumoniae* bacteraemia (49/282 [17.4%] vs 50/715 [7.0%]; P < 0.01), and *E. cloacae* bacteraemia (42/195 [21.5%] vs 20/238 [8.4%]; P < 0.01).

Figure 18. Percentage of *Escherichia coli* and *Klebsiella pneumoniae* with extended-spectrum β-lactamase phenotype, by state and territory, and nationally, 2017



	NSW	VIC	QLD	SA	WA	TAS	NT	ACT	Australia
E. coli (n = 4,355)	15.0	15.9	10.6	6.6	12.1	5.7	9.2	13.3	12.6
K. pneumoniae (n = 997)	8.6	19.3	4.5	8.9	8.6	4.5	10.0	14.8	9.8

Table 30: Numbers of isolates with extended-spectrum β-lactamase phenotype, by state and territory, 2017

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,170	794	858	289	771	174	141	158	4,355
ESBL phenotype	177	125	90	19	93	10	13	20	547
Confirmed									
Any ESBL*/number received, n (%)	157/171 (91.8)	115/125 (92.0)	75/88 (85.2)	13/18 (72.2)	89/91 (97.8)	10/10 (100)	12/13 (92.3)	18/20 (90.0)	489/536 (91.2)
CTX-M types	128	100	61	9	77	8	9	16	408
Plasmid-borne AmpC	29	17	17	4	15	2	3	3	90
SHV	2	2	1	0	0	0	0	0	4
Klebsiella pneumoniae	267	197	246	56	152	22	30	27	997
ESBL phenotype	23	39	11	5	13	1	3	4	99
Confirmed									
Any ESBL*/number received, n (%)	18/23 (78.3)	34/39 (87.2)	7/10 (70.0)	3/4 (n/a)	9/15 (60.0)	1/1 (n/a)	2/3 (n/a)	3/4 (n/a)	77/95 (81.1)
CTX-M types	15	33	5	3	6	1	2	2	67
Plasmid-borne AmpC	2	1	1	0	3	0	0	1	8
TEM	14	29	6	2	3	1	2	2	59
Klebsiella oxytoca	58	35	36	22	44	20	2	12	229
ESBL phenotype	4	2	1	1	2	1	0	2	13
Confirmed									
Any ESBL*/number received	0/4	1/2	0/1	0/1	0/2	0/1	0/0	0/2	1/13†
CTX-M types	0	1	0	0	0	0	n/a	0	1
TEM	0	1	0	0	0	0	n/a	0	1
Proteus mirabilis	65	38	47	22	38	11	5	9	235
ESBL phenotype	4	2	0	1	1	0	0	0	8
Confirmed									
Any ESBL*/number received	3/4	2/2	0/0	1/1	0/1	0/0	0/0	0/0	6/8
CTX-M types	1	1	n/a	0	0	n/a	n/a	n/a	2
Plasmid-borne AmpC	2	0	n/a	1	0	n/a	n/a	n/a	3
TEM	0	1	n/a	0	0	n/a	n/a	n/a	1
Salmonella species (non-typhoidal)	20	15	28	5	39	2	21	4	135
ESBL phenotype	0	1	1	0	0	0	0	0	2
CTX-M types	0	1	0	0	0	0	0	0	1
Plasmid-borne AmpC	0	0	1	0	0	0	0	0	1

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

Based on the tests performed in this study, ESBLs were more common among *E. coli* (11.2% confirmed) and *K. pneumoniae* (7.7% confirmed) than among other species. For *Enterobacter* species with cefepime MIC greater than 1 mg/L, 29 of 64 *E. cloacae* (45%; 6.7% overall) contained an ESBL. Of identified ESBLs, *E. cloacae* contained the following types: TEM and SHV (*n* = 14), CTX-M group 1 and TEM (*n* = 7), CTX-M group 1 only (*n* = 7), CTX-M group 9 only (*n* = 4), CTX-M group 1 and Group 9 only (*n* = 1), and TEM only (*n* = 9). Seven of 35 *E. cloacae* with ESBLs also contained carbapenemases ($bla_{\text{IMP-4}}$ [*n* = 5], $bla_{\text{VIM-1}}$ [*n* = 1], $bla_{\text{IMP-4+OXA-23}}$ [*n* = 1]).

The majority (92%) of *K. oxytoca* isolates with a ceftriaxone-resistant phenotype were presumably hyperproducers of K1 β-lactamase, the natural chromosomal enzyme in this species, with characteristic resistance to piperacillin–tazobactam and borderline resistance to cefepime, but

susceptibility to ceftazidime. This pattern is not typical of other types of gram-negative β-lactamases.

As expected, the CTX-M-type ESBL genes were prominent in *E. coli*. Of 489 confirmed ESBLs, 408 (83.4%; range 69.2–87.0%) had CTX-M types detected by consensus primers targeting CTX-M group 1 (*n* = 214), CTX-M group 9 (*n* = 186), CTX-M group 1 and CTX-M group 9 (*n* = 6), and CTX-M group 8/25 (*n* = 2). Among *K. pneumoniae* with confirmed ESBLs, 67 of 77 (87.0%) contained CTX-M types: CTX-M group 1 (*n* = 57) and CTX-M group 9 (*n* = 10).

Plasmid-borne AmpC β-lactamases

Plasmid-borne AmpC β-lactamases have recently emerged internationally as a growing gram-negative resistance problem. They are the result of mobilisation of natural chromosomally located genes from common and uncommon species of Enterobacterales onto transmissible plasmids, and transmission into more common pathogens. There are currently six separate classes of plasmid-borne AmpC β-lactamases. Like ESBLs, these enzymes confer resistance to the important third-generation cephalosporins, such as ceftriaxone and ceftazidime. Routine phenotypic detection methods have not yet been developed. Nevertheless, it is possible to exploit a special feature of these enzymes: their ability to inactivate the cephamycins, represented by cefoxitin. *Enterobacter* species already naturally possess chromosomally encoded AmpC enzymes.

The proportions of *E. coli* and *K. pneumoniae* with elevated cefoxitin MICs were low. Only 54% (85/157) of *E. coli* and 15% (8/55) of *K. pneumoniae* with cefoxitin MIC ≥32 mg/L that were available for molecular confirmation were confirmed to contain plasmid-borne *ampC* genes (Table 31).

The bla_{CMY} gene was found in 64% (54/85) of *E. coli* with plasmid-borne *ampC* genes; bla_{DHA} was found in all *K. pneumoniae* with plasmid-borne *ampC* genes.

Carbapenemase genes were detected in five of the cefoxitin-resistant *K. pneumoniae* (bla_{IMP-4}, *n* = 3; bla_{KPC-2}, *n* = 1; bla_{NDM-1}, n = 1) and one *E. coli* bla_{IMP-4}) that did not have plasmid-borne *ampC* genes. Nine *E. coli* with a cefoxitin MIC of <32 mg/L also contained bla_{CMY}.

Table 31: Numbers of isolates with presumptive plasmid-borne AmpC β-lactamase production, by state and territory, 2017

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,170	794	858	288	770	174	141	158	4,353
Cefoxitin MIC ≥32 mg/L (%)	50 (4.3%)	35 (4.4%)	33 (3.8%)	6 (2.1%)	26 (3.4%)	2 (1.1%)	5 (3.5%)	5 (3.2%)	162 (3.7%)
Confirmed/number received	27/46	17/35	16/33	3/5	14/26	2/2	3/5	3/5	85/157
bla_{CMY}	20	6	14	0	8	1	3	2	54
bla_{DHA}	7	11	2	3	6	1	0	1	31
Klebsiella pneumoniae	267	197	246	55	152	22	30	27	996
Cefoxitin MIC ≥32 mg/L (%)	14 (5.2%)	14 (7.1%)	11 (4.5%)	1 (1.8%)	13 (8.6%)	0 (0.0%)	1 (3.3%)	2 (7.4%)	56 (5.6%)
Confirmed/number received	2/14	1/14	1/11	0/1	3/12	0/0	0/1	1/2	8/55
bla_{DHA}	2	1	1	0	3	0	0	1	8

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

Carbapenemases

Twenty-seven (0.34%) isolates from 25 patients were found to harbour a carbapenemase gene (Table 32). The *bla*$_{IMP-4}$ gene was detected in 12 isolates: *E. cloacae* (eight), *K. pneumoniae* (three), *E. coli* (one) – one *E. cloacae* and one *K. pneumoniae* were from the same patient. *bla* $_{OXA-181}$ was detected in four *E. coli* and one *K. pneumoniae* – one *E. coli* and one *K. pneumoniae* from the same patient. *bla*$_{OXA-23}$ was detected in three *A. baumannii*. *bla*$_{NDM-1}$ was detected in two *K. pneumoniae*. *bla*$_{KPC-2}$ was detected in one *K. pneumoniae* and *bla*$_{KPC-3}$ in one *E. coli*. *bla*$_{VIM-1}$ was detected in one *E. cloacae* and *bla*$_{VIM-5}$ in one *P. aeruginosa*; and *bla*$_{GES-5}$ was detected in one *P. aeruginosa*. Thirteen of 15 Enterobacterales with confirmed metallo-β-lactamases also contained plasmid-mediated quinolone resistance genes (*aac[6']-Ib-cr* alone or with *qnrB* or *qnrA*).

Two *E. cloacae* demonstrated carbapenemase activity by the carbapenem inactivation method, but were negative for IMP, VIM, KPC, NDM, OXA-48-like, SIM, GIM, SPM, BIC, DIM, AIM, GES, SME, IMI and FRI carbapenemases. Both isolates contained ACT-28, or ACT-12-like AmpC genes.

Overall prevalence of carbapenemase genes among Enterobacterales was 0.31% (22/7,100). It was 0.29% (2/697) for *P. aeruginosa* and 2.7% (3/113) for *Acinetobacter* species.

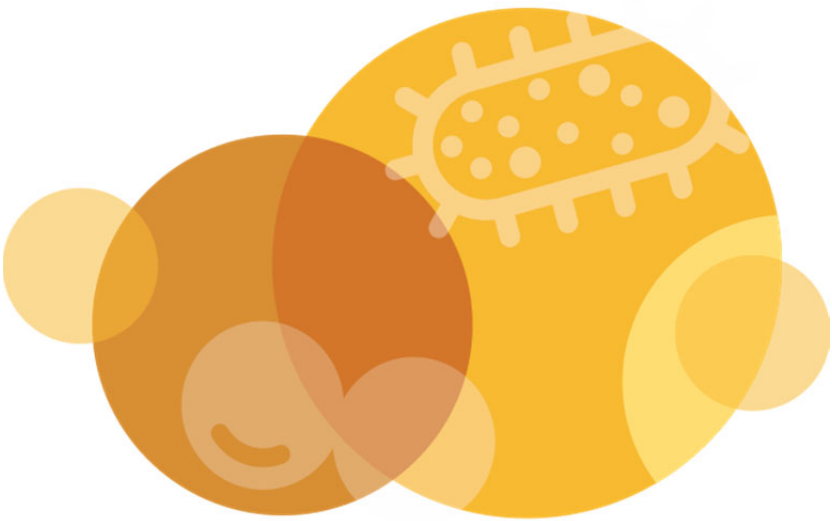


Table 32: Number of carbapenemases and associated resistance genes, by species, and state and territory, 2017

Gene	State or territory	Species	Meropenem MIC (mg/L)	ESBL type*	PMQR gene†	RMT
bla$_{IMP-4}$ (*n* = 12)	NSW	*E. cloacae* (*n* = 1)	≥16	–§	*aac(6')-Ib-cr*, *qnrB*	–§
	NSW	*E. cloacae* (*n* = 1)	≥16	–§	*aac(6')-Ib-cr*, *qnrB, qnrA*	–§
	NSW	*E. cloacae* (*n* = 1)	≥16	–§	*aac(6')-Ib-cr*	–§
	NSW	*E. cloacae* (*n* = 1)	≥16	–§	*qnrB*	–§
	NSW	*K. pneumoniae* (*n* = 1)	≤0.25	–§	*qnrB*	–§
	NSW	*K. pneumoniae* (*n* = 1)	4	–§	*qnrB*	–§
	Qld	*E. cloacae* (*n* = 2)#	≥16	–§	*aac(6')-Ib-cr*, *qnrB*	–§
	Qld	*K. pneumoniae* (*n* = 1)#	≥16	–§	*aac(6')-Ib-cr*, *qnrB*	–§
	WA	*E. cloacae* (*n* = 1)	≥16	–§	*qnrB*	–§
	ACT	*E. cloacae* (*n* = 1)	≥16	CTX-M-15	*aac(6')-Ib-cr*, *qnrB1*	–§
	ACT	*E. coli* (*n* = 1)	≥16	–§	*qnrB*	–§
bla$_{OXA-181}$ (*n* = 5)	NSW	*E. coli* (*n* = 1)	≥16	CMY-146,	*qnrS*	–§
	NSW	*E. coli* (*n* = 1)	1	CTX-M-15	*aac(6')-Ib-cr*, *qnrS*	–§
	Qld	*E. coli* (*n* = 1)	2	CTX-M-15	*qnrS*	–§
	Qld	*E. coli* (*n* = 1)**	0.5	CTX-M-15	*qnrS*	–§
	Qld	*K. pneumoniae* (*n* = 1)**	0.5	–§	*qnrS*	–§
bla$_{OXA-23}$ (*n* = 3)	Qld	A. baumannii (n = 2)	≥16	–§	–§	*armA*
	WA	*A. baumannii* (*n* = 1)	≥16	–§	–§	*armA*
bla$_{KPC-3}$ (*n* = 1)	NSW	*E. coli* (*n* = 1)	≥16	–§	–§	–§
bla$_{KPC-2}$ (*n* = 1)	Vic	*K. pneumoniae* (*n* = 1)	≥16	–§	–§	–§
bla$_{NDM-1}$ (*n* = 2)	NSW	*K. pneumoniae* (*n* = 1)	≥16	CTX-M-15	–§	*rmtB*
	Vic	*K. pneumoniae* (*n* = 1)	≥16	DHA-1 CTX-M-15	*qnrB*	*rmtC*
bla$_{VIM-1}$ (*n* = 1)	NSW	*E. cloacae* (*n* = 1)	≥16	CTX-M-14	–§	–§
bla$_{VIM-5}$ (*n* = 1)	Vic	*P. aeruginosa* (*n* = 1)	≥16	–§	–§	–§
bla$_{GES-5}$ (*n* = 1)	Qld	*P. aeruginosa* (*n* = 1)	≥16	–§	–§	–§

ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance; RMT = 16S rRNA methyltransferase

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

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

§ Not detected

\# *bla*$_{IMP-4}$ from the same patient

** *bla*$_{OXA-181}$, from the same patient

Plasmid-mediated quinolone resistance

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

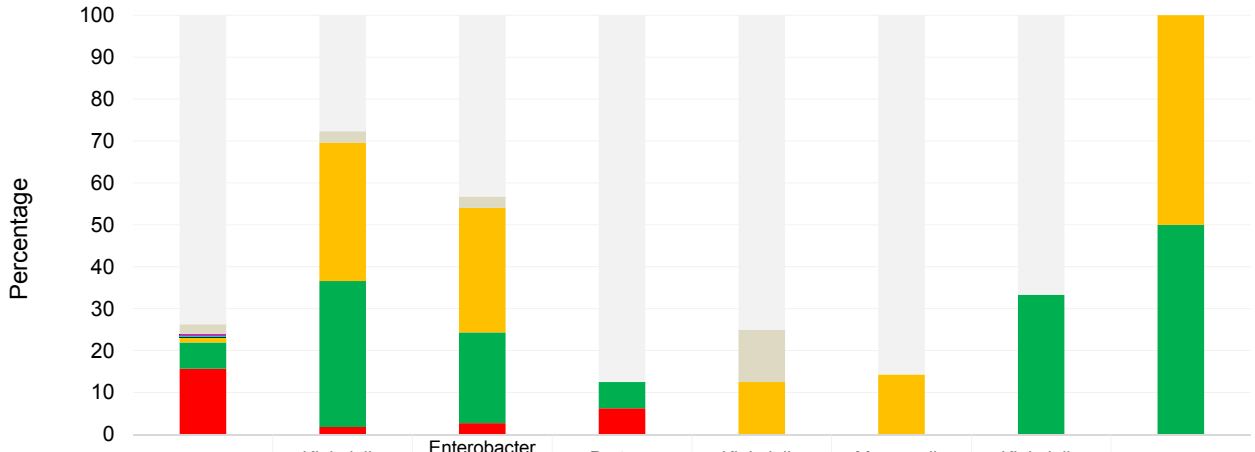
Of isolates with ciprofloxacin MIC greater than 0.25 mg/L, 24% of *E. coli,* 72% of *K. pneumoniae* and 56% of *E. cloacae* were confirmed to contain PMQRs (Table 33). The proportion and type of PMQR determinant found among isolates with ciprofloxacin MIC greater than 0.25 mg/L varied among the different species (Figure 19). The *aac(6')-Ib-cr* gene, with or without *qnr*, was dominant, and was present in eight of the nine species.

Table 33: Number and percentage of isolates with plasmid-mediated quinolone resistance, by species, and state and territory, 2017

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli									
Percent ciprofloxacin MIC >0.25 mg/L* (*n*)	20.3 (237)	20.9 (166)	15.6 (134)	11.1 (32)	19.9 (153)	6.9 (12)	18.4 (26)	15.2 (24)	18.0 (784)
Number confirmed/number received (%)	62/229 (27.1)	36/165 (21.8)	33/130 (25.4)	6/31 (19.4)	38/149 (25.5)	3/12 (25.0)	5/25 (20.0)	4/24 (16.7)	187/765 (24.4)
aac(6')Ib-cr	39	24	24	5	26	0	3	2	123
aac(6')Ib-cr; qnrB	2	1	1	0	1	1	0	0	6
aac(6')Ib-cr; qnrS	2	0	1	0	0	0	0	0	3
aac(6')Ib-cr; oqxAB	0	0	0	0	1	0	0	0	1
qnrS	14	8	7	0	8	2	2	1	42
qnrB	2	1	0	1	2	0	0	0	6
qnrB; qnrS	1	0	0	0	0	0	0	0	1
qnrS; oqxAB	0	1	0	0	0	0	0	0	1
QepA	1	0	0	0	0	0	0	1	2
oqxAB	1	1	0	0	0	0	0	0	2
Klebsiella pneumoniae									
Percent ciprofloxacin MIC >0.25 mg/L* (*n*)	10.5 (28)	21.8 (43)	7.7 (19)	7.3 (4)	7.9 (12)	0.0 (0)	6.7 (2)	14.8 (4)	11.2 (112)
Number confirmed/number received (%)	17/28 (60.7)	35/42 (83.3)	11/19 (57.9)	2/3 n/a	9/11 (81.8)	–†	2/2 n/a	2/4 n/a	78/109 (71.6)
aac(6')-Ib-cr	2	0	0	0	0	n/a	0	0	2
aac(6')-Ib-cr + qnrB	5	18	5	1	3	n/a	2	2	36
aac(6')-Ib-cr + qnrS	0	1	0	0	0	n/a	0	0	1
qnrS	7	12	4	1	4	n/a	0	0	28
qnrB	3	4	2	0	2	n/a	0	0	11
Enterobacter cloacae									
Percent ciprofloxacin MIC >0.25 mg/L* (*n*)	9.6 (13)	10.7 (8)	4.7 (5)	11.5 (3)	5.5 (3)	11.8 (2)	28.6 (2)	10.0 (1)	8.5 (37)
Number confirmed/number received (%)	9/12 (75.0)	3/8 n/a	1/5 n/a	2/3 n/a	1/3 n/a	2/2 n/a	1/2 n/a	1/1 n/a	20/37 (55.6)
aac(6')Ib-cr	1	0	0	0	0	0	0	0	1
aac(6')Ib-cr; qnrB	3	0	1	1	0	1	0	1	7
aac(6')Ib-cr; qnrA	2	1	0	0	0	0	0	0	3
aac(6')Ib-cr; qnrA; qnrB	1	0	0	0	0	0	0	0	1
qnrA	1	0	0	1	1	0	1	0	4
qnrB	0	1	0	0	0	1	0	0	2
qnrB; qnrS	0	1	0	0	0	0	0	0	1
qnrS	1	0	0	0	0	0	0	0	1

MIC = minimum inhibitory concentration; n/a = not applicable (insufficient numbers)
* Concentration used to select isolates for molecular testing
† No isolates

Figure 19. Proportion of plasmid-mediated quinolone resistance genes among gram-negative species with ciprofloxacin MIC >0.25 mg/L, 2017



	Escherichia coli (n = 784)	Klebsiella pneumoniae (n = 112)	Enterobacter cloacae complex (n = 37)	Proteus mirabilis (n = 16)	Klebsiella oxytoca (n = 8)	Morganella morganii (n = 7)	Klebsiella aerogenes (n = 6)	Other species (n = 4)
Not detected	73.7	27.7	43.2	87.5	75.0	85.7	66.7	0.0
Not available	2.4	2.7	2.7	0.0	12.5	0.0	0.0	0.0
Qnr + oqxAB	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CR + oqxAB	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
QepA	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
oqxAB	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CR + Qnr	1.1	33.0	29.7	0.0	12.5	14.3	0.0	50.0
Qnr	6.3	34.8	21.6	6.3	0.0	0.0	33.3	50.0
CR	15.7	1.8	2.7	6.3	0.0	0.0	0.0	0.0

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

Other species: *C. freundii* (n = 3), *Enterobacter* species (n = 1)

Escherichia coli sequence type 131

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

Most of the isolates with an ESBL phenotype harboured genes of the CTX-M type (408/536; 76.1%) (Table 34). Fifty-three per cent (112/214) of the *E. coli* with CTX-M group 1 types (CTX-M-15 like) were found to belong to the O25b-ST131 lineage. O25b-ST131 accounted for 57.3% (176/307) of *E. coli* ESBL phenotypes that were ciprofloxacin resistant (MIC >1 mg/L), but only 4.8% (11/229) of ciprofloxacin-susceptible ESBL phenotypes. O25b-ST131 often carried *bla*CTX-M-15 and *aac(6')-Ib-cr*.

Table 34: Number of *Escherichia coli* with ESBL phenotype, by O25b-ST131 clone and ciprofloxacin resistance, 2017

		CTX-M types			Ciprofloxacin MIC	
Clone	Total	CTX-M-15-like	CTX-M-15like + CTX-M 14 like	Non-CTX-M-15	>1 mg/L	≤1 mg/L
O25b-ST131	187	112	5	56	176	11
Non-O25b-ST131	349	120	1	132	131	218
Total	536	214	6	188	307	229

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

Plasmid-mediated colistin determinants

Because colistin is currently only available on the Phoenix™ cards, only 805 (10.2%) isolates from two laboratories were tested for colistin susceptibility. Excluding intrinsically resistant species, 7/752 (0.9%) had colistin MIC >2 mg/L (*E. coli, n* = 3; *Edwardsiella hoshinae*, *n* = 1; *E. asburiae*, *n* = 1; *K. pneumoniae*, *n* = 1; and *K. aerogenes*, n = 1).

All referred isolates were screened for the presence of plasmid-mediated colistin determinants, *mcr-1*, *mcr-2* and *mcr-3*, regardless of the resistance profile. Of 1,407 (19.0%) isolates (which excluded intrinsically resistant species) available, no mobile colistin resistance genes were detected.

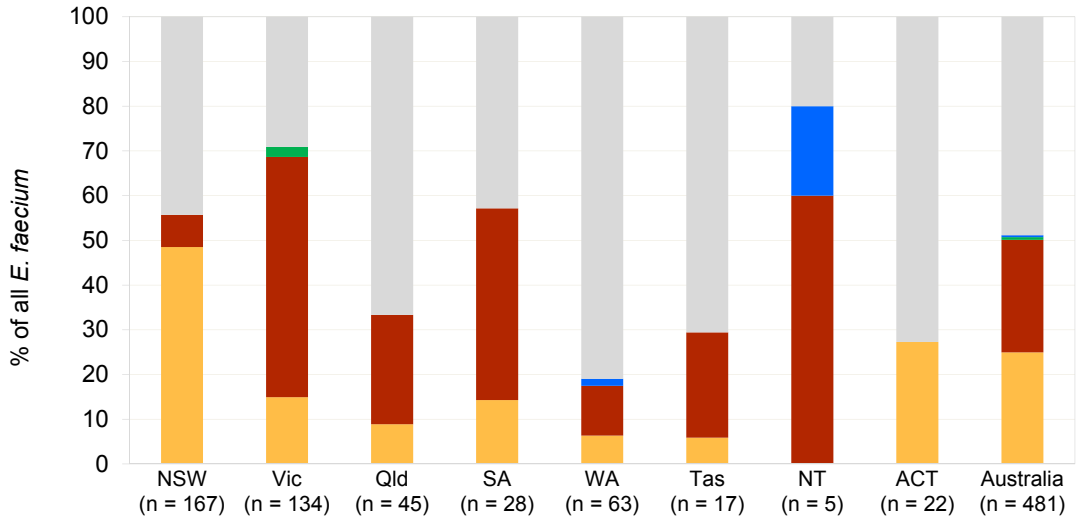
3.10.2. Molecular epidemiology of *Enterococcus faecium van* genes

PCR results for *vanA* and *vanB* genes were available for 479 (99.6%) of the 481 *E. faecium* isolates. *van* genes were detected in 50.9% (244/479) of *E. faecium*; *vanA* in 120 (25.1%), *vanB* in 121 (25.3%), and *vanA* and *vanB* in three (0.6%) isolates (Figure 20).

For vancomycin-resistant *E. faecium* (MIC > 4 mg/L), *vanA* was detected in 113/226 (50.0%), *vanB* in 110 (48.7%), and *vanA* and *vanB* in three (1.3%).

In 18 of 253 (7.1%) vancomycin-susceptible *E. faecium*; *van* genes were detected: 7 with *vanA* and 11 with *vanB*. All isolates had vancomycin MIC ≤ 2 mg/L.

Figure 20: Vancomycin genotype of *Enterococcus faecium* isolates, by state and territory, and nationally, 2017



	NSW (n = 167)	Vic (n = 134)	Qld (n = 45)	SA (n = 28)	WA (n = 63)	Tas (n = 17)	NT (n = 5)	ACT (n = 22)	Australia (n = 481)
not vanA or vanB (n = 235)	44.3	29.1	66.7	42.9	81.0	70.6	20.0	72.7	48.9
Not determined (n = 2)	0.0	0.0	0.0	0.0	1.6	0.0	20.0	0.0	0.4
vanA and vanB (n = 3)	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	0.6
vanB (n = 121)	7.2	53.7	24.4	42.9	11.1	23.5	60.0	0.0	25.2
vanA (n = 120)	48.5	14.9	8.9	14.3	6.3	5.9	0.0	27.3	24.9

Multilocus sequence type

Of the 481 *E. faecium* isolates reported, 461 (95.8%) were available for typing by whole genome sequencing (Table 35). Based on the MLST, 64 sequence types (STs) were identified. Overall 80.0% of *E. faecium* could be characterised into nine STs: ST17 (n = 72); ST1421, formerly known as M-type 1 (n = 70); ST796 (n = 63); ST1424, formerly known as M-type 3 (n = 62); ST80 (n = 42); ST555 (n = 21); ST203 (n = 14); ST18 (n = 14); and ST78 (n = 11). The *pstS* housekeeping gene is absent in the M-type isolates. M-type 1 was initially identified in 2015. In 2017, there were five M-type single locus variants. There were 39 STs with a single isolate.

ST1421 was detected in all states and territories except the Northern Territory and Western Australia; ST1424 was the predominant ST in New South Wales, but was also detected in Victoria, Queensland and the Australian Capital Territory. ST17 was the predominant ST in Queensland and Western Australia. ST796 was the predominant ST in Victoria, and ST555 was the predominant ST in South Australia.

The distribution of vancomycin-resistant *E. faecium* sequence types throughout Australia states and territories is shown in Figure 21.

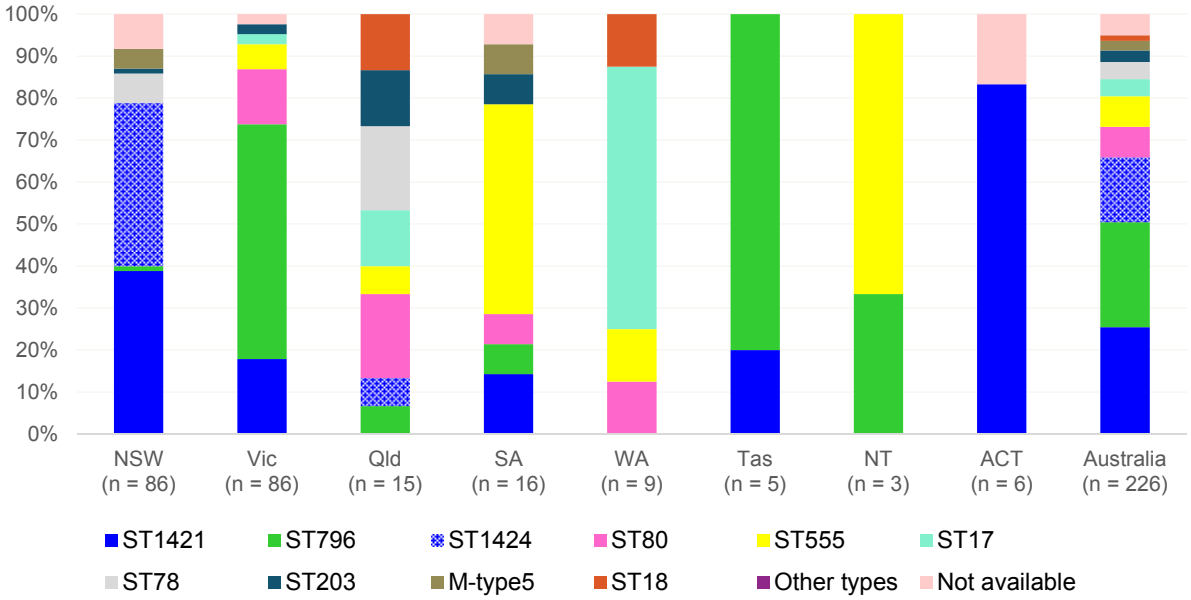
Table 35: *Enterococcus faecium* MLST, by state and territory, 2017

	Percentage, % (*n*)								
MLST	**NSW**	**Vic**	**QLD**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST17*	3.8 (6)	10.0 (13)	45.5 (20)	3.8 (1)	52.5 (32)	0.0 (0)	0.0 (0)	0.0 (0)	15.6 (72)
ST1421	25.9 (41)	12.3 (16)	2.3 (1)	7.7 (2)	0.0 (0)	5.9 (1)	0.0 (0)	42.9 (9)	15.2 (70)
ST796†	2.5 (4)	40.0 (52)	2.3 (1)	3.8 (1)	0.0 (0)	23.5 (4)	25.0 (1)	0.0 (0)	13.7 (63)
ST1424	36.1 (57)	0.8 (1)	2.3 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	14.3 (3)	13.4 (62)
ST80	4.4 (7)	14.6 (19)	9.1 (4)	3.8 (1)	9.8 (6)	5.9 (1)	0.0 (0)	19.0 (4)	9.1 (42)
ST555§	0.0 (0)	3.8 (5)	2.3 (1)	30.8 (8)	6.6 (4)	5.9 (1)	50.0 (2)	0.0 (0)	4.6 (21)
ST203	2.5 (4)	3.1 (4)	6.8 (3)	3.8 (1)	0.0 (0)	11.8 (2)	0.0 (0)	0.0 (0)	3.0 (14)
ST18§	0.6 (1)	3.1 (4)	6.8 (3)	0.0 (0)	3.3 (2)	0.0 (0)	0.0 (0)	19.0 (4)	3.0 (14)
ST78†	5.1 (8)	0.0 (0)	6.8 (3)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	2.4 (11)
Other types (n = 55)	19.0 (30)	12.3 (16)	15.9 (7)	46.2 (12)	27.9 (17)	47.1 (8)	25.0 (1)	4.8 (1)	20.0 (92)
Total	**158**	**130**	**44**	**26**	**61**	**17**	**4**	**21**	**461**

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

* includes three slv
† Includes one slv
§ Included two slv

Figure 21: Distribution of vancomycin-resistant *Enterococcus faecium* sequence types, by state and territory, 2017



MLST and *van* genes

The *vanA* gene alone was detected in nine STs; ST1421 (*n* = 59), ST1424 (*n* = 34), ST80 (*n* = 9), M-type 5 (*n* = 5), and one each of ST17, ST203, ST262, ST546, and ST789. The *vanB* gene alone was detected in 12 STs: ST796 (*n* = 59), ST555 (*n* = 16), ST78 (*n* = 11), ST80 (*n* = 10), ST17 (*n* = 9), ST203 (*n* = 5), ST18 (*n* = 4), and one each of ST341, ST479, ST992, ST1423, and ST1424 (Table 36). Isolates with both *vanA* and *vanB* genes were found in ST796 (*n* = 1) and ST233 (*n* = 1).

Table 36: *Enterococcus faecium* MLST harbouring *vanA* and/or *vanB* genes, 2017

MLST	*vanA*, % (*n*)	*vanB*, % (*n*)	*vanA* and *vanB*, % (*n*)	*vanA* or *vanB* not detected, % (n)	Total, *n*
ST17†	1.4 (1)	12.5 (9)	0.0 (0)	86.1 (62)	72
ST1421 (M-type 1)	84.3 (59)	0.0 (0)	0.0 (0)	15.7 (11)	70
ST796§	0.0 (0)	93.7 (59)	1.6 (1)	4.8 (3)	63
ST1424 (M-type 3)	54.8 (34)	1.6 (1)	0.0 (0)	43.5 (27)	62
ST80	21.4 (9)	23.8 (10)	0.0 (0)	54.8 (23)	42
ST555#	0.0 (0)	76.2 (16)	0.0 (0)	23.8 (5)	21
ST203	7.1 (1)	35.7 (5)	0.0 (0)	57.1 (8)	14
ST18#	0.0 (0)	28.6 (4)	0.0 (0)	71.4 (10)	14
ST78§	0.0 (0)	100.0 (11)	0.0 (0)	0.0 (0)	11
Other types (n = 55)	8.7 (8)	4.3 (4)	1.1 (1)	85.9 (79)	92
Total	**24.3 (112)**	**25.8 (119)**	**0.4 (2)**	**49.5 (228)**	**461**

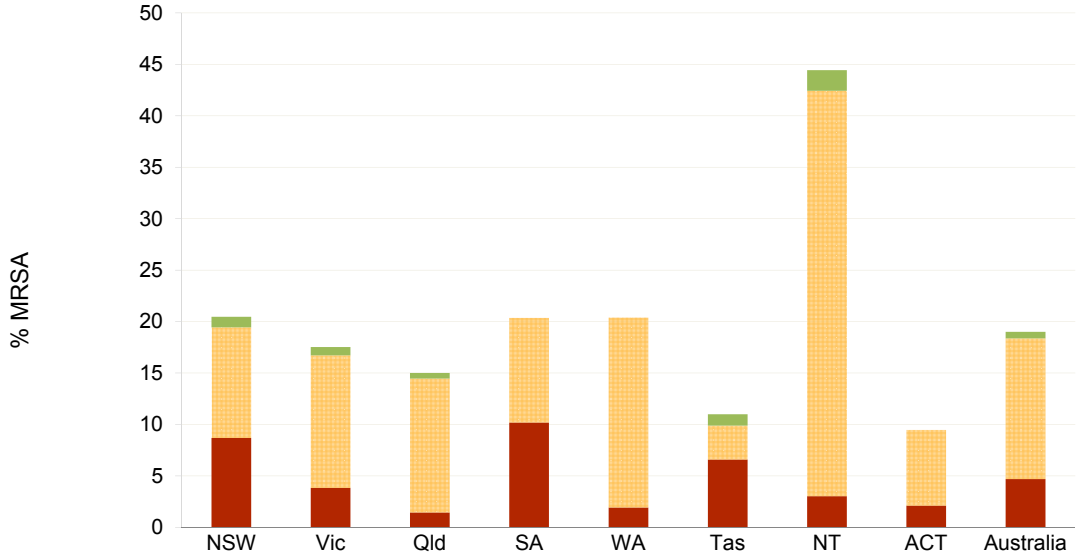
MLST = multi-locus sequence type; slv = single locus variant(s)

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

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

Of the 478 MRSA reported, 462 (96.7%) were available for typing by whole genome sequencing. There were significant differences among the states and territories in the percentage and types of MRSA clones. Prevalence of MRSA ranged from 9.5% in the Australian Capital Territory to 44.4% in the Northern Territory (Figure 22).

Figure 22: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, 2017



	NSW (n = 139)	Vic (n= 64)	Qld (n = 83)	SA (n = 34)	WA (n = 95)	Tas (n = 10)	NT (n = 44)	ACT (n = 9)	Australia (n = 478)
Not available (n = 16)	1.0	0.8	0.5	0.0	0.0	1.1	2.0	0.0	0.6
Community associated (n = 344)	10.8	12.9	13.0	10.2	18.5	3.3	39.4	7.4	13.7
Healthcare associated (n = 118)	8.7	3.8	1.4	10.2	1.9	6.6	3.0	2.1	4.7

MRSA = methicillin-resistant *Staphylococcus aureus*

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), ST5-II (NY/Japan EMRSA or USA100) (Tables 37, 38).

PVL-associated genes were not identified in HA-MRSA. Note: Although four PVL positive ST22-IV isolates were identified, one each in New South Wales, Victoria, Queensland and South Australia, PVL positive ST22-IV, which are frequently isolated in the South Asian subcontinent, 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. ST239-III was identified in all states and territories except Western Australia and the Australian Capital Territory. ST5-II was identified in New South Wales and Queensland (Table 39).

Community-associated MRSA

Based on the MLST and SCC*mec* type, 39 CA-MRSA clones were identified. PVL was detected in 16 CA-MRSA clones. Overall 49.7% of CA MRSA were PVL positive (Tables 37, 38).

The most frequently isolated CA-MRSA clone, ST93-IV (Qld CA-MRSA), was isolated in all states except Tasmania (Table 40).

Of the hospital-onset MRSA, 60.9% (84/138) were caused by CA-MRSA.

Table 37: MRSA clones, association, place of onset and PVL carriage, 2017

Clone	Clonal complex	Total, *n*	Community onset, % (*n*)*	Hospital onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)†	22	90	58.9 (53)	41.1 (37)	0.0 (0)
ST239-III (Aus2/3 EMRSA)§	8	25	32.0 (8)	68.0 (17)	0.0 (0)
ST5-II (NY/Japan, USA100)	5	3	–** (3)	0.0 (0)	0.0 (0)
Total HA-MRSA		118	54.2 (64)	45.8 (54)	0.0 (0)
Community-associated					
ST93-IV (Qld CA-MRSA)†	Singleton	113	85.0 (96)	15.0 (17)	93.8 (106)
ST45-V	45	44	61.4 (27)	38.6 (17)	34.1 (15)
ST5-IV§	5	39	66.7 (26)	33.3 (13)	23.1 (9)
ST1-IV (WA1 MRSA)#	1	34	76.5 (26)	23.5 (8)	2.9 (1)
ST78-IV (WA2 MRSA)†	78	16	81.3 (13)	18.8 (3)	12.5 (2)
ST30-IV (SWP MRSA)	30	10	90.0 (9)	10.0 (1)	70.0 (7)
ST8-IV#		10	80.0 (8)	20.0 (2)	100.0 (10)
ST5-V		8	–** (6)	–** (2)	0.0 (0)
ST97-IV		8	–** (6)	–** (2)	0.0 (0)
ST6-IV§		7	–** (5)	–** (2)	–** (4)
ST953-IV		6	–** (4)	–** (2)	0.0 (0)
ST22-IV (PVL positive)		4	–** (3)	–** (1)	–** (4)
ST59-V		4	–** (3)	–** (1)	–** (4)
ST188-IV		4	–** (1)	–** (3)	0.0 (0)
ST762-IV		4	–** (3)	–** (1)	0.0 (0)
Other (n = 24)		33	77.8 (24)	22.2 (9)	25.9 (9)
Total CA-MRSA		344	75.6 (260)	24.4 (84)	49.7 (171)
MRSA		**462**	**324**	**138**	

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

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

Table 38: MRSA clones, association, place of onset, 2017

Clone	Clonal complex	Community onset, % (*n*)*	Hospital onset, % (*n*)*	Total, % (*n*)
Healthcare-associated				
ST22-IV (EMRSA-15)†	22	16.4 (53)	26.8 (37)	19.5 (90)
ST239-III (Aus2/3 EMRSA)§	8	2.5 (8)	12.3 (17)	5.4 (25)
ST5-II (NY/Japan, USA100)	5	–** (3)	0.0 (0)	0.6 (3)
Total HA-MRSA		19.8 (64)	39.1 (54)	25.5 (118)
Community-associated				
ST93-IV (Qld CA-MRSA)†	Singleton	29.6 (96)	12.3 (17)	24.5 (113)
ST45-V	45	8.3 (27)	12.3 (17)	9.5 (44)
ST5-IV§	5	8.0 (26)	9.4 (13)	8.4 (39)
ST1-IV (WA1 MRSA)#	1	8.0 (26)	–‡ (8)	7.4 (34)
ST78-IV (WA2 MRSA)†	78	4.0 (13)	–‡ (3)	3.5 (16)
ST30-IV (SWP MRSA)	30	–‡ (9)	–‡ (1)	2.2 (10)
ST8-IV#		–‡ (8)	–‡ (2)	2.2 (10)
ST5-V		–‡ (6)	–‡ (2)	1.7 (8)
ST97-IV		–‡ (6)	–‡ (2)	1.7 (8)
ST6-IV§		–‡ (5)	–‡ (2)	1.5 (7)
ST953-IV		–‡ (4)	–‡ (2)	1.3 (6)
ST22-IV (PVL positive)		–‡ (3)	–‡ (1)	0.9 (4)
ST59-V		–‡ (3)	–‡ (1)	0.9 (4)
ST188-IV		–‡ (1)	–‡ (3)	0.9 (4)
ST762-IV		–‡ (3)	–‡ (1)	0.9 (4)
Other (n = 24)		7.4 (24)	–‡ (9)	7.1 (33)
Total CA-MRSA		80.2 (260)	60.9 (84)	74.5 (344)
MRSA		**70.1 (324)**	**29.9 (138)**	**462**

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

* Percentage of all MRSA
† includes three slv
§ Includes one slv
# Included two slv
** Insufficient numbers (<10) to calculate percentage

Table 39: Healthcare-associated MRSA clones, by state and territory, 2017

Clone	Percentage, % (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15) *	71.2 (42)	92.9 (13)	50.0 (4)	82.4 (14)	100 (9)	83.3 (5)	33.3 (1)	100 (2)	76.3 (90)
ST239-III (Aus2/3 EMRSA) †	27.1 (16)	7.1 (1)	25.0 (2)	17.6 (3)	0.0 (0)	16.7 (1)	66.7 (2)	0.0 (0)	21.2 (25)
ST5-II (NY/Japan, USA100)	– § (1)	– § (0)	– § (2)	– § (0)	– § (0)	– § (0)	– § (0)	– § (0)	– § (3)
Total	59	14	8	17	9	6	3	2	118

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

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

Table 40: Major community-associated MRSA clones (> 10 isolates) by state and territory and PVL carriage, 2017

	Percentage, % (*n*)								
Clone	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST93-IV (Qld CA-MRSA)*	20.5 (15)	19.1 (9)	37.5 (27)	17.6 (3)	32.6 (28)	–† (0)	74.4 (29)	–† (2)	32.8 (113)
Number PVL positive	14	7	27	3	28	0	26	1	106
Number PVL negative	1	2	0	0	0	0	3	1	7
ST45-V	39.7 (29)	23.4 (11)	1.4 (1)	5.9 (1)	1.2 (1)	0.0 (0)	0.0 (0)	–† (1)	12.8 (44)
Number PVL positive	10	4	0	0	1	0	0	0	15
Number PVL negative	19	7	1	1	0	0	0	1	29
ST5-IV§	6.8 (5)	8.5 (4)	18.1 (13)	17.6 (3)	11.6 (10)	0.0 (0)	10.3 (4)	0.0 (0)	11.3 (39)
Number PVL positive	0	0	0	1	7	0	1	0	9
Number PVL negative	5	4	13	2	3	0	3	0	30
ST1-IV#	1.4 (1)	4.3 (2)	11.1 (8)	17.6 (3)	14.0 (12)	–† (3)	7.7 (3)	—† (2)	9.9 (34)
Number PVL positive	1	0	0	0	0	0	0	0	1
Number PVL negative	0	2	8	3	12	3	3	2	33
ST78-IV*	1.4 (1)	2.1 (1)	1.4 (1)	11.8 (2)	12.8 (11)	0.0 (0)	0.0 (0)	0.0 (0)	4.7 (16)
Number PVL positive	0	0	1	0	1	0	0	0	2
Number PVL negative	1	1	0	2	10	0	0	0	14
ST8-IV#	4.1 (3)	6.4 (3)	2.8 (2)	0.0 (0)	2.3 (2)	0.0 (0)	0.0 (0)	0.0 (0)	2.9 (10)
Number PVL positive	3	3	2	0	2	0	0	0	10
Number PVL negative	0	0	0	0	0	0	0	0	0
ST30-IV	4.1 (3)	2.1 (1)	4.2 (3)	5.9 (1)	2.3 (2)	0.0 (0)	0.0 (0)	0.0 (0)	2.9 (10)
Number PVL positive	2	0	2	1	2	0	0	0	7
Number PVL negative	1	1	1	0	0	0	0	0	3
Other clones (n = 32)	21.9 (16)	34.0 (16)	23.6 (17)	23.5 (4)	23.3 (20)	0.0 (0)	7.7 (3)	–† (2)	22.7 (78)
Number PVL positive	9	6	3	2	0	0	0	1	21
Number PVL negative	7	10	14	2	20	0	3	1	57
Total	**73**	**47**	**72**	**17**	**86**	**3**	**39**	**7**	**344**
PVL positive	39	20	35	7	41	0	27	2	171
PVL negative	34	27	37	10	45	3	12	5	173

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

* includes three slv
† Insufficient numbers (<10) to calculate percentage
§ Includes one slv
# Included two slv

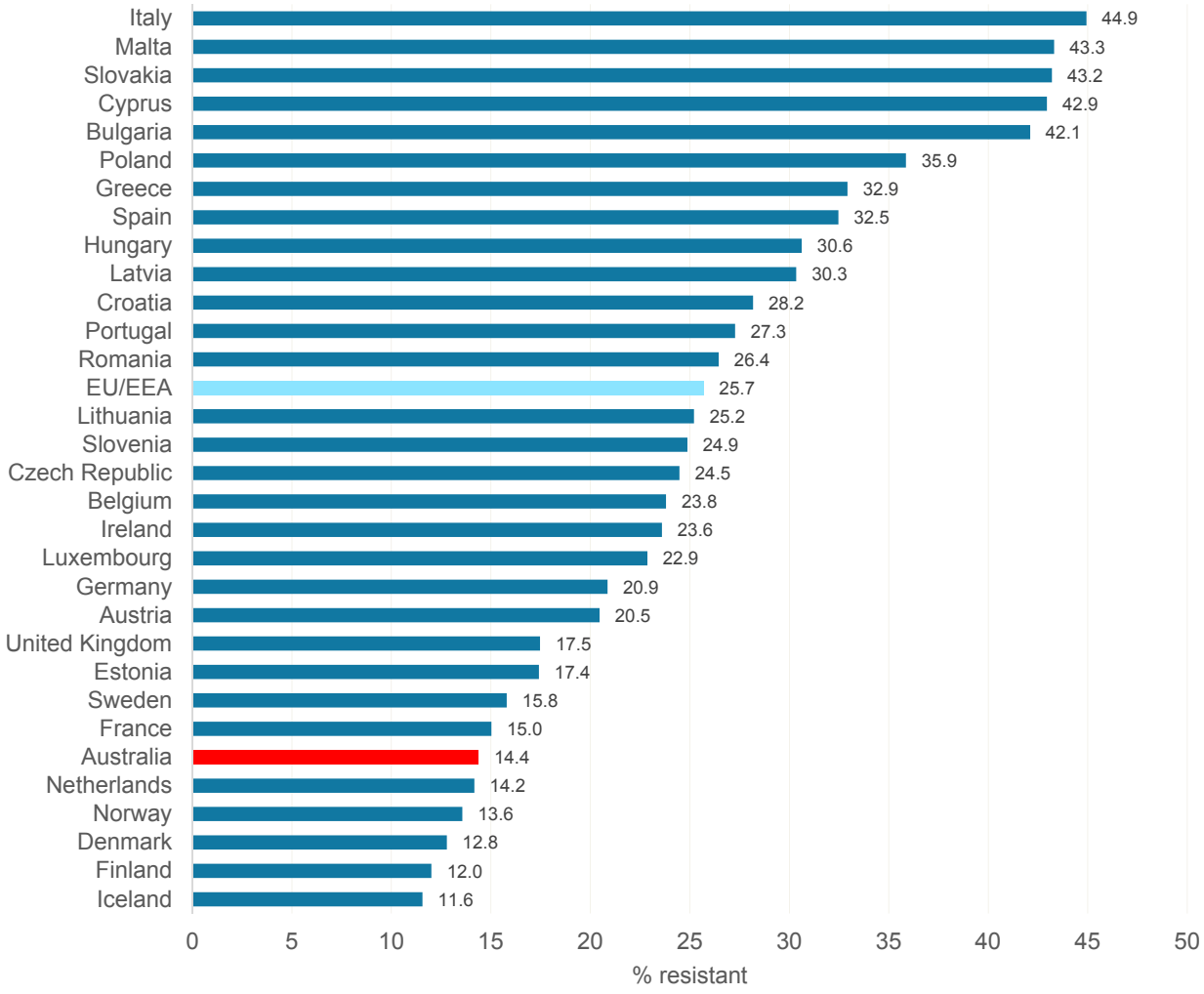
4. International comparisons

Data from AGAR can be compared with data from the European Antimicrobial Resistance Surveillance Network (EARs-Net) program,[42] as both programs examine resistance in bacterial pathogens found in blood culture.

Rates of resistance to fluoroquinolone in *E. coli* and *K. pneumoniae* (represented by resistance to ciprofloxacin) remain very low in Australia compared with most European countries (Figures 23 and 24). Resistance to third-generation cephalosporins in these two species, is similarly low by comparison, although not as low as for fluoroquinolones (Figures 25 and 26).

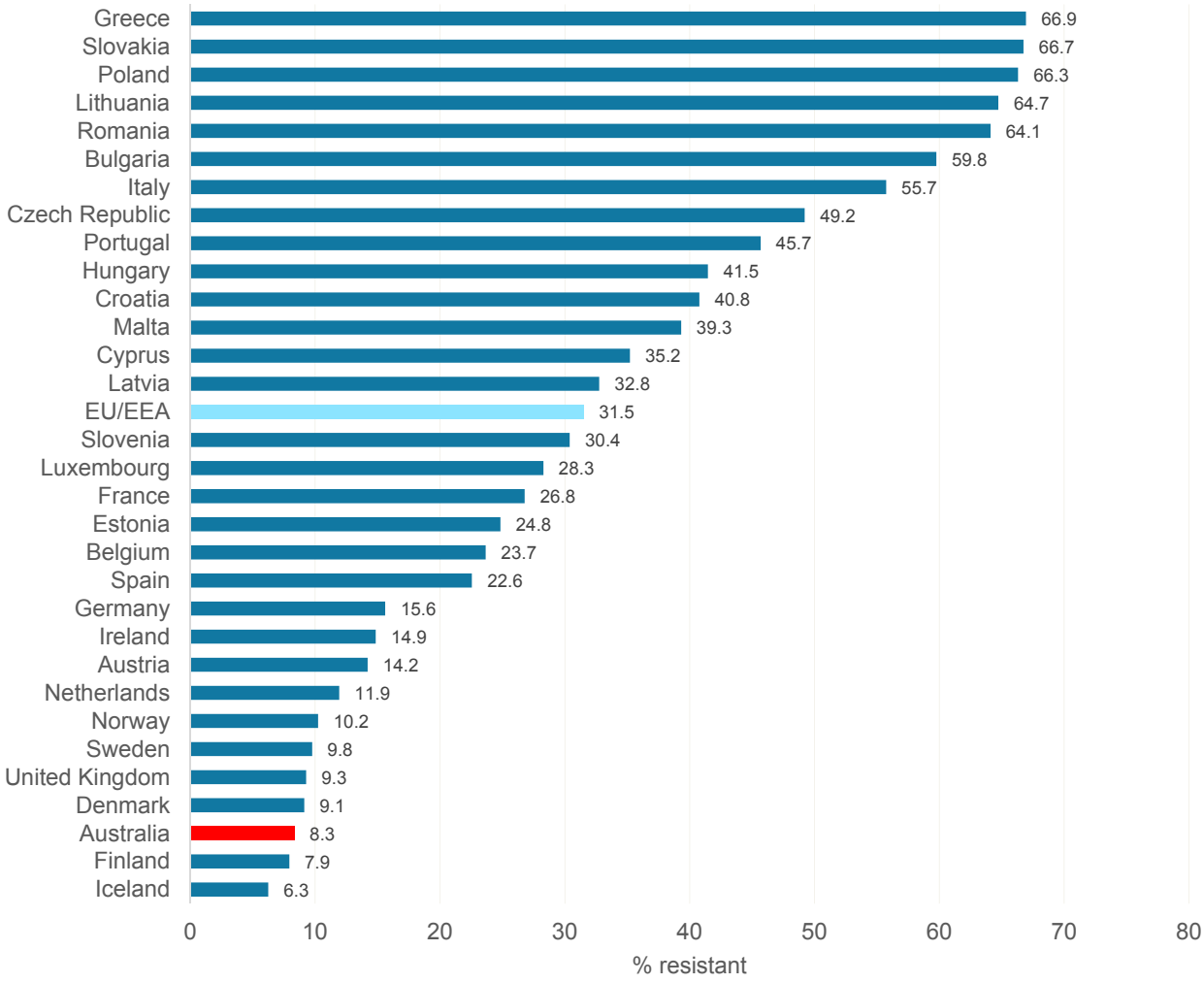
Australia ranks towards the middle in rates of resistance to methicillin in *S. aureus* (Figure 27), and higher than any European country in rates of resistance to vancomycin in *E. faecium* (Figure 28).

Figure 23: Comparison of *Escherichia coli* rates of resistance to ciprofloxacin in Australia and European countries, 2017



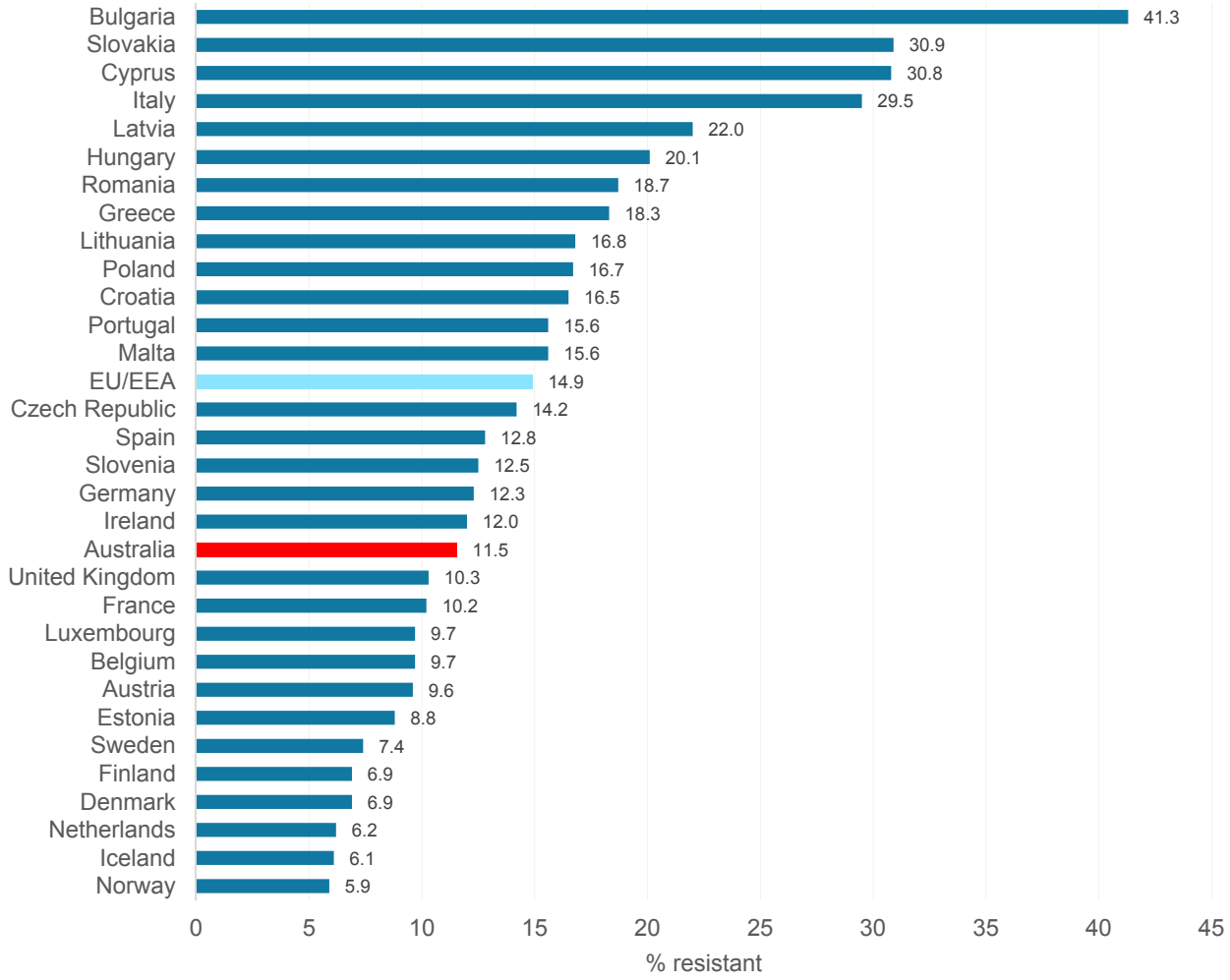
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 24: Comparison of *Klebsiella pneumoniae* rates of resistance to ciprofloxacin in Australia and European countries, 2017



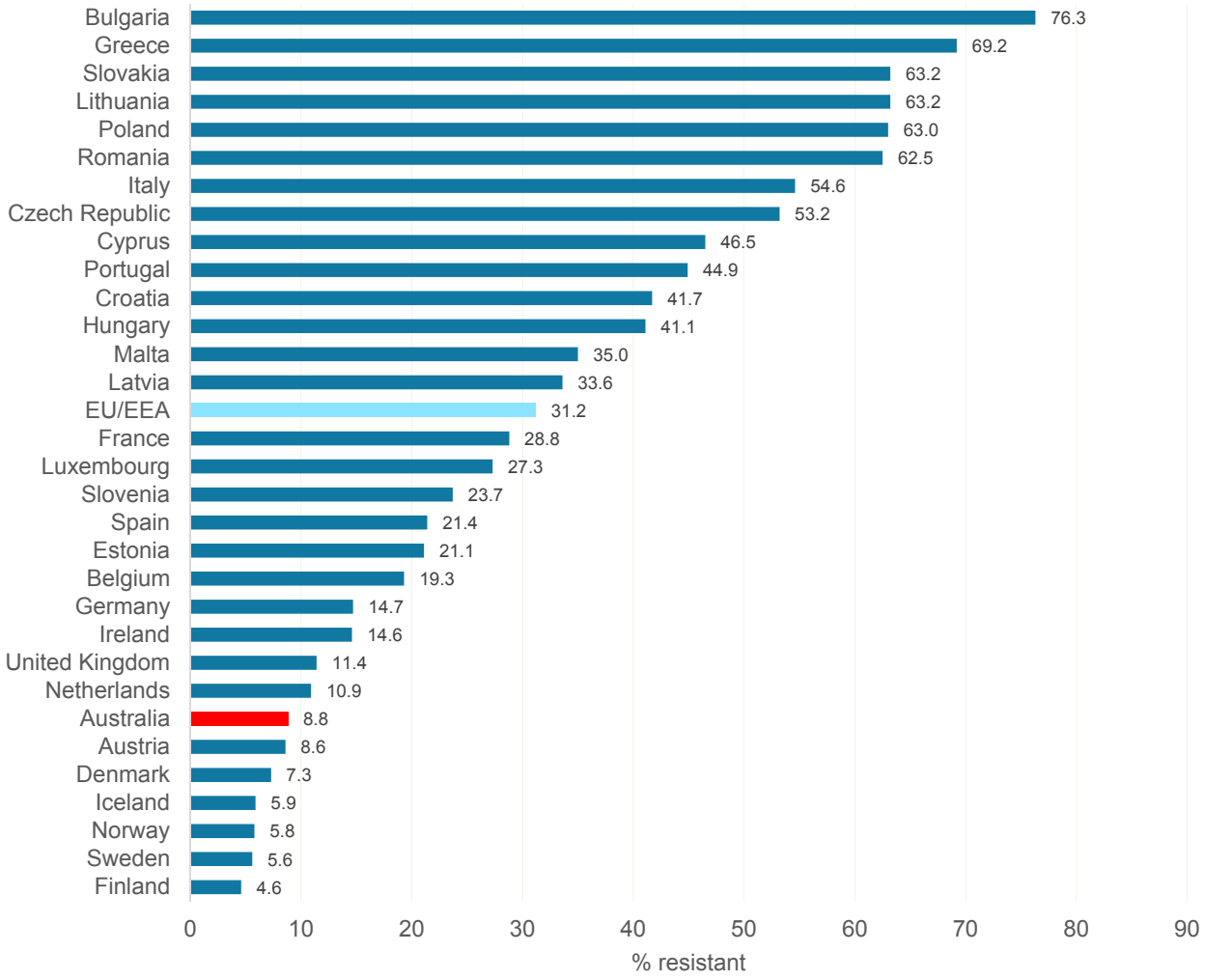
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 25: Comparison of *Escherichia coli* rates of resistance to third-generation cephalosporins in Australia and European countries, 2017



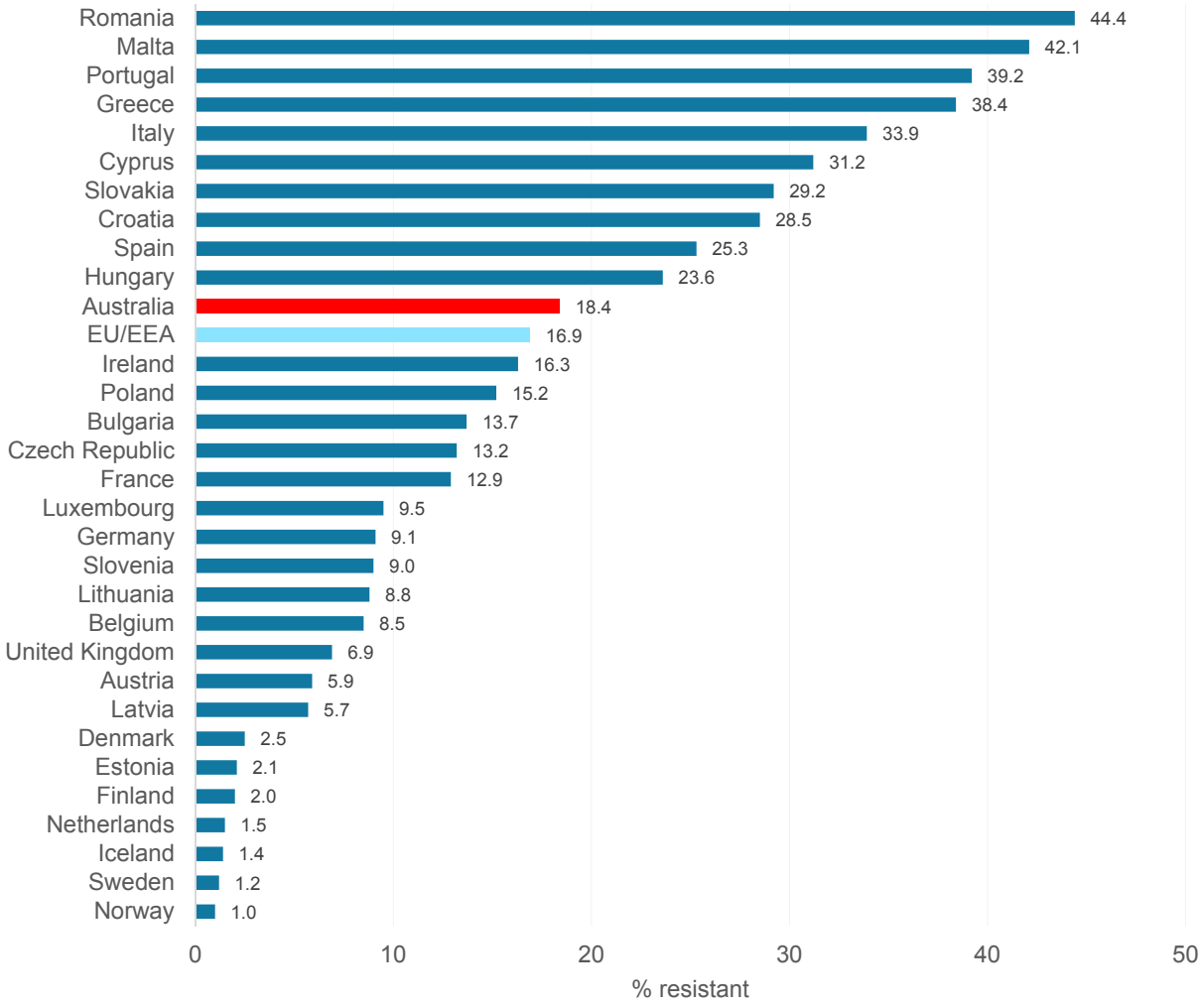
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 26: Comparison of *Klebsiella pneumoniae* rates of resistance to third-generation cephalosporins in Australia and European countries, 2017



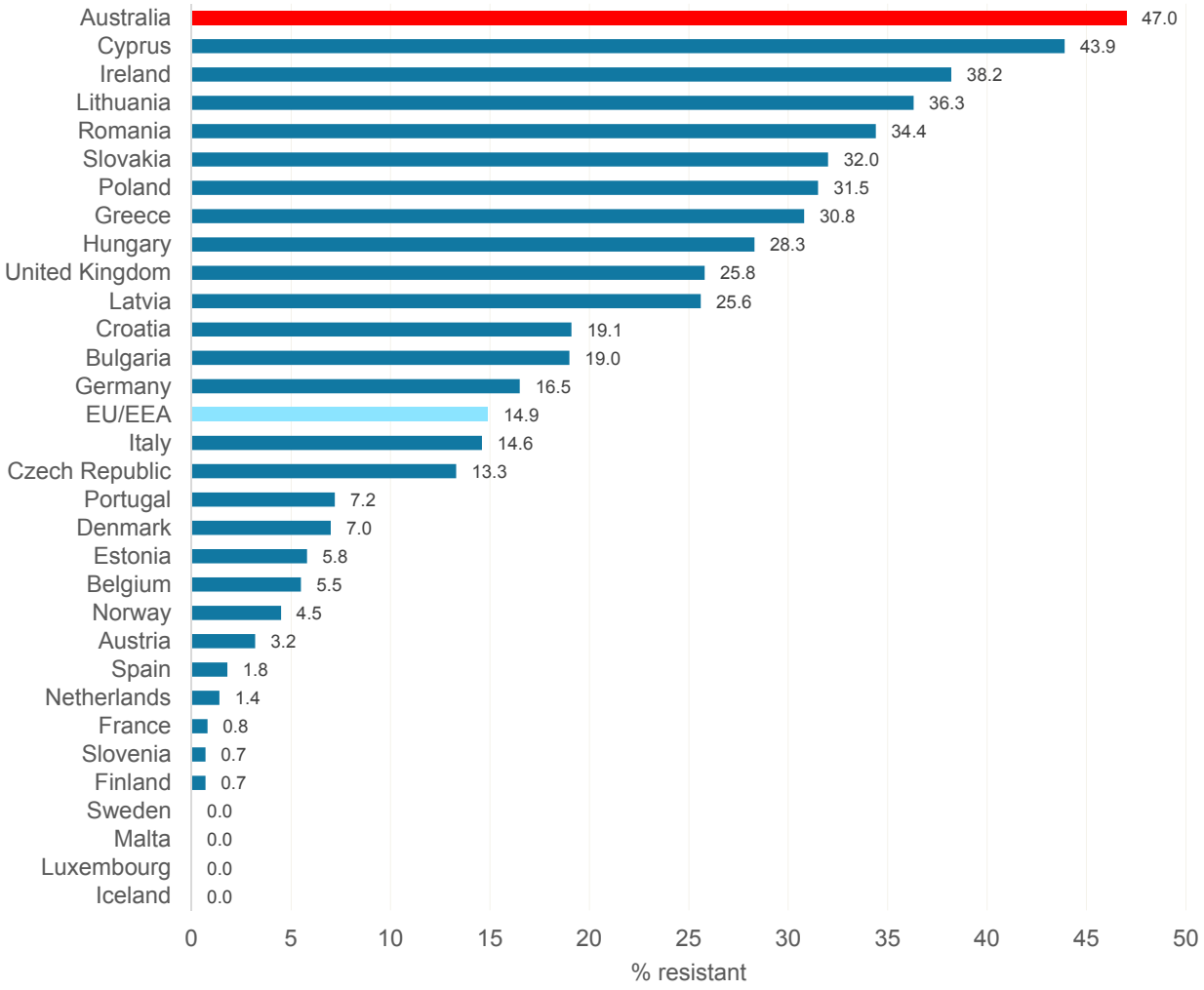
EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Figure 27: Comparison of *Staphylococcus aureus* rates of resistance to methicillin in Australia and European countries, 2017



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

Figure 28: Comparison of *Enterococcus faecium* rates of resistance to vancomycin in Australia and European countries, 2017



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

5. Limitations of the study

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

- The data are not denominator controlled, and there is currently no consensus on an appropriate denominator for such surveys; hospital size, patient throughput, patient complexity and local antibiotic use patterns all influence the types of resistance that are likely to be observed
- Although data have been collected from 36 large hospitals across Australia, it is not yet clear how representative the sample is of Australia as a whole, because the proportion of the population that is served by the laboratories that participate in AGAR is not accurately known. Further, it is likely that the proportion of the population served differs in each state and territory
- Because of the formulation of amoxicillin– clavulanic acid in both the Vitek® and Phoenix™ cards used, interpretation using EUCAST guidelines for this agent was not possible
- Concentration ranges of some antimicrobial agents in both the Vitek® and Phoenix™ cards limit the ability to accurately identify ‘susceptible’ for some combinations of antimicrobial agents and species.
- Data is classified into hospital- and community-onset infections; healthcare-associated community-onset infection
- ns may be included in the community-onset group.

6. Discussion and conclusions

AGAR data show that in 2017, the majority of episodes of bacteraemia in Australia had their onset in the community. The most frequent clinical manifestations of episodes of bacteraemia for the GNSOP and the AESOP were urinary tract infection, biliary tract infection and intra-abdominal infections. However, episodes with no focus and setting also accounted for high proportions of clinical manifestations for enterococcal bacteraemia overall, and for *E. faecalis* and *E. faecium*. For the ASSOP, the most frequent principal clinical manifestations were osteomyelitis/septic arthritis, skin and skin structure and device-related infection without metastatic focus. Strategies to reduce blood stream infections should take this information on clinical manifestation into account.

AGAR data show a longitudinal trend of increasing *E. coli* non-susceptibility to key anti-gram negative antimicrobial agents, such as ceftriaxone and ciprofloxacin. Rates of non-susceptibility to amoxicillin–clavulanic acid in *E. coli* (22.0%) are no longer substantially different from rates of non-susceptibility to ciprofloxacin (18.0%); there are no substantial differences between these rates for hospital and community settings. The steady rise in resistance to fluoroquinolones is more striking in hospital-onset bacteraemia, with an increase from 16.1% to 21.1% between 2013 and 2017. In 2017, rates of non-susceptibility for *K. pneumoniae* to amoxicillin–clavulanic acid (9.4%) and ciprofloxacin (11.2%), were lower than for *E. coli.*

Emerging fluoroquinolone resistance in Australia is a concern. A little over a decade ago, ciprofloxacin-resistance rates were consistently between 1 to 4%.[24, 43] 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 historically relied on as 'rear-guard' oral antibiotics, can no longer be considered a reliable antibiotic in these circumstances. Despite this concerning increase, the percentage of fluoroquinolone-resistant *E. coli* in Australia remains low in comparison to northern European countries.[42] Because fluoroquinolone resistance is often linked to cephalosporin resistance caused by ESBLs of the CTX-M type, fluoroquinolone use alone may not be solely responsible for the increase. It is possible that the high use of oral cephalosporins is driving this resistance.

Fluoroquinolone resistance in *E. coli* can also be linked to the emergence of O25b-ST131. O25b-ST131 is an international clone associated with third-generation cephalosporin and fluoroquinolone resistance, as well as increased virulence. In 2017, ESBL phenotypes were found in 12.6% of *E. coli* and 9.8% of *K. pneumoniae* isolates submitted to AGAR; O25b-ST131 accounted for 57% of *E. coli* ESBL phenotypes that were ciprofloxacin resistant. This reflects the dynamics of clonal spread of resistance, leading to rapid international, and now Australian, emergence of clones such as O25b-ST131. It shows how quickly resistance successes can be undermined, and also demonstrates the value of regular surveillance in identifying rapid changes in resistance.

When ESBLs first arose globally, they were more common in hospital-onset infections in *K. pneumoniae* (TEM, SHV); as a result, there is a perception that ESBLs are primarily a hospital problem. However, this is no longer the case, with 77.0% of ESBL *E. coli* bacteraemias now community-onset. This indicates that a substantial reservoir of resistance exists in the community, particularly in the elderly and in long-term residential care settings.[44] If the rate continues to rise, it will potentially affect the application of therapeutic guidelines for empirical treatment of severe infections. Current Australian guidelines recommend third-generation cephalosporins for empirical treatment for many conditions, partly to minimise prescribing of broader-spectrum antibiotics. The AGAR data suggest that customised patient risk assessment may be required in empirical treatment decisions. Rates of *E. coli* resistance to ceftriaxone continue to rise in hospital-onset bacteraemia (from 13.0% in 2016 to 15.5% in 2017), however community-onset ceftriaxone resistance has remained steady (11.1% in 2016 and 10.4% in 2017).

To date, carbapenemase-producing Enterobacterales (CPE) remain uncommon (0.1% in *E. coli* and 0.7% in *K. pneumoniae*). The overall low rates of CPE bacteraemia are encouraging; however, some organisms harbour them more commonly; 3.2% of *Enterobacter cloacae* complex infections harbour a carbapenemase in hospital-onset infections. Examining previous and current AGAR surveys, most CPEs are endemic in origin.[45, 46] Twelve of the 27 CPEs were due to the IMP-4 gene, which has previously been reported predominantly in eastern Australia. However, one *E. cloacae* complex harbouring *bla* $_{IMP-4}$ was isolated in Western Australia. The 15 non-IMP-4 isolates are thought to be introductions of individual CPEs into hospitals by patients who acquired the isolates overseas; these isolates have the potential for secondary local transmission, as occurred recently in Victoria with KPC- producing *K. pneumoniae*.[47] This reinforces the importance of infection control programs to limit transmission of CPE.[6]

Colistin susceptibility testing cannot be performed on the current Vitek® susceptibility cards. No mobile colistin resistance genes, a concerning genetic resistance for last line antimicrobials, were detected from all isolates referred for molecular testing.

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 Australian public hospitals in 2016-17 was 5.7 days.[48] Thirty-day all-cause mortality due to *E. faecium* in 2017 was high (27.7%); 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*, *E. cloacae* complex and *S. aureus* hospital-onset infections exceeds community-onset infections.

The emergence of penicillin-resistant clonal complex 17 *E. faecium* bacteraemia is a worldwide phenomenon. In addition to penicillin resistance, the isolates are often multidrug resistant, with high-level gentamicin resistance and vancomycin resistance. The limited therapeutic options may be a factor in the differing 30-day all-cause mortality between *E. faecium* (27.7%) and *E. faecalis* (14.3%).

In the 2017 survey, 50.9% of *E. faecium* harboured *vanA* or *vanB* genes, or both. Vancomycin, which until recently was the mainstay of therapy for *E. faecium*, can no longer be recommended empirically; agents with less certain efficacy such as linezolid are the alternative.
For almost two decades, and unlike in most other countries where vancomycin resistance is a problem, vancomycin resistance in Australia has been dominated by the *vanB* genotype. However, in the 2017 survey, 50% of vancomycin resistant *E. faecium* bacteraemias were due to *vanA*. This type of vancomycin resistance has emerged rapidly in the past six years, particularly in New South Wales, where it is now the dominant genotype. This in turn has reduced the overall teicoplanin susceptibility of *E. faecium* in Australia.

The percentage of *E. faecium* bacteraemia isolates that are resistant to vancomycin in Australia is significantly higher than that seen in almost all European countries. In 2017, the European Union/European Economic Area (EU/EEA) population-weighted mean percentage was 14.9%; most other countries are below 35%, except for Cyprus (43.9%), Ireland (38.2%), and Lithuania (36.3%).[42]

Although infection control strategies will be imperative in control of this organism, many antimicrobials have been implicated in the development of vancomycin non-susceptible *E. faecium.* Vancomycin, used commonly as an empiric therapeutic choice for MRSA, and other broad-spectrum antibiotics, such as third generation cephalosporins, are widely used in Australia.

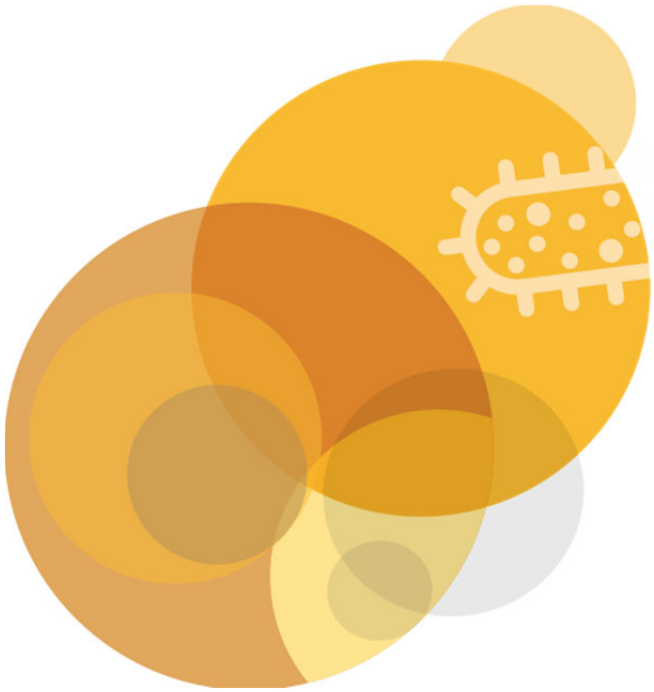
The overall rates of MRSA increased from 18.1% in 2015[49] to 19.0% in the 2017 study. This compares with the 2017 EU/EEA population-weighted mean MRSA percentage of 16.9%, ranging from 1.0% in Norway to 44.4% in Romania.[42]

The rate of community-onset SABs that are methicillin-resistant is increasing. Additionally, CA-MRSA clones are an increasing source of hospital-onset bacteraemia (particularly ST45-V and ST5-IV). Although HA-MRSA strains, for example, ST22-IV, were more frequently found in community-onset bacteraemia, this may be due to previous hospital exposure or onset in a long-term care facility. The molecular characterisation of MRSA contained within this report aids in identifying opportunities for control of MRSA blood stream infections in the Australian setting.

The rapidly changing picture of MRSA in Australia, drawing from 15 years of AGAR surveillance, is further explored in *MRSA: A tale of three types*.[50] This technical paper will be updated as appropriate by AGAR and the Commission to provide further information on the issue.

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

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



Abbreviations

Abbreviation	Term
AGAR	Australian Group on Antimicrobial Resistance
ANCU	*AURA National Coordinating Unit*
APAS	Australian Passive AMR Surveillance
AURA	Antimicrobial Use and Resistance in Australia
CI	confidence interval
CLSI	Clinical and Laboratory Standards Institute
ESBL	extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
MIC	minimum inhibitory concentration

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Institution	AGAR members
Alfred Hospital, Vic	Denis Spelman and Rose Bernhard
Alice Springs Hospital, NT	James McLeod
Austin Hospital, Vic	Paul Johnson and Frances Hurren
Canberra Hospital, ACT	Peter Collignon and Susan Bradbury
Concord Hospital, NSW	Thomas Gottlieb and Graham Robertson
John Hunter Hospital, NSW	Rod Givney and Ian Winney
Joondalup Hospital, WA	Shalinie Perera and Ian Meyer
Lady Cilento Children's Hospital, Qld	Clare Nourse and Janet Wallace
Launceston General Hospital, Tas	Pankaja Kalukottege and Kathy Wilcox
Monash Children's Hospital, Vic	Tony Korman and Despina Kotsanas
Monash Health (Monash Medical Centre), Vic	Tony Korman and Despina Kotsanas
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Pathology Queensland Central Laboratory, Qld	Graeme Nimmo and Narelle George
Pathology Queensland Gold Coast Hospital, Qld	Petra Derrington and Cheryl Curtis
Pathology Queensland Prince Charles Hospital, Qld	Robert Horvath and Laura Martin
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Reference laboratories

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Appendix A. Study design

Thirty-six institutions participated in the 2017 survey. All states and territories were represented. The laboratories that participated in AGAR collected all isolates from different patient episodes of bacteraemia for either all isolates or up to 200 isolates for the Gram- negative Sepsis Outcome Program. In patients with more than one isolate, a new episode was defined as a new positive blood culture more than two weeks after the initial positive culture.

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

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

Table A1: Level of participation of laboratories that contributed data on gram-negative* bacteraemia, by state and territory, 2017

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

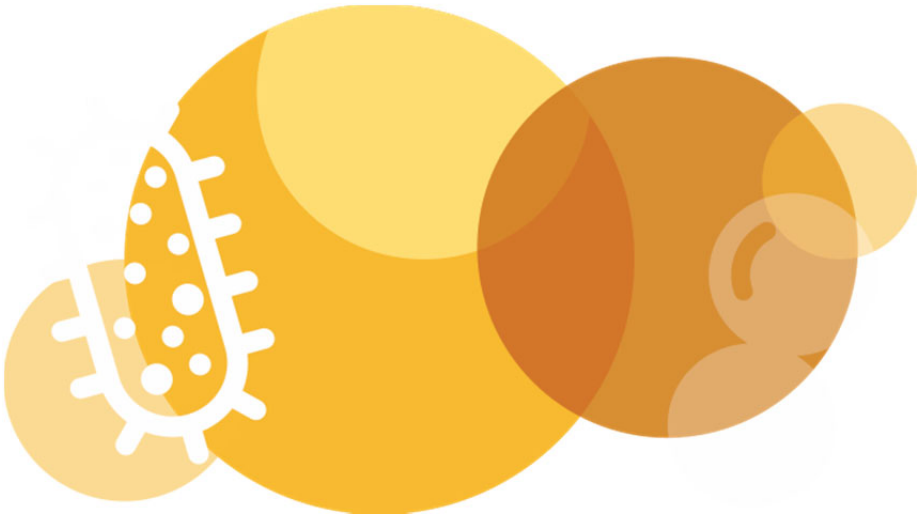
* Enterobacterales, *Acinetobacter* species and *Pseudomonas aeruginosa*

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

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

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

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



Appendix B. Methods

Species identification

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

Susceptibility testing

Testing was performed using two commercial semi-automated methods: Vitek 2 (bioMérieux) (*n* = 32) and Phoenix (BD) (*n* = 4), which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution. Commercially available Vitek 2 AST-N246 and AST-N247 cards or Phoenix NMIC-203 and NMIC-404 cards were used by all participants throughout the survey period.

The CLSI M100-A28[26] and the EUCAST v8.1[27] breakpoints from January 2018 were used in the analysis. For analysis of cefazolin, breakpoints of ≤4 mg/L for susceptible and ≥8 mg/L for resistant were applied, because of the restricted MIC range available on the commercial cards (recognising that the January 2018 breakpoint is susceptible ≤2 mg/L).

Antimicrobials tested

The antimicrobials tested is shown in Table B1.

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

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v8.0†		
	S	SDD	I	R	S	I	R
Benzylpenicillin							
Enterococcus spp.	≤8		–§	≥16	–#	–#	–#
Staphylococcus aureus	≤0.12		–§	≥0.25	≤0.125	–§	>0.125
Amikacin							
Acinetobacter spp.	≤16		32	≥64	≤8	16	>16
Enterobacterales	≤16		32	≥64	≤8	16	>16
Pseudomonas spp.	≤16		32	≥64	≤8	16	>16
Amoxicillin–clavulanic acid							
Enterobacterales	≤8/4		16/8	≥32/16	≤8**	–§	>8**
Enterococcus spp.	–#		–#	–#	≤4**	8**	>8**
Ampicillin							
Enterobacterales	≤8		16	≥32	≤8	–§	>8
Enterococcus spp.	≤8		–§	≥16	≤4	8	>8
Aztreonam (Phoenix card)							
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤1	2–16	>16
Cefazolin (Australian)‡	≤2		4	≥8	≤2	4	>4
Cefepime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤2	4–8	–§	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	8	–§	>8
Cefalexin	–#		–#	–#	≤16	–§	>16

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v8.0†		
	S	SDD	I	R	S	I	R
Cefalotin	≤8		16	≥32	–[#]	–[#]	–[#]
Cefoxitin	≤8		16	≥32	–[#]	–[#]	–[#]
Ceftazidime							
Acinetobacter spp.	≤8		16	≥32	–[#]	–[#]	–[#]
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤8	–[§]	>8
Ceftriaxone							
Acinetobacter spp.	≤8		16–32	≥64	–[#]	–[#]	–[#]
Enterobacterales	≤1		2	≥4	≤1	2	>2
Chloramphenicol (Phoenix card)	≤8		16	≥32	≤8	–[§]	≥16
Ciprofloxacin							
Acinetobacter spp.	≤1		2	≥4	≤1	–[§]	>1
Enterobacterales	≤1		2	≥4	≤0.25	0.5	>0.5
Salmonella spp.[§§]	≤0.06		0.12–0.5	≥1	≤0.06	–[§]	>0.06
Enterococcus spp.[##]	≤1		2	≥4	≤4	–[§]	>4
Staphylococcus aureus	≤1		2	≥4	≤1	–[§]	>1
Pseudomonas spp.	≤1		2	≥4	≤0.5	–[§]	>0.5
Clindamycin							
Staphylococcus aureus	≤0.5		1–2	≥4	≤0.25	0.5	>0.5
Colistin (Phoenix card)							
Acinetobacter spp.	≤2		–[§]	≥4	≤2	–[§]	>2
Enterobacterales	–[#]		–[#]	–[#]	≤2	–[§]	>2
Pseudomonas spp.	≤2		–[§]	≥4	≤2	–[§]	>2
Daptomycin							
Enterococcus spp.	≤4		–[#]	–[#]	–[#]	–[#]	–[#]
Staphylococcus aureus	≤1		–[#]	–[#]	≤1	–[§]	>1
Doxycycline (Phoenix card)							
Enterococcus spp.	≤4		8	≥16	–[#]	–[#]	–[#]
Staphylococcus aureus	≤4		8	≥16	≤1	2	>2
Ertapenem (Phoenix card)	≤0.5		1	≥2	≤0.5	1	>1
Erythromycin							
Enterococcus spp.	≤0.5		1–4	≥8	–[#]	–[#]	–[#]
Staphylococcus aureus	≤0.5		1–4	≥8	≤1	2	>2
Fosfomycin (Phoenix card)	≤64		128	≥256	≤32	–[§]	>32
Fusidic acid							
Staphylococcus aureus	–[#]		–[#]	–[#]	≤1	–[§]	>1
Gentamicin							
Acinetobacter spp.	≤4		8	≥16	≤4	–[§]	>4
Enterobacterales	≤4		8	≥16	≤2	4	>4
Pseudomonas spp.	≤4		8	≥16	≤4	–[§]	>4
Staphylococcus aureus	≤4		8	≥16	≤1	–[§]	>1
Imipenem (Phoenix card)							
Acinetobacter spp.	≤2		4	≥8	≤2	4–8	>8
Enterobacterales	≤1		2	≥4	≤2	4–8	>8
Enterococcus spp.	-		-	-	≤4	8	>8
Pseudomonas spp.	≤2		4	≥8	≤4	8	>8

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v8.0†		
	S	SDD	I	R	S	I	R
Linezolid							
Enterococcus spp.	≤2		4	≥8	≤4	–§	>4
Staphylococcus aureus	≤4		–§	≥8	≤4	–§	>4
Meropenem							
Acinetobacter spp.	≤2		4	≥8	≤2	4–8	>8
Enterobacterales	≤1		2	≥4	≤2	4–8	>8
Pseudomonas spp.	≤2		4	≥8	≤2	4–8	>8
Nitrofurantoin							
Enterobacterales	≤32		64	≥128	≤64††	–§	>64
Enterococcus spp.	≤32		64	≥128	≤64††	–§	>64
Staphylococcus aureus	≤32		64	≥128	–#	–#	–#
Norfloxacin							
Enterobacterales	≤4		8	≥16	≤0.5	1	>1
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	≤16	–§	>16
Rifampicin							
Enterococcus spp.	≤1		2	≥4	–#	–#	–#
Staphylococcus aureus	≤1		2	≥4	≤0.06***	0.12–0.5	>0.5
Teicoplanin							
Enterococcus spp.	≤8		16	≥32	≤2	–§	>2
Staphylococcus aureus	≤8		16	≥32	≤2	–§	>2
Tetracycline							
Acinetobacter spp.	≤4		8	≥16	–#	–#	–#
Enterobacterales	≤4		8	≥16	–#	–#	–#
Enterococcus spp.	≤4		8	≥16	–#	–#	–#
Staphylococcus aureus	≤4		8	≥16	≤1	2	>2
Ticarcillin–clavulanic acid							
Acinetobacter spp.	≤16/2		32/2–64/2	≥128/2	–#	–#	–#
Enterobacterales	≤16/2		32/2–64/2	≥128/2	≤8	16	>16
Pseudomonas spp.	≤16/2		32/2–64/2	≥128/2	≤16	–§	>16
Tigecycline (Phoenix card)	–#		–#	–#	≤1	2	≥4
Tobramycin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	>4
Enterobacterales	≤4		8	≥16	≤2	4	>4
Pseudomonas spp.	≤4		8	≥16	≤4	–§	>4
Trimethoprim							
Enterobacterales	≤8		–§	≥16	≤2	4	>4

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v8.0†		
	S	SDD	I	R	S	I	R
Enterococcus spp.	–#		–#	–#	≤0.03	0.06–1	>1
Staphylococcus aureus	≤8		–§	≥16	≤2	4	>4
Trimethoprim–sulfamethoxazole							
Acinetobacter spp.	≤2/38		–§	≥4/76	≤2/38	4/76	>4/76
Enterobacterales	≤2/38		–§	≥4/76	≤2/38	4/76	>4/76
Enterococcus spp.	–#		–#	–#	≤0.03§§§	0.06–1	>1
Staphylococcus aureus	≤2/38		–§	≥4/76	≤2	4	>4
Vancomycin							
Enterococcus spp.	≤4		8–16	≥32	≤4	–§	>4
Staphylococcus aureus	≤2		4–8	≥16	≤2	–§	>2

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate; R = resistant; S = sensitive; SDD = sensitive dose dependent

* The breakpoints selected to identify resistance are described in *Performance Standards for Antimicrobial Susceptibility Testing: Twenty-seventh informational supplement*, CLSI document M100-S28, January 2018.

† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 8.0, 2018 (www.eucast.org)

§ No category defined

No guidelines for indicated species

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

‡ The concentration range available on the current Vitek card restricts the ability to identify the susceptible category. For analysis, breakpoints of ≤4 mg/L for susceptible and ≥8 mg/L for resistant were applied.

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

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

†† Breakpoints apply to *E. coli* only.

‡‡ Breakpoints apply to *E. faecalis* only.

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

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

All referred isolates were screened using real-time polymerase chain reaction (PCR) platform (LC-480) and published primers for the presence of bla_{TEM} and bla_{SHV}, CTX-M-type genes (groups 1, 2, 9, 8/25), plasmid-borne AmpC (bla_{CIT}, bla_{DHA}, bla_{EBC}, bla_{ACC}, bla_{FOX}, bla_{MOX}), and carbapenemases genes (bla_{IMP}, bla_{NDM}, bla_{KPC}, $bla_{OXA-48-like}$, bla_{VIM}, bla_{GES}, bla_{SME}, bla_{IMI}).[28-30]

PCRs were also used to detect bla_{IMP} types, known plasmid-mediated quinolone resistance mechanisms (*qnr*, efflux [*qepA*, *oqxAB*] and *aac* (*6')-Ib-cr*), aminoglycoside ribosomal methyltransferases (armA, rmtB, rmtC, rmtF), and mobile colistin resistance genes (mcr-1, mcr-2, mcr-3)[31-36]. All referred *E. coli* were examined for membership of the O25b-ST131 clone.[37] All isolates with demonstrated carbapenemase activity and any amikacin resistant isolates were also screened for OXA-23-like, -24, and -58 carbapenemases.[38]

All gram-negative isolates with carbapenemase activity, *E. faecium* and MRSA were subjected to whole genome sequencing using the Illumina MiSeq platform. Data were analysed using the Nullarbor bioinformatic pipeline.[39] The pipeline was used to identify the multi-locus sequence type and the resistome.

Quality control

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

Data validation

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

- Null values in the mandatory fields
- Missing MIC data
- Age ≥100 or <0 years
- Date of collection > discharge date
- Discharge date < date of admission
- Date of admission < date of birth
- Date of admission < date of collection + two days.

Appendix C. Susceptibility to antimicrobial agents

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

Table C1: Susceptibility (CLSI and EUCAST) to antimicrobial agents in indicator species of national priority, by state and territory, 2017

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	8	12	18	6	8	1	8	1	62
	%R	n/a	0.0, 0.0	11.1, 11.1	n/a	na	n/a	n/a	n/a	3.2, 3.2
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%R	0.7, 0.7	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	0.2, 0.2
Escherichia coli	n	1,170	794	858	289	771	174	141	158	4,355
	%R	0.2, 0.3	0.0, 0.4	0.1, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.2
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%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	58	35	36	22	44	20	2	12	229
	%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
Klebsiella pneumoniae	n	267	197	246	56	152	22	30	27	997
	%R	0.4, 0.4	0.5, 0.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 3.3	0.0, 0.0	0.2, 0.3
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%R	0.0, 0.0	2.6, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.4, 0.4
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	195	87	204	57	86	15	15	30	689
	%R	0.0, 0.0	2.3, 4.6	0.5, 1.5	0.0, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.4, 1.2
Amoxicillin–clavulanic acid										
Escherichia coli	n	1,170	794	858	288	771	174	141	158	4,354
	%I	15.4, –†	12.1, –†	11.4, –†	12.5, –†	15.6, –†	15.5, –†	12.8, –†	12.0, –†	13.6, –†
	%R	8.9, –†	8.9, –†	10.3, –†	5.6, –†	7.4, –†	5.2, –†	5.7, –†	7.6, –†	8.4, –†
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%I	3.4, –†	5.7, –†	2.8, –†	0.0, –†	0.0, –†	5.0, –†	n/a	16.7, –†	3.5, –†

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	10.3, –[†]	8.6, –[†]	5.6, –[†]	9.1, –[†]	4.5, –[†]	5.0, –[†]	n/a	25.0, –[†]	8.3, –[†]
Klebsiella pneumoniae	n	267	197	246	54	152	22	30	27	995
	%I	3.4, –[†]	6.6, –[†]	4.5, –[†]	1.9, –[†]	3.3, –[†]	0.0, –[†]	6.7, –[†]	0.0, –[†]	4.1, –[†]
	%R	4.5, –[†]	6.6, –[†]	4.5, –[†]	5.6, –[†]	5.9, –[†]	4.5, –[†]	6.7, –[†]	7.4, –[†]	5.3, –[†]
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%I	3.1, –[†]	5.3, –[†]	4.3, –[†]	4.5, –[†]	13.2, –[†]	9.1, –[†]	n/a	n/a	5.5, –[†]
	%R	4.6, –[†]	2.6, –[†]	0.0, –[†]	4.5, –[†]	2.6, –[†]	0.0, –[†]	n/a	n/a	2.6, –[†]
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%I	0.0, –[†]	7.1, –[†]	0.0, –[†]	n/a	0.0, –[†]	n/a	0.0, –[†]	n/a	0.8, –[†]
	%R	0.0, –[†]	0.0, –[†]	3.6, –[†]	0.0, –[†]	0.0, –[†]	n/a	0.0, –[†]	n/a	0.8, –[†]
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%I	n/a	0.0, –[†]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –[†]
	%R	n/a	0.0, –[†]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –[†]
Ampicillin										
Enterococcus faecalis	n	187	119	101	31	94	31	10	28	601
	%I	–[§], 0.0	–[§], 0.0	–[§], 1.0	–[§], 0.0	–[§], 0.0	–[§], 0.0	–[§], 0.0	–[§], 0.0	–[§], 0.2
	%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	167	134	45	28	63	17	5	22	481
	%I	–[§], 0.0	–[§], 0.7	–[§], 0.0	–[§], 0.0	–[§], 0.0	–[§], 0.0	n/a	–[§], 0.0	–[§], 0.2
	%R	89.2, 89.2	92.5, 92.5	95.6, 95.6	85.7, 85.7	81.0, 81.0	88.2, 88.2	n/a	95.5, 95.5	89.6, 89.6
Escherichia coli	n	1,170	794	858	288	770	174	141	158	4,353
	%I	1.7, –[§]	1.4, –[§]	1.3, –[§]	2.1, –[§]	0.9, –[§]	1.1, –[§]	0.7, –[§]	1.9, –[§]	1.4, –[§]
	%R	55.2, 56.9	54.2, 55.5	51.6, 52.9	41.7, 43.8	56.6, 57.5	40.8, 42.0	58.9, 59.6	48.7, 50.6	53.0, 54.4
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%I	0.0, –[§]	2.6, –[§]	0.0, –[§]	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	n/a	0.4, –[§]
	%R	15.4, 15.4	23.7, 26.3	8.5, 8.5	18.2, 18.2	21.1, 21.1	18.2, 18.2	n/a	n/a	16.6, 17.0
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%I	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	0.0, –[§]	n/a	0.0, –[§]	n/a	0.0, –[§]
	%R	10.5, 10.5	14.3, 14.3	7.1, 7.1	n/a	7.7, 7.7	n/a	9.5, 9.5	n/a	8.4, 8.4
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%I	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	8.3, 8.3	n/a	n/a	n/a	n/a	n/a	n/a	6.5, 6.5
Benzylpenicillin										

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Enterococcus faecalis	n	187	117	101	30	91	16	10	28	580
	%R/– [#]	0.0, – [#]	0.0, – [#]	1.0, – [#]	0.0, – [#]	1.1, – [#]	0.0, – [#]	0.0, – [#]	0.0, – [#]	0.3, – [#]
Enterococcus faecium	n	165	132	44	28	63	10	5	22	469
	%R/– [#]	89.7, – [#]	94.7, – [#]	95.5, – [#]	85.7, – [#]	84.1, – [#]	100, – [#]	n/a	95.5, – [#]	91.3, – [#]
Staphylococcus aureus	n	676	364	553	166	465	91	99	95	2,509
	%R	81.7, 81.7	82.1, 82.1	79.4, 79.4	84.9, 84.9	83.9, 83.9	72.5, 72.5	88.9, 88.9	73.7, 73.7	81.5, 81.5
Cefazolin										
Enterobacter cloacae complex	n	136	75	107	26	55	12	7	10	428
	%R	97.1, 97.1	100, 100	97.2, 97.2	96.2, 96.2	98.2, 98.2	91.7, 91.7	n/a	100, 100	97.7, 97.7
Escherichia coli	n	1,170	794	858	288	771	127	141	158	4,307
	%R	25.5, 25.5	23.3, 23.3	20.2, 20.2	15.6, 15.6	24.9, 24.9	22.0, 22.0	19.1, 19.1	20.3, 20.3	22.8, 22.8
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	2	1	5	103
	%R	91.1, 91.1	95.8, 95.8	90.0, 90.0	n/a	76.9, 76.9	n/a	n/a	n/a	90.3, 90.3
Klebsiella oxytoca	n	58	35	36	22	44	13	2	12	222
	%R	60.3, 60.3	71.4, 71.4	72.2, 72.2	54.5, 54.5	70.5, 70.5	76.9, 76.9	n/a	75.0, 75.0	67.1, 67.1
Klebsiella pneumoniae	n	267	197	246	55	152	16	30	27	990
	%R	11.2, 11.2	21.3, 21.3	8.1, 8.1	16.4, 16.4	9.9, 9.9	6.3, 6.3	10.0, 10.0	14.8, 14.8	12.5, 12.5
Proteus mirabilis	n	65	38	47	22	38	8	5	9	232
	%R	16.9, 16.9	28.9, 28.9	8.5, 8.5	18.2, 18.2	23.7, 23.7	n/a	n/a	n/a	18.5, 18.5
Cefoxitin										
Escherichia coli	n	1,170	794	858	288	770	174	141	158	4,353
	%R/– [#]	4.3, – [#]	4.4, – [#]	3.8, – [#]	2.1, – [#]	3.4, – [#]	1.1, – [#]	3.5, – [#]	3.2, – [#]	3.7, – [#]
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%R/– [#]	5.2, – [#]	2.9, – [#]	0.0, – [#]	4.5, – [#]	0.0, – [#]	0.0, – [#]	n/a	0.0, – [#]	2.2, – [#]
Klebsiella pneumoniae	n	267	197	246	55	152	22	30	27	996
	%R/– [#]	5.2, – [#]	7.1, – [#]	4.5, – [#]	1.8, – [#]	8.6, – [#]	0.0, – [#]	3.3, – [#]	7.4, – [#]	5.6, – [#]
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%R/– [#]	1.5, – [#]	0.0, – [#]	0.0, – [#]	0.0, – [#]	0.0, – [#]	0.0, – [#]	n/a	n/a	0.4, – [#]
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%R/– [#]	0.0, – [#]	0.0, – [#]	3.6, – [#]	n/a	0.0, – [#]	n/a	0.0, – [#]	n/a	0.8, – [#]
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%R/– [#]	n/a	0.0, – [#]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, – [#]
Cefepime										
Acinetobacter baumannii complex	n	7	12	18	6	8	1	8	1	61
	%R/– [#]	n/a	0.0, – [#]	22.2, – [#]	n/a	n/a	n/a	n/a	n/a	8.2, – [#]
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%NS**	11.0,	5.3,	1.9,	7.7,	5.5,	11.8,	n/a	10.0,	6.9, 14.5

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		19.1	13.3	9.3	19.2	9.1	23.5		20.0	
Escherichia coli	n	1,170	794	858	288	771	174	141	158	4,354
	%NS**	7.7, 10.7	4.9, 9.9	3.1, 7.1	3.8, 3.8	4.8, 9.1	3.4, 4.6	3.5, 6.4	3.2, 10.1	5.1, 8.7
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%NS**	0.0, 2.2	0.0, 4.2	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	0.0, 1.9
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%NS**	0.0, 0.0	2.9, 5.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.9
Klebsiella pneumoniae	n	267	197	246	56	152	22	30	27	997
	%NS**	4.1, 5.2	4.6, 15.7	2.0, 3.3	7.1, 7.1	4.6, 4.6	4.5, 4.5	6.7, 6.7	3.7, 7.4	4.0, 6.9
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%NS**	0.0, 0.0	5.3, 5.3	0.0, 0.0	0.0, 0.0	2.6, 2.6	0.0, 0.0	n/a	n/a	1.3, 1.3
Pseudomonas aeruginosa	n	195	87	204	57	86	15	15	30	689
	%R	3.1, 6.2	4.6, 5.7	2.0, 3.9	5.3, 17.5	2.3, 4.7	0.0, 0.0	6.7, 13.3	10.0, 13.3	3.3, 6.5
Salmonella species (non-typhoidal)	n	18	14	28	4	39	2	21	4	130
	%NS**	0.0, 0.0	7.1, 7.1	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.8, 0.8
Salmonella species (typhoidal)	n	4	12	7	1	4	0	1	1	30
	%NS**	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Ceftazidime										
Acinetobacter baumannii	n	7	12	18	6	8	1	8	1	61
	%NS	n/a	25.0, –#	27.8, –#	n/a	n/a	n/a	n/a	n/a	24.6, –#
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%NS	27.2, 28.7	37.3, 38.7	18.7, 24.3	23.1, 26.9	14.5, 21.8	23.5, 23.5	n/a	30.0, 30.0	24.9, 28.2
Escherichia coli	n	1,170	794	858	289	771	174	141	158	4,355
	%NS	9.1, 13.7	5.7, 12.7	5.2, 9.4	2.1, 6.2	6.6, 11.4	4.0, 5.7	4.3, 6.4	3.8, 10.1	6.3, 11.1
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%NS	42.2, 44.4	45.8, 50.0	20.0, 20.0	n/a	23.1, 30.8	n/a	n/a	n/a	41.3, 45.2
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%NS	0.0, 0.0	0.0, 2.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.4
Klebsiella pneumoniae	n	267	197	246	56	152	22	30	27	997
	%NS	6.0, 7.5	12.7, 16.2	1.6, 4.1	1.8, 5.4	3.9, 8.6	4.5, 4.5	6.7, 10.0	11.1, 14.8	5.8, 8.6
Proteus mirabilis	n	65	38	47	21	38	11	5	9	234
	%NS	1.5, 4.6	2.6, 5.3	0.0, 0.0	0.0, 4.8	2.6, 2.6	0.0, 0.0	n/a	n/a	1.3, 3.0
Pseudomonas aeruginosa	n	195	85	203	57	86	15	15	30	686
	%NS/R	8.2, 8.2	8.2, 8.2	6.9, 6.9	22.8, 22.8	8.1, 8.1	0.0, 0.0	6.7, 6.7	20.0, 20.0	9.3, 9.3
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%NS	0.0, 0.0	7.1, 7.1	3.6, 3.6	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.5, 1.5

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%NS	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Ceftriaxone										
Acinetobacter baumannii complex	n	7	12	18	3	8	1	8	0	57
	%NS/– [#]	n/a	66.7, – [#]	77.8, – [#]	n/a	n/a	n/a	n/a	n/a	77.2, – [#]
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%NS	28.7, 28.7	40.0, 40.0	23.4, 23.4	26.9, 26.9	20.0, 20.0	23.5, 23.5	n/a	30.0, 30.0	27.9, 27.9
Escherichia coli	n	1,170	794	858	289	771	174	141	158	4,355
	%NS	13.8, 13.8	14.1, 14.1	9.4, 9.4	4.2, 4.2	11.3, 11.3	5.2, 5.2	9.2, 9.2	11.4, 11.4	11.3, 11.3
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%NS	44.4, 44.4	45.8, 45.8	20.0, 20.0	n/a	30.8, 30.8	n/a	n/a	n/a	43.3, 43.3
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%NS	6.9, 6.9	5.7, 5.7	2.8, 2.8	4.5, 4.5	4.5, 4.5	5.0, 0.0	n/a	16.7, 16.7	5.7, 5.7
Klebsiella pneumoniae	n	267	197	246	56	152	22	30	27	997
	%NS	7.9, 7.9	19.8, 19.8	3.3, 3.3	7.1, 7.1	5.9, 5.9	4.5, 4.5	6.7, 6.7	14.8, 14.8	8.8, 8.8
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%NS	3.1, 3.1	5.3, 5.3	0.0, 0.0	0.0, 0.0	2.6, 2.6	0.0, 0.0	n/a	n/a	2.1, 2.1
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%NS	0.0, 0.0	7.1, 7.1	3.6, 3.6	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	1.5, 1.5
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%NS	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Ciprofloxacin										
Acinetobacter baumannii complex	n	8	12	18	6	8	2	8	1	63
	%NS/R	n/a	0.0, 0.0	16.7, 16.7	n/a	n/a	n/a	n/a	n/a	6.3, 6.3
Enterococcus faecalis	n	185	118	95	31	91	16	10	0	546
	%NS/R	14.1, 10.8	14.4, 13.6	25.3, 16.8	29.0, 22.6	9.9, 5.5	6.2, 6.2	20.0, 20.0	n/a	16.1, 12.3
Enterococcus faecium	n	165	133	40	28	63	10	5	0	444
	%NS/R	92.7, 87.3	93.2, 91.7	92.5, 90.0	89.3, 85.7	88.9, 79.4	100, 100	n/a	n/a	92.3, 87.8
Staphylococcus aureus	n	671	365	553	166	465	91	99	95	2,505
	%NS	16.7, 16.7	11.8, 11.8	4.7, 4.7	13.3, 13.3	6.5, 6.5	8.8, 8.8	4.0, 4.0	6.3, 6.3	10.0, 10.0
Methicillin-resistant *S. aureus*	n	137	64	83	34	95	10	44	9	476
	%NS/R	67.9, 67.9	56.2, 56.2	21.7, 21.7	55.9, 55.9	18.9, 18.9	60.0, 60.0	9.1, 9.1	n/a	41.6, 41.6
Methicillin-susceptible *S. aureus*	n	676	364	553	166	465	91	99	95	2,509
	%NS/R	3.6, 3.6	2.3, 2.3	1.7, 1.7	2.3, 2.3	3.2, 3.2	2.5, 2.5	0.0, 0.0	2.3, 2.3	2.6, 2.6
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%NS	5.9, 9.6	1.3, 10.7	0.0, 4.7	7.7, 11.5	0.0, 5.5	11.8, 11.8	n/a	0.0, 10.0	3.0, 8.5

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	n	1,170	794	858	288	770	174	141	158	4,353
	%NS	14.1, 20.3	12.6, 20.9	10.7, 15.6	6.6, 11.1	14.2, 19.9	4.6, 6.9	12.1, 18.4	11.4, 15.2	12.1, 18.0
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%NS	2.2, 4.4	0.0, 12.5	0.0, 0.0	n/a	0.0, 7.7	n/a	n/a	n/a	1.0, 5.8
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%NS	5.2, 6.9	0.0, 2.9	0.0, 2.8	0.0, 0.0	0.0, 2.3	0.0, 5.0	n/a	0.0, 0.0	1.3, 3.5
Klebsiella pneumoniae	n	267	197	246	55	152	22	30	27	996
	%NS	3.0, 10.5	10.2, 21.8	2.0, 7.7	1.8, 7.3	3.3, 7.9	0.0, 0.0	6.7, 6.7	11.1, 14.8	4.4, 11.2
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%NS	4.6, 10.8	5.3, 10.5	0.0, 0.0	4.5, 4.5	5.3, 7.9	0.0, 0.0	n/a	n/a	3.4, 6.8
Salmonella species (non-typhoidal)	n	19	12	28	4	39	2	21	4	129
	%R‡	0.0, –‡	8.3, –‡	14.3, –‡	n/a	2.6, –‡	n/a	0.0, –‡	n/a	4.7, –‡
Salmonella species (typhoidal)	n	5	6	7	1	4	0	1	1	25
	%NR‡	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	88.0, –‡
Pseudomonas aeruginosa	n	194	86	203	56	86	15	15	30	685
	%NS/R	4.1, 5.2	7.0, 15.1	5.5, 10.8	5.4, 14.3	3.5, 8.1	0.0, 0.0	6.7, 6.7	10.0, 20.0	5.1, 9.8
Clindamycin (inducible + constitutive resistance)										
Staphylococcus aureus	n	495	345	553	75	465	91	99	95	2,218
	%NS/%R	17.0, 17.0	15.4, 15.4	11.2, 11.2	20.0, 20.0	16.6, 16.6	13.2, 13.2	29.3, 29.3	10.5, 10.5	15.4, 15.4
Methicillin-resistant *S. aureus*	n	99	60	83	15	95	10	44	9	415
	%NS/%R	41.4, 41.4	36.7, 36.7	19.3, 19.3	60.0, 60.0	31.6, 31.6	60.0, 60.0	43.2, 43.2	n/a	34.9, 34.9
Methicillin-susceptible *S. aureus*	n	396	285	470	60	370	81	55	86	1,803
	%NS/%R	10.9, 10.9	10.9, 10.9	9.8, 9.8	10.0, 10.0	12.7, 12.7	7.4, 7.4	18.2, 18.2	9.3, 9.3	10.9, 10.9
Daptomycin										
Enterococcus faecalis	n	186	116	100	31	92	17	10	28	580
	%NS	1.1, –#	0.0, –#	0.0, –#	0.0, –#	0.0, –#	0.0, –#	0.0, –#	0.0, –#	0.3, –#
Staphylococcus aureus	n	679	365	553	167	466	91	99	95	2,515
	%NS	0.7, 0.7	0.3, 0.3	0.0, 0.0	0.0, 0.0	0.2, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.3
Methicillin-resistant *S. aureus*	n	139	64	83	34	95	10	44	9	478
	%NS	0.7, 0.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.1, 1.1	0.0, 0.0	0.0, 0.0	n/a	0.4, 0.4
Methicillin-susceptible *S. aureus*	n	540	300	470	133	371	81	55	86	2,037
	%NS	0.7, 0.7	0.3, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
Erythromycin										
Staphylococcus aureus	n	677	365	553	166	465	91	99	95	2,511
	%NS	20.7, 19.4	17.8, 16.4	14.1, 11.6	21.7, 21.1	17.4, 16.8	13.2, 11.0	30.3, 30.3	10.5, 7.4	18.0, 16.5
Methicillin-resistant	n	138	64	83	34	95	10	44	9	477

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
S. aureus	%NS	49.3, 49.3	43.7, 43.8	26.5, 26.5	61.8, 61.8	33.7, 32.6	60.0, 60.8	45.5, 45.5	n/a	41.7, 41.5
Methicillin-susceptible *S. aureus*	n	539	301	470	132	370	81	55	86	2,034
	%NS	13.4, 11.7	12.3, 10.6	11.9, 8.9	11.4, 10.6	13.2, 12.7	7.4, 4.9	18.2, 18.2	9.3, 5.8	12.4, 10.7
Fusidic acid										
Staphylococcus aureus	n	677	365	553	166	465	91	99	95	2,511
	%R	–[#], 3.4	–[#], 1.6	–[#], 6.3	–[#], 2.4	–[#], 1.3	–[#], 1.1	–[#], 6.1	–[#], 3.2	–[#], 3.3
Methicillin-resistant *S. aureus*	n	138	64	83	34	95	10	44	9	477
	%R	–[#], 3.6	–[#], 4.7	–[#], 6.0	–[#], 0.0	–[#], 2.1	–[#], 0.0	–[#], 9.1	n/a	–[#], 4.0
Methicillin-susceptible *S. aureus*	N	539	301	470	132	370	81	55	86	2,034
	%R	–[#], 3.3	–[#], 1.0	–[#], 6.4	–[#], 3.0	–[#], 1.1	–[#], 1.2	–[#], 3.6	–[#], 3.5	–[#], 3.2
Gentamicin										
Acinetobacter baumannii complex	n	8	12	18	6	8	2	8	1	63
	%R	n/a	0.0, 0.0	11.1, 11.1	n/a	n/a	n/a	n/a	n/a	6.3, 6.3
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%R	10.3, 10.3	4.0, 4.0	6.5, 6.5	7.7, 7.7	1.8, 3.6	11.8, 11.8	n/a	10.0, 10.0	6.9, 7.4
Escherichia coli	n	1,170	794	58	288	770	174	141	158	4,353
	%R	8.2, 8.3	9.6, 9.6	7.1, 7.5	5.2, 5.2	10.1, 10.1	3.4, 3.4	9.9, 9.9	12.7, 12.7	8.4, 8.5
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%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	58	35	36	22	44	20	2	12	229
	%R	0.0, 0.0	0.0, 0.0	2.8, 2.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
Klebsiella pneumoniae	n	267	197	246	55	152	22	30	27	996
	%R	4.9, 4.9	6.6, 9.1	2.4, 2.4	5.5, 5.5	3.9, 3.9	4.5, 4.5	0.0, 0.0	7.4, 7.4	4.4, 4.9
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%R	3.1, 4.6	7.9, 10.5	0.0, 0.0	4.5, 9.1	2.6, 2.6	0.0, 0.0	n/a	n/a	3.4, 4.7
Pseudomonas aeruginosa	n	194	87	203	56	86	15	15	30	686
	%R	2.1, 4.1	3.4, 4.6	1.0, 3.0	5.4, 5.4	2.3, 4.7	0.0, 0.0	0.0, 6.7	0.0, 3.3	2.0, 3.9
Staphylococcus aureus	n	677	365	553	166	465	91	99	95	2,511
	%R	5.2, 8.7	2.5, 3.0	1.8, 2.0	2.4, 2.4	0.9, 1.1	1.1, 1.1	7.1, 8.1	2.1, 3.2	2.9, 4.1
Methicillin-resistant *S. aureus*	n	138	64	83	34	95	10	44	9	477
	%R	22.5, 33.3	10.9, 14.1	9.6, 9.6	11.8, 11.8	3.2, 3.2	10.0, 10.0	13.6, 13.6	n/a	12.8, 16.6
Methicillin-susceptible *S. aureus*	n	539	301	470	132	370	81	55	86	2,034
	%R	0.7, 2.4	0.7, 0.7	0.4, 0.6	0.0, 0.0	0.3, 0.5	0.0, 0.0	1.8, 3.6	1.2, 1.2	0.5, 1.1
Linezolid										
Enterococcus faecalis	n	186	119	102	31	94	17	10	28	580
	%NS/R	0.0, 0.0	0.8, 0.0	2.9, 0.0	3.2, 0.0	2.1, 0.0	3.2, 0.0	0.0, 0.0	0.0, 0.0	1.3, 0.0

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Enterococcus faecium	n	167	134	45	28	63	17	5	22	481
	%NS/R	0.6, 0.0	2.2, 0.0	0.0, 0.0	3.6, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.0, 0.0
Staphylococcus aureus	n	679	365	553	167	466	91	99	95	2,515
	%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	139	64	83	34	95	10	44	9	478
	%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	n/a	0.0, 0.0
Methicillin-susceptible *S. aureus*	n	540	300	470	133	371	81	55	86	2,037
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Meropenem										
Acinetobacter baumannii complex	n	8	12	18	6	8	2	8	1	63
	%NS	n/a	0.0, 0.0	11.1, 11.1	n/a	n/a	n/a	n/a	n/a	4.8, 4.8
Enterobacter cloacae complex	n	136	75	106	26	54	17	7	10	431
	%NS	4.4, 4.4	0.0, 0.0	1.9, 1.9	0.0, 0.0	1.9, 1.9	0.0, 0.0	n/a	10.0, 10.0	2.3, 2.3
Escherichia coli	n	1,170	794	858	289	769	174	141	158	4,353
	%NS	0.3, 0.3	0.0, 0.0	0.1, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.6, 0.6	0.1, 0.1
Klebsiella (*Enterobacter*) *aerogenes*	n	44	24	10	3	13	3	1	5	103
	%NS	0.0, 0.0	4.2, 4.2	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	1.0, 1.0
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae	n	267	197	244	56	152	22	30	27	995
	%NS	1.5, 1.5	1.0, 1.0	0.8, 0.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.8, 0.8
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%NS	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	194	86	203	57	86	15	15	30	686
	%NS	10.8, 10.9	9.3, 9.3	4.9, 4.9	7.0, 7.0	8.1, 8.1	0.0, 0.0	13.3, 13.3	6.7, 6.7	7.9, 7.9
Mupirocin (high-level)										
Staphylococcus aureus	n	677	365	553	165	465	91	99	95	2,510
	%R	0.9, 0.9	0.3, 0.3	4.9, 4.9	0.0, 0.0	0.4, 0.4	2.2, 2.2	1.0, 1.0	1.1, 1.1	1.6, 1.6
Methicillin-resistant *S. aureus*	n	138	64	83	34	95	10	44	9	477
	%R	2.2, 2.2	0.0, 0.0	7.2, 7.2	0.0, 0.0	1.1, 1.1	0.0, 0.0	0.0, 0.0	n/a	2.1, 2.1
Methicillin-susceptible *S. aureus*	n	539	301	470	131	370	81	55	86	2,033
	%R	0.6, 0.6	0.3, 0.3	4.5, 4.5	0.0, 0.0	0.3, 0.3	2.5, 2.5	1.8, 1.8	1.2, 1.2	1.5, 1.5

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Nitrofurantoin										
Enterococcus faecalis	n	187	118	100	31	90	31	10	28	595
	%R	0.0, 0.0	0.8, 0.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
Enterococcus faecium	n	161	133	42	28	63	17	5	22	471
	%R	73.3, –[#]	24.1, –[#]	66.7, –[#]	42.9, –[#]	60.3, –[#]	23.5, –[#]	n/a	77.3, –[#]	53.1, –[#]
Enterobacter cloacae complex	n	126	75	107	26	55	17	7	10	423
	%R	11.1, –[#]	6.7, –[#]	5.6, –[#]	38.5, –[#]	9.1, –[#]	11.8, –[#]	n/a	10.0, –[#]	10.6, –[#]
Escherichia coli	n	1,170	794	858	288	770	174	141	158	4,353
	%R	0.6, 0.6	0.3, 0.3	1.2, 1.2	1.4, 1.4	1.3, 1.3	0.6, 0.6	0.7, 0.7	1.3, 1.3	0.8, 0.8
Klebsiella (*Enterobacter*) *aerogenes*	n	43	24	10	3	13	3	1	5	102
	%R	34.9, –[#]	41.7, –[#]	20.0, –[#]	n/a	38.5, –[#]	n/a	n/a	n/a	34.3, –[#]
Klebsiella oxytoca	n	53	35	36	22	44	20	2	12	224
	%R	0.0, –[#]	0.0, –[#]	8.3, –[#]	4.5, –[#]	0.0, –[#]	0.0, –[#]	n/a	0.0, –[#]	1.8, –[#]
Klebsiella pneumoniae	n	259	197	246	55	152	22	30	27	988
	%R	19.3, –[#]	23.9, –[#]	19.1, –[#]	34.5, –[#]	28.3, –[#]	13.6, –[#]	23.3, –[#]	44.4, –[#]	23.1, –[#]
Proteus mirabilis	n	63	38	47	22	38	11	5	0	224
	%R	82.5, –[#]	92.1, –[#]	87.2, –[#]	86.4, –[#]	81.6, –[#]	90.9, –[#]	n/a	n/a	86.2, –[#]
Salmonella species (non-typhoidal)	n	17	14	28	4	39	2	21	0	125
	%R	11.8, –[#]	14.3, –[#]	7.1, –[#]	n/a	12.8, –[#]	n/a	4.8, –[#]	n/a	9.6, –[#]
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	0	30
	%R	n/a	0.0, –[#]	n/a	n/a	n/a	n/a	n/a	n/a	3.3, –[#]
Oxacillin										
Staphylococcus aureus	n	677	365	552	166	464	90	99	95	2,508
	%R	19.5, 19.5	16.4, 16.4	14.7, 14.7	19.9, 19.9	19.4, 19.4	15.6, 15.6	42.4, 42.4	9.5, 9.5	18.4, 18.4
Piperacillin–tazobactam										
Acinetobacter baumannii complex	n	8	12	16	6	7	1	4	1	55
	%R	n/a	16.7, nd	25.0, nd	n/a	n/a	n/a	n/a	n/a	12.7, nd
Enterobacter cloacae complex	n	104	65	94	20	37	15	7	9	351
	%R	26.0, 31.7	43.1, 43.1	11.7, 20.2	5.0, 10.0	13.5, 18.9	20.0, 20.0	n/a	n/a	22.5, 27.6
Escherichia coli	n	1,170	790	855	288	770	173	141	158	4,345
	%R	3.2, 5.0	2.4, 7.8	3.5, 6.8	2.4, 4.4	2.7, 9.2	1.7, 4.8	0.7, 7.2	1.3, 3.3	2.8, 6.5
Klebsiella (*Enterobacter*) *aerogenes*	n	45	23	10	3	13	3	1	5	103
	%R	31.1, 40.0	47.8, 56.5	20.0, 20.0	n/a	30.8, 30.8	n/a	n/a	n/a	33.0, 42.7
Klebsiella oxytoca	n	58	35	36	22	44	19	2	12	228
	%R	13.8, 13.8	14.3, 14.3	2.8, 8.3	9.1, 9.1	4.5, 4.5	5.3, 5.3	n/a	25.0, 33.3	9.6, 11.0
Klebsiella pneumoniae	n	266	195	244	55	151	22	30	27	990
	%R	4.1,	3.6,	3.3,	3.6,	4.6,	0.0,	3.3,	3.7,	3.7, 7.3

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		7.5	8.2	6.1	9.1	7.3	4.5	3.3	11.1	
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%R	0.0, 1.5	0.0, 2.6	0.0, 0.0	0.0, 4.5	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 1.3
Pseudomonas aeruginosa	n	193	85	204	57	85	15	15	30	684
	%R	7.3, 14.0	8.2, 12.9	4.4, 9.8	14.0, 24.6	1.2, 9.4	0.0, 0.0	0.0, 13.3	16.7, 26.7	6.4, 13.2
Salmonella species (non-typhoidal)	n	19	13	28	4	39	2	21	4	130
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Rifampicin										
Staphylococcus aureus	n	677	365	553	166	465	44	99	95	2,464
	%NS	0.4, 0.6	1.4, 1.4	1.3, 1.3	0.6, 0.6	0.0, 0.0	0.0, 0.0	1.0, 1.0	0.0, 0.0	0.7, 0.7
Methicillin-resistant *S. aureus*	n	138	64	83	34	95	7	44	9	474
	%NS	0.7, 0.7	4.7, 4.7	3.6, 3.6	2.9, 2.9	0.0, 0.0	n/a	2.3, 2.3	n/a	1.9, 1.9
Methicillin-susceptible *S. aureus*	n	539	301	470	132	370	37	55	86	1,990
	%NS	0.2, 0.6	0.7, 0.7	0.6, 0.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.5
Teicoplanin										
Enterococcus faecalis	n	187	119	101	31	94	31	10	28	601
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Enterococcus faecium	n	167	134	45	28	63	17	5	22	481
	%NS/R	41.9, 45.5	16.4, 17.2	11.1, 13.3	17.9, 17.9	4.8, 4.8	5.9, 5.9	n/a	18.2, 27.3	22.9, 24.9
Staphylococcus aureus	n	677	365	553	166	465	91	99	95	2,511
	%NS/R	0.0, 0.1	0.0, 0.3	0.0, 0.2	0.0, 0.0	0.0, 0.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.2
Tetracycline										
Enterococcus faecalis	n	139	118	93	13	91	16	10	28	508
	%R	71.9, –[#]	77.1, –[#]	77.4, –[#]	61.5, –[#]	70.3, –[#]	93.8, –[#]	100, –[#]	89.3, –[#]	75.8, –[#]
Enterococcus faecium	n	124	133	41	13	63	10	5	22	411
	%R	35.5, –[#]	82.0, –[#]	85.4, –[#]	61.5, –[#]	73.0, –[#]	60.0, –[#]	n/a	68.2, –[#]	65.2, –[#]
Staphylococcus aureus	n	496	365	553	75	465	91	99	95	2,239
	%R	11.5, 11.7	4.4, 4.7	2.9, 2.9	6.7, 6.7	3.9, 3.9	3.3, 3.3	3.0, 3.0	3.2, 3.2	5.4, 5.5
Methicillin-resistant *S. aureus*	n	100	64	83	15	95	10	44	9	420
	%R	34.0, 34.0	14.1, 15.6	10.8, 10.8	20.0, 20.0	3.2, 3.2	10.0, 10.0	6.8, 6.8	n/a	15.0, 15.2
Methicillin-susceptible *S. aureus*	n	396	301	470	60	370	81	55	86	1,819
	%R	5.8, 6.1	2.3, 2.3	1.5, 1.5	3.3, 3.3	4.1, 4.1	2.5, 2.5	0.0, 0.0	2.3, 2.3	3.2, 3.2
Ticarcillin–clavulanic acid										
Acinetobacter baumannii complex	n	5	12	18	4	8	1	8	1	57
	%R	n/a	0.0,	11.1,	n/a	n/a	n/a	n/a	n/a	5.3, nd

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
			nd	nd						
Enterobacter cloacae complex	n	102	75	107	9	55	17	7	10	382
	%R	30.4, 31.4	40.0, 41.3	17.8, 24.3	n/a	14.5, 23.6	23.5, 23.5	n/a	30.0, 50.0	25.9, 30.4
Escherichia coli	n	815	794	858	168	770	174	141	158	3,878
	%R	11.8, 24.5	6.8, 15.1	9.4, 18.8	4.2, 10.7	9.2, 18.6	5.2, 14.9	7.8, 17.0	7.0, 13.9	8.8, 18.4
Klebsiella (*Enterobacter*) *aerogenes*	n	36	24	10	1	13	3	1	5	93
	%R	30.6, 41.7	45.8, 50.0	20.0, 20.0	n/a	23.1, 38.5	n/a	n/a	n/a	31.2, 43.0
Klebsiella oxytoca	n	40	35	36	13	44	20	2	12	202
	%R	10.0, 15.0	8.6, 14.3	5.6, 5.6	0.0, 0.0	4.5, 4.5	5.0, 10.0	n/a	25.0, 41.7	7.4, 10.9
Klebsiella pneumoniae	n	196	197	246	29	152	22	30	27	898
	%R	7.7, 9.7	7.1, 15.2	4.9, 8.9	13.8, 17.2	6.6, 9.2	4.5, 4.5	6.7, 13.3	7.4, 11.1	6.7, 10.9
Proteus mirabilis	n	44	38	47	10	38	11	5	9	202
	%R	0.0, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.5
Pseudomonas aeruginosa	n	155	85	203	24	86	15	15	30	613
	%R	13.5, 52.3	15.3, 57.6	14.3, 57.6	25.0, 75.0	10.5, 55.8	20.0, 60.0	13.3, 53.3	30.0, 56.7	15.0, 56.6
Salmonella species (non-typhoidal)	n	14	14	28	4	39	2	21	4	126
	%R	0.0, 0.0	0.0, 7.1	0.0, 3.6	n/a	0.0, 0.0	n/a	0.0, 4.8	n/a	0.0, 2.4
Salmonella species (typhoidal)	n	4	12	7	1	4	0	1	1	30
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Tobramycin										
Acinetobacter baumannii complex	n	8	12	18	6	8	2	8	1	63
	%R	n/a	0.0, 0.0	11.1, 11.1	n/a	n/a	n/a	n/a	n/a	6.3, 6.3
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%R	9.6, 11.0	4.0, 4.0	3.7, 5.6	7.7, 11.5	0.0, 3.6	11.8, 11.8	n/a	10.0, 10.0	5.8, 7.6
Escherichia coli	n	1,170	794	858	289	771	174	141	158	4,355
	%R	4.5, 9.4	3.7, 10.3	3.6, 8.4	2.4, 5.9	4.0, 11.3	2.3, 3.4	2.1, 11.3	2.5, 12.0	3.7, 9.4
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%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	58	35	36	22	44	20	2	12	229
	%R	0.0, 5.2	0.0, 0.0	0.0, 2.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 1.7
Klebsiella pneumoniae	n	267	197	246	56	152	22	30	27	997
	%R	3.4, 5.2	9.6, 14.2	1.6, 3.3	3.6, 5.4	2.6, 3.3	4.5, 4.5	6.7, 6.7	11.1, 11.1	4.4, 6.4
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%R	1.5, 4.6	5.3, 7.9	0.0, 0.0	0.0, 4.5	2.6, 2.6	0.0, 0.0	n/a	n/a	1.7, 3.8
Pseudomonas aeruginosa	n	195	87	204	57	86	15	15	30	689
	%R	1.5, 2.1	1.1, 2.3	0.5, 0.5	3.5, 3.5	2.3, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.3, 1.6

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Trimethoprim										
Enterobacter cloacae complex	n	135	75	107	26	55	17	7	10	432
	%R	21.5, 21.5	17.3, 17.3	22.4, 22.4	34.6, 34.6	18.2, 18.2	11.8, 11.8	n/a	20.0, 20.0	21.1, 21.1
Escherichia coli	n	1,170	794	858	288	771	173	141	158	4,353
	%R	33.6, 33.7	34.6, 34.6	34.8, 35.1	24.7, 25.0	35.1, 35.4	16.8, 16.8	46.1, 46.1	33.5, 33.5	33.4, 33.6
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%R	2.2, 4.4	8.3, 12.5	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	2.9, 4.8
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%R	6.9, 6.9	2.9, 2.9	5.6, 5.6	9.1, 9.1	4.5, 6.8	0.0, 0.0	n/a	8.3, 8.3	5.2, 5.7
Klebsiella pneumoniae	n	267	197	246	55	152	22	30	27	996
	%R	17.2, 18.0	25.4, 25.9	13.4, 14.6	12.7, 12.7	11.8, 13.2	9.1, 9.1	23.3, 23.3	25.9, 25.9	17.1, 17.9
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%R	20.0, 20.0	26.3, 28.9	12.8, 12.8	22.7, 22.7	13.2, 13.2	18.2, 18.2	n/a	n/a	19.1, 19.6
Salmonella species (non-typhoidal)	n	19	14	28	4	39	2	21	4	131
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	2.6, 2.6	n/a	0.0, 0.0	n/a	0.8, 0.8
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%R	n/a	8.3, 8.3	n/a	n/a	n/a	n/a	n/a	n/a	6.5, 6.5
Trimethoprim–sulfamethoxazole										
Acinetobacter baumannii complex	n	7	12	18	6	8	2	8	1	62
	%R	n/a	0.0, 0.0	11.1, 11.1	n/a	n/a	n/a	n/a	n/a	12.9, 11.3
Enterobacter cloacae complex	n	136	75	107	26	55	17	7	10	433
	%R	20.6, 20.6	16.0, 16.0	22.4, 22.4	30.8, 30.8	18.2, 16.4	11.8, 11.8	n/a	20.0, 20.0	20.1, 19.9
Escherichia coli	n	1,169	794	857	287	770	174	141	158	4,350
	%R	32.1, 32.1	32.2, 32.1	32.9, 32.7	22.3, 22.3	32.3, 32.3	14.4, 13.8	41.1, 41.1	31.6, 31.6	31.2, 31.1
Klebsiella (*Enterobacter*) *aerogenes*	n	45	24	10	3	13	3	1	5	104
	%R	0.0, 0.0	8.3, 8.3	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	n/a	1.9, 1.9
Klebsiella oxytoca	n	58	35	36	22	44	20	2	12	229
	%R	6.9, 6.9	2.9, 2.9	2.8, 2.8	0.0, 0.0	2.3, 2.3	0.0, 0.0	n/a	8.3, 8.3	3.5, 3.5
Klebsiella pneumoniae	n	267	197	246	54	152	22	30	27	998
	%R	16.1, 15.7	25.4, 23.9	13.0, 13.0	9.3, 9.3	10.5, 10.5	9.1, 9.1	23.3, 23.3	18.5, 18.5	16.1, 15.7
Proteus mirabilis	n	65	38	47	22	38	11	5	9	235
	%R	16.9, 16.9	18.4, 18.4	10.6, 10.6	18.2, 18.2	10.5, 10.5	18.2, 18.2	n/a	n/a	14.9, 14.9
Salmonella species (non-typhoidal)	n	119	14	28	4	39	2	21	4	131
	%R	0.0, 0.0	7.1, 0.0	0.0, 0.0	n/a	5.1, 2.6	n/a	0.0, 0.0	n/a	2.3, 0.8
Salmonella species (typhoidal)	n	5	12	7	1	4	0	1	1	31
	%R	n/a	8.3,	n/a	n/a	n/a	n/a	n/a	n/a	6.5, 6.5

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
			8.3							
Staphylococcus aureus	n	676	365	553	164	465	91	99	95	2,508
	%R	3.8, 3.7	3.6, 3.6	4.3, 4.0	4.9, 4.9	5.4, 4.7	1.1, 1.1	6.1, 3.0	2.1, 2.1	4.2, 3.8
Methicillin-resistant *S. aureus*	n	137	64	83	33	95	10	44	9	475
	%R	10.9, 10.9	12.5, 12.5	14.5, 13.3	18.2, 18.2	14.7, 13.7	10.0, 10.0	11.4, 6.8	n/a	12.8, 12.0
Methicillin-susceptible *S. aureus*	n	539	301	470	131	370	81	55	86	2,033
	%R	2.0, 1.9	1.7, 1.7	2.6, 2.3	1.5, 1.5	3.0, 2.4	0.0, 0.0	1.8, 0.0	2.3, 2.3	2.2, 1.9
Vancomycin										
Enterococcus faecalis	n	187	119	101	31	94	31	10	28	601
	%NS/R	0.0, 0.0	1.7, 1.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.3
Enterococcus faecium	n	167	134	45	28	63	17	5	22	481
	%NS/R	51.5, 51.5	64.2, 64.2	33.3, 33.3	57.1, 57.1	14.3, 14.3	29.4, 29.4	n/a	27.3, 27.3	47.0, 47.0
Staphylococcus aureus	n	677	365	553	166	465	91	99	95	2,511
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate; n/a = insufficient numbers (<10) to calculate; nd = no breakpoints defined; NR = susceptible plus intermediate (concentration range limitation); NS = sensitive dose dependent or intermediate plus resistant; R = resistant

* 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 guidelines for indicated species

** NS category for cefepime includes CLSI sensitive dose dependent for Enterobacterales.

‡ 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.

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–D13 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.

Acinetobacter baumannii complex is not included because there are few breakpoints to permit analysis.

Table D1: Multiple acquired resistance in *Citrobacter koseri,* by state and territory, 2017

State or territory	Total	Number of drug resistances (non-multi-drug resistant)					Number of drug resistances (multi-drug resistant)							
		0	1	2	3	%	4	5	6	7	8	9	10	%
NSW	11	11	0	0	0	–*	0	0	0	0	0	0	0	–*
Vic	6	6	0	0	0	–*	0	0	0	0	0	0	0	–*
Qld	11	9	2	0	0	–*	0	0	0	0	0	0	0	–*
SA	2	2	0	0	0	–*	0	0	0	0	0	0	0	–*
WA	9	8	1	0	0	–*	0	0	0	0	0	0	0	–*
Tas	2	2	0	0	0	–*	0	0	0	0	0	0	0	–*
NT	2	2	0	0	0	–*	0	0	0	0	0	0	0	–*
ACT	0	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Total	43	40	3	0	0	100.0	0	0	0	0	0	0	0	0.0

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Note: Antimicrobials were amoxicillin–clavulanic acid (CLSI), piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem.

Table D2: Multiple acquired resistance in *Citrobacter freundii* complex, by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)						
		0	1	2	3	%	4	5	6	7	8	9	%
NSW	9	6	2	0	1	–*	0	0	0	0	0	0	–*
Vic	18	9	2	3	2	–*	2	0	0	0	0	0	–*
Qld	4	2	1	0	1	–*	0	0	0	0	0	0	–*
SA	4	2	0	0	2	–*	0	0	0	0	0	0	–*
WA	10	4	2	0	1	–*	2	1	0	0	0	0	–*
Tas	4	2	1	0	0	–*	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	n/a	n/a
ACT	6	2	2	1	0	–*	0	0	0	0	1	0	–*
Total	55	27	10	4	7	87.3	5	1	0	0	1	0	12.7

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Notes: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem. *Citrobacter freundii* complex includes *Citrobacter braakii* (n = 5), *Citrobacter werkmani*i (n = 2) and *Citrobacter sedlakii* (n = 1).

Table D3: Multiple acquired resistance in *Enterococcus faecium* (vancomycin resistant) by state and territory, 2017

State or territory	Total	Number of drug resistances (non-multidrug resistant)				
		0	1	2	3	%
NSW	86	0	0	2	84	100
Vic	86	0	0	0	86	100
Qld	13	0	0	0	13	–*
SA	16	0	0	0	16	–*
WA	9	0	0	0	9	–*
Tas	4	0	0	0	4	–*
NT	3	0	0	0	3	–*
ACT	0	n/a	n/a	n/a	n/a	n/a
Total	217	0	0	2	215	100

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Notes: Antimicrobials were ampicillin, ciprofloxacin, and linezolid

Table D4: Multiple acquired resistance in *Enterococcus faecium* (vancomycin susceptible) by state and territory, 2017

State or territory	Total	Number of drug resistances (non-multidrug resistant)				
		0	1	2	3	%
NSW	79	16	5	58	0	100
Vic	47	8	3	36	0	100
Qld	27	2	2	23	0	–*
SA	12	4	0	8	0	–*
WA	54	12	1	41	0	100
Tas	6	0	0	6	0	–*
NT	2	1	0	1	0	–*
ACT	0	n/a	n/a	n/a	n/a	n/a
Total	227	43	11	173	0	100

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Notes: Antimicrobials were ampicillin, ciprofloxacin, and linezolid

Table D5: Multiple acquired resistance in *Klebsiella aerogenes*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)						
		0	1	2	3	%	4	5	6	7	8	9	%
NSW	44	20	4	1	16	93.2	3	0	0	0	0	0	6.8
Vic	23	9	3	0	7	–*	2	1	0	1	0	0	–*
Qld	10	8	0	0	2	–*	0	0	0	0	0	0	–*
SA	3	0	0	1	2	–*	0	0	0	0	0	0	–*
WA	13	8	1	0	4	–*	0	0	0	0	0	0	–*
Tas	3	0	0	0	3	–*	0	0	0	0	0	0	–*
NT	1	1	0	0	0	–*	0	0	0	0	0	0	–*
ACT	5	2	0	1	1	–*	1	0	0	0	0	0	–*
Total	102	48	8	3	35	92.2	6	1	0	1	0	0	7.8

* Not applicable (insufficient numbers)
Note: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem.

Table D6: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)							
		0	1	2	3	%	4	5	6	7	8	9	10	11	%
NSW	58	14	30	6	4	93.1	4	0	0	0	0	0	0	0	6.9
Vic	35	9	18	2	4	94.3	0	2	0	0	0	0	0	0	5.7
Qld	36	10	19	2	4	97.2	0	1	0	0	0	0	0	0	2.8
SA	22	8	9	3	1	–*	1	0	0	0	0	0	0	0	–*
WA	44	12	25	5	0	95.5	1	1	0	0	0	0	0	0	4.5
Tas	12	3	8	0	1	–*	0	0	0	0	0	0	0	0	–*
NT	2	1	1	0	0	–*	0	0	0	0	0	0	0	0	–*
ACT	12	2	5	1	2	–*	2	0	0	0	0	0	0	0	–*
Total	221	59	115	19	16	94.6	8	4	0	0	0	0	0	0	5.4

* Not applicable (insufficient numbers)
Note: Antimicrobials were amoxicillin–clavulanic acid (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem.

Table D7: Multiple acquired resistance in *Morganella morganii*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)						
		0	1	2	3	%	4	5	6	7	8	9	%
NSW	29	26	2	1	0	–*	0	0	0	0	0	0	–*
Vic	16	10	2	2	1	–*	0	1	0	0	0	0	–*
Qld	13	11	0	1	0	–*	1	0	0	0	0	0	–*
SA	1	1	0	0	0	–*	0	0	0	0	0	0	–*
WA	9	8	0	0	1	–*	0	0	0	0	0	0	–*
Tas	1	1	0	0	0	–*	0	0	0	0	0	0	–*
NT	4	2	1	0	1	–*	0	0	0	0	0	0	–*
ACT	5	4	0	0	0	–*	1	0	0	0	0	0	–*
Total	78	63	5	4	3	96.2	2	1	0	0	0	0	3.8

* Not applicable (insufficient numbers)
Note: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem.

Table D8: Multiple acquired resistance in *Proteus mirabilis*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)									
		0	1	2	3	%	4	5	6	7	8	9	10	11	12	%
NSW	65	30	20	6	4	92.3	2	1	1	1	0	0	0	0	0	7.7
Vic	38	20	9	1	2	84.2	3	1	0	0	0	2	0	0	0	15.8
Qld	47	36	6	4	1	100.0	0	0	0	0	0	0	0	0	0	0.0
SA	21	7	10	0	1	–*	1	1	1	0	0	0	0	0	0	–*
WA	38	23	7	2	4	94.7	1	0	0	0	0	1	0	0	0	5.3
Tas	8	5	2	0	0	–*	1	0	0	0	0	0	0	0	0	–*
NT	5	4	1	0	0	–*	0	0	0	0	0	0	0	0	0	–*
ACT	9	5	2	1	0	–*	0	1	0	0	0	0	0	0	0	–*
Total	231	130	57	14	12	92.2	8	4	2	1	0	3	0	0	0	7.8

* Not applicable (insufficient numbers)
Note: Antimicrobials were ampicillin, amoxicillin–clavulanic acid (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem.

Table D9: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)		
		0	1	2	3	%	4	5	%
NSW	193	150	19	15	7	99.0	2	0	1.0
Vic	85	65	10	5	1	95.3	2	2	4.7
Qld	203	165	21	9	5	98.5	2	1	1.5
SA	56	38	4	8	4	96.4	1	1	3.6
WA	85	72	4	3	3	96.5	3	0	3.5
Tas	15	15	0	0	0	–*	0	0	–*
NT	15	12	1	1	1	–*	0	0	–*
ACT	30	19	5	2	3	96.7	1	0	3.3
Total	682	536	64	43	24	97.8	11	4	2.2

* Not applicable (insufficient numbers)
Note: Antimicrobials were ceftazidime, ciprofloxacin, piperacillin–tazobactam, tobramycin and meropenem.

Table D10: Multiple acquired resistance in *Salmonella* species (non-typhoidal), by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)						
		0	1	2	3	%	4	5	6	7	8	9	%
NSW	18	16	2	0	0	–*	0	0	0	0	0	0	–*
Vic	11	9	1	1	0	–*	0	0	0	0	0	0	–*
Qld	28	22	5	0	0	–*	1	0	0	0	0	0	–*
SA	4	4	0	0	0	–*	0	0	0	0	0	0	–*
WA	39	34	4	1	0	100.0	0	0	0	0	0	0	0.0
Tas	2	2	0	0	0	–*	0	0	0	0	0	0	–*
NT	21	19	2	0	0	–*	0	0	0	0	0	0	–*
ACT	4	4	0	0	0	–*	0	0	0	0	0	0	–*
Total	127	110	14	2	0	99.2	1	0	0	0	0	0	0.8

* Not applicable (insufficient numbers)
Notes: Antimicrobials were ampicillin, amoxicillin–clavulanic acid (CLSI), piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, ciprofloxacin, trimethoprim and meropenem.

Table D11: Multiple acquired resistance in *Salmonella* species (typhoidal), by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)						
		0	1	2	3	%	4	5	6	7	8	9	%
NSW	4	1	2	0	1	–*	0	0	0	0	0	0	–*
Vic	6	0	6	0	0	–*	0	0	0	0	0	0	–*
Qld	7	2	5	0	0	–*	0	0	0	0	0	0	–*
SA	1	0	1	0	0	–*	0	0	0	0	0	0	–*
WA	4	0	4	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	0	1	0	0	–*	0	0	0	0	0	0	–*
ACT	1	0	1	0	0	–*	0	0	0	0	0	0	–*
Total	24	3	20	0	1	–*	0	0	0	0	0	0	–*

n/a = not applicable (no isolates)
* Not applicable (insufficient numbers)
Note: Antimicrobials were ampicillin, amoxicillin–clavulanic acid (CLSI), piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, ciprofloxacin, trimethoprim and meropenem.

Table D12: Multiple acquired resistance in *Serratia marcescens*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non- multi-drug resistant)					Number of drug resistances (multi-drug resistant)						
		0	1	2	3	%	4	5	6	7	8	9	%
NSW	42	38	2	1	1	100.0	0	0	0	0	0	0	0.0
Vic	22	19	1	1	1	–*	0	0	0	0	0	0	–*
Qld	38	36	1	1	0	100.0	0	0	0	0	0	0	0.0
SA	11	10	0	1	0	–*	0	0	0	0	0	0	–*
WA	1	1	0	0	0	–*	0	0	0	0	0	0	–*
Tas	6	6	0	0	0	–*	0	0	0	0	0	0	–*
NT	1	0	1	0	0	–*	0	0	0	0	0	0	–*
ACT	5	5	0	0	0	–*	0	0	0	0	0	0	–*
Total	126	115	5	4	2	100.0	0	0	0	0	0	0	0.0

* Not applicable (insufficient numbers)
Notes: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim and meropenem.

Table D13: Multiple acquired resistance in *Staphylococcus aureus*, by state and territory, 2017

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)										
		0	1	2	3	%	4	5	6	7	8	9	10	11	12	13	14	%
NSW	578	77	293	102	48	90.0	18	16	11	13	0	0	0	0	0	0	0	10.0
Vic	364	54	205	56	22	92.6	14	5	4	3	1	0	0	0	0	0	0	7.4
Qld	552	90	303	92	45	96.0	13	4	0	3	1	1	0	0	0	0	0	4.0
SA	163	20	92	22	12	89.6	10	3	1	3	0	0	0	0	0	0	0	10.4
WA	464	60	240	106	47	97.6	6	3	1	1	0	0	0	0	0	0	0	2.4
Tas	44	10	24	4	3	93.2	2	0	0	1	0	0	0	0	0	0	0	6.8
NT	99	7	40	22	24	93.9	2	1	1	2	0	0	0	0	0	0	0	6.1
ACT	95	23	50	16	3	96.8	2	0	1	0	0	0	0	0	0	0	0	3.2
Total	2,359	341	1,247	420	204	93.8	67	32	19	26	2	1	0	0	0	0	0	6.2

MDR = multi-drug resistant
Note: Antimicrobials were benzylpenicillin, ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin (CLSI), oxacillin, rifampicin, trimethoprim-sulfamethoxazole, tetracyclines (tetracycline, Vitek; doxycycline, Phoenix) and vancomycin.

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