AUSTRALIAN COMMISSION
ON SAFETY AND QUALITY IN HEALTH CARE

AURA
Antimicrobial Use and Resistance in Australia

AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Sepsis Outcome Programs

2015 report

AGAR

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

Level 5, 255 Elizabeth Street, Sydney NSW 2000
Phone: (02) 9126 3600
Fax: (02) 9126 3613

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

ISBN: 978-1-925224-75-7

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

Coombs G, Daley D, Gottlieb T, Turnidge JD, Bell JM. Australian Group on Antimicrobial Resistance: Sepsis Outcome Programs 2015 report. Sydney: ACSQHC; 2017.

Contents

Summary

As part of the Antimicrobial Use and Resistance in Australia (AURA) Surveillance System, the Australian Commission on Safety and Quality in Health Care (the Commission) funds the Australian Group on Antimicrobial Resistance (AGAR), a component of the Australian Society for Antimicrobials, to:

- Conduct targeted surveillance of selected pathogens
- Collect demographic, treatment and outcome data, and data on antimicrobial resistance rates
- Analyse and report on these data.

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. AGAR prepares a detailed annual report for each of these programs for publication on its website.

The AURA National Coordinating Unit (ANCU) is expanding the range of analyses of, and reports on, AURA Surveillance System data to provide greater access to surveillance data. This report brings together the key findings of the 2015 AGAR sepsis outcome programs.

In 2015, AGAR collected data on 10,739 episodes of bacteraemia across Australia. Where the place of onset was known, approximately three-quarters of episodes had their onset in the community.

Key findings from analysis of the 2015 AGAR data include the following:

- Of all vancomycin-resistant *Enterococcus faecium* bacteraemias nationally, 36% were caused by strains harbouring vanA genes; this type of vancomycin resistance has emerged very rapidly in the past five years, particularly in New South Wales, where it is now the dominant type
- The Commission will more closely examine the impact of these changes in resistance and the need for development of targeted resources to promote enhanced infection control practice
- There was no significant difference in 30-day all-cause mortality between infections caused by vancomycin-resistant and vancomycin-non-susceptible *E. faecium*
- During the decade to 2015, fluoroquinolone resistance rates in *Escherichia coli* increased from less than 1% to rates that are now consistent with those in some northern European countries; the overall rate in 2015 was 12.6%, and for community-onset *E. coli* bacteraemias, it was 11.6%
- The Commission will work with AGAR in undertaking further data anlyses of whether shared resistance with other antimicrobials (or so-called co-resistance) is contributing to this increased resistance. The health impact of increasing community rates of resistance will also be examined
- Of all *E. coli* bacteraemias, 83.6% have their onset in the community
- Carbapenemase-producing Enterobacteriaceae remains an uncommon form of resistance
- Overall, rates of methicillin-resistant *Staphylococcus aureus* (MRSA) do not appear to be increasing (18.2% in 2015); however, the rate of community-onset *S. aureus* bacteraemias that are methicillin resistant is increasing, and community-associated clones of MRSA are an increasing source of hospital-onset bacteraemia
- The Commission will update its technical paper on MRSA evolution in Australia to provide further information on this issue
- There is high use of broad-spectrum β-lactam agents – mainly ceftriaxone and piperacillin–tazobactam – in treatment of sepsis caused by gram-negative organisms. A proportion of this use appears to be unnecessary. Broad spectrum agents are associated with greater risks of adverse effects and the development of antimicrobial resistance. Ceftriaxone is a strong driver of *Clostridium difficile* diarrhoea, and can select

for extended-spectrum beta-lactamase (ESBL) producing organisms. Where narrower-spectrum agents are appropriate, changing to these agents is important.

Additional highlights from each of the surveys for 2015 are set out below.

Gram-negative species

- A total of 7,330 episodes of gram-negative bacteraemia were reported; Enterobacteriaceae accounted for 89.6%, followed by *Pseudomonas aeruginosa* (9.0%) and *Acinetobacter* species
- Of the Enterobacteriaceae, three genera – *Escherichia* (61.0%), *Klebsiella* (18.5%) and *Enterobacter* (7.4%) – contributed 86.9% of all isolates. The most frequent clinical manifestation was urinary tract infection. The overall 30-day mortality was 14.1% (10.7% in *E. coli*, 18.4% in *P. aeruginosa*)
- Of patients with bacteraemia caused by Enterobacteriaceae, 47.4% had a length of stay following bacteraemia less than 7 days; however, 16.3% of patients with *P. aeruginosa* bacteraemia had a length of stay more than 30 days
- Extended-spectrum β-lactamase (ESBL) phenotypes were found in 11.5% of *E. coli* and 7.7% of *Klebsiella pneumoniae* episodes; ESBL phenotypes were significantly more likely to be found among hospital- than community-onset episodes
- Most (85.5%) *E. coli* with an ESBL phenotype harboured genes of the CTX-M type; O25b-ST131 accounted for 74% of *E. coli* ESBL phenotypes that were ciprofloxacin resistant.

Enterococcus species

- A total of 1,014 episodes of enterococcal bacteraemia were reported; the majority (95.3%) of enterococcal bacteraemia episodes were caused by *E. faecalis* or *E. faecium*.
- The overall 30-day mortality was 20.2% (26.1% in *E. faecium*, 15.8% in *E. faecalis*). The most frequent clinical manifestation for *E. faecalis* was urinary tract infection; for *E. faecium*, it was biliary tract infection
- The length of stay following enterococcal bacteraemia was more than 30 days for 21.1% of patients
- Of bloodstream infections caused by *E. faecium*, 50.1% were vancomycin resistant; however, 54.2% of *E. faecium* harboured *vanA* or *vanB* genes. There were 56 *E. faecium* sequence types (STs) of which ST796, ST non-typable, ST555, ST80, ST203 and ST78 were the six most frequently identified; *vanA* genes were detected in five STs, and *vanB* genes in 13 STs.
- 30-day all-cause mortality was not higher for vancomycin-resistant (VRE) versus susceptible strains, suggesting that the current reserve agents used for treatment are effective. However vancomycin resistance prolongs hospital stay, increases the cost of treatment and the risk of acquiring other life-threatening infections during the hospitalisation. As recommended in *AURA 2017: Second Australian Report on antimicrobial use and resistance in human health*, further work on the prevention and control of VRE is to be undertaken.

Staphylococcus aureus

- Staphylococcal sepsis was predominantly a problem that arose in the community, with 70% of cases having their onset there
- A total of 2,398 *S. aureus* bacteraemia episodes were reported, of which 18.2% were methicillin resistant. Of the *S. aureus* bacteraemia episodes, 78% were community onset. There was no significant difference in mortality between community-onset and hospital-onset *S. aureus* bacteraemia.
- The overall 30-day mortality was 15.9% (18.9% in MRSA, 15.2% in methicillin-susceptible *S. aureus* [MSSA]); this is a smaller difference than has been observed in past surveys, due largely to the lower mortality observed with infection caused by community-associated clones, which are more prominent now. This compares favourably with data published previously in Australia and overseas.

- The slightly higher mortality from MRSA sepsis and the predominance of community-onset staphylococcal sepsis highlight the need for raising awareness among clinicians of the risk of resistance and local patterns of disease
- Skin and soft tissue infections were the most common principal clinical manifestation. The length of stay was more than 30 days in 27.6% of patients. Four healthcare-associated clones were identified; 1.4% of healthcare-associated isolates harboured Panton-Valentine leucocidin (PVL)-associated genes.

AGAR data support informed clinical decisions regarding antimicrobial therapy and stewardship programs, and improvements to care of patients with sepsis. The data also inform interventions to prevent and control the spread of resistant organisms.

The Commission's ANCU, AGAR and other relevant experts collaborate on the identification of strategic priorities for surveillance and analysis of antimicrobial resistance.

The AURA Surveillance System and the ANCU support the achievement of the objectives of Australia's first National Antimicrobial Resistance Strategy.[1] The Commission will continue to collaborate with the Australian Society for Antimicrobials to enhance and maintain AGAR as a core element of the AURA Surveillance System, and a key source of data on the emergence of, and trends in, antimicrobial resistance in the human health setting.

1 Background and objectives

The Australian Group on Antimicrobial Resistance (AGAR) is a unique 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 29 laboratories servicing 33 hospitals located 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 methodology, AGAR has collected ongoing data on what is happening in Australia over long periods of time. 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.

1.1 Gram-negative Sepsis Outcome Program

AGAR began surveillance of the key gram-negative pathogens *E. coli* and *Klebsiella* species in 1992. Surveys were conducted every two years until 2008, when annual surveys commenced, alternating between community-onset and hospital-onset infections.* In 2004, another genus of gram-negative pathogens in which resistance can be of clinical importance – *Enterobacter* – was added. *E. coli* is the most common cause of community-onset urinary tract infection, whereas *Klebsiella* species are less common but are known to harbour important resistances. *Enterobacter* species are less common in the community, but of high importance because of their intrinsic resistance to first-line antimicrobials in the community. Taken together, the three groups of species surveyed are considered to be valuable sentinels for multi-drug resistance and emerging resistance in enteric gram-negative bacilli. In 2013, AGAR began the ongoing Enterobacteriaceae Sepsis Outcome Program (EnSOP), which focused on the prospective collection of resistance and demographic data on all isolates from patients with documented bacteraemia. The 2014 survey was the second EnSOP survey. In 2015, *Pseudomonas aeruginosa* and *Acinetobacter* species were added, and the program changed its name to the Gram-negative Sepsis Outcome Program.

Resistances of particular interest include resistance to β-lactams due to β-lactamases, especially extended-spectrum β-lactamases, 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 resistance to reserve agents such as ciprofloxacin and meropenem.

The objectives of the 2015 surveillance program were to:

- Monitor resistance in Enterobacteriaceae, *P. aeruginosa* and *Acinetobacter* species isolated from blood cultures taken from patients presenting to the hospital or already in hospital

* www.agargroup.org/surveys

Table 1: Hospitals that contributed to AGAR, by state and territory, 2015

State or territory	Hospital	
New South Wales	Concord Repatriation General Hospital	Royal Prince Alfred Hospital
	John Hunter Hospital	Westmead Hospital
	Nepean Hospital	Wollongong Hospital
	Royal North Shore Hospital	
Victoria	Alfred Hospital	Royal Women's and Children's Hospital
	Austin Hospital (Austin Health)	St Vincent's Hospital
	Monash Medical Centre (Monash Health)	
Queensland	Cairns Base Hospital	Princess Alexandra Hospital*
	Gold Coast Hospital	Royal Brisbane and Women's Hospital
	Prince Charles Hospital*	Greenslopes Private Hospital†
South Australia	Flinders Medical Centre	Women's and Children's Hospital§
	Royal Adelaide Hospital	
Western Australia	Fiona Stanley Hospital	St John of God Murdoch Hospital
	Joondalup Hospital	Kimberley regional hospitals (Broome, Kununurra, Derby)
	Royal Perth Hospital#	
	Sir Charles Gairdner Hospital	
Tasmania	Royal Hobart Hospital	
Northern Territory	Alice Springs Hospital	Royal Darwin Hospital
Australian Capital Territory	Canberra Hospital	

* Microbiology services provided by Pathology Queensland, Royal Brisbane and Women's Hospital
† 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

- Examine the extent of co-resistance and multi-drug resistance in the major species
- Detect emerging resistance to newer last-line agents such as carbapenems
- Characterise the molecular basis of resistance to third-generation cephalosporins, quinolones and carbapenem
- Monitor the epidemiology of *E. coli* sequence type 131.

1.2 Australian Enterococcal Sepsis Outcome Program

Globally, enterococci are thought to account for approximately 10% of all bacteraemias. In North America and Europe, they are the fourth and fifth leading cause of sepsis, respectively.[2,3] In the 1970s, healthcare-associated enterococcal infections were primarily due to *Enterococcus faecalis*; however, there has been a steadily increasing prevalence of healthcare-associated *E. faecium* infections.[4-6] Worldwide, the increase in healthcare-associated *E. faecium* infections has primarily been due to the expansion of polyclonal hospital-adapted clonal complex (CC) 17 strains. Innately resistant to many classes of antibiotics, *E. faecium* has also 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 pathogens (*E. faecium*, *S. aureus*,

Klebsiella pneumoniae, *Acinetobacter baumannii*, *P. aeruginosa* and *Enterobacter* species) requiring new therapies.[7]

AGAR began surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[8] In 2011, it began the Australian Enterococcal Sepsis Outcome Program.[9] The objective of the program in 2015 was to determine the proportion of *E. faecalis* and *E. faecium* bacteraemia isolates demonstrating antimicrobial resistance, with particular emphasis on:

- Monitoring resistance to ampicillin, glycopeptides and other anti-enterococcal agents
- Examining 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 bloodstream infections.[10] Although serious invasive infection caused by *S. aureus* has a wide variety of manifestations, the organism can be detected in blood cultures in the great majority of cases. Therefore, *S. aureus* bacteraemia (SAB) is considered a very useful marker for serious invasive infection.[11]

Although prolonged antimicrobial therapy and prompt source control are used to treat SAB[12], mortality ranges from 2.5% to 40%.[13-15] Mortality rates are known to vary significantly with patient age, clinical manifestation, comorbidities and methicillin resistance.[16,17] A prospective study of SAB, conducted by 27 laboratories in Australia and New Zealand, found a 30-day all-cause mortality of 20.6%.[18] 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.

AGAR began surveillance of antimicrobial resistance in *S. aureus* in 1986.[19] In 2013, it began the Australian Staphylococcal Sepsis Outcome Program.[9]

The primary objective of the program in 2015 was to determine the proportion of SAB isolates demonstrating antimicrobial resistance, with particular emphasis on:

- Monitoring resistance to methicillin and other important anti-staphylococcal agents
- Examining molecular epidemiology of methicillin-resistant *S. aureus* (MRSA).

2 Summary of methods

Thirty-three hospitals from each state and territory of Australia were enrolled in the 2015 survey. The 29 AGAR laboratories collected either all isolates or up to 200 isolates of Enterobacteriaceae, *Acinetobacter* species and *P. aeruginosa*, and all isolates of *S. aureus* and *Enterococcus* species, from unique patient episodes of bacteraemia from 1 January to 31 December 2015. Approval to conduct the prospective collection 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.

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 – MICs) for each species. The patient's date of birth, gender and postcode of residence were also provided; if they were admitted, the date of admission and date of 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 30 days (including whether the patient died within 30 days), the date of death, and definitive antimicrobial treatment (see Appendix A).

2.2 Species identification

Isolates were identified to species level, where possible, using the routine method for each institution. This included the Vitek® and Phoenix™ automated microbiology systems and, where available, mass spectrometry (MALDI-TOF).

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

2.3 Susceptibility testing

Susceptibility testing of isolates is described in Appendix B. The analysis used breakpoints from the Clinical and Laboratory Standards Institute (CLSI) M100-A26[20] and European Committee on Antimicrobial Susceptibility Testing (EUCAST) v6.0.[21]

2.4 Statistical analysis

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

* www.graphpad.com

3 Results

3.1 Isolates recovered

A total of 7,330 gram-negative isolates (60 species, 21 genera) were reported from 33 participating hospitals. Enterobacteriaceae accounted for 89.6%, followed by *P. aeruginosa* (9.0%) and *Acinetobacter* species (1.4%). Of the Enterobacteriaceae, three genera – *Escherichia* (61.0%), *Klebsiella* (18.5%) and *Enterobacter* (7.4%) – contributed 86.9% of all isolates. The top 10 species by rank were *E. coli* (54.7%), *K. pneumoniae* (13.3%), *P. aeruginosa* (9.0%), *E. cloacae* complex (4.4%), *K. oxytoca* (3.2%), *Proteus mirabilis* (3.0%), *Serratia marcescens* (2.6%), *Enterobacter aerogenes* (1.8%), *Salmonella* species (non-typhoidal) (1.6%) and *Morganella morganii* (1.1%). These 10 species comprised 94.7% of all isolates (Table 2).

Of 2,398 SAB episodes, 435 (18.1%; 95% confidence interval [CI] 16.6–19.7) were methicillin resistant, ranging from 5.9% (95%CI 1.6–15.9) in Tasmania to 38.2% (95%CI 29.6–47.5) in the Northern Territory (Table 2).

There were 1,011 episodes of enterococcal bacteraemias. *E. faecalis* and *E. faecium* accounted for 95.4% of all enterococcal isolates (Table 2).

Table 2: Number of each species recovered, by state and territory, 2015

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Gram-negative species*	1,995	1,293	1,402	777	1,176	142	265	280	7,330
Escherichia coli	1,113	729	691	454	653	79	138	149	4,006
Klebsiella pneumoniae	237	177	189	87	187	18	47	35	977
Pseudomonas aeruginosa	167	74	166	85	107	4	19	36	658
Enterobacter cloacae complex	85	80	65	13	50	14	9	10	326
Klebsiella oxytoca	76	49	45	13	30	8	4	13	238
Proteus mirabilis	66	37	45	24	36	3	6	6	223
Serratia marcescens	67	28	52	9	19	3	3	8	189
Enterobacter aerogenes	34	27	26	11	25	1	3	4	131
Salmonella species (non-typhoidal)	19	21	28	10	10	2	24	1	115
Morganella morganii	26	9	25	7	7	1	0	4	79
Acinetobacter baumannii complex	10	10	20	1	11	2	5	0	59
Citrobacter koseri	21	5	6	10	11	0	1	1	55
Citrobacter freundii	20	9	5	4	2	1	0	4	45
Salmonella species (typhoidal)	5	7	6	5	2	0	0	1	26
Acinetobacter species	3	2	3	5	3	0	4	0	20
Pantoea agglomerans	1	3	4	1	3	0	0	1	13

continued

Table 2: (continued)

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Gram-negative species* (continued)									
Enterobacter species	0	0	0	12	0	0	0	0	12
Raoultella ornithinolytica	6	1	1	0	2	0	0	2	12
Providencia rettgeri	3	0	3	2	2	1	0	0	11
Proteus vulgaris	3	1	0	3	3	0	0	1	11
Other species (*n* = 40)	33	24	22	21	13	5	2	4	124
Enterococcus species	287	237	131	108	152	20	18	58	1,011
Enterococcus faecalis	150	110	96	58	91	12	10	35	562
Percentage vancomycin resistant	1.3	0.9	0	0	0	8.3	0	0	4
Enterococcus faecium	116	120	31	44	53	8	8	22	402
Percentage vancomycin resistant	51.7	63.3	61.3	52.3	11.3	–†	–†	50.0	50.2
Percentage vancomycin susceptible	48.3	36.7	38.7	47.7	88.7	–†	–†	50.0	49.8
Other enterococcal species	21	7	4	6	8	0	0	1	47
Enterococcus casseliflavus	12	2	0	1	1	0	0	0	16
Enterococcus avium	1	2	0	3	4	0	0	1	11
Enterococcus raffinosus	1	2	2	2	0	0	0	0	7
Enterococcus gallinarum	4	0	0	0	3	0	0	0	7
Enterococcus hirae	1	1	2	0	0	0	0	0	4
Enterococcus durans	1	0	0	0	0	0	0	0	1
Enterococcus gilvus	1	0	0	0	0	0	0	0	1
Staphylococcus aureus	590	407	503	262	394	51	110	81	2,398
Percentage methicillin resistant	22.9	15.5	13.5	16.4	17.5	5.9	38.2	14.8	18.1
Percentage methicillin susceptible	77.1	84.5	86.5	83.6	82.5	94.1	61.8	85.2	81.9

* Enterobacteriaceae, *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, 97.0%; *Enterococcus* spp., 98.3%; *S. aureus*, 96.5%). An episode was designated as hospital onset if the first positive blood culture was collected more than 48 hours after admission. If the patient was not admitted, or the first positive blood culture was collected within 48 hours of admission, the episode was designated as community onset.

Information on place of onset of bacteraemia was available for 6,928 (94.5%) gram-negative episodes, 1,008 (99.7%) *Enterococcus* species episodes and 2,397 *S. aureus* episodes (Table 3). For gram-negative species, 74.8% 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

Table 3: Number and percentage of each species recovered, by place of onset, 2015

Organism	Community onset (%)	Hospital onset (%)	Total
Gram-negative species*	5,204 (75.1)	1,724 (24.9)	6,928
Escherichia coli	3,148 (83.6)	617 (16.4)	3,765
Klebsiella pneumoniae	658 (70.4)	276 (29.6)	934
Pseudomonas aeruginosa	362 (57.6)	266 (42.4)	628
Enterobacter cloacae complex	161 (50.9)	155 (49.1)	316
Klebsiella oxytoca	156 (69.6)	68 (30.4)	224
Proteus mirabilis	169 (80.1)	42 (19.9)	211
Serratia marcescens	86 (48.9)	90 (51.1)	176
Enterobacter aerogenes	66 (55.0)	54 (45.0)	120
Salmonella species (non-typhoidal)	97 (87.4)	14 (12.6)	111
Morganella morganii	50 (64.1)	28 (35.9)	78
Acinetobacter baumannii complex	29 (53.7)	25 (46.3)	54
Citrobacter koseri	37 (69.8)	16 (30.2)	53
Citrobacter freundii	32 (72.7)	12 (27.3)	44
Salmonella species (typhoidal)	25 (100)	0 (0.0)	25
Acinetobacter species	13 (72.2)	5 (27.8)	18
Pantoea agglomerans	9 (69.2)	4 (30.8)	13
Enterobacter species	7 (58.3)	5 (41.7)	12
Raoultella ornithinolytica	7 (63.6)	4 (36.4)	11
Providencia rettgeri	10 (90.9)	1 (9.1)	11
Proteus vulgaris	9 (90.0)	1 (10.0)	10
Other gram-negative species (*n* = 40)	73 (64.0)	41 (36.0)	114
Enterococcus species	514 (51.0)	494 (49.0)	1,008
Enterococcus faecalis†	365 (65.3)	194 (34.7)	559
Vancomycin resistant	1§	3§	4
Vancomycin susceptible	363 (65.5)	191 (34.7)	554
Enterococcus faecium	112 (27.9)	290 (72.1)	402
Vancomycin resistant	39 (19.3)	163 (80.7)	202
Vancomycin susceptible	73 (36.5)	127 (63.5)	200
Other *Enterococcus* species (*n* = 7)	37 (78.7)	10 (21.3)	47
Staphylococcus aureus	1,855 (77.4)	542 (22.6)	2,397
Methicillin resistant	313 (72.0)	122 (28.0)	435
Methicillin susceptible	1,542 (78.6)	420 (21.4)	1,962

* Enterobacteriaceae, *Acinetobacter* species and *Pseudomonas aeruginosa*

† One strain was not able to be classified as vancomycin resistant or susceptible.

§ Insufficient numbers (<10) to calculate percentage

(65.3%, 95%CI 61.3–69.1 for *E. faecalis*; and 78.7%, 95%CI 65.1–88.0 for other *Enterococcus* species); however, *E. faecium* episodes were predominantly hospital onset (72.1%; 95%CI 67.6–76.3). The majority of SABs were community onset (77.4%; 95%CI 75.7–79.0).

3.3 Onset versus 30-day all-cause mortality

Information on 30-day all-cause mortality, where place of onset was known, was available for 4,586 (62.6%) episodes involving gram-negative species, 888 (87.8%) involving *Enterococcus* species and 1,986 (82.8%) 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*, *Proteus mirabilis*, *Salmonella* species (non-typhoidal) and *Acinetobacter baumannii* complex (Table 4).

There was a significant difference in the 30-day all-cause mortality between *E. faecium* (26.9%) and *E. faecalis* (15.7%) episodes ($P = 0.0001$). However, there was no significant difference in mortality between vancomycin-resistant and vancomycin-non-susceptible *E. faecium* episodes.

For *S. aureus*, there was no significant difference in mortality between methicillin-susceptible *S. aureus* (MSSA) (15.3%) and MRSA (19.1%) episodes, or between healthcare-associated MRSA (HA-MRSA) and community-associated MRSA (CA-MRSA) clones.

Table 4: Number and percentage of the top 16 species, by place of onset and 30-day all-cause mortality, 2015

	Community onset		Hospital onset		Total		
Organism	**Number**	**Deaths (%)**	**Number**	**Deaths (%)**	**Number**	**Deaths (%)**	**Significance**
Gram-negative species*	3,389	358 (10.6)	1,197	224 (18.7)	4,586	647 (14.1)	
Escherichia coli	2,009	169 (8.4)	422	90 (21.3)	2,431	259 (10.7)	$P < 0.01$
Klebsiella pneumoniae	452	57 (12.6)	195	30 (15.4)	647	87 (13.4)	ns
Pseudomonas aeruginosa	229	42 (18.3)	184	34 (18.5)	413	76 (18.4)	ns
Enterobacter cloacae complex	112	16 (14.3)	117	15 (12.8)	229	31 (13.5)	ns
Klebsiella oxytoca	111	9 (8.1)	44	6 (13.6)	155	15 (9.7)	ns
Proteus mirabilis	111	21 (18.9)	26	10 (38.5)	137	31 (22.6)	$0.01 < P < 0.05$
Serratia marcescens	60	7 (11.7)	71	14 (19.7)	131	21 (16.0)	ns
Enterobacter aerogenes	42	4 (9.5)	38	7 (18.4)	80	11 (13.8)	ns
Salmonella species (non-typhoidal)	61	2 (3.3)	12	3 (25.0)	73	5 (6.8)	$0.01 < P < 0.05$
Morganella morganii	35	5 (14.3)	17	5 (29.4)	52	10 (19.2)	ns

continued

Table 4: (continued)

Organism	Community onset Number	Community onset Deaths (%)	Hospital onset Number	Hospital onset Deaths (%)	Total Number	Total Deaths (%)	Significance
Gram-negative species* (continued)							
Citrobacter koseri	28	2 (7.1)	14	3 (21.4)	42	5 (11.9)	ns
Acinetobacter baumannii complex	21	6 (28.6)	16	0 (0.0)	37	6 (16.2)	0.01 < *P* < 0.05
Citrobacter freundii	24	6 (25.0)	7	3†	31	9 (29.0)	ns
Salmonella species (typhoidal)	13	0 (0.0)	0	0†	13	0 (0.0)	ns
Other gram-negative species (*n* = 53)	81	12 (14.8)	34	4 (11.8)	115	81 (70.4)	
Enterococcus species	437	78 (17.8)	451	104 (23.1)	888	182 (20.5)	
Enterococcus faecalis	311	50 (16.1)	166	25 (15.1)	477	75 (15.7)	ns
Enterococcus faecium	97	24 (24.7)	275	76 (27.6)	372	100 (26.9)	ns
Vancomycin resistant	36	11 (30.6)	154	45 (29.2)	190	56 (29.5)	ns
Vancomycin susceptible	61	13 (21.3)	121	31 (25.6)	182	44 (24.2)	ns
Other enterococcal species (*n* = 7)	29	4 (13.8)	10	3 (30.0)	39	7 (17.9)	ns
Staphylococcus aureus	1,511	242 (16.0)	475	75 (15.8)	1,986	317 (16.0)	
Methicillin resistant	247	48 (19.4)	109	20 (18.3)	356	68 (19.1)	ns
CA-MRSA	162	28 (17.3)	56	10 (17.9)	218	38 (17.4)	ns
HA-MRSA	81	20 (24.7)	49	10 (20.4)	130	30 (23.1)	ns
Methicillin susceptible	1,264	194 (15.3)	366	55 (15.0)	1,630	249 (15.3)	ns

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

* Enterobacteriaceae, *Acinetobacter* species and *Pseudomonas aeruginosa*

† Insufficient numbers (<10) to calculate percentage

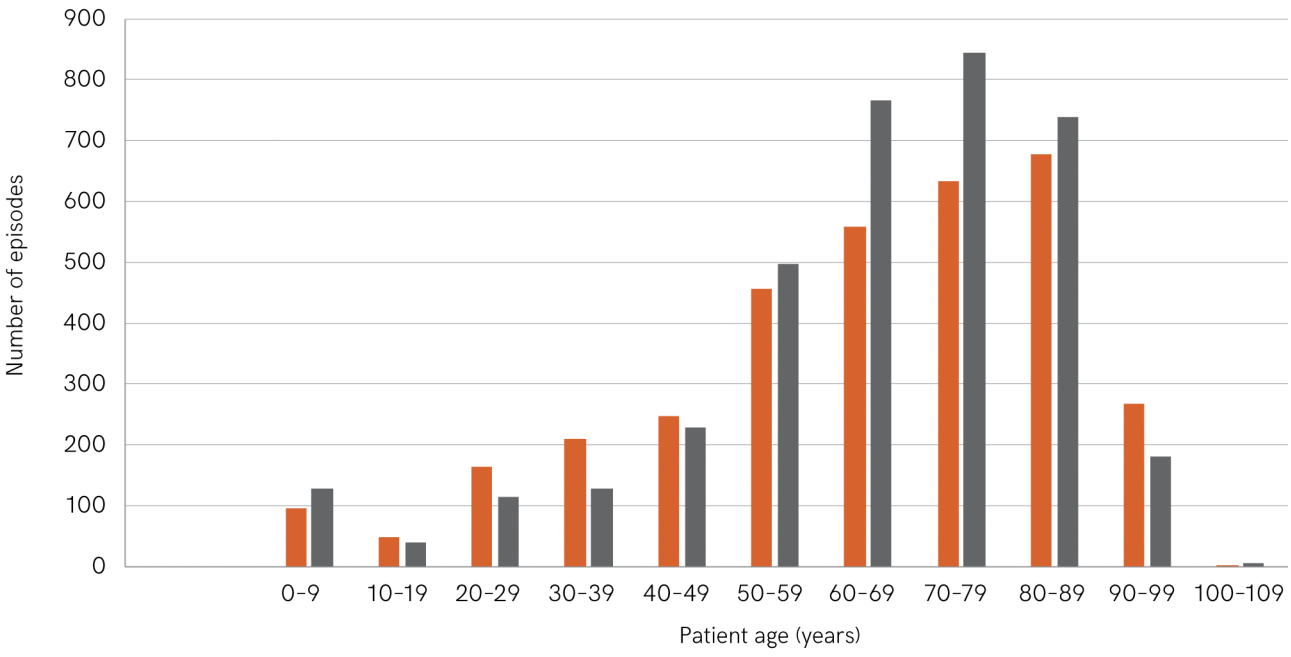
Note: Eight MRSA isolates were not available for typing and therefore could not be characterised as CA-MRSA or HA-MRSA strains.

4 Patient age and gender

Age and gender were available for all patients with enterococcal or staphylococcal bacteraemia and 96.0% of patients with gram-negative bacteraemia. For *Enterococcus* species and *S. aureus*, the majority of episodes were in male patients: 65.6% and 65.0%, respectively. For gram-negative species, the proportion of males was 52.2%.

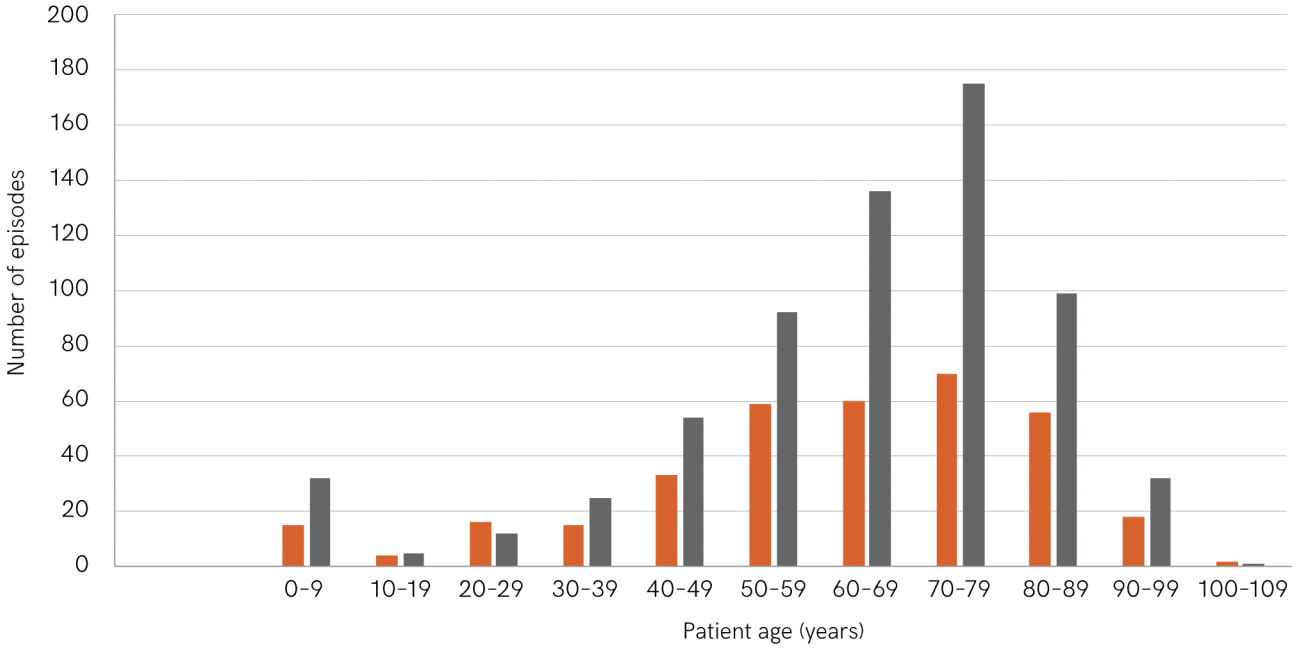
Increasing age was a surrogate risk factor for bacteraemia (Figures 1–3); only 8.4% of gram-negative species episodes, 8.3% of *Enterococcus* species episodes and 14.1% of *S. aureus* episodes were in patients less than 40 years.

Figure 1: Number of episodes of bacteraemia due to gram-negative species, by patient decade of life and gender, 2015



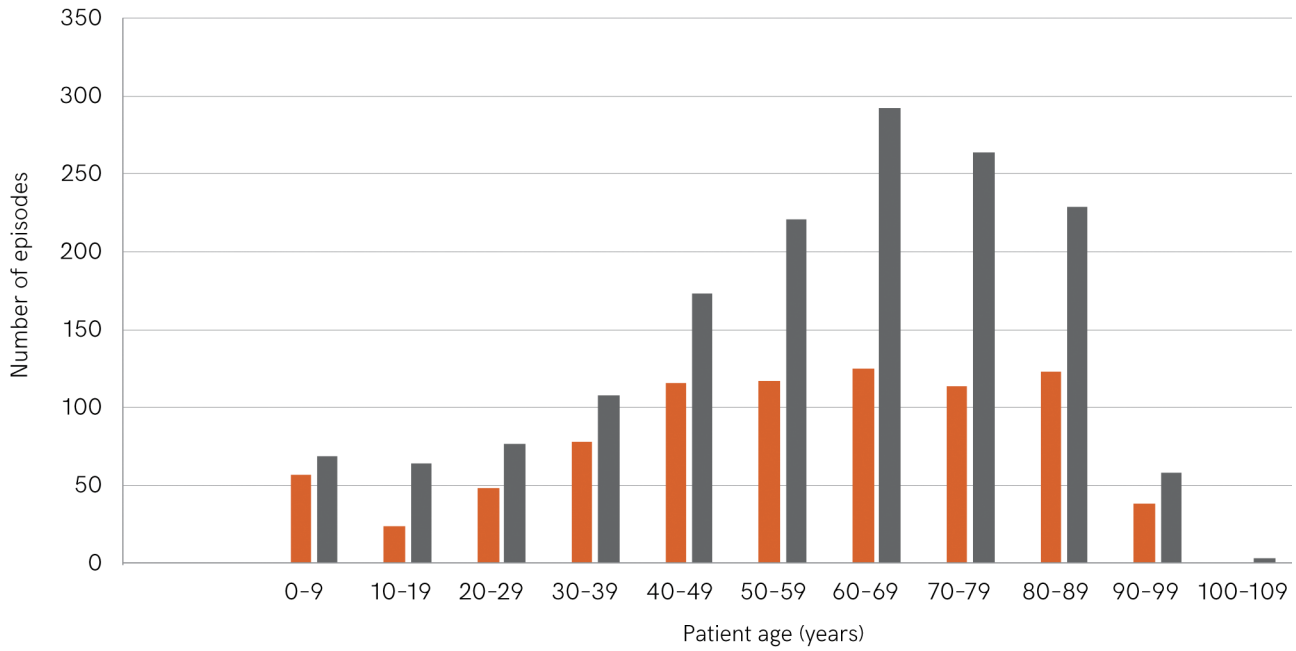
	0-9	10-19	20-29	30-39	40-49	50-59	60-69	70-79	80-89	90-99	100-109
Female (*n* = 3,364)	96	49	164	210	248	457	558	634	678	267	3
Male (*n* = 3,673)	128	39	115	128	229	498	766	844	739	181	6

Figure 2: Number of episodes of bacteraemia due to *Enterococcus* species, by patient decade of life and gender, 2015



	0-9	10-19	20-29	30-39	40-49	50-59	60-69	70-79	80-89	90-99	100-109
Female (*n* = 348)	15	4	16	15	33	59	60	70	56	18	2
Male (*n* = 663)	32	5	12	25	54	92	136	175	99	32	1

Figure 3: Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient decade of life and gender, 2015



	0-9	10-19	20-29	30-39	40-49	50-59	60-69	70-79	80-89	90-99	100-109
Female (*n* = 840)	57	24	48	78	116	117	125	114	123	38	0
Male (*n* = 1,558)	69	64	77	108	173	221	292	264	229	58	3

4.1 Principal clinical manifestation

4.1.1 Gram-negative bacteria

The principal clinical manifestation was documented for 5,085 (69.4%) patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations were urinary tract infection (43.2%), biliary tract infection (15.9%) and other intra-abdominal infection (10.5%) (Table 5).

4.1.2 *Enterococcus* species

For enterococcal bacteraemia, the principal clinical manifestation was known for 949 (93.9%) patient episodes. Overall, the most frequent principal clinical manifestations were biliary tract infection (17.0%), urinary tract infection (16.5%) and other intra-abdominal infection (14.2%) (Table 6).

Of the hospital-onset episodes where data were available, the most frequent principal clinical manifestation was intra-abdominal infection (19.9%). Of the community-onset episodes where data were available, the most frequent principal clinical manifestation was urinary tract infection (24.8%).

The principal manifestation was known for 904 of 972 (93.0%) of the *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 biliary tract infection. Significant differences were seen between *E. faecalis* and *E. faecium* for a number of clinical manifestations.

Table 5: Principal clinical manifestation for gram-negative* bacteraemia, by patient gender, 2015

Principal clinical manifestation	Female (%)	Male (%)	Total (%)	Significance
Urinary tract infection	1,215 (50.7)	981 (36.5)	2,196 (43.2)	$P < 0.01$
Biliary tract infection (including cholangitis)	299 (12.5)	509 (18.9)	808 (15.9)	$P < 0.01$
Intra-abdominal infection other than biliary tract	254 (10.6)	279 (10.4)	533 (10.5)	ns
Other clinical syndrome	138 (5.8)	218 (8.1)	356 (7.0)	$P < 0.01$
Febrile neutropenia	140 (5.8)	200 (7.4)	340 (6.7)	$0.01 < P < 0.05$
No focus	158 (6.6)	176 (6.5)	334 (6.6)	ns
Device-related infection without metastatic focus	78 (3.3)	122 (4.5)	200 (3.9)	$0.01 < P < 0.05$
Skin and skin structure infection	45 (1.9)	100 (3.7)	145 (2.9)	$P < 0.01$
No focus (e.g. in febrile neutropenia)	36 (1.5)	49 (1.8)	85 (1.7)	ns
Osteomyelitis/septic arthritis	16 (0.7)	37 (1.4)	53 (1.0)	$0.01 < P < 0.05$
Device-related infection with metastatic focus	16 (0.7)	19 (0.7)	35 (0.7)	ns
Total	2,395	2,690	5,085	

ns = not significant

* Enterobacteriaceae, *Acinetobacter* species and *Pseudomonas aeruginosa*

Table 6: Principal clinical manifestation for enterococcal bacteraemia, by patient gender, 2015

Principal clinical manifestation	Female (%)	Male (%)	Total (%)	Significance
Biliary tract infection (including cholangitis)	62 (19.3)	99 (15.8)	161 (17.0)	ns
Urinary tract infection	33 (10.3)	124 (19.7)	157 (16.5)	$P < 0.01$
Intra-abdominal infection other than biliary tract	51 (15.9)	84 (13.4)	135 (14.2)	ns
No focus (e.g. in febrile neutropenia)	39 (12.1)	77 (12.3)	116 (12.2)	ns
Device-related infection without metastatic focus	38 (11.8)	58 (9.2)	96 (10.1)	ns
Febrile neutropenia	31 (9.7)	50 (8.0)	81 (8.5)	ns
Other clinical syndrome	21 (6.5)	39 (6.2)	60 (6.3)	ns
Endocarditis, left-sided	16 (5.0)	42 (6.7)	58 (6.1)	ns
Skin and skin structure infection	12 (3.7)	24 (3.8)	36 (3.8)	ns
Osteomyelitis/septic arthritis	6 (1.9)	14 (2.2)	20 (2.1)	ns
Endocarditis, right-sided	6 (1.9)	6 (1.0)	12 (1.3)	ns
Device-related infection with metastatic focus	4 (1.2)	6 (1.0)	10 (1.1)	ns
No focus	2*	4*	6*	na
Pneumonia/empyema	0*	1*	1*	na
Total	321	628	949	

na = not applicable; ns = not significant

* Insufficient numbers (<10) to calculate percentage

Table 7: Principal clinical manifestation for enterococcal bacteraemia, by *Enterococcus* species, 2015

Principal clinical manifestation	*E. faecalis* (%)	*E. faecium* (%)	Significance
Urinary tract infection	130 (25.3)	26 (6.6)	$P < 0.01$
Biliary tract infection (including cholangitis)	52 (10.1)	84 (21.5)	$P < 0.01$
Intra-abdominal infection other than biliary tract	61 (11.9)	70 (17.9)	$0.01 < P < 0.05$
No focus (e.g. in febrile neutropenia)	59 (11.5)	53 (13.6)	ns
Device-related infection without metastatic focus	45 (8.8)	50 (12.8)	ns
Febrile neutropenia	14 (2.7)	65 (16.6)	$P < 0.01$
Endocarditis, left-sided	54 (10.5)	4 (1.0)	$P < 0.01$
Other clinical syndrome	36 (7.0)	20 (5.1)	ns
Skin and skin structure infection	27 (5.3)	6 (1.5)	$0.01 < P < 0.05$
Osteomyelitis/septic arthritis	16 (3.1)	3 (0.8)	$0.01 < P < 0.05$
Endocarditis, right-sided	11 (2.1)	1 (0.3)	$0.01 < P < 0.05$
Device-related infection with metastatic focus	6 (1.2)	4 (1.0)	ns
No focus	2 (0.4)	4 (1.0)	na
Pneumonia/empyema	0 (0.0)	1 (0.3)	na
Total	513	391	

na = not applicable; ns = not significant

4.1.3 *Staphylococcus aureus*

The principal clinical manifestation was known for 2,110 (88.0%) episodes of SAB (Table 8). Overall, the most frequent principal clinical manifestation was skin and skin structure infection (19.8%), followed by osteomyelitis/septic arthritis (19.1%) and device-related infection (16.1%).

Of the hospital-onset SABs where data were available, the most common principal clinical manifestation was device-related infection (35.8%). Of the community-onset SABs where data were available, the most common principal clinical manifestation was osteomyelitis/septic arthritis (22.0%).

4.2 Length of hospital stay following bacteraemic episode

Information on length of stay following bacteraemia was available for 5,432 (74.1%) episodes involving gram-negative species, 937 (92.7%) involving *Enterococcus* species and 2,131 (88.9%) involving *S. aureus*. The majority of patients (45.9%) with a gram-negative bacteraemia had a length of stay less than seven days (Table 9). More than 20.9% of patients remained in hospital for more than 30 days after enterococcal bacteraemia (Table 10), and 27.5% after staphylococcal bacteraemia (Table 11).

Table 8: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient gender, 2015

Principal clinical manifestation	Female (%)	Male (%)	Total (%)	Significance
Skin and skin structure infection	146 (20.0)	272 (19.7)	418 (19.8)	ns
Osteomyelitis/septic arthritis	121 (16.6)	283 (20.5)	404 (19.1)	$0.01 < P < 0.05$
Device-related infection without metastatic focus	122 (16.7)	232 (16.8)	354 (16.8)	ns
No focus	101 (13.8)	172 (12.5)	273 (12.9)	ns
Other clinical syndrome	44 (6.0)	82 (5.9)	126 (6.0)	ns
Pneumonia/empyema	40 (5.5)	83 (6.0)	123 (5.8)	ns
Endocarditis, left-sided	46 (6.3)	75 (5.4)	121 (5.7)	ns
Deep abscess(es), excluding those in the CNS	30 (4.1)	59 (4.3)	89 (4.2)	ns
Endocarditis, right-sided	28 (3.8)	26 (1.9)	54 (2.6)	$P < 0.01$
CNS infection – meningitis, abscess(es)	14 (1.9)	32 (2.3)	46 (2.2)	ns
No focus (e.g. in febrile neutropenia)	11 (1.5)	23 (1.7))	34 (1.6)	ns
Febrile neutropenia	14 (1.9)	17 (1.2)	31 (1.5)	ns
Device-related infection with metastatic focus	13 (1.8)	18 (1.3)	31 (1.5)	ns
Urinary tract infection	0 (0.0)	4 (0.3)	4 (0.2)	na
Intra-abdominal infection other than biliary tract	0 (0.0)	1 (0.1)	1 (0.0)	na
Endocarditis, native valve (unspecified)	0 (0.0)	1 (0.1)	1 (0.0)	na
Total	730	1,380	2,110	

CNS = central nervous system; na = not applicable; ns = not significant

Table 9: Length of stay following gram-negative bacteraemia, by species and place of onset, 2015

Species	Length of stay following bacteraemia (days)				Total
	<7 (%)	7–14 (%)	15–30 (%)	>30 (%)	
Gram-negative species*	2,491 (45.9)	1,625 (29.9)	787 (14.5)	529 (9.7)	5,431
Enterobacteriaceae	2,314 (47.4)	1,438 (29.5)	689 (14.1)	439 (9.0)	4,880
Escherichia coli	1,582 (53.7)	838 (28.4)	340 (11.5)	186 (6.3)	2,946
Community onset	1,458 (59.6)	676 (27.6)	217 (8.9)	97 (4.0)	2,448
Hospital onset	124 (24.9)	162 (32.5)	123 (24.7)	89 (17.9)	498
Klebsiella pneumoniae	264 (36.1)	244 (33.3)	139 (19.0)	85 (11.6)	732
Community onset	232 (45.8)	163 (32.2)	73 (14.4)	38 (7.5)	506
Hospital onset	32 (14.2)	81 (35.8)	66 (29.2)	47 (20.8)	226
Enterobacter cloacae complex	87 (33.3)	72 (27.6)	58 (22.2)	44 (16.9)	261
Community onset	69 (53.1)	40 (30.8)	10 (7.7)	11 (8.5)	130
Hospital onset	18 (13.7)	32 (24.4)	48 (36.6)	33 (25.2)	131
Other Enterobacteriaceae (*n* = 46)	381 (40.5)	284 (30.2)	152 (16.2)	124 (13.2)	941
Pseudomonas aeruginosa	151 (31.9)	163 (34.5)	82 (17.3)	77 (16.3)	473
Community onset	106 (40.2)	96 (36.4)	41 (15.5)	21 (8.0)	264
Hospital onset	45 (21.5)	67 (32.1)	41 (19.6)	56 (26.8)	209
Acinetobacter baumannii complex	10 (22.2)	16 (35.6)	10 (22.2)	9 (20.0)	45
Community onset	9 (36.0)	8 (32.0)	5 (20.0)	3 (12.0)	25
Hospital onset	1 (5.0)	8 (40.0)	5 (25.0)	6 (30.0)	20

* Enterobacteriaceae, *Acinetobacter* species and *Pseudomonas aeruginosa*. These 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.

There were no significant differences in length of stay between *E. faecium* and *E. faecalis* episodes, or between vancomycin-susceptible and vancomycin-non-susceptible *E. faecium* (Table 10). However, for both *E. faecalis* and *E. faecium*, patients with hospital-onset infections had a significantly longer length of stay than those with community-onset infections (31.8% with length of stay >30 days versus 14.9% for *E. faecalis*; 26.4% versus 9.4% for *E. faecium*; $P < 0.01$).

As shown in Table 11, patients with MRSA episodes had a significantly longer length of stay than those with MSSA (32.1% with length of stay >30 days versus 26.5%; $P = 0.0284$). For MRSA episodes, patients with hospital-onset infections had a significantly longer length of stay than those with community-onset infections (28.3% with length of stay >30 days versus 41.4%; $P = 0.0129$).

Table 10: Length of stay following *Enterococcus* species bacteraemia, by vancomycin resistance and place of onset, 2015

Species	Length of stay following bacteraemia (days)				Total
	<7 (%)	7–14 (%)	15–30 (%)	>30 (%)	
All species	217 (23.2)	276 (29.5)	248 (26.5)	196 (20.9)	937
E. faecalis	124 (24.4)	149 (29.3)	129 (25.4)	106 (20.9)	508
E. faecium	81 (21.1)	111 (28.9)	107 (27.9)	85 (22.1)	384
Vancomycin susceptible	43 (23.1)	63 (33.9)	47 (25.3)	33 (17.7)	186
Vancomycin resistant	38 (19.2)	48 (24.2)	60 (30.3)	52 (26.3)	198
Other *Enterococcus* species (*n* = 7)	12 (26.7)	16 (35.6)	12 (26.7)	5 (11.2)	45
Community onset					
E. faecalis	94 (28.6)	105 (31.9)	81 (24.6)	49 (14.9)	329
E. faecium	30 (31.3)	34 (35.4)	23 (24.0)	9 (9.4)	96
Vancomycin resistant	8 (22.9)	16 (45.7)	6 (17.1)	5 (14.3)	35
Vancomycin susceptible	22 (36.1)	18 (29.5)	17 (27.9)	4 (6.6)	61
Hospital onset					
E. faecalis	30 (16.8)	44 (24.6)	48 (26.8)	57 (31.8)	179
E. faecium	51 (17.7)	77 (26.7)	84 (29.2)	76 (26.4)	288
Vancomycin resistant	30 (18.4)	32 (19.6)	54 (33.1)	47 (28.8)	163
Vancomycin susceptible	21 (16.8)	45 (36.0)	30 (24.0)	29 (23.2)	125

Table 11: Length of stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, 2015

Species	Length of stay following bacteraemia (days)				Total
	<7 (%)	7–14 (%)	15–30 (%)	>30 (%)	
Staphylococcus aureus	383 (18.0)	481 (22.6)	680 (31.9)	587 (27.5)	2,131
Methicillin resistant	70 (17.9)	70 (17.9)	126 (32.1)	126 (32.1)	392
Community onset	56 (20.3)	48 (17.4)	94 (34.1)	78 (28.3)	276
Hospital onset	14 (12.1)	22 (19.0)	32 (27.6)	48 (41.4)	116
Methicillin susceptible	313 (18.0)	411 (23.6)	554 (31.9)	461 (26.5)	1,739
Community onset	251 (18.6)	325 (24.1)	421 (31.2)	353 (26.1)	1,350
Hospital onset	62 (15.9)	86 (22.1)	133 (34.2)	108 (27.8)	389

5 Principal antimicrobial treatment and 30-day all-cause mortality

The five principal antimicrobial treatments for the top 12 species and 30-day all-cause mortality (where both treatment and outcome are known) are shown in Tables 12–14.

All-cause mortality is collected because of the well-known difficulty of attributing mortality directly to sepsis, and the lack of consensus definitions for attributable mortality. The results need to be interpreted with caution, because they are not controlled for patient comorbidities, clinician treatment preferences, sepsis due to mixed pathogens, treatment before the initiation of definitive (principal) antimicrobial treatment, or any subsequent oral treatment. Nevertheless, some general conclusions can be drawn.

Notable findings include the significantly higher all-cause mortality seen with *E. coli* sepsis of hospital onset compared with community onset, and sepsis caused by MRSA compared with MSSA. The higher mortality in MSSA sepsis treated with vancomycin, compared with that treated with flucloxacillin and cefazolin, has been noted in previous studies.

The 'not treated' category provides some insights into outcomes when sepsis due to these pathogens is not treated with antimicrobials, although most often the reason for not treating the sepsis is the presence of a rapidly fatal underlying disease. Given that caveat, there was still an observably lower rate of all-cause mortality in enterococcal sepsis than in staphylococcal or gram-negative sepsis.

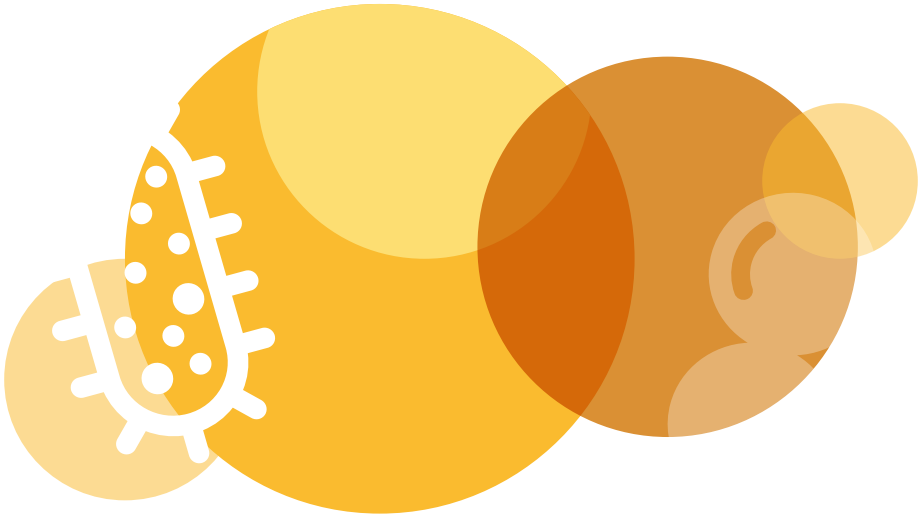


Table 12: Top principal antimicrobial treatments and 30-day all-cause mortality, by place of onset, Enterobacteriaceae, 2015

All episodes			Community onset			Hospital onset		
Agent	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**
Escherichia coli								
Ceftriaxone	784 (34.5)	39 (5.0)	Ceftriaxone	693 (37.1)	25 (3.6)	Piperacillin-tazobactam	149 (36.9)	30 (20.1)
Piperacillin-tazobactam	645 (28.4)	78 (12.1)	Piperacillin-tazobactam	496 (26.6)	48 (9.7)	Ceftriaxone	91 (22.5)	14 (15.4)
Meropenem	261 (11.5)	32 (12.3)	Meropenem	175 (9.4)	14 (8.0)	Meropenem	86 (21.3)	18 (20.9)
Cefazolin	101 (4.4)	7 (6.9)	Amoxicillin	89 (4.8)	0 (0.0)	Cefazolin	14 (3.5)	2 (14.3)
Amoxicillin	94 (4.1)	1 (1.1)	Cefazolin	87 (4.7)	5 (5.7)	Ciprofloxacin	13 (3.2)	1 (7.7)
Other	316 (13.9)	27 (8.5)	Other	270 (14.5)	17 (6.3)	Other	38 (9.4)	10 (26.3)
Not treated	70 (3.1)	57 (81.4)	Not treated	57 (3.1)	47 (82.5)	Not treated	13 (3.2)	10 (76.9)
Total	2,271	241 (10.6)	Total	1,867	156 (8.4)	Total	404	85 (21.0)
Klebsiella pneumoniae								
Piperacillin-tazobactam	254 (42.1)	31 (12.2)	Piperacillin-tazobactam	168 (39.7)	22 (13.1)	Piperacillin-tazobactam	86 (47.5)	9 (10.5)
Ceftriaxone	153 (25.3)	10 (6.5)	Ceftriaxone	128 (30.3)	7 (5.5)	Meropenem	39 (21.5)	10 (25.6)
Meropenem	89 (14.7)	17 (19.1)	Meropenem	50 (11.8)	7 (14.0)	Ceftriaxone	25 (13.8)	3 (12.0)
Ciprofloxacin	28 (4.6)	1 (3.6)	Cefazolin	22 (5.2)	1 (4.5)	Ciprofloxacin	11 (6.1)	1 (9.1)
Cefazolin	23 (3.8)	1 (4.3)	Ciprofloxacin	17 (4.0)	0 (0.0)	Cefepime	4 (na)	0 (na)
Other	39 (6.5)	4 (10.3)	Other	24 (5.7)	2 (8.3)	Other	12 (6.6)	2 (16.7)
Not treated	18 (3.0)	16 (88.9)	Not treated	14 (3.3)	13 (92.9)	Not treated	4 (na)	3 (na)
Total	604	80 (13.2)	Total	423	52 (12.3)	Total	181	28 (15.5)
Pseudomonas aeruginosa								
Piperacillin-tazobactam	208 (52.7)	30 (14.4)	Piperacillin-tazobactam	123 (56.7)	18 (14.6)	Piperacillin-tazobactam	85 (47.8)	12 (14.1)
Meropenem	68 (17.2)	12 (17.6)	Meropenem	24 (11.1)	5 (20.8)	Meropenem	44 (24.7)	7 (15.9)
Ciprofloxacin	29 (7.3)	2 (6.9)	Ciprofloxacin	17 (7.8)	0 (0.0)	Ciprofloxacin	12 (6.7)	2 (16.7)
Ceftazidime	25 (6.3)	3 (12.0)	Ceftazidime	15 (6.9)	1 (6.7)	Ceftazidime	10 (5.6)	2 (20.0)

continued

Table 12: (continued)

All episodes			Community onset			Hospital onset		
Agent	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**
Pseudomonas aeruginosa (continued)								
Cefepime	13 (3.3)	0 (0.0)	Cefepime	7 (na)	0 (na)	Cefepime	6 (na)	0 (na)
Other	29 (7.3)	4 (13.8)	Other	16 (7.4)	2 (12.5)	Other	13 (7.3)	2 (15.4)
Not treated	23 (5.8)	20 (87.0)	Not treated	15 (6.9)	13 (86.7)	Not treated	8 (na)	7 (na)
Total	395	71 (18.0)	Total	217	39 (18.0)	Total	178	32 (18.0)
Enterobacter cloacae								
Meropenem	121 (56.8)	16 (13.2)	Meropenem	52 (51.0)	7 (13.5)	Meropenem	69 (62.2)	9 (13.0)
Piperacillin-tazobactam	38 (17.8)	4 (10.5)	Piperacillin-tazobactam	21 (20.6)	3 (14.3)	Piperacillin-tazobactam	17 (15.3)	1 (5.9)
Ciprofloxacin	26 (12.2)	4 (15.4)	Ciprofloxacin	13 (12.7)	1 (7.7)	Ciprofloxacin	13 (11.7)	3 (23.1)
Cefepime	7 (na)	1 (na)	Cefepime	5 (na)	1 (na)	Cefepime	2 (na)	0 (na)
Ceftriaxone	5 (na)	0 (na)	Ceftriaxone	4 (na)	0 (na)	Amikacin	2 (na)	0 (na)
Other	10 (na)	0 (na)	Other	5 (na)	0 (na)	Other	4 (na)	0 (na)
Not treated	6 (na)	4 (na)	Not treated	2 (na)	2 (na)	Not treated	4 (na)	2 (na)
Total	213	29 (13.6)	Total	102	14 (13.7)	Total	111	15 (13.5)
Klebsiella oxytoca								
Piperacillin-tazobactam	65 (44.2)	5 (7.7)	Piperacillin-tazobactam	45 (43.7)	2 (4.4)	Piperacillin-tazobactam	20 (45.5)	3 (15.0)
Ceftriaxone	37 (25.2)	0 (0.0)	Ceftriaxone	34 (33.0)	0 (0.0)	Meropenem	13 (29.5)	2 (15.4)
Meropenem	23 (15.6)	3 (13.0)	Meropenem	10 (9.7)	1 (10.0)	Ceftriaxone	3 (na)	0 (na)
Ciprofloxacin	5 (na)	1 (na)	Ciprofloxacin	4 (na)	1 (na)	Gentamicin	2 (na)	0 (na)
Gentamicin	5 (na)	0 (na)	Gentamicin	3 (na)	0 (na)	Cefotaxime	2 (na)	0 (na)
Other	9 (na)	1 (na)	Other	4 (na)	0 (na)	Other	4 (na)	1 (na)
Not treated	3 (na)	3 (na)	Not treated	3 (na)	3 (na)			
Total	147	13 (8.8)	Total	103	7 (6.8)	Total	44	6 (13.6)

continued

Table 12: (continued)

All episodes			Community onset			Hospital onset		
Agent	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**
Proteus mirabilis								
Ceftriaxone	39 (31.0)	8 (20.5)	Ceftriaxone	32 (31.4)	5 (15.6)	Piperacillin-tazobactam	12 (50.0)	4 (33.3)
Piperacillin-tazobactam	38 (30.2)	10 (26.3)	Piperacillin-tazobactam	26 (25.5)	6 (23.1)	Ceftriaxone	7 (29.2)	3 (42.9)
Meropenem	10 (7.9)	2 (20.0)	Meropenem	9 (na)	2 (na)	Amoxicillin-clavulanate	1 (na)	0 (na)
Amoxicillin	6 (na)	0 (na)	Ampicillin	6 (na)	0 (na)	Meropenem	1 (na)	0 (na)
Ampicillin	6 (na)	0 (na)	Amoxicillin	6 (na)	0 (na)	Gentamicin	1 (na)	1 (na)
Other	20 (15.9)	4 (20.0)	Other	18 (17.6)	3 (16.7)	Other	0 (na)	0 (na)
Not treated	7 (na)	5 (na)	Not treated	5 (na)	3 (na)	Not treated	2 (na)	2 (na)
Total	126	29 (23.0)	Total	102	19 (18.6)	Total	24	10 (41.7)
Serratia marcescens								
Meropenem	50 (43.9)	5 (10.0)	Meropenem	27 (52.9)	2 (7.4)	Meropenem	23 (36.5)	3 (13.0)
Piperacillin-tazobactam	24 (21.1)	2 (8.3)	Piperacillin-tazobactam	7 (na)	0 (na)	Piperacillin-tazobactam	17 (27.0)	2 (11.8)
Ciprofloxacin	13 (11.4)	2 (15.4)	Ciprofloxacin	7 (na)	1 (na)	Ciprofloxacin	6 (na)	1 (na)
Cefepime	9 (na)	3 (na)	Cefepime	4 (na)	1 (na)	Cefepime	5 (na)	2 (na)
Gentamicin	3 (na)	0 (na)	Gentamicin	2 (na)	0 (na)	Gentamicin	1 (na)	0 (na)
Other	6 (na)	2 (na)	Other	2 (na)	1 (na)	Other	4 (na)	1 (na)
Not treated	9 (na)	7 (na)	Not treated	2 (na)	2 (na)	Not treated	7 (na)	5 (na)
Total	114	21 (18.4)	Total	51	7 (13.7)	Total	63	14 (22.2)
Enterobacter aerogenes								
Meropenem	47 (63.5)	4 (8.5)	Meropenem	23 (60.5)	1 (4.3)	Meropenem	24 (66.7)	3 (12.5)
Piperacillin-tazobactam	11 (14.9)	2 (18.2)	Piperacillin-tazobactam	6 (na)	0 (na)	Piperacillin-tazobactam	5 (na)	2 (na)
Ciprofloxacin	10 (13.5)	3 (30.0)	Ciprofloxacin	5 (na)	1 (na)	Ciprofloxacin	5 (na)	2 (na)

continued

Table 12: (continued)

All episodes			Community onset			Hospital onset		
Agent	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**
Enterobacter aerogenes (continued)								
Gentamicin	2 (na)	0 (na)	Gentamicin	1 (na)	0 (na)	Gentamicin	1 (na)	0 (na)
Cefepime	2 (na)	0 (na)	Cefepime	1 (na)	0 (na)	Cefepime	1 (na)	0 (na)
Other	1 (na)	0 (na)	Other	1 (na)	0 (na)			
Not treated	1 (na)	1 (na)	Not treated	1 (na)	1 (na)			
Total	74	10 (13.5)	Total	38	3 (7.9)	Total	36	7 (19.4)
Salmonella species (non-typhoidal)								
Ceftriaxone	37 (56.9)	0 (0.0)	Ceftriaxone	33 (62.3)	0 (0.0)	Ceftriaxone	4 (na)	0 (na)
Ciprofloxacin	8 (na)	0 (na)	Ciprofloxacin	7 (na)	0 (na)	Piperacillin-tazobactam	4 (na)	2 (na)
Piperacillin-tazobactam	7 (na)	3 (na)	Piperacillin-tazobactam	3 (na)	1 (na)	Meropenem	2 (na)	1 (na)
Amoxicillin	2 (na)	0 (na)	Amoxicillin	2 (na)	0 (na)	Ciprofloxacin	1 (na)	0 (na)
Cefepime	2 (na)	0 (na)	Cefepime	1 (na)	0 (na)	Cefepime	1 (na)	0 (na)
Other	8 (na)	1 (na)	Other	6 (na)	0 (na)			
Not treated	1 (na)	0 (na)	Not treated	1 (na)	0 (na)			
Total	65	4 (6.2)	Total	53	1 (1.9)	Total	12	3 (25.0)

na = not applicable: insufficient numbers (<10) to calculate percentage

Table 13: Top principal antimicrobial treatments and 30-day all-cause mortality, by place of onset, *Staphylococcus aureus,* 2015

All episodes			Community onset			Hospital onset		
Agent	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**
Staphylococcus aureus, methicillin resistant								
Vancomycin	264 (74.8)	36 (13.6)	Vancomycin	181 (73.9)	24 (13.3)	Vancomycin	83 (76.9)	12 (14.5)
Linezolid	17 (4.8)	3 (17.6)	Linezolid	9 (na)	1 (na)	Linezolid	8 (na)	2 (na)
Flucloxacillin	10 (2.8)	4 (40.0)	Flucloxacillin	8 (na)	3 (na)	Daptomycin	4 (na)	0 (na)
Daptomycin	9 (na)	0 (na)	Daptomycin	5 (na)	0 (na)	Flucloxacillin	2 (na)	1 (na)
Other β-lactam	6 (na)	3 (na)	Other β-lactam	4 (na)	3 (na)	Other β-lactam	2 (na)	0 (na)
Other	24 (6.8)	2 (8.3)	Other	22 (9.0)	2 (9.1)	Other	2 (na)	0 (na)
Not treated	23 (6.5)	19 (82.6)	Not treated	16 (6.5)	14 (87.5)	Not treated	7 (na)	5 (na)
Total	353	67 (19.0)	Total	245	47 (19.2)	Total	108	20 (18.5)
Staphylococcus aureus, methicillin susceptible								
Flucloxacillin	1,100 (70.2)	123 (11.2)	Flucloxacillin	864 (71.1)	100 (11.6)	Flucloxacillin	236 (66.9)	23 (9.7)
Cefazolin	147 (9.4)	15 (10.2)	Cefazolin	111 (9.1)	11 (9.9)	Cefazolin	36 (10.2)	4 (11.1)
Vancomycin	83 (5.3)	17 (20.5)	Vancomycin	62 (5.1)	12 (19.4)	Vancomycin	21 (5.9)	5 (23.8)
Other β-lactam	58 (3.7)	21 (36.2)	Other β-lactam	38 (3.1)	17 (44.7)	Other β-lactam	20 (5.7)	4 (20.0)
Benzylpenicillin	47 (3.0)	5 (10.6)	Benzylpenicillin	34 (2.8)	4 (11.8)	Benzylpenicillin	13 (3.7)	1 (7.7)
Other	71 (4.5)	14 (19.7)	Other	60 (4.9)	10 (16.7)	Other	11 (3.1)	4 (36.4)
Not treated	62 (4.0)	46 (74.2)	Not treated	46 (3.8)	34 (73.9)	Not treated	16 (4.5)	12 (75.0)
Total	1,568	241 (15.4)	Total	1,215	188 (15.5)	Total	353	53 (15.0)

na = not applicable: insufficient numbers (<10) to calculate percentage

Note: 'Other β-lactam' means β-lactam or β-lactam plus inhibitor, other than listed elsewhere.

Table 14: Top principal antimicrobial treatments and 30-day all-cause mortality, by place of onset, *Enterococcus* species, 2015

All episodes			Community onset			Hospital onset		
Agent	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**	**Agent**	**Number (%)**	**Deaths (%)**
Enterococcus faecalis								
Piperacillin–tazobactam	100 (21.6)	16 (16.0)	Piperacillin–tazobactam	65 (21.5)	10 (15.4)	Piperacillin–tazobactam	35 (22.0)	6 (17.1)
Amoxicillin	76 (16.5)	6 (7.9)	Amoxicillin	55 (18.2)	4 (7.3)	Vancomycin	35 (22.0)	4 (11.4)
Benzylpenicillin	69 (14.9)	6 (8.7)	Benzylpenicillin	54 (17.8)	6 (11.1)	Amoxicillin	21 (13.2)	2 (9.5)
Vancomycin	64 (13.9)	10 (15.6)	Ampicillin	36 (11.9)	4 (11.1)	Ampicillin	16 (10.1)	2 (12.5)
Ampicillin	52 (11.3)	6 (11.5)	Vancomycin	29 (9.6)	6 (20.7)	Benzylpenicillin	15 (9.4)	0 (0.0)
Other	77 (16.7)	12 (15.6)	Other	48 (15.8)	6 (12.5)	Other	29 (18.2)	6 (20.7)
Not treated	24 (5.2)	15 (62.5)	Not treated	16 (5.3)	13 (81.3)	Not treated	8 (na)	2 (na)
Total	462	71 (15.4)	Total	303	49 (16.2)	Total	159	22 (13.8)
Enterococcus faecium								
Vancomycin	93 (25.3)	15 (16.1)	Vancomycin	24 (25.0)	3 (12.5)	Vancomycin	69 (25.5)	12 (17.4)
Linezolid	72 (19.6)	26 (36.1)	Linezolid	14 (14.6)	9 (64.3)	Linezolid	58 (21.4)	17 (29.3)
Daptomycin	54 (14.7)	10 (18.5)	Piperacillin–tazobactam	14 (14.6)	2 (14.3)	Daptomycin	44 (16.2)	9 (20.5)
Teicoplanin	54 (14.7)	11 (20.4)	Teicoplanin	11 (11.5)	0 (0.0)	Teicoplanin	43 (15.9)	11 (25.6)
Piperacillin–tazobactam	27 (7.4)	8 (29.6)	Daptomycin	10 (10.4)	1 (10.0)	Piperacillin–tazobactam	13 (4.8)	6 (46.2)
Other	33 (9.0)	11 (33.3)	Other	13 (13.5)	4 (30.8)	Other	20 (7.4)	7 (35.0)
Not treated	34 (9.3)	18 (52.9)	Not treated	10 (10.4)	4 (40.0)	Not treated	24 (8.9)	14 (58.3)
Total	367	99 (27.0)	Total	96	23 (24.0)	Total	271	76 (28.0)

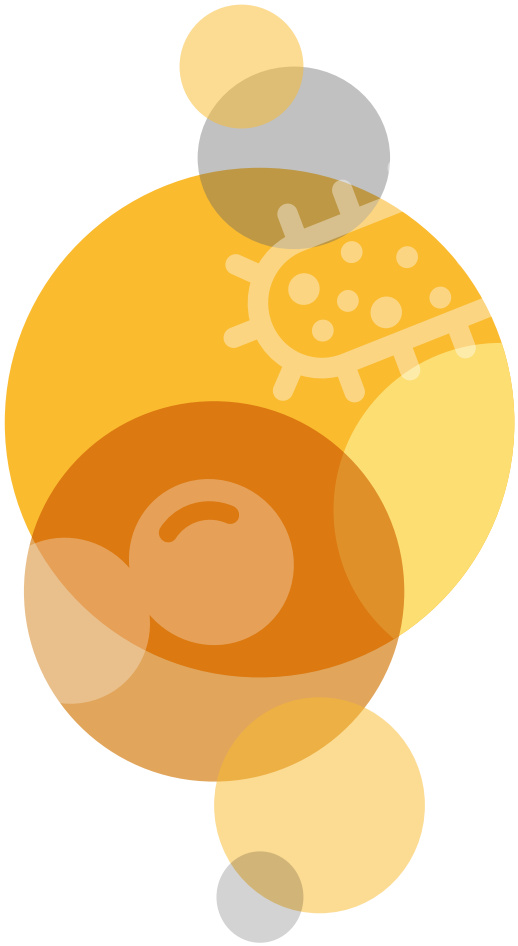
na = not applicable: insufficient numbers (<10) to calculate percentage

6 Susceptibility testing results

6.1 Percentages of non-susceptibility in national priority indicator species

Overall percentages of resistance or non-susceptibility, for both Clinical and Laboratory Standards Institute (CLSI) and European Committee on Antimicrobial Susceptibility Testing (EUCAST), in the indicator species of national priority are shown in Table 15. Resistance by state and territory can be found in Appendix C. For some antimicrobials, the concentration range tested did not distinguish between intermediate susceptibility (I) and resistance (R), and the term non-susceptible (NS) was used to describe these strains. Similarly, NR refers to both susceptible and 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 2015 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.



* www.agargroup.org/surveys

Table 15: Antimicrobial resistances (CLSI and EUCAST), 2015

Species and antimicrobial	Number	CLSI		EUCAST	
		% intermediate (*n*)	% resistant (*n*)	% intermediate (*n*)	% resistant (*n*)
Enterobacter aerogenes					
Piperacillin-tazobactam	130	12.3 (16)	27.7 (36)	3.8 (5)	40.0 (52)
Ceftriaxone	131	1.5 (2)	40.5 (53)	1.5 (2)	40.5 (53)
Ceftazidime	131	0.8 (1)	36.6 (48)	2.3 (3)	37.4 (49)
Cefepime	131	3.1 (4)*	0.8 (1)	0.0 (0)	3.8 (5)
Gentamicin	131	0.0 (0)	3.1 (4)	0.8 (1)	3.1 (4)
Tobramycin	130	1.5 (2)	2.3 (3)	0.0 (0)	3.8 (5)
Amikacin	131	0.0 (0)	0.0 (0)	0.8 (1)	0.0 (0)
Ciprofloxacin	131	0.8 (1)	3.1 (4)	0.8 (1)	3.8 (5)
Meropenem	131	0.0 (0)	1.5 (2)	0.0 (0)	1.5 (2)
Enterobacter cloacae					
Piperacillin-tazobactam	277	4.7 (13)	15.9 (44)	2.2 (6)	20.6 (57)
Ceftriaxone	326	1.2 (4)	24.5 (80)	1.2 (4)	24.5 (80)
Ceftazidime	326	0.3 (1)	22.1 (72)	1.8 (6)	22.4 (73)
Cefepime	326	3.7 (12)	2.1 (7)	8.6 (28)	4.3 (14)
Gentamicin	326	0.6 (2)	6.7 (22)	1.2 (4)	7.4 (24)
Tobramycin	325	5.8 (19)	3.4 (11)	0.3 (1)	9.2 (30)
Amikacin	326	0.0 (0)	0.0 (0)	1.5 (5)	0.0 (0)
Ciprofloxacin	326	1.8 (6)	1.5 (5)	0.6 (2)	3.4 (11)
Meropenem	326	0.3 (1)	3.1 (10)	0.9 (3)	2.1 (7)
Enterococcus faecalis					
Ampicillin	561	–†	0.0 (0)	0.2 (1)	0.0 (0)
Benzylpenicillin	547	–†	2.0 (11)	–§	–§
Ciprofloxacin	521	2.3 (12)	14.8 (77)	–†	10.9 (57)
Daptomycin	539	0.0 (0)	0.2 (1)	–§	–§
Linezolid	561	6.4 (36)	0.2 (1)	–†	0.2 (1)
Teicoplanin	558	0.0 (0)	0.0 (0)	–†	0.0 (0)
Tetracycline	489	0.2 (1)	78.3 (383)	–§	–§
Vancomycin	561	0.4 (2)	0.4 (2)	–†	0.7 (4)
Enterococcus faecium					
Ampicillin	400	0.0 (0)	86.0 (344)	0.8 (3)	86.0 (344)
Benzylpenicillin	391	–†	88.5 (346)	–§	–§
Ciprofloxacin	373	4.3 (16)	87.9 (328)	–†	74.8 (279)
Linezolid	400	3.3 (13)	0.0 (0)	–†	0.0 (0)
Teicoplanin	401	5.7 (23)	11.7 (47)	–†	17.7 (71)

continued

Table 15: (continued)

Species and antimicrobial	Number	CLSI		EUCAST	
		% intermediate (*n*)	% resistant (*n*)	% intermediate (*n*)	% resistant (*n*)
Enterococcus faecium (continued)					
Tetracycline	343	0.6 (2)	57.7 (198)	–§	–§
Vancomycin	402	0.5 (2)	49.8 (200)	–†	50.2 (202)
Escherichia coli					
Ampicillin	3,992	2.1 (83)	53.1 (2,118)	–†	55.1 (2,201)
Amoxicillin–clavulanate	3,995	13.7 (546)	8.7 (349)	–#	–#
Piperacillin–tazobactam	3,974	3.5 (139)	2.8 (112)	1.0 (41)	6.3 (251)
Ceftriaxone	3,994	0.1 (3)	10.5 (420)	0.1 (3)	10.5 (420)
Ceftazidime	3,994	0.3 (12)	5.8 (230)	3.9 (155)	6.1 (242)
Cefepime	3,994	2.0 (79)	3.7 (148)	3.9 (157)	4.8 (191)
Gentamicin	3,994	0.1 (3)	7.8 (311)	0.6 (22)	7.9 (314)
Tobramycin	3,982	5.1 (202)	3.7 (148)	0.7 (28)	8.8 (350)
Amikacin	3,994	0.0 (1)	0.1 (4)	1.6 (62)	0.1 (5)
Ciprofloxacin	3,994	0.3 (13)	12.3 (490)	1.0 (39)	12.6 (503)
Meropenem	3,993	0.0 (1)	0.0 (0)	0.0 (0)	0.0 (0)
Klebsiella pneumoniae					
Amoxicillin–clavulanate	974	4.8 (47)	4.2 (41)	–#	–#
Piperacillin–tazobactam	966	2.9 (28)	3.5 (34)	5.5 (53)	6.4 (62)
Ceftriaxone	974	0.1 (1)	5.7 (56)	0.1 (1)	5.7 (56)
Ceftazidime	974	0.2 (2)	4.7 (46)	2.0 (19)	4.9 (48)
Cefepime	974	0.9 (9)	1.6 (16)	2.5 (24)	2.3 (22)
Gentamicin	974	0.3 (3)	4.2 (41)	0.3 (3)	4.5 (44)
Tobramycin	969	3.1 (30)	2.4 (23)	0.3 (3)	5.5 (53)
Amikacin	974	0.0 (0)	0.1 (1)	0.4 (4)	0.1 (1)
Ciprofloxacin	974	1.8 (18)	2.1 (20)	3.3 (32)	3.9 (38)
Meropenem	974	0.1 (1)	0.3 (3)	0.0 (0)	0.3 (3)
Klebsiella oxytoca					
Amoxicillin–clavulanate	238	4.2 (10)	7.6 (18)	–#	–#
Piperacillin–tazobactam	236	1.3 (3)	8.9 (21)	1.3 (3)	10.2 (24)
Ceftriaxone	237	0.8 (2)	7.6 (18)	0.8 (2)	7.6 (18)
Ceftazidime	238	0.4 (1)	0.8 (2)	0.8 (2)	1.3 (3)
Cefepime	238	0.4 (1)	0.4 (1)	0.4 (1)	0.8 (2)
Gentamicin	238	0.4 (1)	0.8 (2)	0.4 (1)	1.3 (3)
Tobramycin	236	1.3 (3)	0.0 (0)	0.4 (1)	1.3 (3)
Amikacin	238	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)

continued

Table 15: (continued)

Species and antimicrobial	Number	CLSI		EUCAST	
		% intermediate (*n*)	% resistant (*n*)	% intermediate (*n*)	% resistant (*n*)
Klebsiella oxytoca (continued)					
Ciprofloxacin	238	0.0 (0)	0.4 (1)	0.0 (0)	0.4 (1)
Meropenem	238	0.4 (1)	0.4 (1)	0.0 (0)	0.4 (1)
Proteus mirabilis					
Ampicillin	222	0.0 (0)	17.1 (38)	-†	17.1 (38)
Amoxicillin-clavulanate	222	8.6 (19)	1.8 (4)	-#	-#
Piperacillin-tazobactam	219	0.5 (1)	0.5 (1)	0.0 (0)	0.9 (2)
Ceftriaxone	222	0.0 (0)	2.3 (5)	0.0 (0)	2.3 (5)
Ceftazidime	222	0.0 (0)	1.4 (3)	0.5 (1)	1.4 (3)
Cefepime	222	0.5 (1)	0.9 (2)	0.5 (1)	0.9 (2)
Gentamicin	222	1.4 (3)	0.5 (1)	2.3 (5)	1.8 (4)
Tobramycin	221	0.9 (2)	0.9 (2)	0.0 (0)	1.8 (4)
Amikacin	222	0.0 (0)	0.0 (0)	1.4 (3)	0.0 (0)
Ciprofloxacin	222	0.5 (1)	3.6 (8)	0.5 (1)	4.1 (9)
Meropenem	221	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin-tazobactam	647	6.8 (44)	7.1 (46)	-†	13.9 (90)
Ceftazidime	653	5.1 (33)	5.4 (35)	-†	10.4 (68)
Cefepime	654	5.4 (35)	2.6 (17)	-†	8.0 (52)
Gentamicin	654	0.9 (6)	2.4 (16)	-†	3.4 (22)
Tobramycin	649	0.2 (1)	2.2 (14)	-†	2.3 (15)
Amikacin	654	0.3 (2)	0.5 (3)	1.7 (11)	0.8 (5)
Ciprofloxacin	653	2.5 (16)	3.8 (25)	0.0 (0)	6.3 (41)
Meropenem	653	4.0 (26)	4.1 (27)	5.5 (36)	2.6 (17)
Salmonella species (non-typhoidal)					
Ampicillin	114	0.0 (0)	8.8 (10)	-†	8.8 (10)
Amoxicillin-clavulanate	114	1.8 (2)	2.6 (3)	-#	-#
Piperacillin-tazobactam	114	0.9 (1)	0.0 (0)	0.0 (0)	0.9 (1)
Ceftriaxone	114	0.0 (0)	2.6 (3)	0.0 (0)	2.6 (3)
Ceftazidime	114	0.0 (0)	1.8 (2)	0.0 (0)	1.8 (2)
Cefepime	114	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Gentamicin	114	0.0 (0)	1.8 (2)	0.9 (1)	1.8 (2)
Tobramycin	114	0.0 (0)	0.9 (1)	1.8 (2)	0.9 (1)
Amikacin	114	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Ciprofloxacin	114	-**	1.8 (2)	-**	6.1 (7)

continued

Table 15: (continued)

Species and antimicrobial	Number	CLSI		EUCAST	
		% intermediate (*n*)	% resistant (*n*)	% intermediate (*n*)	% resistant (*n*)
Salmonella species (non-typhoidal) (continued)					
Meropenem	114	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	142	–‡	–‡	–‡	–‡
Ceftriaxone	189	0.5 (1)	3.2 (6)	0.5 (1)	3.2 (6)
Ceftazidime	189	0.0 (0)	1.1 (2)	0.0 (0)	1.1 (2)
Cefepime	189	0.5 (1)	0.0 (0)	0.5 (1)	0.5 (1)
Gentamicin	189	0.0 (0)	2.1 (4)	0.0 (0)	2.1 (4)
Tobramycin	188	9.6 (18)	1.6 (3)	9.6 (18)	11.2 (21)
Amikacin	189	0.0 (0)	0.5 (1)	0.0 (0)	0.5 (1)
Ciprofloxacin	189	0.5 (1)	0.5 (1)	1.6 (3)	1.1 (2)
Meropenem	189	0.0 (0)	0.5 (1)	0.0 (0)	0.5 (1)
Staphylococcus aureus					
Benzylpenicillin	2,397	–†	82.3 (1972)	–†	82.3 (1972)
Ciprofloxacin	2,398	0.4 (9)	10.2 (245)	–†	10.3 (254)
Clindamycin	2,398	0.0 (0)	3.3 (78)	0.2 (5)	3.3 (78)
Daptomycin	2,397	0.6 (6)§§	–†	–†	0.3 (6)
Erythromycin	2,398	4.2 (100)	12.4 (298)	0.3 (8)	13.7 (328)
Gentamicin	2,398	1.0 (24)	2.6 (62)	–†	4.0 (97)
Linezolid	2,397	0.0 (0)	0.0 (0)	–†	0.0 (0)
Oxacillin	2,396	–§	17.6 (421)	–†	17.6 (421)
Rifampicin	2,347	0.1 (2)	0.6 (13)	–##	0.6 (15)##
Trimethoprim–sulfamethoxazole	2,398	–§	4.0 (96)	0.2 (5)	3.8 (91)
Teicoplanin	2,398	0.0 (0)	0.0 (0)	0.0 (0)	0.1 (2)
Tetracycline	2,139	0.1 (3)	5.0 (107)	0.5 (11)	5.1 (110)
Vancomycin	2,397	0.0 (0)	0.0 (0)	–§	0.0 (0)

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate susceptibility; R = resistant

* Includes sensitive dose dependent category for CLSI

† No category defined

§ No guidelines for indicated species

\# For susceptibility testing purposes, EUCAST fixes the concentration of clavulanate at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines. 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 determine 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.

6.2 Antimicrobial resistance by place of onset

Antimicrobial resistances (CLSI and EUCAST) by place of onset, where known, in indicator species are shown in Table 16.

Table 16: Antimicrobial resistances (CLSI, EUCAST), by place of onset, 2015

		Community onset		Hospital onset	
Species and antimicrobial	**Number**	**%I**	**%R**	**%I**	**%R**
Enterobacter aerogenes					
Community onset, 54%; hospital onset, 46%					
Piperacillin-tazobactam	119	6.1, 3.0	28.8, 34.8	18.9, 3.8	28.3, 47.2
Ceftriaxone	120	0.0, 0.0	37.9, 37.9	3.7, 3.7	44.4, 44.4
Ceftazidime	120	1.5, 1.5	33.3, 34.8	0.0, 3.7	42.6, 42.6
Cefepime	120	3.0, 0.0*	1.5, 4.5	3.7, 0.0*	0.0, 3.7
Gentamicin	120	0.0, 1.5	3.0, 3.0	0.0, 0.0	1.9, 1.9
Tobramycin	119	0.0, 0.0	3.0, 3.0	1.9, 0.0	1.9, 3.8
Amikacin	120	0.0, 0.0	0.0, 0.0	0.0, 1.9	0.0, 0.0
Ciprofloxacin	120	1.5, 1.5	3.0, 4.5	0.0, 0.0	3.7, 3.7
Meropenem	120	0.0, 0.0	1.5, 1.5	0.0, 0.0	1.9, 1.9
Enterobacter cloacae					
Community onset, 51%; hospital onset, 49%					
Piperacillin-tazobactam	270	7.8, 0.7	8.5, 16.3	1.6, 3.9	24.8, 26.4
Ceftriaxone	316	0.6, 0.6	18.6, 18.6	1.9, 1.9	30.3, 30.3
Ceftazidime	316	0.6, 2.5	16.1, 16.8	0.0, 1.3	27.7, 27.7
Cefepime	316	2.5, 6.8*	1.2, 2.5	4.5, 11.0*	2.6, 5.2
Gentamicin	316	1.2, 0.6	5.0, 6.2	0.0, 1.9	7.7, 7.7
Tobramycin	315	5.6, 0.0	1.3, 6.9	6.5, 0.6	4.5, 11.0
Amikacin	316	0.0, 1.2	0.0, 0.0	0.0, 1.3	0.0, 0.0
Ciprofloxacin	316	0.6, 0.0	0.0, 0.6	3.2, 0.6	3.2, 6.5
Meropenem	316	0.6, 1.2	2.5, 1.2	0.0, 0.6	3.2, 2.6

continued

Table 16: (continued)

Species and antimicrobial	Number	Community onset		Hospital onset	
		%I	%R	%I	%R
Enterococcus faecalis					
Community onset, 65%; hospital onset, 35%					
Ampicillin	558	–†, 0.0	0.0, 0.0	–†, 0.0	0.0, 0.0
Benzylpenicillin	544	–†, –§	1.1, –§	–†, –§	3.7, –§
Ciprofloxacin	518	2.7, –†	12.6, 9.3	1.6, –†	19.0, 15.2
Daptomycin	536	0.0#, –§	–†, –§	0.5#, –§	–†, –§
Linezolid	558	5.2, –†	0.3, 0.3	8.2, –†	0.0, 0.0
Teicoplanin	555	0.0, –†	0.0, 0.0	0.0, –†	0.0, 0.0
Tetracycline	486	0.0, –†	77.5, –§	0.6, –†	79.4, –§
Vancomycin	558	0.0, –†	0.3, 0.3	1.0, –†	0.5, 1.5
Enterococcus faecium					
Community onset, 28%; hospital onset, 72%					
Ampicillin	400	–†, 0.0	68.8, 68.8	–§, 0.0	92.7, 92.7
Benzylpenicillin	391	–†, –§	71.6, –§	–†, –§	95.0, –§
Ciprofloxacin	373	9.6, –†	72.1, 68.5	2.2, –†	94.1, 92.7
Linezolid	400	4.5, –†	0.0, 0.0	2.8, –†	0.0, 0.0
Teicoplanin	401	4.5, –†	7.1, 11.6	6.2, –†	13.5, 19.7
Tetracycline	343	2.1, –†	43.8, –§	0.0, –†	63.2, –§
Vancomycin	402	0.0, –†	34.8, 34.8	0.7, –†	55.5, 56.2
Escherichia coli					
Community onset, 83%; hospital onset, 17%					
Ampicillin	3,751	2.2, –†	50.9, 53.1	1.5, –†	61.6, 63.1
Amoxicillin–clavulanate	3,754	12.8, –**	7.7, –**	18.5, –**	13.0, –**
Piperacillin–tazobactam	3,733	3.1, 1.0	2.1, 5.2	4.9, 1.3	6.7, 11.7
Ceftriaxone	3,753	0.1, 0.1	9.1, 9.1	0.0, 0.0	15.8, 15.8
Ceftazidime	3,753	0.3, 3.5	5.0, 5.3	0.5, 5.7	8.5, 8.9
Cefepime	3,753	1.7*, 3.5	3.3, 4.2	2.8*, 5.2	6.0, 7.5
Gentamicin	3,753	0.1, 0.6	7.4, 7.5	0.0, 0.7	8.5, 8.5
Tobramycin	3,741	4.9, 0.8	3.4, 8.3	4.8, 0.7	4.6, 9.3
Amikacin	3,753	0.0, 1.3	0.0, 0.1	0.0, 2.6	0.3, 0.3
Ciprofloxacin	3,753	0.3, 0.9	11.3, 11.6	0.7, 1.8	15.1, 15.8
Meropenem	3,752	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

continued

Table 16: (continued)

Species and antimicrobial	Number	Community onset		Hospital onset	
		%I	%R	%I	%R
Klebsiella pneumoniae					
Community onset, 70%; hospital onset, 30%					
Amoxicillin–clavulanate	932	4.3, –**	2.3, –**	6.2, –**	9.1, –**
Piperacillin–tazobactam	925	2.8, 4.9	1.4, 4.1	3.7, 7.0	8.1, 11.7
Ceftriaxone	932	0.0, 0.0	5.0, 5.0	0.4, 0.4	7.3, 7.3
Ceftazidime	932	0.2, 1.4	3.7, 3.8	0.4, 3.6	6.9, 7.3
Cefepime	932	0.9*, 2.0	1.1, 1.8	0.7*, 3.6	2.9, 2.9
Gentamicin	932	0.3, 0.2	3.8, 4.1	0.4, 0.7	5.5, 5.8
Tobramycin	927	2.9, 0.3	2.0, 4.9	4.0, 0.4	3.3, 7.3
Amikacin	932	0.0, 0.3	0.2, 0.2	0.0, 0.7	0.0, 0.0
Ciprofloxacin	932	1.7, 2.7	1.8, 3.5	1.8, 5.1	2.9, 4.7
Meropenem	932	0.0, 0.0	0.3, 0.3	0.4, 0.0	0.4, 0.4
Klebsiella oxytoca					
Community onset, 70%; hospital onset, 30%					
Amoxicillin–clavulanate	224	1.9, –**	5.1, –**	8.8, –**	13.2, –**
Piperacillin–tazobactam	222	0.0, 1.3	5.2, 5.2	4.4, 1.5	16.2, 20.6
Ceftriaxone	223	0.0, 0.0	5.8, 5.8	1.5, 1.5	13.4, 13.4
Ceftazidime	224	0.6, 0.6	0.0, 0.6	0.0, 1.5	2.9, 2.9
Cefepime	224	0.6*, 0.6	0.6, 1.3	0.0, 0.0	0.0, 0.0
Gentamicin	224	0.6, 0.6	0.0, 0.6	0.0, 0.0	2.9, 2.9
Tobramycin	222	0.6, 0.6	0.0, 0.6	2.9, 0.0	0.0, 2.9
Amikacin	224	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Ciprofloxacin	224	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.5, 1.5
Meropenem	224	0.6, 0.0	0.0, 0.0	0.0, 0.0	1.5, 1.5
Proteus mirabilis					
Community onset, 80%; hospital onset, 20%					
Ampicillin	210	0.0, –†	19.6, 19.5	0.0, –†	7.3, 7.3
Amoxicillin–clavulanate	210	9.5, –**	1.8, –**	4.9, –**	0.0, –**
Piperacillin–tazobactam	207	0.6, 0.0	0.6, 1.2	0.0, 0.0	0.0, 0.0
Ceftriaxone	210	0.0, 0.0	1.2, 1.2	0.0, 0.0	4.9, 4.9
Ceftazidime	210	0.0, 0.0	1.2, 1.2	0.0, 0.0	2.4, 2.4
Cefepime	210	0.6*, 0.6	0.6, 0.6	0.0, 0.0	2.4, 2.4
Gentamicin	210	0.6, 1.8	0.6, 1.2	4.9, 4.9	0.0, 4.9
Tobramycin	209	0.6, 0.0	0.6, 1.2	2.5, 0.0	2.5, 5.0

continued

Table 16: (continued)

Species and antimicrobial	Number	Community onset		Hospital onset	
		%I	%R	%I	%R
Proteus mirabilis (continued)					
Amikacin	210	0.0, 0.6	0.0, 0.0	0.0, 4.9	0.0, 0.0
Ciprofloxacin	210	0.0, 0.6	4.1, 4.1	2.4, 0.0	2.4, 4.9
Meropenem	209	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Pseudomonas aeruginosa					
Community onset, 57%; hospital onset, 43%					
Piperacillin-tazobactam	617	5.9, -†	3.4, 9.3	8.0, -†	11.9, 19.9
Ceftazidime	623	4.5, -†	2.8, 7.3	6.0, -†	8.6, 14.7
Cefepime	624	0.0, -†	0.8, 5.9	0.0, -†	4.1, 10.2
Gentamicin	624	0.8, -†	0.6, 1.4	0.8, -†	5.3, 6.0
Tobramycin	619	0.3, -†	0.3, 0.6	0.0, -†	4.6, 4.6
Amikacin	624	0.0, 1.4	0.0, 0.0	0.8, 2.3	1.1, 1.9
Ciprofloxacin	623	2.5, 0.0	3.1, 5.7	1.9, 0.0	5.3, 7.4
Meropenem	623	3.1, 3.9	2.2, 1.4	4.9, 7.2	6.8, 4.5
Salmonella species (non-typhoidal)					
Community onset, 87%; hospital onset, 13%					
Ampicillin	110	0.0, -†	7.3, 7.3	0.0, -†	21.4, 21.4
Amoxicillin-clavulanate	110	2.1, -**	1.0, -**	0.0, -**	14.3, -**
Piperacillin-tazobactam	110	0.0, 0.0	0.0, 0.0	7.1, 0.0	0.0, 7.1
Ceftriaxone	110	0.0, 0.0	2.1, 2.1	0.0, 0.0	7.1, 7.1
Ceftazidime	110	0.0, 0.0	1.0, 1.0	0.0, 0.0	7.1, 7.1
Cefepime	110	0.0*, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Gentamicin	110	0.0, 0.0	1.0, 1.0	0.0, 0.0	7.1, 7.1
Tobramycin	110	0.0, 2.1	0.0, 0.0	0.0, 0.0	7.1, 7.1
Amikacin	110	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Ciprofloxacin	110	-‡	1.0, 6.3	-‡	7.1, 7.1
Meropenem	110	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Serratia marcescens					
Community onset, 49%; hospital onset, 51%					
Ampicillin	169	38.6, -†	34.9, 73.5	39.5, -†	36.0, 75.6
Amoxicillin-clavulanate	176	22.1, -†	59.3, -†	21.1, -†	65.6, -†
Piperacillin-tazobactam	132	-§§	-§§	-§§	-§§
Ceftriaxone	176	0.0, 0.0	0.0, 0.0	1.1, 1.1	5.6, 5.6
Ceftazidime	176	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.2, 2.2

continued

Table 16: (continued)

Species and antimicrobial	Number	Community onset		Hospital onset	
		%I	%R	%I	%R
Serratia marcescens (continued)					
Cefepime	176	0.0§, 0.0	0.0, 0.0	1.1, 1.1	0.0, 1.1
Gentamicin	176	0.0, 0.0	0.0, 0.0	0.0, 0.0	4.4, 4.4
Tobramycin	175	7.1, 11.8	0.0, 7.1	13.3, 7.8	3.3, 16.7
Amikacin	176	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.1, 1.1
Ciprofloxacin	176	1.2, 1.2	0.0, 1.2	0.0, 1.2	1.1, 1.1
Meropenem	176	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.1, 1.1
Staphylococcus aureus					
Community onset, 77%; hospital onset, 23%					
Benzylpenicillin	2,396	–†, –†	82.5, 82.5	–†, –†	81.7, 81.7
Ciprofloxacin	2,397	0.3, –†	8.6, 8.9	0.6, –†	15.9, 16.4
Clindamycin	2,397	0.0, 0.2	2.6, 2.6	0.0, 0.2	5.5, 5.5
Daptomycin	2,396	0.2#, –§	–†, 0.2	0.4#, –§	–†, 0.4
Erythromycin	2,397	4.4, 0.3	11.5, 12.7	3.3, 0.6	15.7, 17.0
Gentamicin	2,397	0.6, –§	1.8, 2.8	2.4, –§	5.4, 8.3
Linezolid	2,396	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Oxacillin	2,395	–§, –§	16.1, 16.1	–§, –§	22.5, 22.5
Rifampicin	2,346	0.1, –##	0.3, 0.3	0.2, –##	1.5, 1.7
Trimethoprim–sulfamethoxazole	2,397	–§, 0.1	3.3, 3.2	–§, 0.6	6.3, 5.7
Teicoplanin	2,397	0.0, 0.1	0.0, 0.0	0.0, 0.0	0.0, 0.0
Tetracycline	2,138	0.1, 0.5	3.8, 3.9	0.2, 0.4	9.0, 9.2
Vancomycin	2,396	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 susceptibility; R = resistant

* Includes sensitive dose dependent category for CLSI

† No category defined

§ No guidelines for indicated species

Non-susceptible, resistance not defined

** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanate 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 determine 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.

6.3 Multi-drug resistance

The most problematic pathogens are those with multiple acquired resistances. Although there is no agreed benchmark for the definition of multi-drug resistance, acquired resistance to more than three agents has been chosen as the definition 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, where applicable.

Only isolates for which the full range of antimicrobial agents was tested were included for determination of multi-drug resistance. EUCAST breakpoints were used throughout in the analysis. For cefazolin, the EUCAST-approved Australian National Advisory Committee guidelines were used. For amoxicillin-clavulanate, CLSI breakpoints were used, because both the Vitek and Phoenix cards used the CLSI formulation for this agent.

Acinetobacter baumannii complex has not been included because there are too few breakpoints to permit analysis.

Multiple acquired resistances for key species are shown in Tables 17 to 23. The agents included for each species are listed in the notes after each table. For other common species, refer to Appendix D.

Table 17: Multiple acquired resistance in *Enterobacter cloacae* complex, by state and territory, 2015

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	%
NSW	57	39	3	2	6	87.7	2	1	2	2	0	0	0	12.3
Vic	77	49	6	0	7	80.5	5	3	5	2	0	0	0	19.5
Qld	64	42	4	0	6	81.3	4	3	2	3	0	0	0	18.8
SA	13	10	2	1	0	100.0	0	0	0	0	0	0	0	0.0
WA	41	29	0	2	4	85.4	4	2	0	0	0	0	0	14.6
Tas	11	7	1	2	0	90.9	0	1	0	0	0	0	0	9.1
NT	9	6	1	0	1	88.9	0	1	0	0	0	0	0	11.1
ACT	5	5	0	0	0	100.0	0	0	0	0	0	0	0	0.0
Total	277	187	17	7	24	84.8	15	11	9	7	0	0	0	15.2

MDR = multi-drug resistant

Note: Antimicrobials were piperacillin-tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table 18: Multiple acquired resistance in *Enterococcus faecalis*, by state and territory, 2015

		Number of drug resistances (non-MDR)					Number of drug resistances (MDR)		
State or territory	Total	0	1	2	3	%	4	5	%
NSW	149	134	15	0	0	100.0	0	0	0.0
Vic	109	92	16	1	0	100.0	0	0	0.0
Qld	83	73	9	1	0	100.0	0	0	0.0
SA	43	40	3	0	0	100.0	0	0	0.0
WA	91	83	8	0	0	100.0	0	0	0.0
Tas	0*	na	na	na	na	na	na	na	na
NT	10	7	3	0	0	100.0	0	0	0.0
ACT	35	30	5	0	0	100.0	0	0	0.0
Total	520	459	59	2	0	100.0	0	0	0.0

MDR = multi-drug resistant; na = not applicable

* Ciprofloxacin minimum inhibitory concentrations not provided

Note: Antimicrobials were ampicillin, ciprofloxacin, nitrofurantoin, vancomycin, linezolid.

Table 19: Multiple acquired resistance in *Enterococcus faecium*, by state and territory, 2015

		Number of drug resistances (non-MDR)					Number of drug resistances (MDR)	
State or territory	Total	0	1	2	3	%	4	%
NSW	114	16	8	48	42	100.0	0	0.0
Vic	120	12	0	32	76	100.0	0	0.0
Qld	28	5	0	5	18	100.0	0	0.0
SA	27	1	11	14	1	100.0	0	0.0
WA	53	11	0	36	6	100.0	0	0.0
Tas	1	0	0	1	0	100.0	0	0.0
NT	8	1	0	1	6	100.0	0	0.0
ACT	22	1	0	10	11	100.0	0	0.0
Total	373	47	19	147	160	100.0	0	0.0

MDR = multi-drug resistant

Note: Antimicrobials were ampicillin, ciprofloxacin, linezolid, vancomycin.

Table 20: Multiple acquired resistance in *Escherichia coli*, by state and territory, 2015

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	1,106	418	161	159	99	75.7	59	47	30	67	23	24	10	9	0	0	24.3
Vic	604	215	103	96	57	78.0	30	33	19	26	14	7	3	1	0	0	22.0
Qld	676	285	96	118	69	84.0	44	28	11	10	5	5	3	2	0	0	16.0
SA	452	225	59	48	45	83.4	28	15	10	11	3	5	3	0	0	0	16.6
WA	573	216	105	86	59	81.3	41	14	11	21	7	10	3	0	0	0	18.7
Tas	49	25	7	9	2	87.8	4	1	1	0	0	0	0	0	0	0	12.2
NT	137	47	26	24	13	80.3	7	8	5	3	1	1	2	0	0	0	19.7
ACT	146	66	23	21	14	84.9	4	3	6	6	0	1	2	0	0	0	15.1
Total	3,743	1,497	580	561	358	80.0	217	149	93	144	53	53	26	12	0	0	20.0

MDR = multi-drug resistant

Note: Antimicrobials were ampicillin, amoxicillin–clavulanate (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, nitrofurantoin, trimethoprim, meropenem.

Table 21: Multiple acquired resistance in *Klebsiella pneumoniae*, by state and territory, 2015

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	235	170	25	14	5	91.1	5	1	2	6	3	4	0	0	8.9
Vic	150	108	12	4	2	84.0	5	2	4	4	4	4	0	1	16.0
Qld	184	136	27	8	3	94.6	3	1	0	1	1	4	0	0	5.4
SA	85	65	12	1	2	94.1	2	0	1	0	0	1	1	0	5.9
WA	164	128	12	8	5	93.3	5	1	2	1	0	2	0	0	6.7
Tas	9	7	1	0	1	100.0	0	0	0	0	0	0	0	0	0.0
NT	47	33	3	4	3	91.5	3	0	0	0	0	1	0	0	8.5
ACT	35	20	9	3	0	91.4	2	0	0	0	1	0	0	0	8.6
Total	909	667	101	42	21	91.4	25	5	9	12	9	16	1	1	8.6

MDR = multi-drug resistant

Note: Antimicrobials were amoxicillin–clavulanate (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table 22: Multiple acquired resistance in *Staphylococcus aureus* (methicillin resistant), by state and territory, 2015

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	107	17	25	24	9	70.1	20	11	1	0	0	0	0	0	0	29.9
Vic	63	15	23	12	6	88.9	3	2	2	0	0	0	0	0	0	11.1
Qld	62	33	17	9	1	96.8	1	1	0	0	0	0	0	0	0	3.2
SA	9	2	3	2	1	88.9	0	1	0	0	0	0	0	0	0	11.1
WA	69	24	27	10	6	97.1	2	0	0	0	0	0	0	0	0	2.9
Tas	0*	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na
NT	42	23	11	1	0	83.3	0	7	0	0	0	0	0	0	0	16.7
ACT	12	3	6	1	0	83.3	2	0	0	0	0	0	0	0	0	16.7
Total	364	117	112	59	23	85.4	28	22	3	0	0	0	0	0	0	14.6

MDR = multi-drug resistant; na = not applicable

* Nitrofurantoin and rifampicin minimum inhibitory concentrations not provided

Note: Antimicrobials were ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin (CLSI), rifampicin, trimethoprim–sulfamethoxazole, tetracycline, vancomycin.

Table 23: Multiple acquired resistance in *Staphylococcus aureus* (methicillin susceptible), by state and territory, 2015

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	389	80	265	30	13	99.7	1	0	0	0	0	0	0	0	0	0	0.3
Vic	344	86	217	33	7	99.7	0	1	0	0	0	0	0	0	0	0	0.3
Qld	385	81	247	45	12	100.0	0	0	0	0	0	0	0	0	0	0	0.0
SA	85	21	59	3	2	100.0	0	0	0	0	0	0	0	0	0	0	0.0
WA	325	64	219	37	5	100.0	0	0	0	0	0	0	0	0	0	0	0.0
Tas	0*	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na
NT	68	10	40	16	1	98.5	1	0	0	0	0	0	0	0	0	0	1.5
ACT	69	13	46	6	4	100.0	0	0	0	0	0	0	0	0	0	0	0.0
Total	1,665	355	1,093	170	44	99.8	2	1	0	0	0	0	0	0	0	0	0.2

MDR = multi-drug resistant; na = not applicable

* Nitrofurantoin and rifampicin minimum inhibitory concentrations not provided

Note: Antimicrobials were benzylpenicillin, ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin (CLSI), rifampicin, trimethoprim–sulfamethoxazole, tetracycline, vancomycin.

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

Multi-drug resistances by onset setting (community or hospital) and 30-day all-cause mortality for the most common species are shown in Table 24.

Table 24: Multi-drug resistance, by onset setting and 30-day all-cause mortality, 2015

		Total		Community onset		Hospital onset	
Species	**Category***	**Number**	**Deaths (%)**	**Number**	**Deaths (%)**	**Number**	**Deaths (%)**
Escherichia coli	Total	2,272	244 (10.7)	1,880	162 (8.6)	392	82 (20.9)
	Non-MDR (≤3)	1,734	178 (10.3)	1,475	124 (8.4)	259	54 (20.8)
	MDR (>3)	538	66 (12.3)	405	38 (9.4)	133	28 (21.1)
Enterobacter cloacae complex	Total	200	23 (11.5)	99	12 (12.1)	101	11 (10.9)
	Non-MDR (≤3)	167	16 (9.6)	89	8 (9.0)	78	8 (10.3)
	MDR (>3)	33	7 (21.2)	10	4 (40.0)	23	3 (13.0)
Enterococcus faecalis	Total	385	70 (18.2)	246	47 (19.1)	139	23 (16.5)
	Non-MDR (≤3)	385	70 (18.2)	246	47 (19.1)	139	23 (16.5)
	MDR (>3)	0	na	0	na	0	na
Enterococcus faecium	Total	300	79 (26.3)	78	16 (20.5)	222	63 (28.4)
	Non-MDR (≤3)	194	47 (24.2)	61	14 (23.0)	133	33 (24.8)
	MDR (>3)	106	32 (30.2)	17	2 (11.8)	89	30 (33.7)
Klebsiella pneumoniae	Total	610	84 (13.8)	431	55 (12.8)	179	29 (16.2)
	Non-MDR (≤3)	548	74 (13.5)	395	50 (12.7)	153	24 (15.7)
	MDR (>3)	62	10 (16.1)	36	5 (13.9)	26	5 (19.2)
Staphylococcus aureus	Total	1,697	270 (15.9)	1,278	203 (15.9)	419	67 (16.0)
	Non-MDR (≤3)	1,562	238 (15.2)	1,198	181 (15.1)	364	57 (15.7)
	MDR (>3)	135	32 (23.7)	80	22 (27.5)	55	10 (18.2)
Staphylococcus aureus, methicillin resistant	Total	299	53 (17.7)	202	36 (17.8)	97	17 (17.5)
	Non-MDR (≤3)	222	39 (17.6)	159	27 (17.0)	63	12 (19.0)
	MDR (>3)	77	14 (18.2)	43	9 (20.9)	34	5 (14.7)
Staphylococcus aureus, methicillin susceptible	Total	1,398	217 (15.5)	1,076	167 (15.5)	322	50 (15.5)
	Non-MDR (≤3)	1,390	214 (0.0)	1,073	166 (0.0)	317	48 (0.0)
	MDR (>3)	8	3†	3	1†	5	2†
Pseudomonas aeruginosa	Total	406	75 (18.5)	228	42 (18.4)	178	33 (18.5)
	Non-MDR (≤3)	397	70 (17.6)	228	42 (18.4)	169	28 (16.6)
	MDR (>3)	9	5†	0	na	9	5†
	Non-MDR (≤2)	388	68 (17.5)	225	42 (18.7)	163	26 (16.0)
	MDR (>2)	18	7 (38.9)	3	0 (0.0)	15	7 (46.7)

MDR = multi-drug resistant; na = not applicable

* MDR is defined in Section 6.3. For *P. aeruginosa*, resistance to more than two agents was also included.

† Insufficient numbers (<10) to calculate percentage

7 Trend analysis (2013–2015)

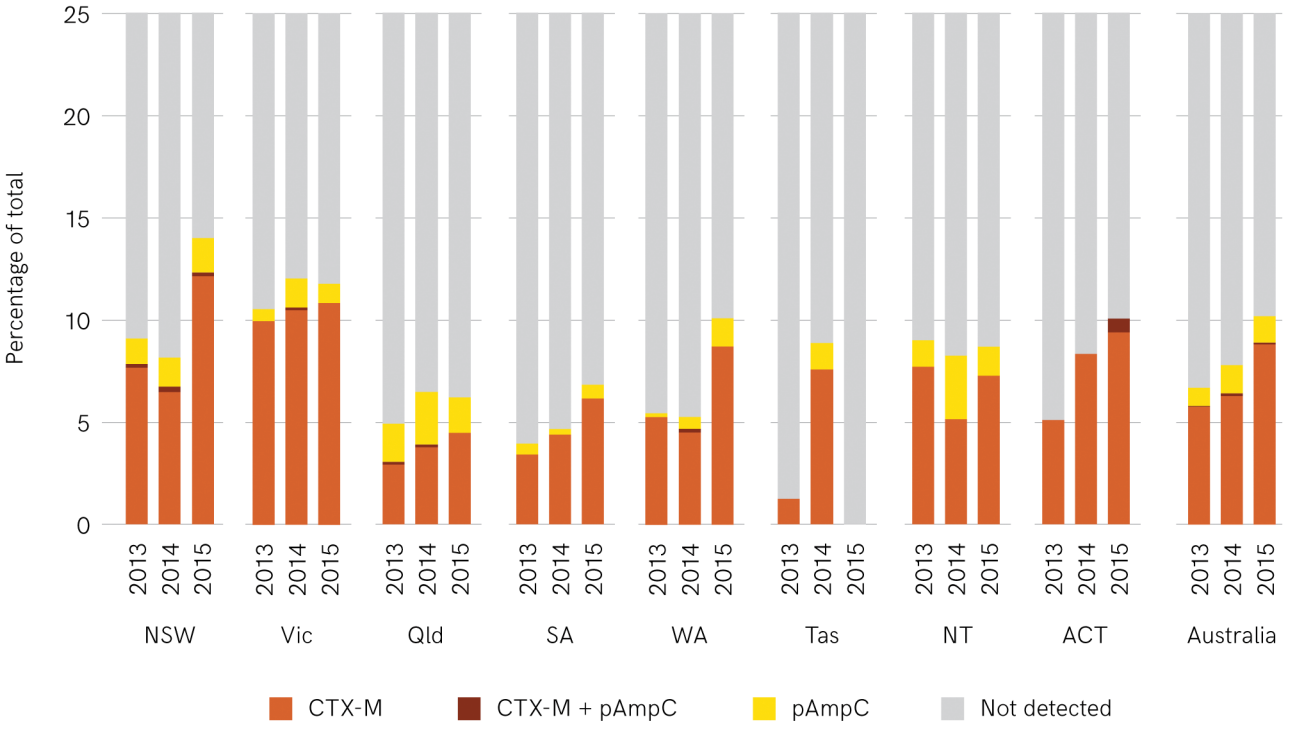
7.1 Gram-negative species

Trend data were available for Enterobacteriaceae for the period 2013 to 2015. *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–clavulanate, as both the Vitek and Phoenix cards used the CLSI formulation for this agent.

7.1.1 Extended-spectrum β-lactamases

Nationally, there was a significant increase in the proportion of *E. coli* with CTX-M-type (see Section 8.1.1) and/or plasmid-borne AmpC β-lactamases (CTX-M types; χ^2 for linear trend = 25.95, $P < 0.001$). Most of this increase was driven by the sharp increases in CTX-M types seen in New South Wales and Western Australia (Figure 4).

Figure 4: Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Escherichia coli* by state and territory, and nationally, 2013–2015



SHV or 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 extended-spectrum β-lactamases (ESBLs).

The proportion of *K. pneumoniae* with CTX-M-type or plasmid-borne AmpC β-lactamases remained steady during the period 2013–2015, although regional variations were seen (Figure 5).

7.1.2 *Escherichia coli*

Non-susceptibility to key anti-gram-negative antimicrobial agents showed a steady increase from 2013 to 2015 (Figure 6). There was a significant increase in non-susceptibility to ciprofloxacin (χ^2 for linear trend = 8.64, $P < 0.01$).

7.1.3 *Klebsiella pneumoniae*

There was a decrease in non-susceptibility among *K. pneumoniae* in 2015 compared with 2014 (Figure 7).

Figure 5: Proportion of CTX-M-type and plasmid-borne AmpC β-lactamases in *Klebsiella pneumoniae* by state and territory, and nationally, 2013–2015

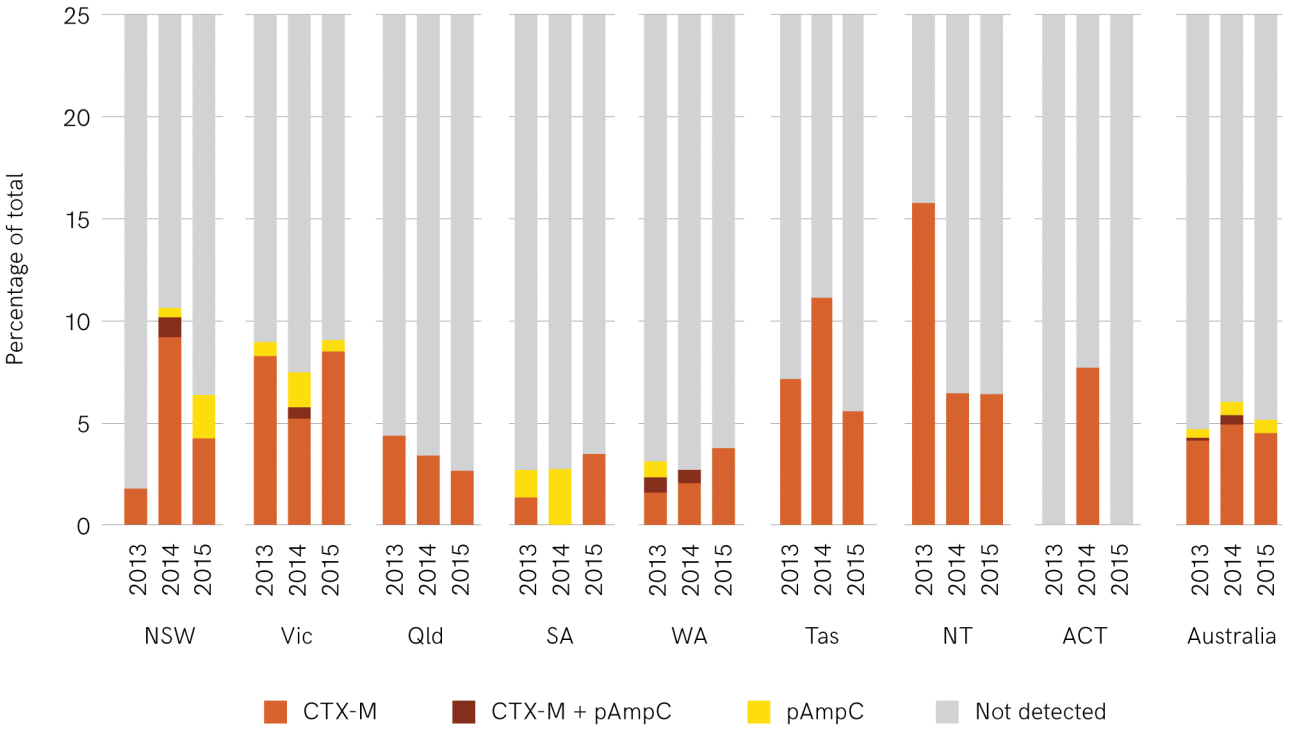
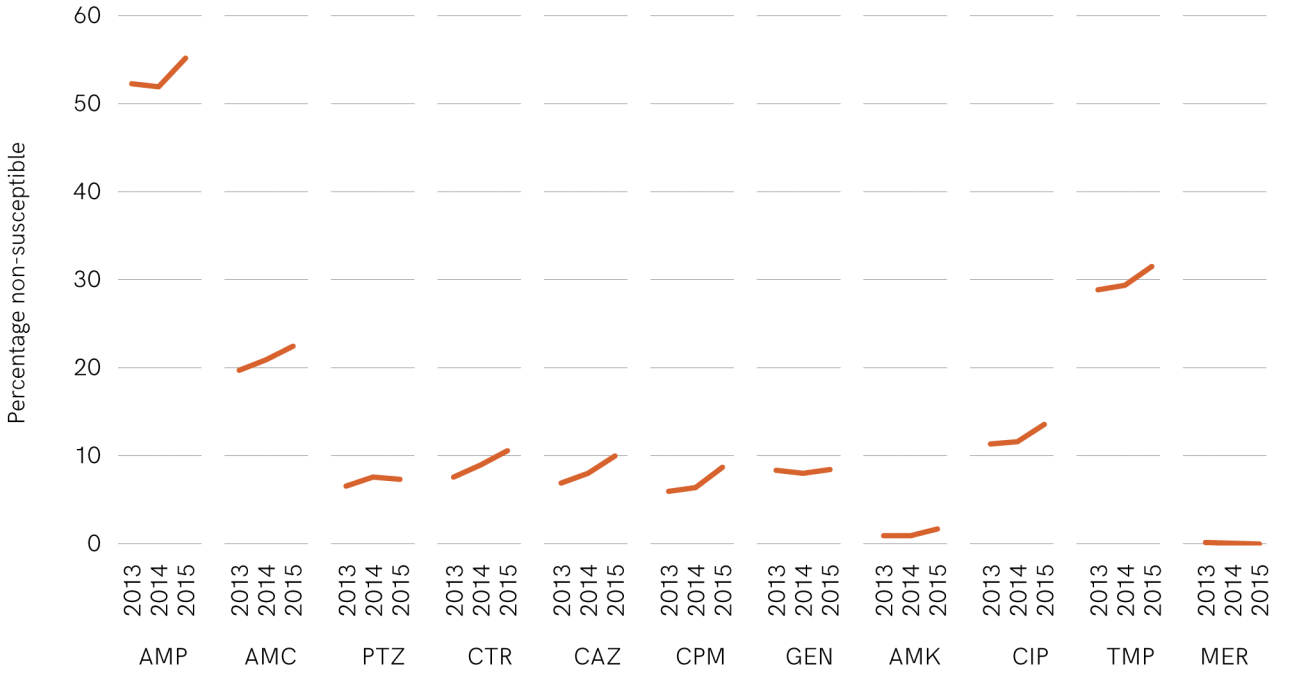
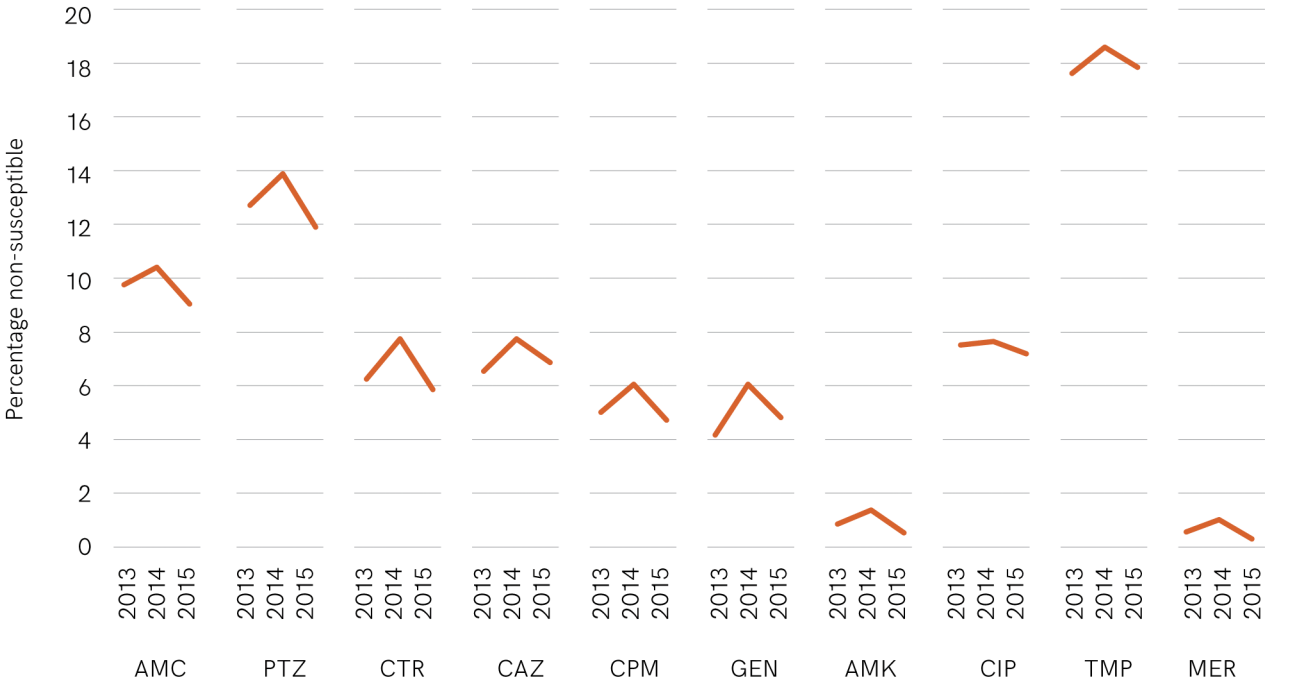


Figure 6: Non-susceptibility of *Escherichia coli* to key antimicrobials (EUCAST), Australia, 2013–2015



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

Figure 7: Non-susceptibility of *Klebsiella pneumoniae* to key antimicrobials (EUCAST), Australia, 2013–2015

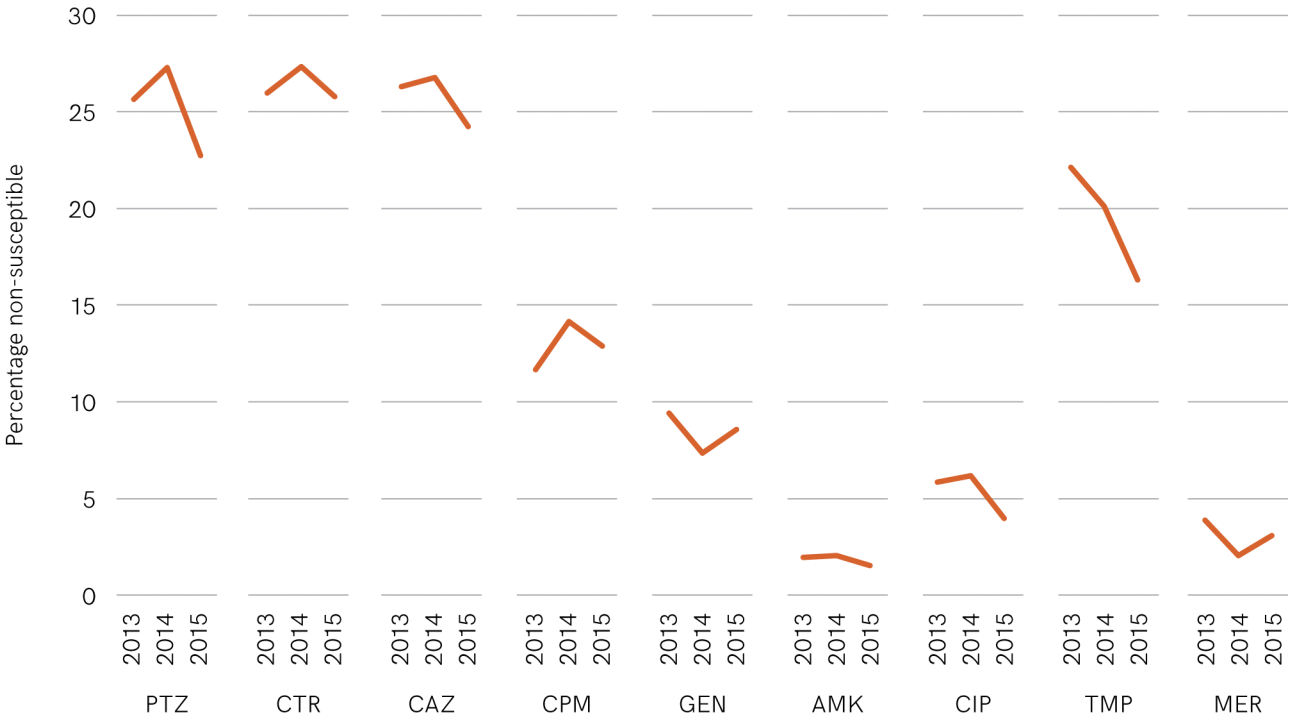


AMC = amoxicillin–clavulanate (2:1 ratio); AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; TMP = trimethoprim

7.1.4 *Enterobacter cloacae* complex

There were no significant differences in non-susceptibility to key antimicrobials for *E. cloacae* over the three-year period 2013–2015 (Figure 8).

Figure 8: Non-susceptibility of *Enterobacter cloacae* to key antimicrobials (EUCAST), Australia, 2013–2015



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

7.2 *Enterococcus* species

7.2.1 Vancomycin-resistant *Enterococcus faecium*

The proportion of vancomycin-resistant enterococcus (*Enterococcus faecium*) (VRE) by state and territory is shown in Table 25. Although VRE was detected in both the Northern Territory and Tasmania, total numbers for each year were less than 10.

7.2.2 *Enterococcus faecalis*

Non-susceptibility (EUCAST) to key antimicrobial agents for *E. faecalis* by state and territory is shown in Table 26. Both ciprofloxacin non-susceptibility and high-level gentamicin resistance were lower in all states in 2015 than in 2014; resistance to all other agents remained constant. The only significant trend over the years 2013–2015 was a decrease in ciprofloxacin non-susceptibility in New South Wales (χ^2 for trend, P = 0.0410).

Table 25: Number and percentage of vancomycin-resistant *Enterococcus faecium*, by state and territory, 2013–2015

State or territory	2013		2014		2015			
	Total	% R (*n*)	Total	% R (*n*)	Total	% R (*n*)	*P**	Trend†
NSW	107	43.9 (47)	104	50.0 (52)	116	51.7 (60)	ns	
Vic	80	53.8 (43)	94	66.0 (62)	120	63.3 (76)	ns	
Qld	37	40.5 (15)	37	40.5 (15)	31	61.3 (19)	ns	
SA	32	59.4 (19)	46	56.5 (26)	44	52.3 (23)	ns	
WA	42	4.8 (2)	50	20.0 (10)	53	11.3 (6)	ns	
Tas	5	0§	7	1§	8	1§	na	
NT	3	3§	1	0§	8	6§	na	
ACT	18	33.3 (6)	41	24.4 (10)	22	50.0 (11)	ns	
Australia	324	41.7 (135)	380	46.3 (176)	402	50.2 (202)	0.0213	

na = not applicable; ns = not significant; R = resistant

* χ^2 for trend

† Bar graphs for the years 2013, 2014 and 2015, with highest point shaded red

§ Insufficient numbers to calculate percentage

Table 26: Number and percentage of non-susceptible *Enterococcus faecalis* (EUCAST), by state and territory, 2013–2015

Antimicrobial	Year	Number tested	Number non-susceptible (%)								
			NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ampicillin	2013	477	1 (0.8)	0	0	0	0	0	0	0	1 (0.2)
	2014	522	0	0	2 (2.0)	1 (2.0)	0	0	0	0	3 (0.6)
	2015	561	0	0	1 (1.1)	0	0	0	0	0	1 (0.2)
Vancomycin	2013	477	1 (0.8)	1 (0.9)	0	0	0	0	0	0	2 (0.4)
	2014	522	0	0	1 (1.0)	0	0	0	0	0	1 (0.2)
	2015	561	2 (1.3)	1 (0.9)	0	0	0	1 (8.3)	0	0	4 (0.7)
Teicoplanin	2013	476	1 (0.8)	0	0	0	0	1 (9.1)	0	0	2 (0.4)
	2014	521	0	0	0	0	0	0	0	0	0 (0.0)
	2015	558	0	0	0	0	0	0	0	0	0 (0.0)
Ciprofloxacin	2013	439	30 (24.6)	12 (11.3)	11 (14.9)	14 (37.8)	7 (9.9)	na	1 (24.6)	4 (17.4)	79 (18.0)
	2014	477	31 (23.1)	24 (20.0)	14 (15.7)	12 (37.5)	7 (11.1)	na	3 (23.1)	14 (42.4)	105 (22.0)
	2015	521	22 (14.8)	17 (15.5)	8 (9.6)	11 (25.6)	8 (8.8)	na	3 (14.8)	5 (14.3)	74 (14.2)
Nitrofurantoin	2013	468	1 (0.8)	0	0	1 (2.3)	0	1 (9.1)	0	0	3 (0.6)
	2014	521	0	0	1 (1.0)	1 (2.0)	0	0	0	0	2 (0.4)
	2015	558	0	0	1 (1.1)	0	0	0	0	0	1 (0.2)
Gentamicin (high level)	2013	408	34 (40.0)	36 (34.0)	24 (27.6)	6 (31.6)	20 (28.2)	2 (18.2)	2 (33.3)	7 (30.4)	131 (32.1)
	2014	519	56 (42.4)	46 (38.7)	35 (34.3)	18 (35.3)	18 (28.6)	4 (30.8)	3 (50.0)	18 (54.5)	198 (38.2)
	2015	544	41 (29.3)	29 (27.4)	24 (25.5)	16 (28.1)	21 (23.3)	3 (25.0)	4 (40.0)	12 (34.3)	150 (27.6)
Linezolid	2013	477	0	0	0	0	0	0	0	0	0 (0.0)
	2014	522	0	0	1 (1.1)	0	0	0	0	0	0 (0.0)
	2015	561	0	0	0	0	0	0	0	0	1 (0.2)

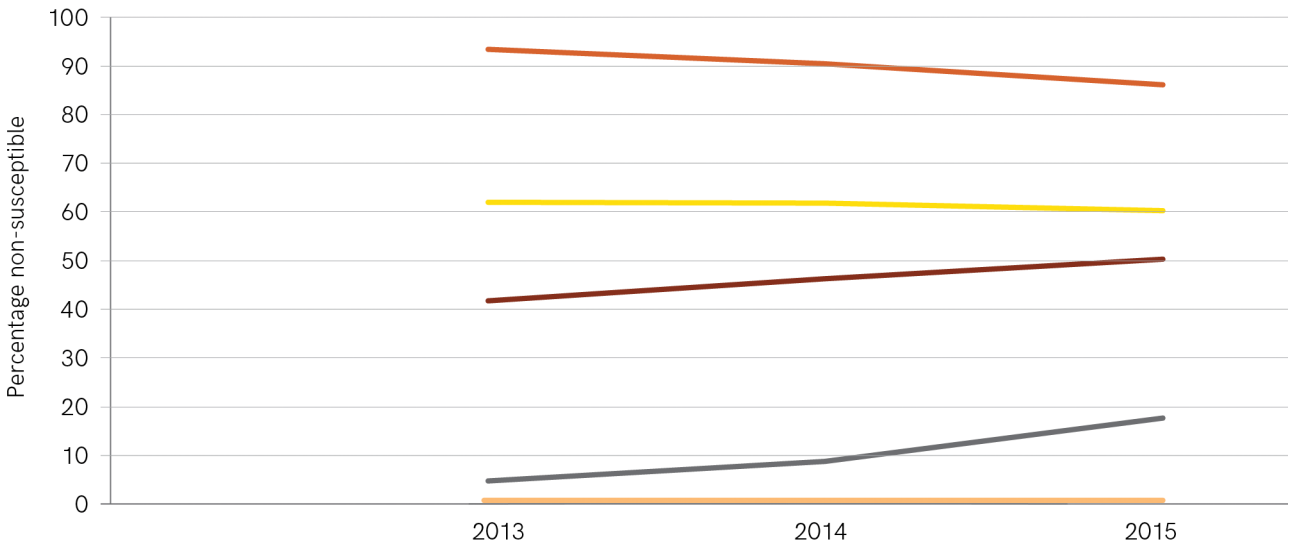
EUCAST = European Committee on Antimicrobial Susceptibility Testing; na = not applicable

7.2.3 *Enterococcus faecium*

For *E. faecium*, there was a significant decrease (χ^2 for trend, $P = 0.0027$) in ampicillin resistance from 2013 to 2015, and a significant increase in vancomycin resistance ($P = 0.0213$) and teicoplanin resistance ($P < 0.0001$) (Figure 9). No teicoplanin-resistant strains were detected in either the Northern Territory or Tasmania; all other states and territories except South Australia and Western Australia had a significant increase. This increase was due to the increased prevalence of *E. faecium* carrying *vanA* genes in these regions. Linezolid resistance has remained at less than 0.5%.

Non-susceptibility to key antimicrobial agents for *E. faecium* is shown in Table 27.

Figure 9: Non-susceptibility of *Enterococcus faecium* to key antimicrobials (EUCAST), Australia, 2013–2015



	2013	2014	2015
Ampicillin	93.5	90.5	86.8
Vancomycin	41.7	46.3	50.2
Teicoplanin	4.7	8.8	17.7
Linezolid	0.0	0.3	0.0
Gentamicin (high level)	62.0	61.8	60.5

EUCAST = European Committee on Antimicrobial Susceptibility Testing

Table 27: Number and percentage of non-susceptible *Enterococcus faecium* (EUCAST), by state and territory, 2013–2015

			Number non-susceptible (%)								
Antimicrobial	**Year**	**Total**	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
Ampicillin	2013	321	97 (90.7)	75 (93.8)	32 (88.9)	31 (96.9)	**41 (97.6)**	5 (100.0)	3 (100.0)	16 (100.0)	**300 (93.5)**
	2014	379	92 (89.3)	88 (93.6)	32 (86.5)	41 (89.1)	**47 (94.0)**	5 (71.4)	0	38 (92.7)	**343 (90.5)**
	2015	400	99 (86.1)	108 (90.0)	25 (83.3)	41 (93.2)	**42 (79.2)**	4 (50.0)	7 (87.5)	21 (95.5)	**347 (86.8)**
Vancomycin	2013	324	47 (43.9)	43 (53.8)	15 (40.5)	19 (59.4)	2 (4.8)	0	3 (100.0)	6 (33.3)	**135 (41.7)**
	2014	380	52 (50.0)	62 (66.0)	15 (40.5)	26 (56.5)	10 (20.0)	1 (14.3)	0	10 (24.4)	**176 (46.3)**
	2015	402	60 (51.7)	76 (63.3)	19 (61.3)	23 (52.3)	6 (11.3)	1 (12.5)	6 (75.0)	11 (50.0)	**202 (50.2)**
Teicoplanin	2013	321	10 (9.3)	2 (2.5)	2 (5.6)	1 (3.1)	0	0	0	0	15 (4.7)
	2014	377	30 (29.1)	1 (1.1)	0	0	1 (2.0)	0	0	1 (2.4)	33 (8.8)
	2015	401	39 (33.9)	15 (12.5)	6 (19.4)	1 (2.3)	3 (5.7)	0	0	7 (31.8)	71 (17.7)
Gentamicin (high level)	2013	271	64 (77.1)	41 (51.3)	28 (77.8)	**2 (33.3)**	13 (31.0)	3 (60.0)	3 (100.0)	14 (87.5)	168 (62.0)
	2014	377	72 (70.6)	54 (57.4)	25 (69.4)	**31 (67.4)**	20 (40.0)	1 (14.3)	0	30 (73.2)	233 (61.8)
	2015	387	67 (65.7)	71 (59.2)	19 (63.3)	**36 (81.8)**	14 (26.4)	2 (25.0)	6 (75.0)	19 (86.4)	234 (60.5)
Linezolid	2013	321	0	0	0	0	0	0	0	0	0
	2014	378	1 (1.0)	0	0	0	0	0	0	0	1 (0.3)
	2015	400	0	0	0	0	0	0	0	0	0

EUCAST = European Committee on Antimicrobial Susceptibility Testing

Note: Tinted cells indicate a significant trend.

7.3 *Staphylococcus aureus*

7.3.1 Methicillin-resistant *Staphylococcus aureus*

The proportion of *S. aureus* that is methicillin resistant throughout Australia remained constant over the years 2013–2015, although there were notable variations at state and territory level (Figure 10).

There was a significant decrease in erythromycin (χ^2 for linear trend = 5.006, P = 0.0253) and clindamycin (χ^2 for linear trend = 5.966, P = 0.0146) non-susceptible MRSA from 2013 to 2015 (Figure 11).

Figure 10: Proportion of methicillin-resistant *Staphylococcus aureus,* by state and territory, and nationally, 2013–2015

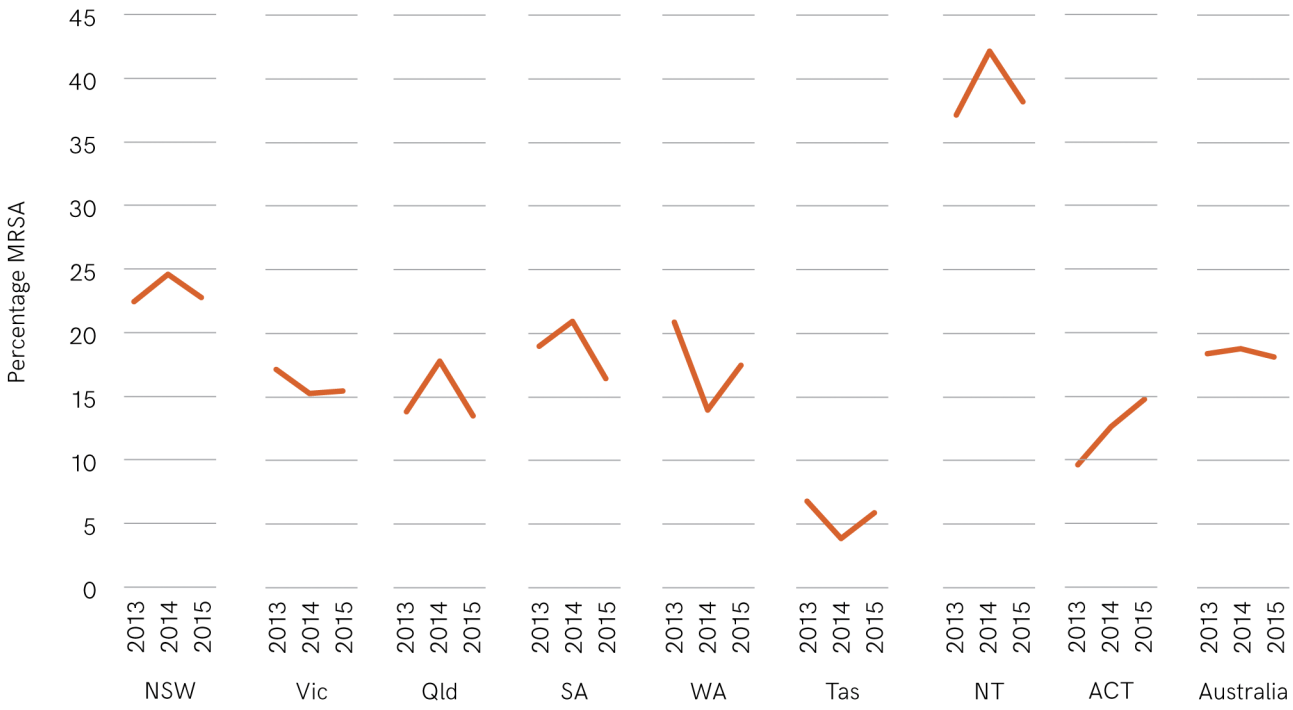
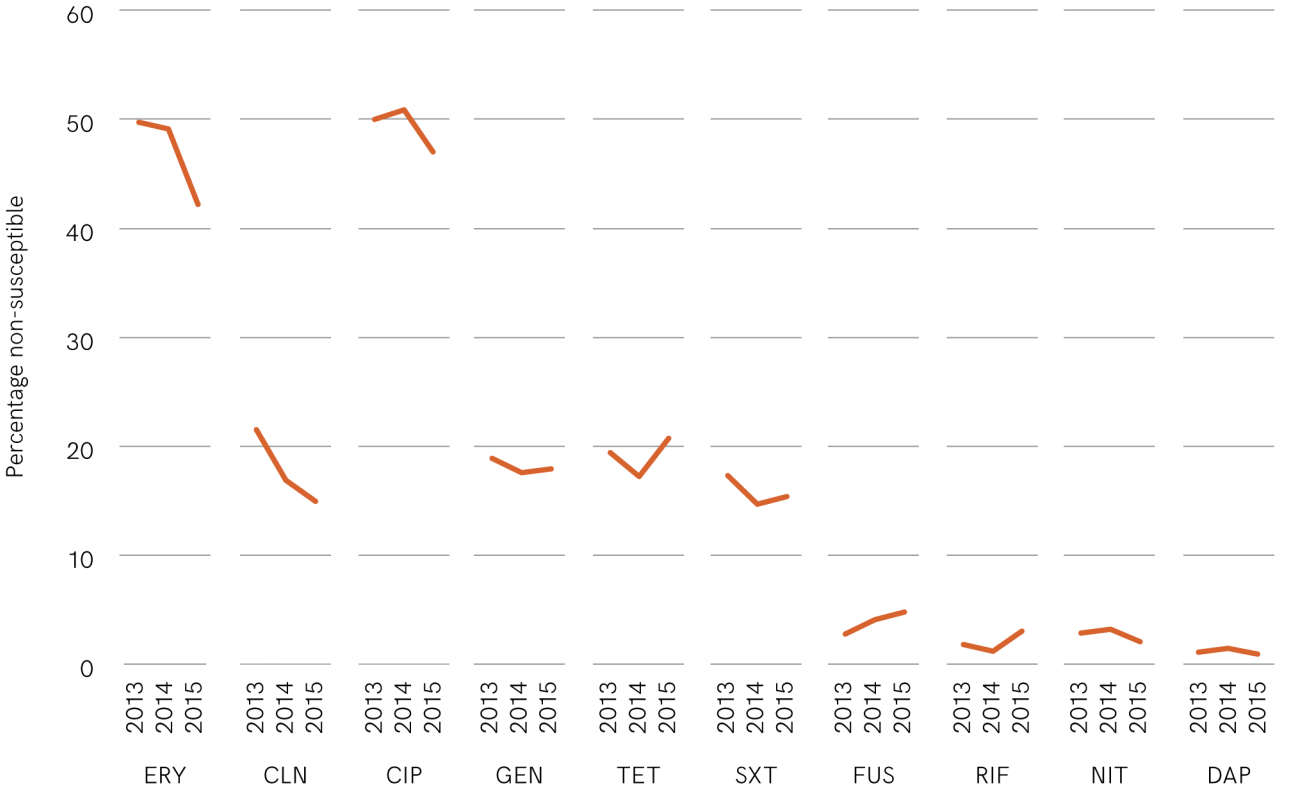


Figure 11: Non-susceptibility of methicillin-resistant *Staphylococcus aureus* to key antimicrobials (EUCAST), Australia, 2013–2015



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 = tetracycline

7.3.2 Methicillin-susceptible *Staphylococcus aureus*

There was a significant decrease in erythromycin (χ^2 for linear trend = 9.479, P = 0.0021) and clindamycin (χ^2 for linear trend = 18.54, $P \leq 0.0001$) non-susceptibility in MSSA from 2013 to 2015, as shown in Figure 12. There was also a decrease in daptomycin non-susceptibility (χ^2 for linear trend = 3.875, P = 0.0490).

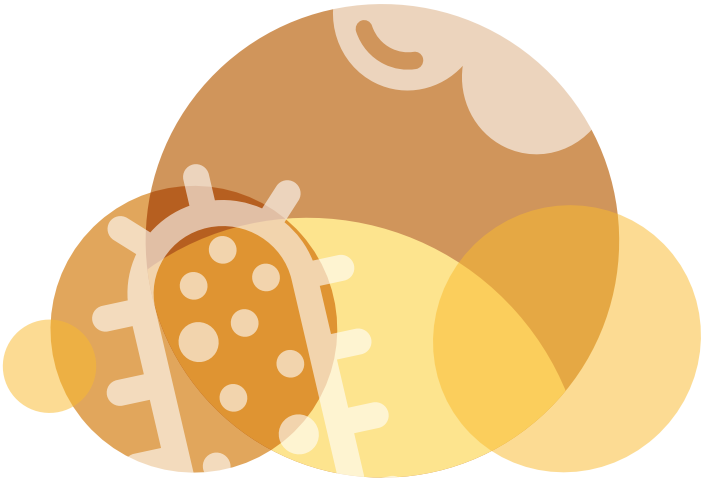
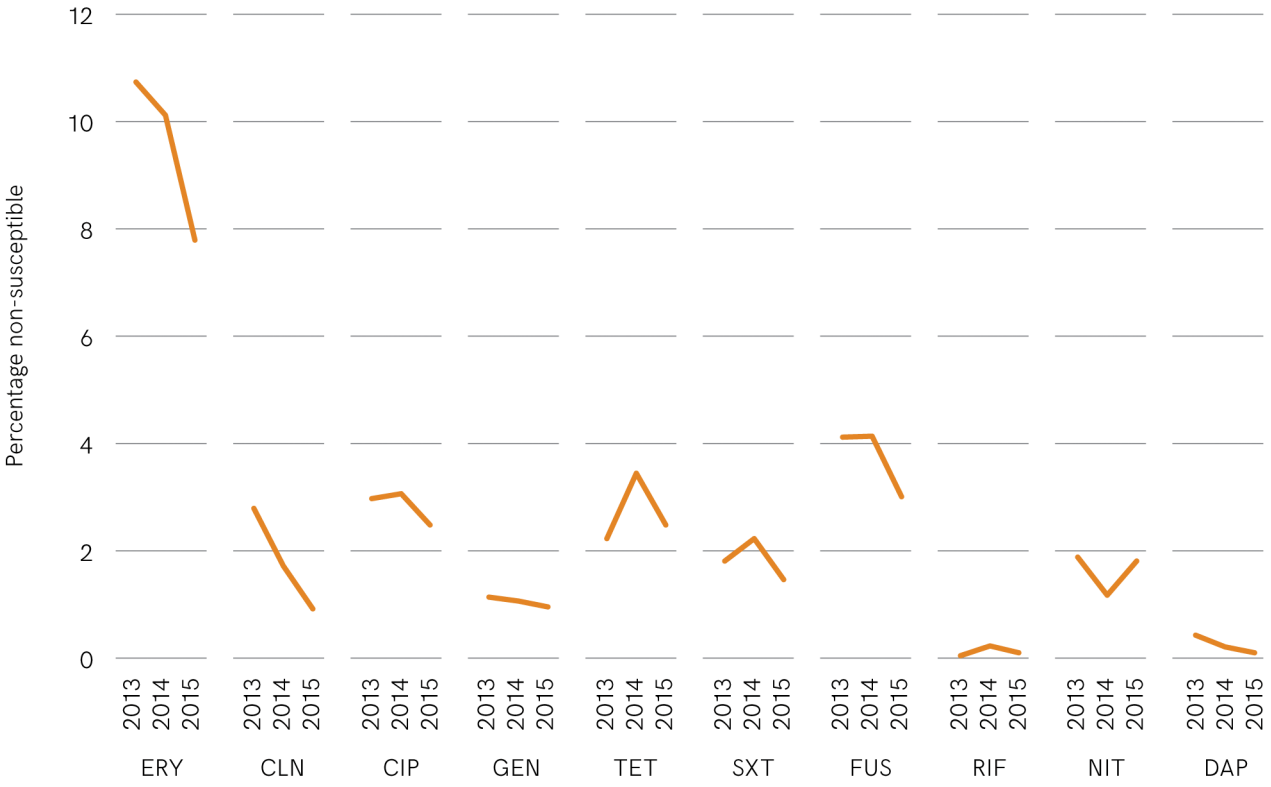
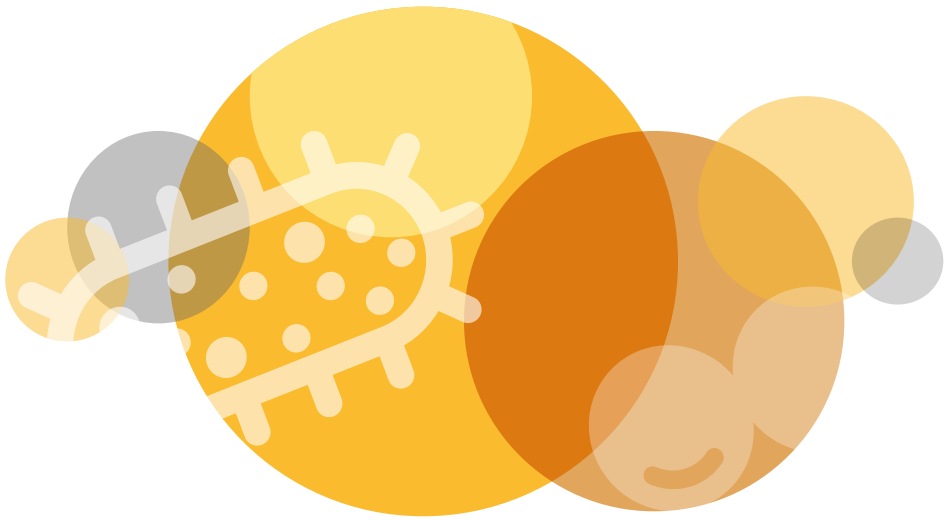


Figure 12: Non-susceptibility of methicillin-susceptible *Staphylococcus aureus* to key antimicrobials (EUCAST), Australia, 2013–2015



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 = tetracycline



8 Molecular studies

8.1 Gram-negative organisms

8.1.1 Extended-spectrum β-lactamases

ESBLs are important problem resistances internationally, especially in hospital practice. Initially, they 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* strains in 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, because third-generation cephalosporins are not widely used in that setting; it is likely 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 a useful therapeutic alternative for infections in patients presenting from the community, as evidenced by the frequency with which ceftriaxone was used for treatment in this survey. ESBL-producing strains frequently 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 strains will be captured using the CLSI/EUCAST ceftriaxone 'susceptible' breakpoint of 1 mg/L. The 'susceptible' breakpoint of 4 mg/L for ceftazidime is less sensitive for ESBL detection, but an MIC of greater than 1 mg/L is more sensitive. **Isolates with either ceftriaxone or ceftazidime MICs above 1 mg/L were selected for molecular testing**.

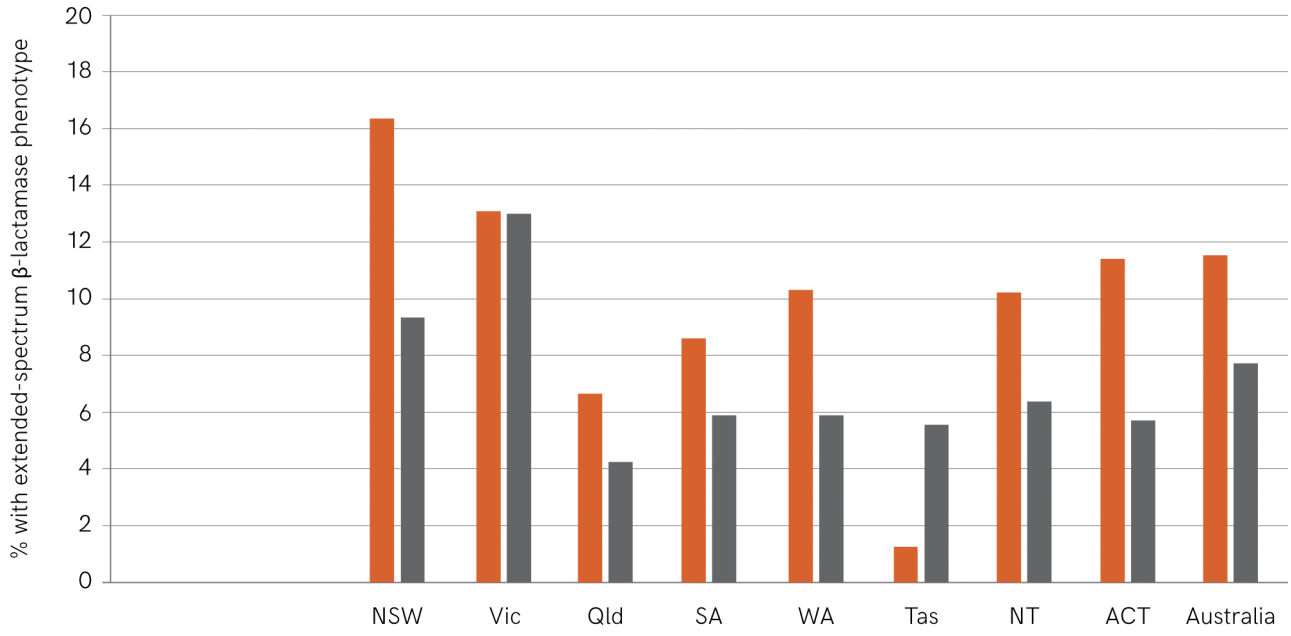
Neither ceftriaxone nor ceftazidime testing will identify ESBL production in *Enterobacter* species because of their intrinsic chromosomal AmpC β-lactamase. In these species, cefepime MICs of greater than 0.25 mg/L are suggestive that an isolate of this genus harbours an ESBL.[22] However, because of card range limitations, **isolates with a cefepime MIC greater than 1 mg/L were selected for molecular testing**.

Molecular testing involved screening for TEM, SHV, CTX-M and plasmid-borne *ampC* genes. TEM screening does not accurately discriminate between TEM-1/2 genes, which encode narrow-spectrum β-lactamases, and TEM genes with higher numbers that encode ESBLs. Similarly, SHV screening does not discriminate between SHV-1/11 genes, which are narrow-spectrum β-lactamases, and SHV genes that encode ESBLs. SHV-1 is the dominant natural chromosomal enzyme of *K. pneumoniae* leading to natural ampicillin and amoxicillin resistance. **Therefore, *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* strains that are resistant to ceftriaxone and/or ceftazidime (MIC >1 mg/L), and their variation across states and territories, are shown in Figure 13. The presumptive and confirmed ESBLs by state and territory are shown in Table 28.

Based on the tests performed in this study, ESBLs were more common among *E. coli* (10.2% confirmed) and *K. pneumoniae* (5.4% confirmed) than among other species. For *Enterobacter* species with cefepime MIC greater than 1 mg/L, 22 of 42 *E. cloacae* (52%; 6.7% overall) and 2 of 4 *E. aerogenes* contained an ESBL. Of identified ESBLs, *E. cloacae* contained the following types: TEM and SHV-types (n = 10), CTX-M group 1 and TEM (n = 2),

Figure 13: Percentage of *Escherichia coli* and *Klebsiella pneumoniae* with extended-spectrum β-lactamase phenotype, by state and territory, and nationally, 2015



	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
E. coli (*n* = 3,994)	16.4	13.1	6.7	8.6	10.3	1.3	10.2	11.4	11.5
K. pneumoniae (*n* = 974)	9.3	13.0	4.2	5.9	5.9	5.6	6.4	5.7	7.7

CTX-M group 9 only (*n* = 2), and TEM only (*n* = 8). Eight of 22 *E. cloacae* with ESBLs also contained $bla_{\text{IMP-4}}$ carbapenemases.

The majority (67%) of *K. oxytoca* isolates with an ESBL phenotype were hyperproducers of K1 β-lactamase, the natural chromosomal enzyme in this species, rather than ESBL producers. Hyperproducers of K1 β-lactamase are consistently resistant to piperacillin–tazobactam and have borderline resistance to cefepime, but remain susceptible to ceftazidime. This pattern is not typical of other types of gram-negative β-lactamases.

There was a notable presence of CTX-M enzymes in *E. coli*. Of 408 confirmed ESBLs, 349 (85.5%; range 68.3–93.8%) had CTX-M types: CTX-M group 1 (*n* = 204), CTX-M group 9 (*n* = 142), and CTX-M group 1 plus CTX-M group 9 (*n* = 3). Among *K. pneumoniae* with confirmed ESBLs, 44 of 53 (83.0%) contained CTX-M types: CTX-M group 1 (*n* = 37) and CTX-M group 9 (*n* = 7).

ESBL phenotypes were significantly more likely to be found among hospital- than community-onset episodes of *E. coli* bacteraemia (103/615 [16.7%] vs 319/3,138 [10.2%]; $P < 0.01$) and *K. pneumoniae* bacteraemia (32/275 [11.6%] vs 40/657 [6.1%]; $P \leq 0.01$). No significant difference was noted among *E. cloacae* for hospital versus community onset.

8.1.2 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 Enterobacteriaceae 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.

Table 28: Numbers of isolates with extended-spectrum β-lactamase phenotype, by state and territory, 2015

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,107	727	691	454	650	79	137	149	3,994
ESBL phenotype	181	95	46	39	67	1	14	17	460
Confirmed									
Any ESBL*/number received	151/162	86/92	41/45	32/38	64/66	1/1	12/14	16/17	408/435
CTX-M types	135	78	28	28	55	0	10	15	349
Plasmid-borne AmpC	18	7	12	3	9	0	2	1	52
SHV	1	2	2	1	1	0	0	1	14
Klebsiella pneumoniae	237	177	189	87	187	18	47	35	977
ESBL phenotype	22	23	8	5	11	1	3	2	75
Confirmed									
Any ESBL*/number received	15/19	17/23	6/7	3/5	7/11	1/1	3/3	1/2	53/71
CTX-M types	10	15	5	3	7	1	3	0	44
Plasmid-borne AmpC	4	1	0	0	0	0	0	0	5
TEM	9	13	5	1	5	1	2	1	37
Klebsiella oxytoca	76	49	45	13	30	8	4	13	238
ESBL phenotype	10	3	3	3	2	0	0	1	22
Confirmed									
Any ESBL*/number received	0/9	2/3	1/3	0/3	0/2	0/0	0/0	0/1	3/21†
CTX-M types	0	1	0	0	0	na	na	0	1
TEM	0	0	1	0	0	na	na	0	1
SHV	1	1	1	0	0	na	na	0	2
Proteus mirabilis	66	37	45	24	36	3	6	6	223
ESBL phenotype	1	2	1	0	1	0	0	0	5
Confirmed									
Any ESBL*/number received	1/1	1/2	1/1	0/0	1/1	0/0	0/0	0/0	4/5
CTX-M types	1	0	0	na	0	na	na	na	1
Plasmid-borne AmpC	0	1	0	na	1	na	na	na	2
TEM	1	0	1	na	1	na	na	na	3
Salmonella species (non-typhoidal)	19	21	28	10	10	2	24	1	115
ESBL phenotype	0	3	0	0	0	0	0	0	3
Confirmed									
Any ESBL*/number received	0/0	3/3	0/0	0/0	0/0	0/0	0/0	0/0	3/3
CTX-M types	na	1	na	na	na	na	na	na	1
Plasmid-borne AmpC	na	2	na	na	na	na	na	na	2
TEM	na	2	na	na	na	na	na	na	2

ESBL = extended-spectrum β-lactamase; na = not applicable

* Strains may possess more than one type of ESBL gene.

† See text for an explanation of the low proportion of ESBL.

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 36% (47/129) of cefoxitin-resistant *E. coli* and 14% (6/43) of cefoxitin-resistant *K. pneumoniae* that were available for molecular confirmation were confirmed to contain plasmid-borne *ampC* genes (Table 29). The bla_{CMY} gene was found in 62% (33/53) of isolates with plasmid-borne *ampC* genes. Carbapenamase genes were detected in three of the cefoxitin-resistant *K. pneumoniae* (bla_{IMP-4}, n = 1; bla_{KPC-2}, n = 1; $bla_{NDM+OXA-48}$, n = 1) and one *K. oxytoca* (bla_{IMP-4}) that did not have plasmid-borne *ampC* genes. Four *E. coli* with a cefoxitin MIC of 16 mg/L (intermediate) also contained bla_{CMY}.

Table 29: Numbers of isolates with presumptive plasmid-borne AmpC β-lactamase production, by state and territory, 2015

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,113	729	691	454	653	79	138	149	4,006
Cefoxitin MIC ≥32 mg/L	52 (4.7%)	26 (3.6%)	18 (2.6%)	12 (2.6%)	18 (2.8%)	2 (2.5%)	4 (2.9%)	2 (1.3%)	134 (3.3%)
Confirmed/ number received	18/49	6/26	10/17	3/12	8/17	0/2	2/4	0/2	47/129
bla CMY	10	4	9	3	4	0	2	0	32
bla DHA	8	2	1	0	4	0	0	0	15
Klebsiella pneumoniae	237	177	189	87	187	18	47	35	977
Cefoxitin MIC ≥32 mg/L	21 (8.9%)	7 (4.0%)	6 (3.2%)	2 (2.3%)	8 (4.3%)	0	1 (2.1%)	2 (5.7%)	47 (4.8%)
Confirmed/ number received	5/17	1/7	0/6	0/2	0/8	0/0	0/1	0/2	6/43
bla DHA	4	1	0	0	0	na	0	0	5
bla CMY	1	0	0	0	0	na	0	0	1
Klebsiella oxytoca	76	49	45	13	30	8	4	13	238
Cefoxitin MIC ≥32 mg/L	4 (5.3%)	0 (0.0%)	1 (2.2%)	1 (7.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	6 (2.5%)
Confirmed/ number received	0/4	0/0	0/1	0/1	0/0	0/0	0/0	0/0	0/6

na = not applicable

8.1.3 Carbapenemases

Twenty-two (0.30%) isolates from 20 patients were found to harbour a carbapenemase gene (Table 30). The bla_{IMP-4} gene was detected in 14 strains: *E. cloacae* (8, from 6 patients), *C. freundii* (2), *K. pneumoniae* (1), *K. oxytoca* (1), *R. ornithinolytica* (1) and *S. marcescens* (1); bla_{OXA-48} was detected in 4 *K. pneumoniae* isolates (from 2 patients); bla_{KPC-2} was detected in 1 *K. pneumoniae*; bla_{GES-5} was detected in 1 *P. aeruginosa*; $bla_{NDM + OXA-48}$ was detected in 1 *K. pneumoniae*; and $bla_{IMP-4 + VIM-2}$ was detected in 1 *P. aeruginosa*. Thirteen of 16 isolates with confirmed metallo-β-lactamases also contained plasmid-mediated quinolone resistance genes (*aac(6')-Ib-cr* alone or with *qnrA*, *qnrB* or *qnrS* .

Three *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 and GES carbapenemases. Phenotypic tests indicated a possible serine carbapenemase; however, they did not contain either SME or IMI. These strains were tested for, but did not harbour, bla_{FRI-1}.[23] It is possible that they contain a novel enzyme.

Overall prevalence of carbapenemase genes among Enterobacteriaceae was 0.30% (20/6,567); for *P. aeruginosa*, it was 0.30% (2/660). No carbapenemase genes were detected among 105 *Acinetobacter* species.

8.1.4 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 Enterobacteriaceae. 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*). Twenty-six per cent of *E. coli*, 76% of *K. pneumoniae* and 83% of *E. cloacae* with ciprofloxacin MIC greater than 0.25 mg/L were confirmed to contain PMQRs (Table 31).

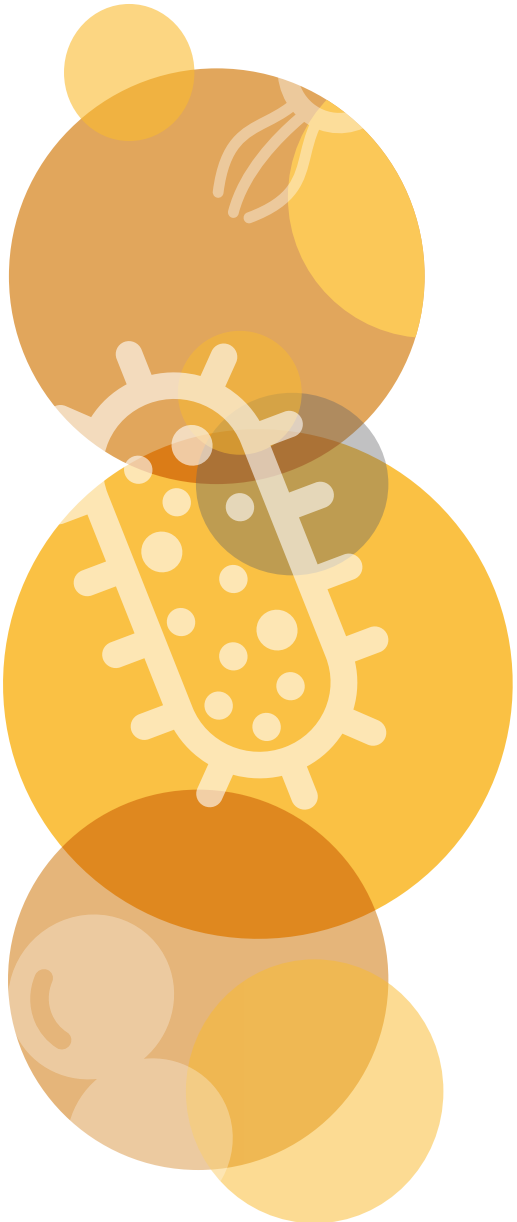


Table 30: Number of carbapenemases and associated resistance genes, by species and state and territory, 2015

Gene	State or territory	Species	Meropenem MIC (mg/L)	ESBL type*	PMQR gene†	16S rRNA methylases
bla$_{IMP-4}$ (*n* = 14)	NSW	*E. cloacae* (*n* = 1)#	≥16	TEM, SHV	*aac(6′)-Ib-cr*, *qnrB*	– §
		E. cloacae (*n* = 1)#	≥16	TEM, CTX-M	*aac(6′)-Ib-cr*, *qnrB*	– §
		E. cloacae (*n* = 1)	≥16	TEM	*qnrB*	– §
		E. cloacae (*n* = 1)	≥16	TEM, SHV	*aac(6′)-Ib-cr*	– §
		E. cloacae (*n* = 1)	1	TEM	*qnrS*	– §
		C. freundii (*n* = 2)	≥16	TEM	*qnrB*	– §
		R. ornithinolytica (*n* = 1)	1	TEM, SHV	*aac(6′)-Ib-cr*, *qnrB*	– §
		S. marcescens (*n* = 1)	≥16	– §	– §	– §
	Qld	*E. cloacae* (*n* = 2)	≥16	TEM	*aac(6′)-Ib-cr*, *qnrB*	– §
		E. cloacae (*n* = 1)	≥16	TEM	*aac(6′)-Ib-cr*, *qnrA*, *qnrB*	– §
		K. oxytoca (*n* = 1)	≥16	TEM, SHV	*qnrB*	– §
	ACT	*K. pneumoniae* (*n* = 1)	≥16	TEM, SHV	– §	– §
bla$_{IMP-4 + VIM-2}$	NSW	*P. aeruginosa* (*n* = 1)	≥16	– §	– §	– §
bla$_{OXA-48}$ (*n* = 4)	Vic	*K. pneumoniae* (*n* = 1)	1	SHV	*qnrB*	– §
		K. pneumoniae (*n* = 1)	0.5	SHV	– §	– §
	Qld	*K. pneumoniae* (*n* = 2)**	1	SHV	– §	– §
bla$_{KPC-2}$	Vic	*K. pneumoniae* (*n* = 1)	≥16	SHV	– §	– §
bla$_{NDM + OXA-48}$	SA	*K. pneumoniae* (*n* = 1)	16	TEM, SHV, CTX-M-15	*aac(6′)-Ib-cr*, *qnrB*	– §
bla$_{GES-5}$	NSW	*P. aeruginosa* (*n* = 1)	≥16	– §	– §	– §

ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance

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

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

§ Not detected

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

** *bla*$_{OXA-48}$ from same patient

Table 31: Number and percentage of isolates with plasmid-mediated quinolone resistance, by species, and state and territory, 2015

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	214	119	72	51	132	7	15	20	630
Ciprofloxacin MIC >0.25 mg/L*	19.3%	16.4%	10.4%	11.2%	20.2%	8.9%	10.9%	13.4%	15.8%
Confirmed/ number received	48/189	41/117	14/72	10/49	31/127	0/7	4/14	5/20	153/595 (25.7%)
aac(6')-Ib-cr	36	33	10	9	23	0	4	2	117
qnrS	8	5	2	1	6	0	0	2	24
qnrB	3	0	1	0	1	0	0	0	5
aac(6')-Ib-cr + qnrB	0	2	1	0	0	0	0	0	3
qepA	1	1	0	0	1	0	0	1	4
Klebsiella pneumoniae	24	24	14	5	16	1	3	2	89
Ciprofloxacin MIC >0.25 mg/L	10.2%	13.6%	7.4%	5.9%	8.6%	5.6%	6.4%	5.7%	9.1%
Confirmed/ number received	18/21	20/23	11/13	2/4	8/15	1/1	2/3	0/2	62/82 (75.6%)
aac(6')-Ib-cr	0	1	0	1	0	0	0	0	2
qnrB	7	8	3	0	4	0	1	0	23
qnrS	3	0	2	0	2	0	0	0	7
qnrA	1	1	2	0	0	0	0	0	4
aac(6')-Ib-cr + qnrB	7	10	4	1	2	1	1	0	26
Enterobacter cloacae	10	7	4	0	2	0	0	1	24
Ciprofloxacin MIC >0.25 mg/L	11.8%	8.8%	6.2%	–†	4.0%	–†	–†	10.0%	7.4%
Confirmed/ number received	7/9	7/7	4/4	–†	0/2	–†	–†	1/1	19/23 (82.6%)
aac(6')-Ib-cr	0	1	0	na	0	na	na	0	1
qnrA	0	2	0	na	0	na	na	0	2
qnrB	0	1	1	na	0	na	na	0	2
qnrS	1	0	0	na	0	na	na	1	2
aac(6')-Ib-cr + qnrA	4	3	0	na	0	na	na	0	7
aac(6')-Ib-cr + qnrB	2	0	3	na	0	na	na	0	5

MIC = minimum inhibitory concentration; na = not applicable

* Concentration used to select strains for molecular testing

† No isolates

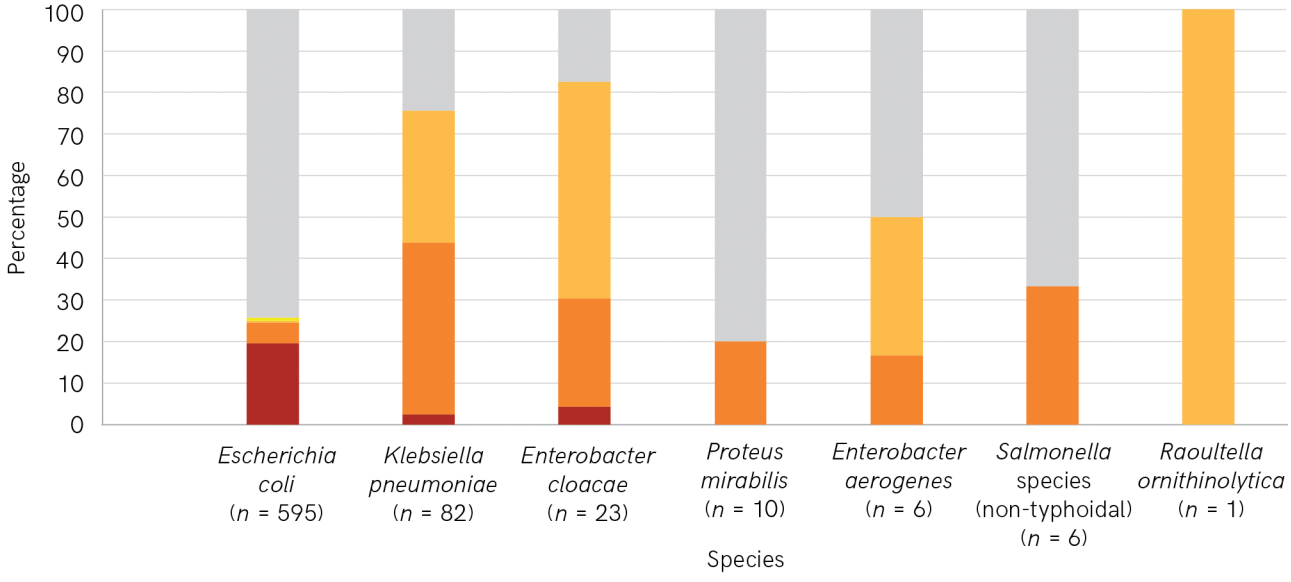
The proportion and type of PMQR determinant found among isolates with ciprofloxacin MIC greater than 0.25 mg/L varied among the different species (Figure 14). The *aac(6')-Ib-cr* gene, with or without *qnr*, was dominant, and was present in five of the seven species.

8.1.5 *Escherichia coli* sequence type 131

Sequence type 131 (O25b-ST131) is the predominant *E. coli* lineage among extraintestinal 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 strains with an ESBL phenotype harboured genes of the CTX-M type (347/431, 80.5%) (Table 32). Sixty-six per cent (132/201) 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 74.3% (200/269) of *E. coli* ESBL phenotypes that were ciprofloxacin resistant (MIC >1 mg/L), but only 5.6% (9/160) of ciprofloxacin-susceptible ESBL phenotypes. Ninety-five per cent (198/209) and 64% (133/209) of O25b-ST131 with an ESBL phenotype were associated with *H30* and *H30*-Rx subclones, respectively, which have a reported association with more antibiotic resistances and greater virulence potential.[24,25] The *H30*-Rx subclone of ST131 often carried $bla_{CTX\text{-}M\text{-}15}$ and *aac(6')-Ib-cr*. As expected, more than 98% of *E. coli* isolates received that were associated with the O25b-ST131 clone belonged to phylogenetic group B2.[26]

Figure 14: Proportion of plasmid-mediated quinolone resistance genes among gram-negative species with ciprofloxacin MIC >0.25 mg/L, 2015



	Escherichia coli (*n* = 595)	*Klebsiella pneumoniae* (*n* = 82)	*Enterobacter cloacae* (*n* = 23)	*Proteus mirabilis* (*n* = 10)	*Enterobacter aerogenes* (*n* = 6)	*Salmonella* species (non-typhoidal) (*n* = 6)	*Raoultella ornithinolytica* (*n* = 1)
Not detected	74.3	24.4	17.4	80.0	50.0	66.7	0.0
qepA	0.7	0.0	0.0	0.0	0.0	0.0	0.0
CR, qnr	0.5	31.7	52.2	0.0	33.3	0.0	100.0
qnr	4.9	41.5	26.1	20.0	16.7	33.3	0.0
CR	19.7	2.4	4.3	0.0	0.0	0.0	0.0

CR = *aac(6')-Ib-cr*; MIC = minimum inhibitory concentration; qnr = *qnrA*, *qnrB* or *qnrS*

Note: Not detected = no PMQR detected; resistance likely due to mutations in DNA gyrase and topoisomerase IV.

Table 32: Number of *Escherichia coli* clones with ESBL phenotype, by O25b-ST131 clone and ciprofloxacin resistance, 2015

Clone/subclone	Total	CTX-M types		Other ESBL types	Ciprofloxacin MIC	
		CTX-M-15-like	Non-CTX-M-15		>1 mg/L	≤1 mg/L
O25b-ST131	209	132	68	9	200	9
H30		129	65	4	198	0
H30-Rx		125	5	3	133	0
Non-O25b-ST131	222	69	78	75	69	151
H30		1	1	1	1	2
H30-Rx		0	0	0	0	0
Total	431	201	146	84	269	160

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

8.2 Molecular epidemiology of *Enterococcus faecium*

8.2.1 *van* genes

Results for *vanA* and *vanB* polymerase chain reaction (PCR) testing were available for 396 (98.5%) of the 402 *E. faecium* isolates. Where determined, *van* genes were detected in 56.6% (224/396) of *E. faecium* isolates: *vanA* in 81 (20.5%), *vanB* in 138 (34.8%), and both *vanA* and *vanB* in 5 (1.3%) (Figure 15).

For vancomycin-resistant *E. faecium* (MIC >4 mg/L), *vanA* was detected in 73 of 199 isolates (36.7%), *vanB* in 121 (60.8%), and both *vanA* and *vanB* in 5 (2.5%).

In 25 of 197 (12.7%) vancomycin-susceptible *E. faecium* isolates, *van* genes were detected: 8 with *vanA* and 17 with *vanB*. All of these strains had a vancomycin MIC of 1 mg/L or less.

8.2.2 Multilocus sequence type

Of the 402 *E. faecium* isolates reported, 391 (97.3%) were available for typing by whole genome sequencing (Table 33). Based on the multilocus sequence type (MLST), 55 sequence types (STs) were identified. Overall, 71.0% of *E. faecium* could be characterised into six STs: ST796 (n = 69), ST non-typable (n = 52), ST555 (n = 49), ST80 (n = 46), ST203 (n = 39) and ST78 (n = 22). For the 52 non-typable MLST isolates, the *pstS* housekeeping gene was absent; however, because the other six housekeeping genes that were present were identical, the isolates were considered a single MLST clone. There were 34 STs with only a single isolate.

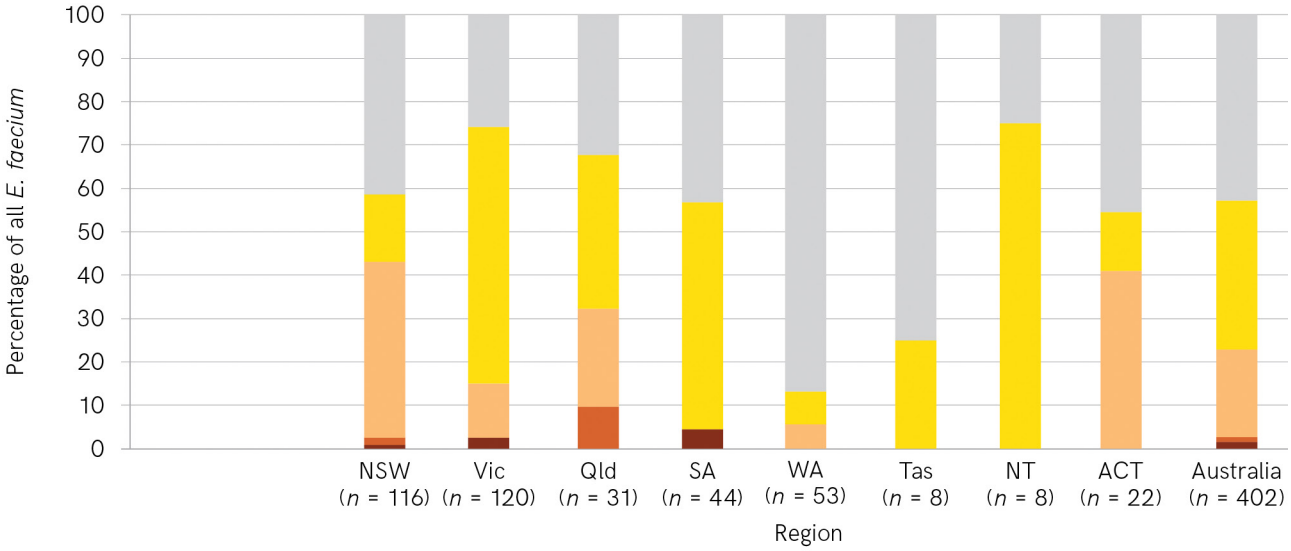
ST796 was predominant in Victoria. ST non-typable was only found in New South Wales and the Australian Capital Territory. ST555 was the predominant ST in Western Australia and South Australia.

The distribution of vancomycin-resistant *E. faecium* sequence types throughout Australian states and territories is shown in Figure 16.

8.2.3 MLST and *van* genes

The *vanA* gene was detected in five STs: ST80 (n = 23), ST203 (n = 8), ST117 (n = 1), ST78 (n = 1) and 45 of the 52 non-typable MLST isolates. The *vanB* gene was detected in 13 STs: ST796 (n = 68); ST555 (n = 23); ST203 (n = 18); ST78 (n = 15); ST17 (n = 2); ST341 (n = 2); and ST117, ST80, ST192, ST789, ST414, ST721 and ST796slv (n = 1 each) (Table 34).

Figure 15: Vancomycin genotype of *Enterococcus faecium* isolates, by state and territory, and nationally, 2015



	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Not *vanA* or *vanB* (*n* = 172)	41.4	25.8	32.3	43.2	86.8	75.0	25.0	45.5	42.8
vanB (*n* = 138)	15.5	59.2	35.5	52.3	7.5	25.0	75.0	13.6	34.3
vanA (*n* = 81)	40.5	12.5	22.6	0.0	5.7	0.0	0.0	40.9	20.1
vanA and *vanB* (*n* = 5)	1.7	0.0	9.7	0.0	0.0	0.0	0.0	0.0	1.2
Not determined (*n* = 6)	0.9	2.5	0.0	4.5	0.0	0.0	0.0	0.0	1.5

Table 33: Number and percentage of *Enterococcus faecium* MLST, by state and territory, 2015

	Number (%)								
MLST	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
796	2 (1.8)	62 (53.0)	3 (9.7)	1 (2.4)	0	1 (12.5)	0	0	69 (17.8)
Non-typable (*pstS* gene absent)	43 (39.4)	0	0	0	0	0	0	9 (40.9)	52 (13.4)
555	1 (0.9)	3 (2.6)	0	16 (39.0)	21 (40.4)	1 (12.5)	6 (75.0)	0	48 (12.4)
80	15 (13.8)	14 (12.0)	3 (9.7)	1 (2.4)	6 (11.5)	0	1 (12.5)	6 (27.3)	46 (11.9)
203	6 (5.5)	10 (8.5)	7 (22.6)	7 (17.1)	3 (5.8)	2 (25.0)	0	4 (18.2)	39 (10.1)
78	12 (11.0)	0	9 (29.0)	0	1 (1.9)	0	0	0	22 (5.7)
17	7 (6.4)	2 (1.7)	1 (3.2)	0	9 (17.3)	0	0	0	19 (4.9)
262	0	1 (0.9)	0	11 (26.8)	0	0	0	0	12 (3.1)
117	5 (4.6)	2 (1.7)	2 (6.5)	0	0	0	0	1 (4.5)	10 (2.6)
Other types	18 (16.5)	23 (19.7)	6 (19.4)	5 (12.2)	12 (23.1)	4 (50.0)	1 (12.5)	2 (9.1)	71 (18.3)
Total	109	117	31	41	52	8	8	22	388

MLST = multilocus sequence type

Figure 16: Distribution of vancomycin-resistant *Enterococcus faecium* sequence types, by state and territory, 2015

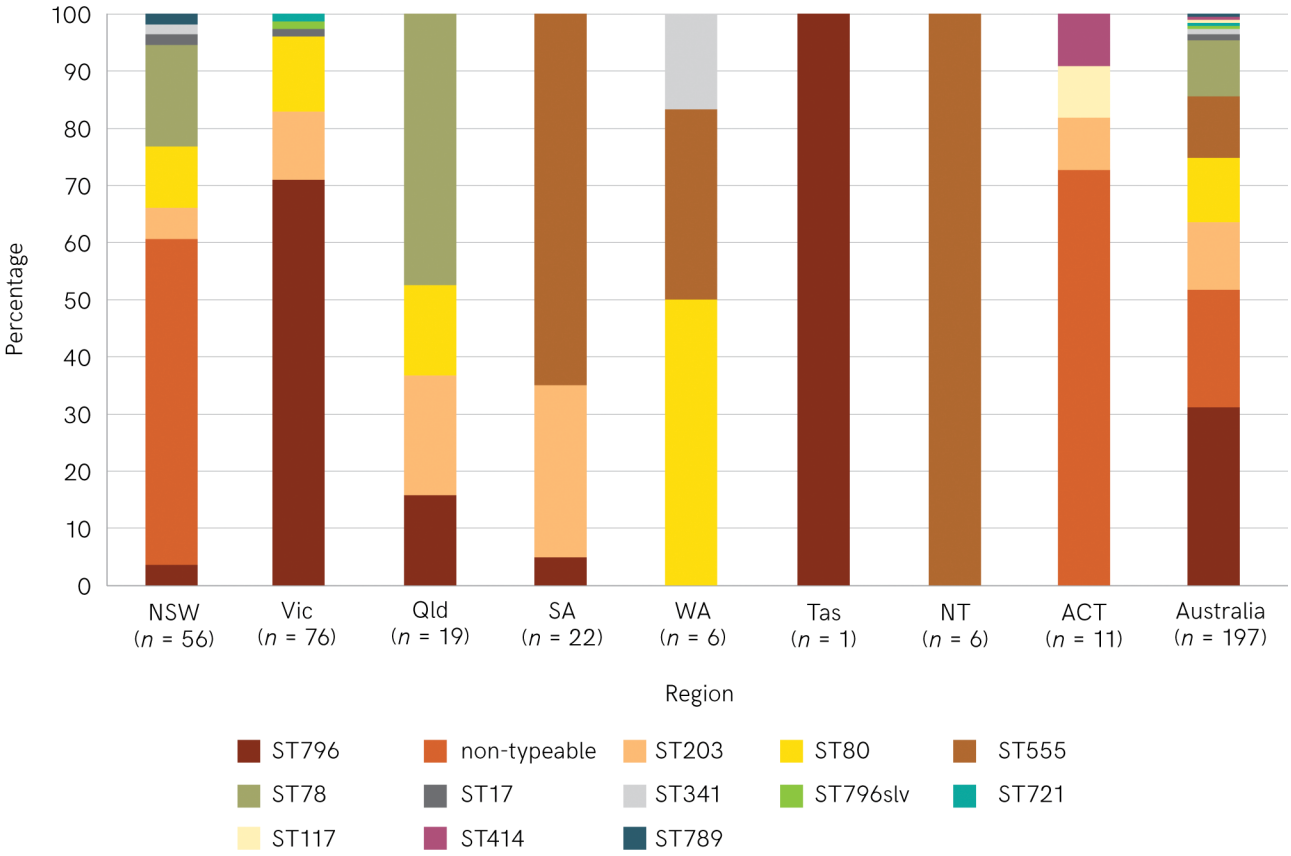


Table 34: Number and percentage of *Enterococcus faecium* MLST harbouring *vanA* and/or *vanB* genes, 2015

MLST	Number (%)				
	vanA	*vanB*	*vanA* and *vanB*	*vanA* or *vanB* not detected	Total
796	0	68 (98.6)	1 (1.4)	0	69
Non-typable (*pstS* gene absent)	45 (86.5)	0	0	7 (13.5)	52
555	0	23 (47.9)	0	25 (52.1)	48
80	23 (50.0)	1 (2.2)	0	22 (47.8)	46
203	8 (20.5)	18 (46.2)	1 (2.6)	12 (30.8)	39
78	1 (4.5)	15 (68.2)	3 (13.6)	3 (13.6)	22
17	0	2 (10.5)	0	17 (89.5)	19
262	0	0	0	12 (100.0)	12
117	1 (10.0)	2 (20.0)	0	7 (70.0)	10
Other types	0	7*	0	64 (16.4)	71
Total	78 (20.1)	136 (35.1)	5 (1.3)	169 (43.6)	388

MLST = multilocus sequence type

* Insufficient numbers (<10) to calculate percentage

8.3 Molecular epidemiology of methicillin-resistant *Staphylococcus aureus*

Of the 435 MRSA reported, 426 (97.9%) 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 5.9% in Tasmania to 38.2% in the Northern Territory (Figure 17).

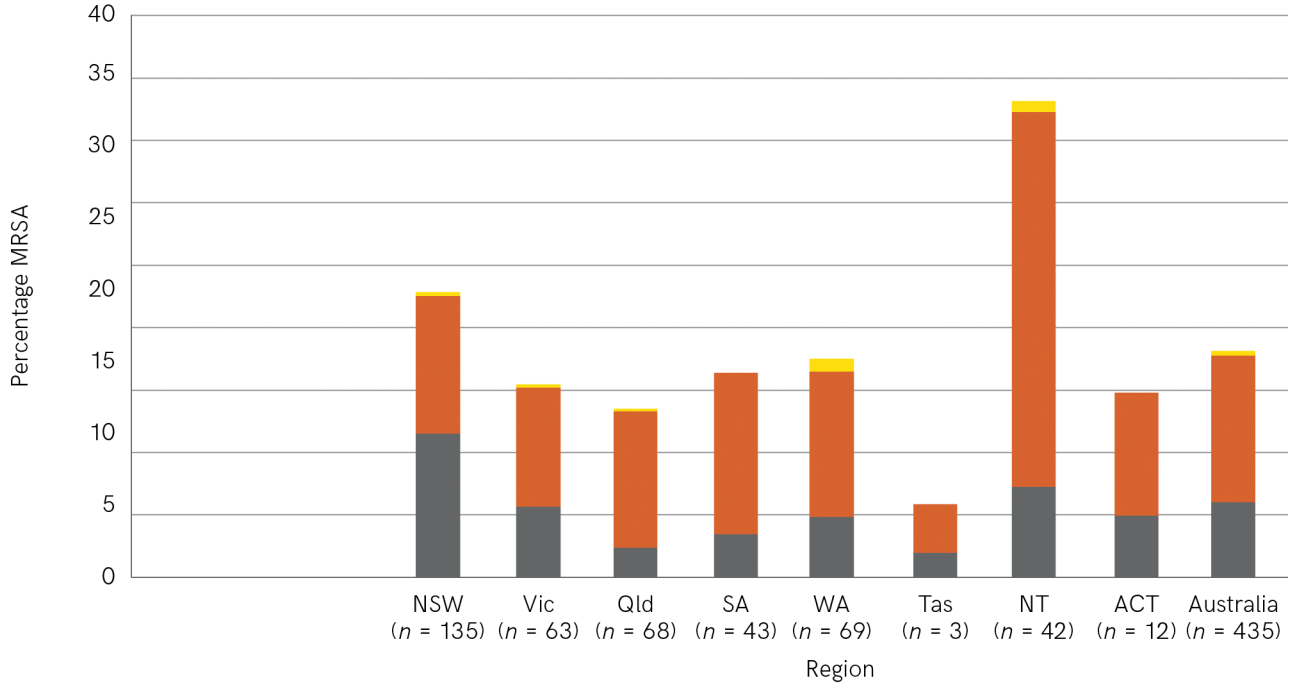
8.3.1 Healthcare-associated MRSA

Based on the MLST and SCC*mec* type, four HA-MRSA clones were identified: ST22-IV (EMRSA-15), ST239-III (Aus 2/3 EMRSA), ST36-II (EMRSA-16) and ST225-II (a single locus variant [slv] of ST5-II, NY/Japan MRSA or USA100) (Table 35).

Panton-Valentine leucocidin (PVL)–associated genes were identified in 1.4% of HA-MRSA. Two PVL-positive ST22-IV were isolated, one each in Western Australia and Victoria. PVL-positive ST22-IV are frequently isolated in the Indian subcontinent and are not related to EMRSA-15.

The most frequently isolated HA-MRSA clone, ST22-IV, was identified in all states and territories. ST239-III was not isolated in the Australian Capital Territory, Tasmania or Western Australia. The single isolates of ST36-II and ST225-II were identified in Western Australia (Table 36).

Figure 17: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, 2015



	NSW (*n* = 135)	Vic (*n* = 63)	Qld (*n* = 68)	SA (*n* = 43)	WA (*n* = 69)	Tas (*n* = 3)	NT (*n* = 42)	ACT (*n* = 12)	Australia (*n* = 435)
Not available (*n* = 9)	0.3	0.2	0.2	0.0	1.0	0.0	0.9	0.0	0.4
Community associated (*n* = 282)	11.0	9.6	10.9	13.0	11.7	3.9	30.0	9.9	11.8
Healthcare associated (*n* = 144)	11.5	5.7	2.4	3.4	4.8	2.0	7.3	4.9	6.0

MRSA = methicillin-resistant *Staphylococcus aureus*

Table 35: Number and proportion of healthcare-associated MRSA clones, by place of onset and PVL carriage, 2015

Clone	Clonal complex	Total (%)†	Community onset*	Hospital onset*	PVL positive (%)
ST22-IV (EMRSA-15)§	22	108 (25.4)	74 (68.5)	34 (31.5)	2 (1.9)
ST239-III (Aus2/3 EMRSA)#	8	34 (8.0)	15 (44.1)	19 (55.9)	0
ST36-II (EMRSA-16/USA200)	30	1 (0.2)	1 (100)	0	0
ST225-II (NY/Japan/USA100 variant)	5	1 (0.2)	1 (100)	0	0
Total		144 (33.8)	91 (63.2)	53 (36.8)	2 (1.4)

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

* Percentage of the clone

† Percentage of all MRSA

§ Includes two isolates identified as ST22slv-IV (MLST allele submitted to MLST database curator)

Includes four isolates identified as ST239slv

Table 36: Number and percentage of healthcare-associated MRSA clones, by state and territory, 2015

	Number (%)								
Clone	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15)	49 (72.1)	18 (78.3)	11 (91.7)	7 (77.8)	17 (89.5)	1*	1 (12.5)	4 (100)	108 (75.0)
ST239-III (Aus2/3 EMRSA)	19 (27.9)	5 (21.7)	1 (8.3)	2 (22.2)	0	0	7 (87.5)	0	34 (23.6)
ST36-II (EMRSA-16/ USA200)	0	0	0	0	1 (5.3)	0	0	0	1 (0.7)
ST225-II (NY/ Japan/USA100 variant)	0	0	0	0	1 (5.3)	0	0	0	1 (0.7)
Total	68	23	12	9	19	1	8	4	144

MRSA = methicillin-resistant *Staphylococcus aureus*

* Insufficient numbers (<10) to calculate percentage

8.3.2 Community-associated MRSA

Based on the MLST and SCC*mec* type, 36 CA-MRSA clones were identified. PVL was detected in 12 CA-MRSA clones. Overall, 41.5% of CA-MRSA were PVL positive (Table 37).

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

CA-MRSA was the cause of hospital-onset infection in 12.0% (65/542) of all cases.

Table 37: Number and proportion of community-associated MRSA clones, by place of onset and PVL carriage, 2015

Clone	Clonal complex	Total (%)*	Community onset†	Hospital onset†	PVL positive (%)
ST93-IV (Qld CA-MRSA)	Singleton	89 (20.9)	75 (84.3)	14 (15.7)	73 (82.0)
ST45-V (WA84 MRSA)	45	41 (9.6)	25 (61.0)	16 (39.0)	0 (0.0)
ST5-IV	5	34 (8.0)	24 (70.6)	10 (29.4)	18 (52.9)
ST1-IV (WA1 MRSA)	1	30 (7.0)	25 (83.3)	5 (16.7)	1 (3.3)
ST30-IV (SWP MRSA)	30	17 (4.0)	15 (88.2)	2 (11.8)	15 (88.2)
ST78-IV (WA2 MRSA)	78	12 (2.8)	11 (91.7)	1 (8.3)	1 (8.3)
ST5-V	5	7 (1.6)	6§	1§	0
ST872-IV	1	5 (1.2)	2§	3§	0
ST8-IV	8	5 (1.2)	4§	1§	0
ST1-I	1	4 (0.9)	2§	2§	0
ST762-IV	1	3 (0.7)	1§	2§	1§
Other clones (*n* = 25)		35 (8.2)	27 (77.1)	8 (22.9)	8 (22.9)
Total		282	217	65	117 (41.5)

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

* Percentage of all MRSA

† Percentage of the strain

§ Insufficient numbers (<10) to calculate percentage

Table 38: Number and percentage of the major community-associated MRSA clones (>10 isolates), by state and territory, 2015

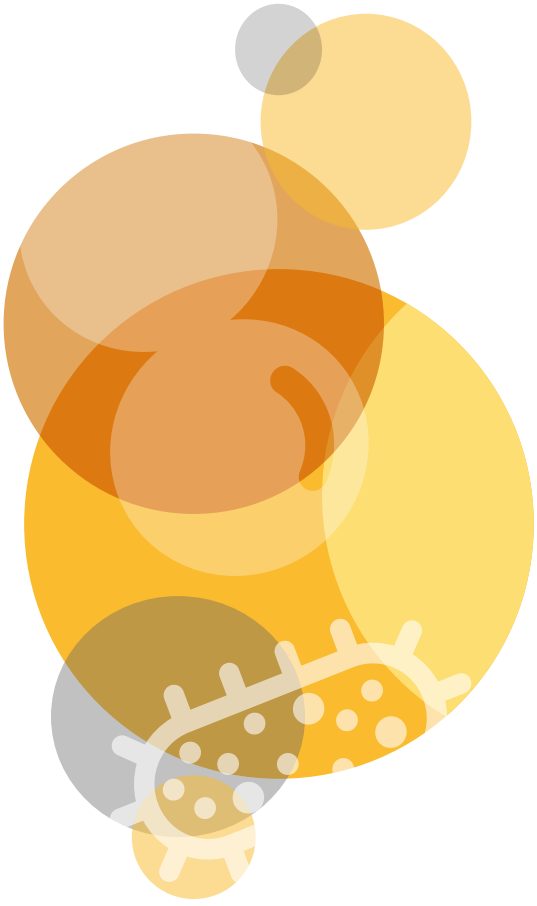
	Number (%)								
Clone	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST93-IV (Qld CA-MRSA)	11 (16.9)	12 (30.8)	18 (32.7)	12 (35.3)	13 (28.3)	0	22 (66.7)	1 (12.5)	89 (31.6)
PVL positive	4	9	13	12	13	0	21	1	73
PVL negative	7	3	5	0	0	0	1	0	16
ST45-V (WA84 MRSA)	31 (47.0)	7 (17.9)	0	1 (2.9)	0	0	0	2 (25.0)	41 (14.5)
PVL positive	0	0	0	0	0	0	0	0	0
PVL negative	31	7	0	1	0	0	0	2	41
ST5-IV	3 (4.6)	1 (2.6)	9 (16.4)	8 (23.5)	7 (15.2)	0	3 (9.1)	3 (37.5)	34 (12.1)
PVL positive	1	1	1	4	7	0	2	2	18
PVL negative	2	0	8	4	0	0	1	1	16
ST1-IV (WA1 MRSA)	10 (15.4)	3 (7.7)	4 (7.3)	4 (11.8)	7 (15.2)	1 (50.0)	1 (3.0)	0	30 (10.6)
PVL positive	0	0	1	0	0	0	0	0	1
PVL negative	10	3	3	4	7	1	1	0	29
ST30-IV (SWP MRSA)	1 (1.5)	3 (7.7)	10 (18.2)	1 (2.9)	1 (2.2)	0	1 (3.0)	0	17 (6.0)
PVL positive	1	3	8	1	0	0	1	0	15
PVL negative	0	0	2	0	0	0	0	0	2
ST78-IV (WA2 MRSA)	2 (3.1)	0	2 (3.6)	1 (2.9)	5 (10.9)	1 (50.0)	0	1 (12.5)	12 (4.3)
PVL positive	1	0	0	0	0	0	0	0	1
PVL negative	1	0	2	1	5	1	0	1	11
Other clones (*n* = 30)	7 (10.8)	13 (33.3)	12 (21.8)	7 (20.6)	13 (28.3)	0	6 (18.2)	1 (12.5)	59 (20.9)
PVL positive	0	2	3	2	2	0	0	0	9
PVL negative	7	11	9	5	11	0	6	1	50
Total	65	39	55	34	46	2	33	8	282
PVL positive	7	15	26	19	23	0	24	3	117
PVL negative	58	24	29	15	23	2	9	5	165

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

9 Limitations of the study

Although this study is comprehensive in its coverage of Australia, and the methodology follows 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; institution 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 33 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 these laboratories is not known; further, it is likely that the proportion of the population served differs across the state and territory groupings used in this report
- Because of the formulation of amoxicillin–clavulanate 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 determine 'susceptible' for some combinations of antimicrobial agents and species.



10 Discussion and conclusions

AGAR is a core component of the Antimicrobial Use and Resistance in Australia (AURA) program. As a targeted surveillance program, which focuses on selected pathogens and collects demographic, treatment and outcome data in addition to data on resistance rates, AGAR allows healthcare professionals to make informed clinical decisions and improve patient care. AGAR surveys have been conducted regularly since 1985. Since 2013, they have focused on bacteraemia and have become aligned with the European Antimicrobial Resistance Surveillance Network (EARS-Net), which enables benchmarking and better predictions of future trends. The Commission will continue to ensure that comparative data and analyses are available on its website to inform infection control and antimicrobial stewardship policy and practice.

AGAR participants are from all states and territories, and provide information on the most common serious bacterial infections, primarily presenting or occurring in tertiary healthcare organisations. In 2015, AGAR collected data on 10,739 episodes of bacteraemia Australia-wide. Where the place of onset was known, approximately three-quarters of episodes had their onset in the community.

The conservative approach to fluoroquinolone use taken in community and hospital health care in Australia means that ciprofloxacin resistance, particularly in *E. coli*, is important. Fluoroquinolones are relied on as 'rearguard' oral antibiotics, particularly for deep-seated gram-negative infections. There is a community perception that resistance to this class in Australia is uncommon, but this is not supported by the current AGAR data. Over the last decade, resistance to ciprofloxacin in *E. coli* has increased from less than 1% resistance[27] to rates comparable with those in some northern European countries. The current ciprofloxacin resistance rates in *E. coli* in Australia are around 12%, with minimal difference between hospital and community-onset *E. coli* bacteraemias (which make up 83.6% of *E. coli* bacteraemias overall). It is possible that, because fluoroquinolone resistance is frequently linked to cephalosporin resistance caused by ESBLs of the CTX-M type, the high use of oral cephalosporins in the community is driving this increase (as described in *AURA 2017: First Australian report on antimicrobial use and resistance in human health*[28]). The Commission will work with AGAR in undertaking further data analyses to determine whether shared resistance with other antimicrobials (so-called co-resistance) is contributing to this increased resistance. The health impact of increasing community rates of resistance will also be exmined.

Fluoroquinolone resistance in *E. coli* can also be linked to the emergence of a major clone. O25b-ST131 is an international clone associated with third-generation cephalosporin and fluoroquinolone resistance, as well as increased virulence within its subtypes. In the 2015 survey, O25b-ST131 accounted for 74% of *E. coli* ESBL phenotypes (ceftriaxone or ceftazidime MICs >1 mg/L) 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 picking up rapid changes in resistance.

So far, carbapenemase-producing Enterobacteriaceae (CPE) remains uncommon (<0.1% in *E. coli*; 0.3% in *K. pneumoniae*). Examining previous and current AGAR surveys, a majority of CPEs are endemic in origin (IMP).[27] The remainder

are believed to be introductions of individual CPEs into hospitals by patients who have acquired their strains overseas; these strains have the potential for secondary local transmission, as occurred recently in Victoria with KPC-producing *K. pneumoniae*.[29] The importance of infection control in limiting the transmission of CPE cannot be overestimated.[30]

ESBL phenotypes were found in 11.5% of *E. coli* and 7.7% of *K. pneumoniae*. This is a continuing trend of ESBLs, especially in *E. coli*, the commonest organism reported in the Sepsis Outcome Programs 2015 report. [67] [10] Incidence of ESBLs has been increasing, especially in *E. coli* (the most common cause of Gram-negative sepsis). When ESBLs first arose, they were more common in hospital-onset infections in *K. pneumoniae* (TEM, SHV); as a result, there has been a perception that ESBLs are a hospital problem. This is no longer the case, with 84% of *E. coli* bacteraemia being community onset. The 2015 AGAR findings show that standard therapy with third-generation cephalosporins may be ineffective in 11% of cases.

Although the overall rates of MRSA do not appear to be increasing (18.2% in 2015), the rate of community-onset *S. aureus* bacteraemias that are methicillin resistant is increasing. Conversely community-associated clones of MRSA are an increasing source of hospital-onset bacteraemia (particularly ST93 and ST5, both usually PVL positive). Although HA-MRSA strains (for example ST22) were more frequently found in community-onset bacteraemias, this may reflect either prior hospital exposure or onset in long-term care facilities; the AGAR data are not able to sufficiently differentiate between these. 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*.[31] This paper will be updated based on the 2015 AGAR data to provide further information on this issue.

The slightly higher mortality from MRSA sepsis and the predominance of community-onset staphylococcal sepsis highlight the need for raising awareness among clinicians of the risk of resistance and local patterns of disease.

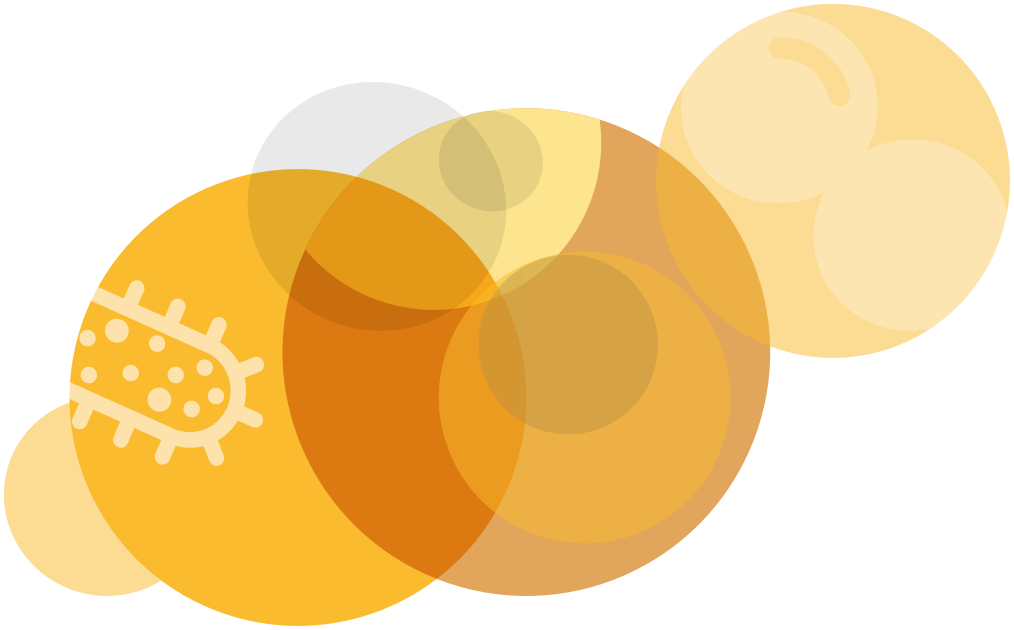
The emergence of *E. faecium* in enterococcal bacteraemia is a worldwide phenomenon that remains unexplained. Unlike *E. faecalis*, which is largely community in onset, *E. faecium* bacteraemia is mostly of hospital onset. It has clinical consequences — penicillins are preferred therapy, but cannot be used because of the high rate of resistance. This means that the use of vancomycin for treatment of enterococcal sepsis has become more common, potentially acting as a driver for selection of VRE. Furthermore, there is a difference in the 30-day all-cause mortality between *E. faecium* (26.9%) and *E. faecalis* (15.7%). This may be a consequence of underlying patient comorbidities and/or limited therapeutic choices. Notably, 54.2% of *E. faecium* harboured *vanA* or *vanB* genes in 2015. Thus, vancomycin, the mainstay of therapy until recently, cannot be used, and agents with uncertain efficacy must be used instead. It is striking that, in 2015, 36% of vancomycin-resistant *E. faecium* bacteraemias nationally were caused by strains harbouring *vanA*. This type of vancomycin resistance has emerged very rapidly in the past five years, particularly in New South Wales, where it is now the dominant type.

For nearly two decades, and unlike in most other countries where VRE has become a problem, VRE in Australia was dominated by the *vanB* genotype. In 2015, there was no significant difference in mortality between vancomycin-resistant and vancomycin-non-susceptible *E. faecium*. This challenges the general belief that instituting early appropriate therapy is important, and suggests that the mortality associated with enterococcal bacteraemia (which is higher than for *S. aureus* bacteraemia) is much more likely to be related to patient comorbidities. The Commission will more closely examine the impact of these changes in resistance and the need for targeted resources to promote enhanced infection control practice.

Another notable feature of the AGAR findings is the heavy dependence on broad-spectrum β-lactam agents – mainly ceftriaxone and piperacillin-tazobactam – in gram-negative sepsis. These were the dominant agents of choice for definitive treatment across Australia. A proportion of this use appears to be unnecessary. Broad spectrum agents are associated with greater risks of adverse effects

and the development of antimicrobial resistance. Ceftriaxone is a strong driver of *Clostridium difficile* diarrhoea, and can select for extended-spectrum beta-lactamase (ESBL) producing organisms. Changing to narrower spectrum agents, where appropriate, is an important role of antimicrobial stewarsdship teams.

From the findings noted above, it is clear that AGAR surveillance is a key component in Australia's response to the problem of increasing antimicrobial resistance. It defines where Australia stands in relation to antimicrobial resistance in human health. The next important question is how these data are communicated and used by healthcare networks, across different speciality networks, and in informing the national response to antimicrobial resistance.



Abbreviations

Abbreviation	Term
AGAR	Australian Group on Antimicrobial Resistance
AURA	Antimicrobial use and resistance in Australia
CA-MRSA	community-associated methicillin-resistant *Staphylococcus aureus*
CI	confidence interval
CLSI	Clinical and Laboratory Standards Institute
CPE	carbapenem-producing Enterobacteriaceae
ESBL	extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
HA-MRSA	healthcare-associated methicillin-resistant *Staphylococcus aureus*
MIC	minimum inhibitory concentration
MLST	multilocus sequence type
MRSA	methicillin-resistant *Staphylococcus aureus*
MSSA	methicillin-susceptible *Staphylococcus aureus*
PMQR	plasmid-mediated quinolone resistance
PVL	Panton-Valentine leucocidin
SAB	*Staphylococcus aureus* bacteraemia
ST	sequence type
VRE	vancomycin-resistant enterococcus

Acknowledgements

Participating members of AGAR:

Alfred Hospital, Vic	Denis Spelman and Amanda Dennison
Alice Springs Hospital, NT	James McLeod
Austin Health, Vic	Paul Johnson and Peter Ward
Concord Hospital, NSW	Thomas Gottlieb and Graham Robertson
John Hunter Hospital, NSW	Rodney Givney and Ian Winney
Joondalup Hospital, WA	Shalinie Perera and Ian Meyer
Nepean Hospital, NSW	James Branley and Donna Barbaro
Pathology Queensland, Cairns Base Hospital, Qld	Enzo Binotto and Bronwyn Thomsett
Pathology Queensland, Central Laboratory, Qld	Graeme Nimmo and Narelle George
Pathology Queensland, Gold Coast Hospital, Qld	Petra Derrington and Sharon Dal-Cin
Pathology Queensland, Prince Charles Hospital, Qld	Robert Horvath and Laura Martin
Pathology Queensland, Princess Alexandra Hospital, Qld	Naomi Runnegar and Joel Douglas
PathWest Laboratory Medicine WA, Fiona Stanley Hospital	David McGechie and Denise Daley
PathWest Laboratory Medicine WA, Queen Elizabeth II Medical Centre	Ronan Murray and Jacinta Bowman
PathWest Laboratory Medicine WA, remote WA	Michael Leung
PathWest Laboratory Medicine WA, Royal Perth Hospital	Owen Robinson and Geoffrey Coombs
Royal Darwin Hospital, NT	Rob Baird and Jann Hennessy
Royal Hobart Hospital, Tas	Louise Cooley and David Jones
Royal North Shore Hospital, NSW	George Kotsiou and Peter Huntington
Royal Prince Alfred Hospital, NSW	Sebastian van Hal and Bradley Watson
Royal Women's and Children's Hospital, Vic	Andrew Daley and Gena Gonis
SA Pathology, Flinders Medical Centre, SA	Kelly Papanaoum and Nicholas Wells
SA Pathology, Royal Adelaide Hospital, SA	Morgyn Warner and Kija Smith
SA Pathology, Women's and Children's Hospital, SA	Morgyn Warner and Kija Smith
Southern Health (Monash Medical Centre), Vic	Tony Korman and Despina Kotsanas
St John of God Pathology, WA	Sudha Pottumarthy-Boddu and Fay Kappler
St Vincent's Hospital, Vic	Mary Jo Waters and Lisa Brenton
Sullivan Nicolaides Pathology, Qld	Jenny Robson and Georgia Peachey
The Canberra Hospital, ACT	Peter Collignon and Susan Bradbury
Westmead Hospital, NSW	Jon Iredell and Andrew Ginn
Wollongong Hospital, NSW	Peter Newton and Melissa Hoddle

Reference laboratories:

We also gratefully acknowledge Ms Yung Thin Lee and Dr Stanley Pang, Antimicrobial Resistance Laboratory, School of Veterinary and Life Sciences, Murdoch University, Western Australia; and the Australian Centre for Antimicrobial Resistance Ecology (ACARE), The University of Adelaide, South Australia.

APPENDIX A

Study design

Thirty-three hospitals participated in the 2015 survey. All states and territories were represented. The 29 laboratories that participated in AGAR collected all isolates from different patient episodes of bacteraemia for the Australian Staphylococcal Sepsis Outcome Program and the Australian Enterococcal Sepsis Outcome Program, and 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 three levels of enrolment: Bronze, Silver and Gold (Tables A1–A3). At Bronze level, participating laboratories provided date of collection, date of birth, gender, postcode and admission date. At Silver level, participating laboratories provided discharge date, device-related infection, principal clinical manifestation, intensive care unit (ICU) admission, outcome at 30 days and date of death. At Gold level, participating laboratories provided discharge date, device-related infection, principal clinical manifestation, ICU admission, outcome at 30 days, date of death and principal antimicrobial treatment.

Table A1: Level of participation of laboratories that contributed data on gram-negative* bacteraemia, by state and territory, 2015

		Level of participation		
State or territory	Number of hospitals	Bronze	Silver	Gold
New South Wales	7	1	0	6
Victoria	5	1	0	4
Queensland	6	1	1	4
South Australia	3	2	0	1
Western Australia	8	5	0	3
Tasmania	1	0	0	1
Northern Territory	2	1	0	1
Australian Capital Territory	1	1	0	0
Total	33	12	1	20

* Enterobacteriaceae, *Acinetobacter* species and *Pseudomonas aeruginosa*

Table A2: Level of participation of hospitals that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2015

State or territory	Number of hospitals	Level of participation		
		Bronze	Silver	Gold
New South Wales	7	0	0	7
Victoria	5	1	0	4
Queensland	6	1	1	4
South Australia	3	0	0	3
Western Australia	8	5	0	3
Tasmania	1	0	0	1
Northern Territory	2	1	0	1
Australian Capital Territory	1	0	0	1
Total	33	8	1	24

Table A3: Level of participation of hospitals that contributed data on enterococcal bacteraemia, by state and territory, 2015

State or territory	Number of hospitals	Level of participation		
		Bronze	Silver	Gold
New South Wales	7	0	0	7
Victoria	5	1	0	4
Queensland	6	0	1	5
South Australia	3	0	0	3
Western Australia	8	5	0	3
Tasmania	1	0	0	1
Northern Territory	2	1	0	1
Australian Capital Territory	1	0	0	1
Total	33	7	1	25

APPENDIX B

Methods

Species identification

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

Susceptibility testing

Testing was performed using two commercial semi-automated methods: Vitek 2 (bioMérieux) (*n* = 27) and Phoenix (BD) (*n* = 2), which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution. Commercially available Vitek 2 AST-N246, AST-N247 and P612 cards, or Phoenix NMIC-203 and PMIC-84 cards were used by all participants throughout the survey period.

The Clinical and Laboratory Standards Institute (CLSI) M100-A26[1] and European Committee on Antimicrobial Susceptibility Testing (EUCAST) v6.0[2] breakpoints from January 2016 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 minimum inhibitory concentration (MIC) range available on the commercial cards, recognising that the January 2016 breakpoint is actually susceptible ≤2 mg/L.

Antimicrobials tested

Table B1 shows the antimicrobials tested.

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

	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v6.0†		
Antimicrobial agent	**S**	**SDD**	**I**	**R**	**S**	**I**	**R**
Benzylpenicillin							
Enterococcus spp.	≤8		–§	≥16	–#	–#	–#
Staphylococcus aureus	≤0.12		–§	≥0.25	≤0.125	–#	≥0.25
Amikacin							
Acinetobacter spp.	≤16		32	≥64	≤8	16	≥32
Enterobacteriaceae	≤16		32	≥64	≤8	16	≥32
Pseudomonas spp.	≤16		32	≥64	≤8	16	≥32
Amoxicillin–clavulanate							
Enterobacteriaceae	≤8/4		16/8	≥32/16	≤8**	–§	≥16
Enterococcus spp.	–#		–#	–#	≤4	8	≥16

Table B1: (continued)

	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v6.0†		
Antimicrobial agent	**S**	**SDD**	**I**	**R**	**S**	**I**	**R**
Ampicillin							
Enterobacteriaceae	≤8		16	≥32	≤8	–#	≥16
Enterococcus spp.	≤8		–§	≥16	≤4	8	≥16
Aztreonam (Phoenix card)							
Enterobacteriaceae	≤4		8	≥16	≤1	2-4	≥8
Pseudomonas spp.	≤8		16	≥32	≤1	2-16	≥32
Cefazolin (Australian)‡	≤2		4	≥8	≤2	4	≥8
Cefepime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacteriaceae	≤2	4-8	–#	≥16	≤1	2-4	≥8
Pseudomonas spp.	≤8		16	≥32	8	–§	≥16
Cefoxitin	≤8		16	≥32	–#	–#	–#
Cephalothin	≤8		16	≥32	–#	–#	–#
Cefalexin	–#		–#	–#	≤16	–§	≥32
Ceftazidime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacteriaceae	≤4		8	≥16	≤1	2-4	≥8
Pseudomonas spp.	≤8		16	≥32	≤8	–§	≥16
Ceftriaxone							
Acinetobacter spp.	≤8		16-32	≥64	–#	–#	–#
Enterobacteriaceae	≤1		2	≥4	≤1	2	≥4
Chloramphenicol (Phoenix card)	≤8		16	≥32	≤8	–§	≥16
Ciprofloxacin							
Acinetobacter spp.	≤1		2	≥4	≤1	–§	≥2
Enterobacteriaceae	≤1		2	≥4	≤0.5	1	≥2
Salmonella spp.§§	≤0.06		0.12-0.5	≥1	≤0.06	–§	≥0.12
Enterococcus spp.##	≤1		2	≥4	≤4	–§	≥8
Staphylococcus aureus	≤1		2	≥4	≤1	–§	≥2
Pseudomonas spp.	≤1		2	≥4	≤0.5	1	≥2
Clindamycin							
Staphylococcus aureus	≤0.5		1-2	≥4	≤0.25	0.5	≥1

Table B1: (continued)

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v6.0†		
	S	SDD	I	R	S	I	R
Colistin (Phoenix card)							
Acinetobacter spp.	≤2		4	≥8	≤2	–§	≥4
Enterobacteriaceae	–#		–#	–#	≤2	–§	≥4
Pseudomonas spp.	≤2		4	≥8	≤4	–§	≥8
Daptomycin							
Enterococcus spp.	≤4		–#	–#	–#	–#	–#
Staphylococcus aureus	≤1		–#	–#	≤1	–§	≥2
Doxycycline (Phoenix card)							
Enterococcus spp.	≤4		8	≥16	–#	–#	–#
Staphylococcus aureus	≤4		8	≥16	≤1	2	≥4
Ertapenem (Phoenix card)	≤0.5		1	≥2	≤0.5	1	≥2
Erythromycin							
Enterococcus spp.	≤0.5		1-4	≥8	–#	–#	–#
Staphylococcus aureus	≤0.5		1-4	≥8	≤1	2	≥4
Fosfomycin (Phoenix card)	≤64		128	≥256	≤32	–§	≥64
Fusidic acid							
Staphylococcus aureus	–#		–#	–#	≤1	–§	≥2
Gentamicin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	≥8
Enterobacteriaceae	≤4		8	≥16	≤2	4	≥8
Pseudomonas spp.	≤4		8	≥16	≤4	–§	≥8
Staphylococcus aureus	≤4		8	≥16	≤1	–§	≥2
Imipenem (Phoenix card)							
Acinetobacter spp.	≤2		4	≥8	≤2	4-8	≥16
Enterobacteriaceae	≤1		2	≥4	≤2	4-8	≥16
Pseudomonas spp.	≤2		4	≥8	≤4	8	≥16
Linezolid							
Enterococcus spp.	≤2		4	≥8	≤4	–§	≥8
Staphylococcus aureus	≤4		8	≥16	≤4	–§	≥8
Meropenem							
Acinetobacter spp.	≤2		4	≥8	≤2	4-8	≥16
Enterobacteriaceae	≤1		2	≥4	≤2	4-8	≥16
Pseudomonas spp.	≤2		4	≥8	≤2	4-8	≥16

continued

Table B1: (continued)

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v6.0†		
	S	SDD	I	R	S	I	R
Nitrofurantoin							
Enterobacteriaceae	≤32		64	≥128	≤64††	–§	≥128
Enterococcus spp.	≤32		64	≥128	≤64‡‡	–§	≥128
Staphylococcus aureus	≤32		64	≥128	–	–	–
Norfloxacin							
Enterobacteriaceae	≤4		8	≥16	≤0.5	1	≥2
Pseudomonas spp.	≤4		8	≥16	–	–	–
Oxacillin							
Staphylococcus aureus	≤2		–§	≥4	–#	–#	–#
Piperacillin-tazobactam							
Acinetobacter spp.	≤16/4		32/4-64/4	≥128/4	–#	–#	–#
Enterobacteriaceae	≤16/4		32/4-64/4	≥128/4	≤8	16	≥32
Pseudomonas spp.	≤16/4		32/4-64/4	≥128/4	≤16	–§	≥32
Rifampicin							
Enterococcus spp.	≤1		2	≥4	–#	–#	–#
Staphylococcus aureus	≤1		2	≥4	≤0.06***	0.12-0.5	≥1
Teicoplanin							
Enterococcus spp.	≤8		16	≥32	≤2	–§	≥4
Staphylococcus aureus	≤8		16	≥32	≤2	–§	≥4
Tetracycline							
Acinetobacter spp.	≤4		8	≥16	–#	–#	–#
Enterobacteriaceae	≤4		8	≥16	–#	–#	–#
Enterococcus spp.	≤4		8	≥16	–#	–#	–#
Staphylococcus aureus	≤4		8	≥16	≤1	2	≥4
Ticarcillin-clavulanate							
Acinetobacter spp.	≤16/2		32/2-64/2	≥128/2	–#	–#	–#
Enterobacteriaceae	≤16/2		32/2-64/2	≥128/2	≤8	16	≥32
Pseudomonas spp.	≤16/2		32/2-64/2	≥128/2	≤16	–§	≥32
Tigecycline (Phoenix card)	–#		–#	–#	≤1	2	≥4
Tobramycin							
Acinetobacter spp.	≤4		8	≥16	≤4	–§	≥8
Enterobacteriaceae	≤4		8	≥16	≤2	4	≥8
Pseudomonas spp.	≤4		8	≥16	≤4	–§	≥8

continued

Table B1: (continued)

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v6.0†		
	S	SDD	I	R	S	I	R
Trimethoprim							
Enterobacteriaceae	≤8		–§	≥16	≤2	4	≥8
Enterococcus spp.	–#		–#	–#	≤0.03	0.06–1	≥2
Staphylococcus aureus	≤8		–§	≥16	≤2	4	≥8
Trimethoprim–sulfamethoxazole							
Acinetobacter spp.	≤2/38		–	≥4/76	≤2/38	4/76	≥8/152
Enterobacteriaceae	≤2/38		–	≥4/76	≤2/38	4/76	≥8/152
Enterococcus spp.	–#		–#	–#	≤0.03§§§	0.06–1	≥2
Staphylococcus aureus	≤2		–§	≥4	≤2	4	≥8
Vancomycin							
Enterococcus spp.	≤4		8–16	≥32	≤4	–§	≥8
Staphylococcus aureus	≤2		4–8	≥16	≤2	–§	≥4

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 determine resistance are described in Performance Standards for Antimicrobial Susceptibility Testing: Twenty-fifth Informational Supplement, CLSI document M100-S26, January 2016.

† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 6.0, 2016 (http://www.eucast.org)

§ No category defined

No guidelines for indicated species

** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanate at 2 mg/L, rather than the 2:1 ratio used in CLSI guidelines. 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 determine 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 determine 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 Enterobacteriaceae 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 (SA Pathology) for molecular confirmation of resistance.

All referred isolates were screened for the presence of the bla_{TEM} and bla_{SHV} genes using a real-time polymerase chain reaction (PCR) platform (LC-480) and published primers.[3,4] A multiplex real-time TaqMan PCR was used to detect CTX-M-type genes.[5] Strains were probed for plasmid-borne AmpC enzymes using the method described by Pérez-Pérez and Hanson,[6] and subjected to molecular tests for MBL (bla_{VIM}, bla_{IMP}, and bla_{NDM}), bla_{KPC} and $bla_{OXA\text{-}48\text{-}like}$ genes using real-time PCR.[7,8] Known plasmid-mediated quinolone resistance mechanisms (*qnr*, efflux [*qepA*, *oqxAB*], and *aac(6')-Ib-cr*) were examined by PCR on all referred isolates with ciprofloxacin MIC >0.25 mg/L using published methods.[9,10] All referred *E. coli* were examined for phylogenetic group and membership of the O25b-ST131 clone and its *H30*- and *H30*-Rx subclones.[11-13]

All available vancomycin-resistant *E. faecium* and methicillin-resistant *S. aureus* were characterised by whole genome sequencing using the Illumina MiSeq platform. Data were analysed using the Nullarbor platform.[14] The pipeline was used to determine the multilocus sequence type, the SCC*mec* type, and the presence of Panton-Valentine leucocidin-associated genes (*S. aureus*) and *van* genes (*Enterococcus* species).

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 B references

1. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. CLSI document M100S. Wayne, PA: Clinical and Laboratory Standards Institute; 2016.
2. European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 6.0, valid from 2016-01-01. Available from: http://www.eucast.org
3. Chia JH, Chu C, Su LH, Chiu CH, Kuo AJ, Sun CF, et al. Development of a multiplex PCR and SHV melting-curve mutation detection system for detection of some SHV and CTX-M beta-lactamases of *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterobacter cloacae* in Taiwan. J Clin Microbiol 2005;43:4486–91.
4. Hanson ND, Thomson KS, Moland ES, Sanders CC, Berthold G, Penn RG. Molecular characterization of a multiply resistant *Klebsiella pneumoniae* encoding ESBLs and a plasmid-mediated AmpC. J Antimicrob Chemother 1999;44:377-80.
5. Birkett CI, Ludlam HA, Woodford N, Brown DF, Brown NM, Roberts MT, et al. Real-time TaqMan PCR for rapid detection and typing of genes encoding CTX-M extended-spectrum beta-lactamases. J Med Microbiol 2007;56:52–5.
6. Perez-Perez FJ, Hanson ND. Detection of plasmid-mediated AmpC beta-lactamase genes in clinical isolates by using multiplex PCR. J Clin Microbiol 2002;40:2153–62.
7. Mendes RE, Kiyota KA, Monteiro J, Castanheira M, Andrade SS, Gales AC, et al. Rapid detection and identification of metallo-beta-lactamase-encoding genes by multiplex real-time PCR assay and melt curve analysis. J Clin Microbiol 2007;45:544–7.
8. Poirel L, Héritier C, Tolün V, Nordmann O. Emergence of oxacillinase-mediated resistance to imipenem in *Klebsiella pneumoniae*. Antimicrob Agents Chemother 2004;48:15–22.
9. Cattoir V, Poirel L, Rotimi V, Soussy CJ, Nordmann P. Multiplex PCR for detection of plasmid-mediated quinolone resistance *qnr* genes in ESBL-producing enterobacterial isolates. J Antimicrob Chemother 2007;60:394–7.
10. Ciesielczuk H, Hornsey M, Choi V, Woodford N, Wareham DW. Development and evaluation of a multiplex PCR for eight plasmid-mediated quinolone-resistance determinants. J Med Microbiol 2013;62:1823–7.
11. Banerjee R, Robicsek A, Kuskowski MA, Porter S, Johnston BD, Sokurenko E, et al. Molecular epidemiology of *Escherichia coli* sequence type 131 and its *H30* and *H30*-Rx subclones among extended-spectrum-beta-lactamase-positive and -negative *E. coli* clinical isolates from the Chicago region, 2007 to 2010. Antimicrob Agents Chemother 2013;57:6385–8.
12. Colpan A, Johnston B, Porter S, Clabots C, Anway R, Thao L, et al. *Escherichia coli* sequence type 131 (ST131) subclone *H30* as an emergent multidrug-resistant pathogen among US veterans. Clin Infect Dis 2013;57:1256–65.
13. Dhanji H, Doumith M, Clermont O, Denamur E, Hope R, Livermore DM, et al. Real-time PCR for detection of the O25b-ST131 clone of *Escherichia coli* and its CTX-M-15-like extended-spectrum beta-lactamases. Int J Antimicrob Agents 2010;36:355–8.
14. Seemann T, Goncalves da Silva A, Bulach DM, Schultz MB, Kwong JC, Howden BP. Nullarbor Github. Available from: https://github.com/tseemann/nullarbor

APPENDIX C

Susceptibility to antimicrobial agents

Overall percentages of resistance or non-susceptibility for the most common gram-negative species – *S. aureus*, *E. faecalis* and *E. faecium* – 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 strains. Similarly, 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, 2015

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Benzylpenicillin										
Enterococcus faecalis	*n*	149	110	94	58	91	0	10	35	547
	%R	2.0, nd	0.9, nd	2.1, nd	0.0, nd	4.4, nd	na	0.0, nd	2.9, nd	2.0, nd
Enterococcus faecium	*n*	115	118	30	44	53	1	8	22	391
	%R	87.8, nd	91.5, nd	83.3, nd	93.2, nd	79.2, nd	na	na	95.5, nd	88.5, nd
Staphylococcus aureus	*n*	590	407	503	261	394	51	110	81	2,397
	%R	84.1, 84.1	77.9, 77.9	80.1, 80.1	88.9, 88.9	80.2, 80.2	86.3, 86.3	90.0, 90.0	80.2, 80.2	82.3, 82.3
Ampicillin										
Escherichia coli	*n*	1,106	727	691	453	650	79	137	149	3,992
	%I	2.2, nd	2.9, nd	1.6, nd	1.3, nd	1.7, nd	2.5, nd	2.9, nd	2.7, nd	2.1, nd
	%R	55.4, 57.6	56.9, 59.8	51.5, 53.1	44.2, 45.5	54.0, 55.7	43.0, 45.6	56.9, 59.9	48.3, 51.0	53.1, 55.1
Enterococcus faecalis	*n*	150	110	95	58	91	12	10	35	561
	%I	nd, 0.0	nd, 0.0	nd, 1.1	nd, 0.0	nd, 0.0	nd, 0.0	nd, 0.0	nd, 0.0	nd, 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*	115	120	30	44	53	8	8	22	400
	%I	nd, 0.9	nd, 1.7	nd, 0.0	nd, 0.0	nd, 0.0	na	na	nd, 0.0	nd, 0.8
	%R	85.2, 85.2	88.3, 88.3	83.3, 83.3	93.2, 93.2	79.2, 79.2	na	na	95.5, 95.5	86.0, 86.0
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%I	0.0, nd	0.0, nd	0.0, nd	0.0, nd	0.0, nd	na	na	na	0.0, nd
	%R	22.7, 22.7	18.9, 18.9	4.5, 4.5	12.5, 12.5	30.6, 30.6	na	na	na	17.1, 17.1

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ampicillin (continued)										
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%I	0.0, nd	0.0, nd	0.0, nd	na	0.0, nd	na	0.0, nd	na	0.0, nd
	%R	5.3, 5.3	23.8, 23.8	10.7, 10.7	na	0.0, 0.0	na	0.0, 0.0	na	8.8, 8.8
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%I	na	na	na	na	na	na	na	na	4.0, nd
	%R	na	na	na	na	na	na	na	na	4.0, 8.0
Amikacin										
Acinetobacter baumannii	*n*	10	10	20	1	11	2	5	0	59
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	na	na	0.0, 0.0
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%R	0.1, 0.1	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.2, 0.2	0.0, 0.0	0.7, 0.7	0.0, 0.7	0.1, 0.1
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%R	0.0, 0.0	0.6, 0.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	0.0, 0.0	0.0, 0.0
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%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	na	0.0, 0.0	0.0, 0.0
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	na	0.0, 0.0
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	na	0.0, 0.0

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Amikacin (continued)										
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0
Salmonella species (typhoidal)	*n*	5	7	5	4	2	0	0	1	25
	%R	na	na	na	na	na	na	na	na	0.0, 0.0
Pseudomonas aeruginosa	*n*	166	74	165	83	107	4	19	36	654
	%R	1.8, 1.8	0.0, 2.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	0.0, 0.0	0.5, 0.8
Amoxicillin-clavulanate										
Escherichia coli	*n*	1,106	727	691	453	650	79	137	149	3,992
	%I	14.1, –†	13.6, –†	15.2, –†	12.8, –†	13.4, –†	10.1, –†	10.2, –†	12.8, –†	13.7, –†
	%R	9.1, –†	10.6, –†	7.8, –†	6.2, –†	8.6, –†	12.7, –†	13.1, –†	3.4, –†	8.7, –†
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%I	3.8, –†	6.8, –†	4.8, –†	2.4, –†	5.3, –†	5.6, –†	6.4, –†	2.9, –†	4.8, –†
	%R	5.1, –†	5.6, –†	3.7, –†	2.4, –†	2.1, –†	5.6, –†	4.3, –†	8.6, –†	4.2, –†
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%I	3.9, –†	6.1, –†	2.2, –†	7.7, –†	0.0, –†	na	na	0.0, –†	4.2, –†
	%R	10.5, –†	4.1, –†	6.7, –†	0.0, –†	10.0, –†	na	na	7.7, –†	7.6, –†
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%I	9.1, –†	5.4, –†	6.8, –†	4.2, –†	19.4, –†	na	na	na	8.6, –†
	%R	1.5, –†	5.4, –†	0.0, –†	0.0, –†	2.8, –†	na	na	na	1.8, –†
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10†	2	24	1	114
	%I	0.0, –†	9.5, –†	0.0, –†	na	0.0, –†	na	0.0, –†	na	1.8, –†
	%R	5.3, –†	9.5, –†	0.0, –†	na	0.0, –†	na	0.0, –†	na	2.6, –†

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Amoxicillin–clavulanate (continued)										
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%I	na	na	na	na	na	na	na	na	8.0, –[†]
	%R	na	na	na	na	na	na	na	na	0.0, –[†]
Cefazolin										
Escherichia coli	*n*	1,107	604	691	453	574	49	137	149	3,764
	%R	25.1, 25.1	24.7, 24.7	20.1, 20.1	18.1, 20.1	19.0, 19.0	10.2, 10.2	21.9, 21.9	18.8, 18.8	21.8, 21.8
Klebsiella pneumoniae	*n*	236	150	189	85	165	9	47	35	916
	%R	10.6, 10.6	16.7, 16.7	9.0, 9.0	8.2, 8.2	8.5, 8.5	na	17.0, 17.0	8.6, 8.6	10.9, 10.9
Klebsiella oxytoca	*n*	76	41	45	13	23	5	4	13	220
	%R	63.2, 63.2	63.4, 63.4	62.2, 62.2	69.2, 69.2	47.8, 47.8	na	na	61.5, 61.5	62.3, 62.3
Enterobacter cloacae complex	*n*	85	74	65	13	48	8	9	10	312
	%R	91.8, 91.8	98.6, 98.6	98.5, 98.5	100, 100	100, 100	na	na	100, 100	96.5, 96.5
Enterobacter aerogenes	*n*	34	20	26	11	23	1	3	4	122
	%R	91.2, 91.2	75.0, 75.0	80.8, 80.8	90.9, 90.9	73.9, 73.9	na	na	na	83.6, 83.6
Proteus mirabilis	*n*	66	34	44	24	27	2	6	6	209
	%R	22.7, 22.7	32.4, 32.4	27.3, 27.3	12.5, 12.5	44.4, 44.4	na	na	na	25.4, 25.4
Salmonella species (non-typhoidal)	*n*	19	16	28	9	9	0	24	1	106
	%R	5.3, 5.3	12.5, 12.5	0.0, 0.0	na	na	na	0.0, 0.0	na	2.8, 2.8
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%R	na	na	na	na	na	na	na	na	4.0, 4.0

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Cefoxitin										
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%R	4.7, nd	3.6, nd	2.6, nd	2.6, nd	2.8, nd	2.5, nd	2.9, nd	1.3, nd	3.4, nd
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%R	8.9, nd	4.0, nd	3.2, nd	2.4, nd	4.3, nd	0.0, nd	2.1, nd	5.7, nd	4.8, nd
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%R	5.3, nd	0.0, nd	2.2, nd	7.7, nd	0.0, nd	na	na	0.0, nd	2.5, nd
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%R	0.0, nd	0.0, nd	0.0, nd	0.0, nd	2.8, nd	na	na	na	0.5, nd
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	0.0, nd	9.5, nd	0.0, nd	na	0.0, nd	na	0.0, nd	na	1.8, nd
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%R	na	na	na	na	na	na	na	na	4.0, nd
Cefepime										
Acinetobacter baumannii	*n*	10	10	20	1	11	0	5	0	57
	%R	0.0, nd	10.0, nd	5.0, nd	na	0.0, nd	na	na	na	3.5, nd
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%NS§	10.0, 13.6	5.4, 9.8	1.6, 3.9	5.5, 6.2	4.6, 7.2	0.0, 0.0	2.9, 8.0	4.7, 9.4	5.7, 8.7
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%NS	4.2, 5.5	3.4, 9.0	1.6, 2.6	3.5, 3.5	1.1, 2.7	0.0, 5.6	2.1, 4.3	0.0, 2.9	2.6, 4.7
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%NS	2.6, 2.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	0.0, 0.0	0.8, 1.3

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Cefepime (continued)										
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%NS	9.4, 12.9	10.0, 18.7	4.6, 13.8	0.0, 0.0	0.0, 12.0	0.0, 7.1	na	0.0, 0.0	5.8, 12.9
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%NS	2.9, 2.9	11.1, 11.1	3.8, 3.8	0.0, 0.0	0.0, 0.0	na	na	na	3.8, 3.8
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%NS	0.0, 0.0	2.7, 2.7	2.3, 2.3	0.0, 0.0	2.8, 2.8	na	na	na	1.4, 1.4
Pseudomonas aeruginosa	*n*	166	74	165	83	107	4	19	36	654
	%R	2.4, 6.6	4.1, 9.5	1.8, 5.5	2.4, 10.8	2.8, 6.5	na	0.0, 15.8	5.6, 16.7	2.6, 8.0
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%NS	na	na	na	na	na	na	na	na	0.0, 0.0
Ceftazidime										
Acinetobacter baumannii	*n*	10	10	20	1	11	0	5	0	57
	%NS	10.0, nd	20.0, nd	25.0, nd	na	0.0, nd	na	na	na	14.0, nd
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%NS	9.9, 14.5	6.3, 11.4	3.2, 5.6	4.4, 7.0	4.8, 8.6	0.0, 1.3	3.6, 8.0	5.4, 9.4	6.1, 9.9
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%NS	6.8, 8.9	9.6, 12.4	3.2, 3.7	2.4, 4.7	2.1, 4.8	5.6, 5.6	2.1, 2.1	2.9, 5.7	4.9, 6.9
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%NS	0.0, 2.6	0.0, 0.0	2.2, 2.2	15.4, 15.4	0.0, 0.0	na	na	0.0, 0.0	1.3, 2.1

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ceftazidime (continued)										
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%NS	23.5, 23.5	27.5, 31.2	23.1, 24.6	0.0, 0.0	20.0, 22.0	28.6, 35.7	na	0.0, 0.0	22.4, 24.2
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%NS	41.2, 47.1	55.6, 55.6	15.4, 19.2	27.3, 27.3	32.0, 32.0	na	na	na	37.4, 39.7
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%NS	0.0, 0.0	2.7, 5.4	2.3, 2.3	0.0, 0.0	2.8, 2.8	na	na	na	1.4, 1.8
Pseudomonas aeruginosa	*n*	166	74	165	82	107	4	19	36	653
	%NS/R	12.0, 12.0	14.9, 14.9	7.3, 7.3	7.3, 7.3	10.3, 10.3	na	5.3, 5.3	19.4, 19.4	10.4, 10.4
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%NS	0.0, 0.0	9.5, 9.5	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	1.8, 1.8
Salmonella species (typhoidal)	*n*	4	7	6	4	2	0	0	1	24
	%NS	na	na	na	na	na	na	na	na	0.0, 0.0
Ceftriaxone										
Acinetobacter baumannii	*n*	10	10	20	1	11	0	5	0	57
	%NS	70.0, nd	90.0, nd	85.0, nd	na	45.5, nd	na	na	na	75.4, nd
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%NS	15.3, 15.3	12.2, 12.2	6.1, 6.1	7.5, 7.5	9.4, 9.4	0.0, 0.0	8.8, 8.8	10.7, 10.7	10.6, 10.6
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%NS	6.8, 6.8	10.7, 10.7	3.7, 3.7	3.5, 3.5	3.7, 3.7	5.6, 5.6	6.4, 6.4	2.9, 2.9	5.9, 5.9
Klebsiella oxytoca	*n*	76	49	45	13	30	7	4	13	237
	%NS	10.5, 10.5	6.1, 6.1	6.7, 6.7	23.1, 23.1	6.7, 6.7	na	na	7.7, 7.7	8.4, 8.4

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ceftriaxone (continued)										
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%NS	24.7, 24.7	32.5, 32.5	29.2, 29.2	0.0, 0.0	22.0, 22.0	28.6, 28.6	na	10.0, 10.0	25.8, 25.8
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%NS	50.0, 50.0	55.6, 55.6	19.2, 19.2	36.4, 36.4	36.0, 36.0	na	na	na	42.0, 42.0
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%NS	1.5, 1.5	5.4, 5.4	2.3, 2.3	0.0, 0.0	2.8, 2.8	na	na	na	2.3, 2.3
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%NS	0.0, 0.0	14.3, 14.3	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	2.6, 2.6
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%NS	na	na	na	na	na	na	na	na	4.0, 4.0
Ciprofloxacin										
Acinetobacter baumannii	*n*	10	10	20	1	11	2	5	0	59
	%NS/R	0.0, 0.0	10.0, 10.0	5.0, 5.0	na	0.0, 0.0	na	na	na	3.4, 3.4
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%NS	16.9, 17.7	13.3, 14.4	8.1, 8.7	8.6, 9.0	14.5, 16.2	3.8, 7.6	8.8, 9.5	10.1, 10.7	12.6, 13.6
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%NS	5.1, 7.2	5.6, 11.9	2.6, 6.3	2.4, 4.7	2.7, 5.9	5.6, 5.6	2.1, 4.3	5.7, 5.7	3.9, 7.2
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	3.3, 3.3	na	na	0.0, 0.0	0.4, 0.4
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%NS	5.9, 8.2	5.0, 5.0	3.1, 3.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	3.4, 4.0

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ciprofloxacin (continued)										
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%NS	0.0, 0.0	11.1, 11.1	7.7, 11.5	0.0, 0.0	0.0, 0.0	na	na	na	3.8, 4.6
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%NS	3.0, 3.0	2.7, 2.7	2.3, 4.5	8.3, 8.3	5.6, 5.6	na	na	na	4.1, 4.5
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R#	10.5, -#	0.0, -#	0.0, -#	na	0.0, -#	na	0.0, -#	na	1.8, -#
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%R#	na	na	na	na	na	na	na	na	56.0, -†
Pseudomonas aeruginosa	*n*	166	74	165	82	107	4	19	36	653
	%NS	3.6, 3.7	10.8, 11.3	5.5, 5.6	9.8, 10.5	5.6, 5.7	na	5.3, 5.6	8.3, 8.6	6.3, 6.5
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%NS/R	19.7, 19.7	12.3, 12.3	4.2, 4.2	6.9, 6.9	8.1, 8.1	2.0, 2.0	8.2, 8.2	8.6, 8.6	10.6, 10.6
Methicillin resistant	*n*	135	63	68	43	69	3	42	12	435
	%NS/R	75.6, 75.6	63.5, 63.5	19.1, 19.1	27.9, 27.9	33.3, 33.3	na	19.0, 19.0	50.0, 50.0	47.1, 47.1
Methicillin susceptible	*n*	455	344	435	219	325	48	68	69	1,963
	%NS/R	3.1, 3.1	2.9, 2.9	1.8, 1.8	2.7, 2.7	2.8, 2.8	0.0, 0.0	1.5, 1.5	1.4, 1.4	2.5, 2.5
Enterococcus faecalis	*n*	149, 140**	110	83	43, 35	91	0	10	35	521, 504
	%NS/R	17.4, 9.3	16.4, 15.5	9.6, 9.6	44.2, 8.6	11.0, 8.8	na	30.0, 30.0	14.3, 14.3	17.1, 11.3
Enterococcus faecium	*n*	144, 89	120	28	27, 4	53	1	8	22	373, 325
	%NS/R	92.1, 83.1	97.5, 90.0	85.7, 82.1	96.3, na	79.2, 79.2	na	na	95.5, 95.5	92.2, 85.8

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Clindamycin										
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%NS	5.8, 6.3	2.9, 2.9	2.0, 2.0	2.7, 3.4	1.0, 1.0	2.0, 2.0	7.3, 7.3	2.5, 2.5	3.3, 3.5
Methicillin resistant	*n*	135	63	68	43	69	3	42	12	435
	%NS	19.3, 20.7	14.3, 14.3	13.2, 13.2	14.0, 16.3	5.8, 5.8	na	16.7, 16.7	8.3, 8.3	14.3, 14.9
Methicillin susceptible	*n*	455	344	435	219	325	48	68	69	1,963
	%NS	1.8, 2.0	0.9, 0.9	0.2, 0.2	0.5, 1.0	0.0, 0.0	2.1, 2.1	1.5, 1.5	1.4, 1.4	0.8, 0.9
Daptomycin										
Enterococcus faecalis	*n*	145	107	92	57	90	0	10	35	536
	%NS	0.0, nd	0.0, nd	1.1, nd	0.0, nd	0.0, nd	na	0.0, nd	0.0, nd	0.2, nd
Staphylococcus aureus	*n*	589	407	503	262	394	51	110	81	2,397
	%NS/R	0.5, 0.5	0.2, 0.2	0.2, 0.2	0.0, 0.0	0.3, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.3
Methicillin resistant	*n*	135	63	68	43	69	3	42	12	435
	%NS/R	0.7, 0.7	1.6, 1.6	1.5, 1.5	0.0, 0.0	1.4, 1.4	na	0.0, 0.0	0.0, 0.0	0.9, 0.9
Methicillin susceptible	*n*	454	344	435	219	325	48	68	69	1,962
	%NS/R	0.4, 0.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
Erythromycin										
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%NS	22.9, 20.5	15.0, 12.0	13.5, 9.7	11.8, 10.7	15.0, 12.7	11.8, 3.9	26.4, 26.4	11.1, 9.9	16.6, 14.0
Methicillin resistant	*n*	135	63	68	43	69	3	42	12	435
	%NS	62.5, 61.5	46.0, 42.9	32.4, 29.4	27.9, 27.9	34.8, 34.8	na	31.0, 31.0	25.0, 25.0	43.5, 42.1

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Erythromycin (continued)										
Methicillin susceptible	*n*	455	344	435	219	325	48	68	69	1,963
	%NS	11.2, 8.4	9.3, 6.4	10.6, 6.7	8.7, 7.3	10.8, 8.0	8.3, 2.1	23.5, 23.5	8.7, 7.2	10.6, 7.8
Fusidic acid										
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%R	nd, 2.9	nd, 2.5	nd, 5.4	nd, 1.9	nd, 2.3	nd, 3.9	nd, 4.5	nd, 6.2	nd, 3.3
Methicillin resistant	*n*	135	63	68	43	69	3	42	12	435
	%R	nd, 4.4	nd, 3.2	nd, 5.9	nd, 9.3	nd, 2.9	na	nd, 7.1	nd, 0.0	nd, 4.8
Methicillin susceptible	*n*	455	344	435	219	325	48	68	69	1,963
	%R	nd, 2.4	nd, 2.3	nd, 5.3	nd, 0.5	nd, 2.2	nd, 4.2	nd, 2.9	nd, 7.2	nd, 3.0
Gentamicin										
Acinetobacter baumannii	*n*	10	10	20	1	11	2	5	0	59
	%R	0.0, 0.0	10.0, 10.0	5.0, 5.0	na	0.0, 0.0	na	na	na	3.4, 3.4
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%R	9.3, 9.4	6.9, 6.9	6.5, 6.7	7.3, 7.3	9.2, 9.2	2.5, 2.5	8.8, 8.8	4.0, 4.7	7.8, 7.9
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%R	5.5, 5.9	3.4, 4.0	3.2, 3.2	4.7, 5.9	2.7, 2.7	5.6, 5.6	10.6, 10.6	2.9, 2.9	4.2, 4.5
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%R	0.0, 0.0	0.0, 2.0	2.2, 2.2	0.0, 0.0	3.3, 3.3	na	na	0.0, 0.0	0.8, 1.3
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%R	12.9, 12.9	3.8, 5.0	9.2, 10.8	0.0, 0.0	0.0, 0.0	7.1, 7.1	na	0.0, 0.0	6.7, 7.4

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Gentamicin (continued)										
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%R	2.9, 2.9	7.4, 7.4	3.8, 3.8	0.0, 0.0	0.0, 0.0	na	na	na	3.1, 3.1
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%R	1.5, 3.0	0.0, 2.7	0.0, 2.3	0.0, 0.0	0.0, 0.0	na	na	na	0.5, 1.8
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	5.3, 5.3	4.8, 4.8	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	1.8, 1.8
Salmonella species (typhoidal)	*n*	5	7	5	4	2	0	0	1	25
	%R	na	na	na	na	na	na	na	na	0.0, 0.0
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%R	5.4, 9.7	2.0, 3.2	0.8, 1.4	3.1, 3.1	0.5, 0.5	0.0, 0.0	7.3, 7.3	0.0, 2.5	2.6, 4.0
Methicillin resistant	*n*	135	63	68	43	69	3	42	12	435
	%R	21.5, 39.3	11.1, 14.3	1.5, 2.9	9.3, 9.3	2.9, 2.9	na	16.7, 16.7	0.0, 8.3	11.5, 17.9
Methicillin susceptible	*n*	455	344	435	219	325	48	68	69	1,963
	%R	0.7, 0.9	0.3, 1.2	0.7, 1.1	1.8, 1.8	0.0, 0.0	0.0, 0.0	1.5, 1.5	0.0, 1.4	0.6, 1.0
Pseudomonas aeruginosa	*n*	166	74	165	83	107	4	19	36	654
	%R	4.8, 5.4	4.1, 6.8	0.6, 1.8	2.4, 2.4	1.9, 1.9	na	0.0, 5.3	0.0, 0.0	2.4, 3.4
Linezolid										
Enterococcus faecalis	*n*	150	110	95	58	91	12	10	35	561
	%NS/R	0.0, 0.0	0.0, 0.0	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
Enterococcus faecium	*n*	115	120	30	44	53	8	8	22	400
	%NS/R	3.5, 0.0	5.0, 0.0	0.0, 0.0	2.3, 0.0	3.8, 0.0	na	na	0.0, 0.0	3.3, 0.0

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Linezolid (continued)										
Staphylococcus aureus	*n*	589	407	503	262	394	51	110	81	2,397
	%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	*n*	135	63	68	43	69	3	42	12	435
	%NS/R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin susceptible	*n*	454	344	435	219	325	48	68	69	1,962
	%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	*n*	10	10	20	1	11	2	5	0	59
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	na	na	0.0, 0.0
Escherichia coli	*n*	1,107	727	691	453	650	79	137	149	3,993
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.3	0.2, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.6	<0.1, 0.0
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%NS	0.0, 0.0	0.6, 0.6	0.0, 0.0	1.2, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.9, 2.9	0.3, 0.3
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%NS	0.0, 0.0	0.0, 0.0	2.2, 2.2	0.0, 0.0	0.0, 0.0	na	na	0.0, 0.0	0.4, 0.4
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%NS	7.1, 5.9	0.0, 0.0	4.6, 4.6	0.0, 0.0	4.0, 4.0	0.0, 0.0	na	0.0, 0.0	3.4, 3.1
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%NS	2.9, 2.9	3.7, 3.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	na	1.5, 1.5
Proteus mirabilis	*n*	66	37	44	24	35	3	6	6	221
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	na	0.0, 0.0

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Meropenem (continued)										
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%NS	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%NS	na	na	na	na	na	na	na	na	0.0, 0.0
Pseudomonas aeruginosa	*n*	166	74	165	82	107	4	19	36	653
	%NS	9.0, 9.0	9.5, 9.5	9.7, 9.7	7.3, 7.3	3.7, 3.7	na	15.8, 15.8	2.8, 2.8	8.1, 8.1
Nitrofurantoin										
Escherichia coli	*n*	1,107	727	691	454	650	79	137	149	3,994
	%R	1.0, 1.0	2.2, 2.2	0.7, 0.7	1.3, 1.3	1.5, 1.5	0.0, 0.0	0.0, 0.0	1.3, 1.3	1.3, 1.3
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%R	30.9, nd	44.1, nd	20.6, nd	35.3, nd	32.6, nd	22.2, nd	38.3, nd	37.1, nd	32.4, nd
Klebsiella oxytoca	*n*	76	49	45	13	30	8	4	13	238
	%R	0.0, nd	0.0, nd	2.2, nd	23.1, nd	0.0, nd	na	na	0.0, nd	2.1, nd
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%R	16.5, nd	25.0, nd	15.4, nd	46.2, nd	20.0, nd	21.4, nd	na	10.0, nd	20.6, nd
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%R	47.1, nd	51.9, nd	46.2, nd	27.3, nd	32.0, nd	na	na	na	43.5, nd
Proteus mirabilis	*n*	66	37	44	24	36	3	6	6	222
	%R	92.4, nd	94.6, nd	100, nd	91.7, nd	91.7, nd	na	na	na	94.6, nd
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	5.3, nd	9.5, nd	7.1, nd	na	40.0, nd	na	0.0, nd	na	8.8, nd

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Nitrofurantoin (continued)										
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%R	na	na	na	na	na	na	na	na	4.0, nd
Staphylococcus aureus	*n*	589	407	448	262	394	0	110	81	2,291
	%R	0.3, nd	0.0, nd	0.0, nd	0.0, nd	0.0, nd	na	0.0, nd	0.0, nd	0.1, nd
Methicillin resistant	*n*	135	63	68	43	69	0	42	12	426
	%R	0.7, nd	0.0, nd	0.0, nd	0.0, nd	0.0, nd	na	0.0, nd	0.0, nd	0.2, nd
Methicillin susceptible	*n*	454	344	386	219	325	0	68	69	1,865
	%R	0.2, nd	0.0, nd	0.0, nd	0.0, nd	0.0, nd	na	0.0, nd	0.0, nd	0.1, nd
Enterococcus faecalis	*n*	149	109	95	57	91	12	10	35	558
	%R	0.0, 0.0	0.0, 0.0	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.2
Enterococcus faecium	*n*	115	120	30	44	53	8	8	22	400
	%R	53.0, nd	20.0, nd	40.0, nd	40.9, nd	28.3, nd	na	na	81.8, nd	38.3, nd
Oxacillin										
Staphylococcus aureus	*n*	587	407	503	262	394	51	110	81	2,395
	%R	22.5, 22.5	14.7, 14.7	13.3, 13.3	15.3, 15.3	16.8, 16.8	3.9, 3.9	37.3, 37.3	14.8, 14.8	17.5, 17.5
Piperacillin-tazobactam										
Acinetobacter baumannii	*n*	10	8	8	1	7	0	1	0	35
	%R	0.0, nd	na	na	na	na	na	na	na	2.9, nd
Escherichia coli	*n*	1,107	726	676	454	649	79	137	146	3,974
	%R	3.4, 6.3	3.2, 7.4	3.3, 7.5	2.0, 4.6	1.8, 5.7	2.5, 5.1	2.9, 6.6	1.4, 3.4	2.8, 6.3

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Piperacillin-tazobactam (continued)										
Klebsiella pneumoniae	*n*	235	176	184	85	186	18	47	35	966
	%R	4.3, 6.4	4.0, 7.4	3.8, 7.1	2.4, 4.7	2.7, 4.3	0.0, 5.6	2.1, 12.8	5.7, 5.7	3.5, 6.4
Klebsiella oxytoca	*n*	76	49	43	13	30	8	4	13	236
	%R	13.2, 14.5	6.1, 6.1	7.0, 7.0	7.7, 15.4	10.0, 10.0	na	na	7.7, 7.7	8.9, 10.2
Enterobacter cloacae complex	*n*	57	77	64	13	41	11	9	5	277
	%R	5.3, 14.0	26.0, 27.3	14.1, 18.8	0.0, 7.7	24.4, 26.8	9.1, 18.2	na	na	15.9, 20.6
Enterobacter aerogenes	*n*	34	27	25	11	25	1	3	4	130
	%R	17.6, 38.2	44.4, 55.6	16.0, 24.0	18.2, 27.3	28.0, 40.0	na	na	na	27.7, 40.0
Proteus mirabilis	*n*	65	37	42	24	36	3	6	6	219
	%R	0.0, 1.5	2.7, 2.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	na	0.5, 0.9
Pseudomonas aeruginosa	*n*	166	74	159	83	107	4	19	35	647
	%R	7.8, 15.7	5.4, 14.9	6.3, 15.1	6.0, 10.8	5.6, 10.3	na	5.3, 10.5	20.0, 20.0	7.1, 13.9
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	5.3, 5.3	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	0.9, 0.9
Salmonella species (typhoidal)	*n*	5	6	5	4	1	0	0	1	22
	%R	na	na	na	na	na	na	na	na	0.0, 0.0
Rifampicin										
Staphylococcus aureus	*n*	590	407	503	262	394	0	110	81	2,347
	%R	1.5, 1.7	0.0, 0.2	0.2, 0.2	0.0, 0.0	0.8, 0.8	na	0.0, 0.0	0.0, 0.0	0.6, 0.6
Methicillin resistant	*n*	135	63	68	43	69	0	42	12	432
	%R	5.9, 5.9	0.0, 1.6	1.5, 1.5	0.0, 0.0	4.3, 4.3	na	0.0, 0.0	0.0, 0.0	2.8, 3.0

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Rifampicin (continued)										
Methicillin susceptible	*n*	455	344	435	219	325	0	68	69	1,915
	%R	0.2, 0.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	0.0, 0.0	0.1, 0.1
Teicoplanin										
Enterococcus faecalis	*n*	149	109	95	57	91	12	10	35	558
	%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*	115	120	31	44	53	8	8	22	401
	%NS/R	33.0, 33.9	12.5, 12.5	19.4, 19.4	2.3, 2.3	5.7, 5.7	na	na	31.8, 31.8	17.5, 17.7
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%NS/R	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1
Tetracycline										
Enterococcus faecalis	*n*	120	110	95	28	91	0	10	35	489
	%R	75.0, nd	82.7, nd	80.0, nd	92.9, nd	69.2, nd	na	90.0, nd	80.0, nd	78.3, nd
Enterococcus faecium	*n*	89	120	30	20	53	1	8	22	343
	%R	34.8, nd	77.5, nd	70.0, nd	90.0, nd	37.7, nd	na	na	36.4, nd	57.5, nd
Staphylococcus aureus	*n*	499	407	503	94	394	51	110	81	2139
	%NS	9.6, 10.0	4.2, 4.4	3.2, 4.4	3.2, 3.2	3.6, 3.8	2.0, 2.0	6.4, 6.4	4.9, 6.2	5.1, 5.7
Methicillin resistant	*n*	107	63	68	9	69	3	42	12	373
	%NS	38.3, 38.3	17.5, 17.5	14.7, 16.2	na	2.9, 2.9	na	16.7, 16.7	8.3, 16.7	20.1, 20.6
Methicillin susceptible	*n*	392	344	435	85	325	48	68	69	1,766
	%NS	1.8, 2.3	1.7, 2.0	1.4, 2.5	0.0, 0.0	3.7, 4.0	2.1, 2.1	0.0, 0.0	4.3, 4.3	2.0, 2.5

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Ticarcillin–clavulanate										
Acinetobacter baumannii	*n*	10	10	20	1	11	0	5	0	57
	%R	0.0, nd	0.0, nd	0.0, nd	na	0.0, nd	na	na	na	0.0, nd
Escherichia coli	*n*	985	726	691	454	650	79	137	149	3,871
	%R	10.4, 25.3	10.2, 22.2	10.6, 19.4	7.9, 20.9	9.2, 18.0	6.3, 13.9	13.1, 19.7	6.7, 14.1	9.8, 21.1
Klebsiella pneumoniae	*n*	213	177	189	85	187	18	47	35	951
	%R	7.0, 10.8	10.7, 13.0	6.3, 7.9	4.7, 10.6	3.2, 8.0	5.6, 11.1	4.3, 8.5	8.6, 11.4	6.5, 10.0
Klebsiella oxytoca	*n*	66	49	45	13	30	8	4	13	228
	%R	12.1, 15.2	6.1, 10.0	8.9, 8.9	7.7, 7.7	10.0, 10.0	na	na	7.7, 7.7	9.2, 11.4
Enterobacter cloacae complex	*n*	74	80	65	13	50	14	9	10	315
	%R	16.2, 23.0	31.3, 31.3	21.5, 26.2	0.0, 0.0	22.0, 22.0	14.3, 21.4	na	0.0, 0.0	21.0, 23.8
Enterobacter aerogenes	*n*	33	27	26	11	25	1	3	4	130
	%R	30.3, 45.5	40.7, 55.6	15.4, 15.4	18.2, 36.4	24.0, 36.0	na	na	na	28.5, 40.0
Proteus mirabilis	*n*	51	37	44	24	36	3	6	6	207
	%R	0.0, 0.0	2.7, 2.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	na	na	0.5, 0.5
Pseudomonas aeruginosa	*n*	166	74	163	83	107	4	19	36	652
	%R	16.3, 53.6	21.6, 52.7	16.6, 50.9	13.3, 48.2	11.2, 45.8	na	26.3, 47.4	22.2, 38.9	16.3, 50.0
Salmonella species (non-typhoidal)	*n*	17	21	28	9	10	2	24	1	112
	%R	5.9, 5.9	9.5, 14.3	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	2.7, 3.6
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%R	na	na	na	na	na	na	na	na	0.0, 8.0

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Tobramycin										
Acinetobacter baumannii	*n*	10	10	20	1	11	2	5	0	59
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	na	na	0.0, 0.0
Escherichia coli	*n*	1,107	727	679	454	650	79	137	149	3,982
	%R	4.7, 10.2	4.4, 9.2	2.1, 6.8	3.7, 7.5	3.7, 10.2	0.0, 2.5	5.1, 11.7	1.3, 4.0	3.7, 8.8
Klebsiella pneumoniae	*n*	236	177	184	85	187	18	47	35	969
	%R	3.0, 6.8	3.4, 6.8	2.2, 3.8	1.2, 5.9	1.6, 3.2	5.6, 5.6	2.1, 10.6	0.0, 2.9	2.4, 5.5
Klebsiella oxytoca	*n*	76	49	43	13	30	8	4	13	236
	%R	0.0, 0.0	0.0, 2.0	0.0, 2.3	0.0, 0.0	0.0, 3.3	na	na	0.0, 0.0	0.0, 1.3
Enterobacter cloacae complex	*n*	85	80	64	13	50	14	9	10	325
	%R	7.1, 14.1	2.5, 10.0	4.7, 12.5	0.0, 0.0	0.0, 0.0	0.0, 7.1	na	0.0, 0.0	3.4, 9.2
Enterobacter aerogenes	*n*	34	27	25	11	25	1	3	4	130
	%R	0.0, 2.9	7.4, 11.1	4.0, 4.0	0.0, 0.0	0.0, 0.0	na	na	na	2.3, 3.8
Proteus mirabilis	*n*	66	37	43	24	36	3	6	6	221
	%R	0.0, 3.0	2.7, 2.7	2.3, 2.3	0.0, 0.0	0.0, 0.0	na	na	na	0.9, 1.8
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	5.3, 5.3	0.0, 0.0	0.0, 0.0	na	0.0, 0.0	na	0.0, 0.0	na	0.9, 0.9
Salmonella species (typhoidal)	*n*	5	7	5	4	2	0	0	1	24
	%R	na	na	na	na	na	na	na	na	0.0, 0.0
Pseudomonas aeruginosa	*n*	166	74	160	83	107	4	19	36	649
	%R	4.2, 4.2	4.1, 4.1	0.6, 1.3	2.4, 2.4	0.9, 0.9	na	0.0, 0.0	0.0, 0.0	2.2, 2.3

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Trimethoprim										
Escherichia coli	*n*	1,107	727	679	454	650	79	137	149	3,982
	%R	34.7, 34.8	32.2, 33.0	30.2, 30.2	24.0, 24.4	30.3, 30.6	15.2, 15.2	35.0, 35.0	30.2, 30.9	31.0, 31.3
Klebsiella pneumoniae	*n*	236	177	184	85	187	18	47	35	969
	%R	14.8, 15.3	18.6, 19.8	15.2, 15.2	12.9, 14.1	10.2, 11.8	22.2, 22.2	17.0, 17.0	31.4, 31.4	15.4, 16.1
Klebsiella oxytoca	*n*	76	49	43	13	30	8	4	13	236
	%R	3.9, 3.9	4.1, 4.1	2.3, 2.3	0.0, 0.0	6.7, 6.7	na	na	0.0, 0.0	3.4, 3.4
Enterobacter cloacae complex	*n*	85	80	64	13	50	14	9	10	325
	%R	16.5, 16.5	20.0, 20.0	18.8, 18.8	15.4, 15.4	2.0, 2.0	21.4, 21.4	na	20.0, 20.0	16.0, 16.0
Enterobacter aerogenes	*n*	34	27	25	11	25	1	3	4	130
	%R	8.8, 8.8	11.1, 11.1	8.0, 8.0	0.0, 0.0	0.0, 0.0	na	na	na	6.2, 6.2
Proteus mirabilis	*n*	66	37	43	24	36	3	6	6	221
	%R	25.8, 25.8	13.5, 16.2	9.3, 11.6	20.8, 20.8	22.2, 22.2	na	na	na	18.1, 19.0
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	5.3, 5.3	9.5, 9.5	3.6, 3.6	na	0.0, 0.0	na	0.0, 0.0	na	4.4, 4.4
Salmonella species (typhoidal)	*n*	5	7	5	4	2	0	0	1	24
	%R	na	na	na	na	na	na	na	na	4.2, 4.2

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Trimethoprim–sulfamethoxazole										
Acinetobacter baumannii	*n*	10	10	20	1	11	2	5	0	59
	%R	0.0, 0.0	0.0, 0.0	5.0, 5.0	na	0.0, 0.0	na	na	na	3.4, 3.4
Escherichia coli	*n*	1,107	727	691	452	648	79	137	149	3,990
	%R	33.1, 33.0	30.9, 30.9	28.8, 28.5	23.2, 23.0	26.5, 26.5	15.2, 15.2	32.8, 32.8	30.2, 30.2	29.3, 29.2
Klebsiella pneumoniae	*n*	236	177	189	85	187	18	47	35	974
	%R	12.7, 12.3	16.9, 16.4	14.8, 14.8	10.6, 9.4	6.4, 6.4	16.7, 16.7	17.0, 14.9	28.6, 28.6	13.3, 12.9
Klebsiella oxytoca	*n*	76	48	45	13	30	8	4	13	237
	%R	2.6, 1.3	4.2, 4.2	2.2, 2.2	0.0, 0.0	6.7, 6.7	na	na	0.0, 0.0	3.0, 2.5
Enterobacter cloacae complex	*n*	85	80	65	13	50	14	9	10	326
	%R	16.5, 16.5	18.8, 18.8	18.5, 18.5	15.4, 15.4	2.0, 2.0	21.4, 21.4	na	20.0, 20.0	15.6, 15.6
Enterobacter aerogenes	*n*	34	27	26	11	25	1	3	4	131
	%R	2.9, 2.9	11.1, 11.1	3.8, 3.8	0.0, 0.0	0.0, 0.0	na	na	na	3.8, 3.8
Enterococcus faecalis	*n*	149	66	95	58	91	0	10	35	504
	%R	nd, 16.8	nd, 21.2	nd, 24.2	nd, 20.7	nd, 15.4	na	nd, 50.0	nd, 22.9	nd, 20.0
Enterococcus faecium	*n*	113	55	30	44	53	1	8	22	326
	%R	nd, 47.8	nd, 83.6	nd, 70.0	nd, 45.5	nd, 62.3	na	na	nd, 59.1	nd, 59.5
Proteus mirabilis	*n*	66	37	43	24	36	3	6	6	221
	%R	19.7, 19.7	8.1, 8.1	6.8, 6.8	20.8, 20.8	20.0, 20.0	na	na	na	14.0, 14.0
Salmonella species (non-typhoidal)	*n*	19	21	28	9	10	2	24	1	114
	%R	5.3, 5.3	9.5, 9.5	3.6, 3.6	na	0.0, 0.0	na	0.0, 0.0	na	4.4, 4.4

continued

Table C1: (continued)

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Trimethoprim–sulfamethoxazole (continued)										
Salmonella species (typhoidal)	*n*	5	7	6	4	2	0	0	1	25
	%R	na	na	na	na	na	na	na	na	4.0, 4.0
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%R	4.9, 4.7	2.5, 2.5	1.4, 1.4	7.3, 7.3	4.3, 4.3	0.0, 0.0	10.0, 6.4	3.7, 3.7	4.0, 3.8
Methicillin resistant	*n*	135	63	68	43	69	3	42	12	435
	%R	16.3, 15.6	12.7, 12.7	1.5, 1.5	23.3, 23.3	18.8, 18.8	na	23.8, 14.3	25.0, 25.0	15.4, 14.3
Methicillin susceptible	*n*	455	344	435	219	325	48	68	69	1,963
	%R	1.5, 1.5	0.6, 0.6	1.4, 1.4	4.1, 4.1	1.2, 1.2	0.0, 0.0	1.5, 1.5	0.0, 0.0	1.5, 1.5
Vancomycin										
Enterococcus faecalis	*n*	149	109	95	57	91	12	10	35	558
	%NS	1.3, 1.3	0.9, 0.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	8.3, 8.3	0.0, 0.0	0.0, 0.0	0.7, 0.7
Enterococcus faecium	*n*	116	120	31	44	53	8	8	22	402
	%NS	51.7, 51.7	62.5, 63.3	58.1, 61.3	52.3, 52.3	11.3, 11.3	na	na	50.0, 50.0	49.8, 50.2
Staphylococcus aureus	*n*	590	407	503	262	394	51	110	81	2,398
	%NS	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate; na = 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 clavulanate 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.

§ NS category for cefepime includes CLSI sensitive dose dependent for Enterobacteriaceae.

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

** The concentration range on the Phoenix card prohibits interpretation for *Enterococcus* species. Figures reflect the number of isolates that can be interpreted using CLSI and EUCAST, respectively.

APPENDIX D

Multiple acquired resistance by species and state or territory

0The most problematic pathogens are those with multiple acquired resistances. Although there is no agreed benchmark for the definition of multi-drug resistance, acquired resistance to more than three agents has been chosen to define multi-drug 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 the purposes of this analysis, resistance included intermediate susceptibility, where applicable.

Only isolates where the full range of antimicrobial agents was tested were included for determination of multi-drug resistance. The agents included for each species are listed in the notes after each table. EUCAST breakpoints have been used throughout in the analysis. For cefazolin, the EUCAST-approved Australian National Advisory Committee guidelines were used. For amoxicillin–clavulanate, CLSI breakpoints were used, because both the Vitek and Phoenix cards used the CLSI formulation for this agent.

Acinetobacter baumannii complex has not been included because there are too few breakpoints to permit analysis.

Table D1: Multiple acquired resistance in *Citrobacter koseri*, by state and territory, 2015

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	20	16	2	0	1	95.0	0	1	0	0	0	0	0	0	5.0
Vic	4	4	0	0	0	100.0	0	0	0	0	0	0	0	0	0.0
Qld	6	5	1	0	0	100.0	0	0	0	0	0	0	0	0	0.0
SA	10	9	1	0	0	100.0	0	0	0	0	0	0	0	0	0.0
WA	10	8	2	0	0	100.0	0	0	0	0	0	0	0	0	0.0
Tas	0	na	na	na	na	na	na	na	na	na	na	na	na	na	na
NT	1	0	0	0	0	0.0	0	0	0	1	0	0	0	0	100.0
ACT	1	1	0	0	0	100.0	0	0	0	0	0	0	0	0	0.0
Total	52	43	6	0	1	96.2	0	1	0	1	0	0	0	0	3.8

MDR = multi-drug resistant; na = not applicable (no isolates)

Note: Antimicrobials were amoxicillin–clavulanate (CLSI), piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D2: Multiple acquired resistance in *Citrobacter freundii*, by state and territory, 2015

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	%
NSW	19	8	0	2	5	78.9	2	1	1	0	0	0	0	21.1
Vic	9	8	0	0	0	88.9	0	1	0	0	0	0	0	11.1
Qld	4	3	0	0	1	100.0	0	0	0	0	0	0	0	0.0
SA	4	3	0	0	1	100.0	0	0	0	0	0	0	0	0.0
WA	2	1	0	1	0	100.0	0	0	0	0	0	0	0	0.0
Tas	1	0	1	0	0	100.0	0	0	0	0	0	0	0	0.0
NT	0	na	na	na	na	na	na	na	na	na	na	na	na	na
ACT	4	3	0	0	1	100.0	0	0	0	0	0	0	0	0.0
Total	43	26	1	3	8	88.4	2	2	1	0	0	0	0	11.6

MDR = multi-drug resistant; na = not applicable (no isolates)

Note: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D3: Multiple acquired resistance in *Enterobacter aerogenes*, by state and territory, 2015

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	%
NSW	34	15	2	1	14	94.1	1	1	0	0	0	0	0	5.9
Vic	27	12	0	0	10	81.5	1	1	1	2	0	0	0	18.5
Qld	25	17	2	2	2	92.0	1	0	0	1	0	0	0	8.0
SA	11	7	0	1	3	100.0	0	0	0	0	0	0	0	0.0
WA	25	14	2	0	9	100.0	0	0	0	0	0	0	0	0.0
Tas	1	0	0	0	1	100.0	0	0	0	0	0	0	0	0.0
NT	3	2	0	0	1	100.0	0	0	0	0	0	0	0	0.0
ACT	4	1	0	0	3	100.0	0	0	0	0	0	0	0	0.0
Total	130	68	6	4	43	93.1	3	2	1	3	0	0	0	6.9

MDR = multi-drug resistant

Note: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D4: Multiple acquired resistance in *Enterococcus faecium* (vancomycin resistant), by state and territory, 2015

State or territory	Total	Number of drug resistances (non-MDR)				
		0	1	2	3	%
NSW	58	0	16	42	0	100.0
Vic	76	0	0	76	0	100.0
Qld	18	0	0	18	0	100.0
SA	13	0	12	1	0	100.0
WA	6	0	0	6	0	100.0
Tas	0*	na	na	na	na	na
NT	6	0	0	6	0	100.0
ACT	11	0	0	11	0	100.0
Total	188	0	28	160	0	100.0

MDR = multi-drug resistant; na = not applicable (no isolates)

* Ciprofloxacin minimum inhibitory concentrations not provided

Note: Antimicrobials were ampicillin, ciprofloxacin, linezolid.

Table D5: Multiple acquired resistance in *Enterococcus faecium* (vancomycin susceptible), by state and territory, 2015

	Number of drug resistances (non-MDR)			Number of drug resistances (MDR)		
State or territory	Total	0	1	2	3	%
NSW	56	16	8	32	0	100.0
Vic	44	12	0	32	0	100.0
Qld	10	5	0	5	0	100.0
SA	14	1	11	2	0	100.0
WA	47	11	0	36	0	100.0
Tas	1	0	0	1	0	100.0
NT	2	1	0	1	0	100.0
ACT	11	1	0	10	0	100.0
Total	185	47	19	119	0	100.0

MDR = multi-drug resistant

Note: Antimicrobials were ampicillin, ciprofloxacin, linezolid.

Table D6: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, 2015

		Number of drug resistances (non-MDR)					Number of drug resistances (MDR)								
State or territory	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	%
NSW	76	23	36	3	8	92.1	6	0	0	0	0	0	0	0	7.9
Vic	41	15	22	0	1	92.7	2	1	0	0	0	0	0	0	7.3
Qld	43	16	23	0	1	93.0	2	0	0	1	0	0	0	0	7.0
SA	13	2	8	0	0	76.9	3	0	0	0	0	0	0	0	23.1
WA	23	9	10	0	2	91.3	1	1	0	0	0	0	0	0	8.7
Tas	4	1	2	1	0	100.0	0	0	0	0	0	0	0	0	0.0
NT	4	1	3	0	0	100.0	0	0	0	0	0	0	0	0	0.0
ACT	13	5	7	0	0	92.3	1	0	0	0	0	0	0	0	7.7
Total	217	72	111	4	12	91.7	15	2	0	1	0	0	0	0	8.3

MDR = multi-drug resistant

Note: Antimicrobials were amoxicillin–clavulanate (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D7: Multiple acquired resistance in *Morganella morganii*, by state and territory, 2015

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	%
NSW	26	17	5	3	1	100.0	0	0	0	0	0	0	0	0.0
Vic	9	6	1	2	0	100.0	0	0	0	0	0	0	0	0.0
Qld	25	22	2	0	0	96.0	0	1	0	0	0	0	0	4.0
SA	7	4	1	1	0	85.7	0	0	1	0	0	0	0	14.3
WA	7	6	0	0	0	85.7	0	1	0	0	0	0	0	14.3
Tas	1	0	1	0	0	100.0	0	0	0	0	0	0	0	0.0
NT	0	na	na	na	na	na	na	na	na	na	na	na	na	na
ACT	4	4	0	0	0	100.0	0	0	0	0	0	0	0	0.0
Total	79	59	10	6	1	96.2	0	2	1	0	0	0	0	3.8

MDR = multi-drug resistant; na = not applicable (no isolates)

Note: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D8: Multiple acquired resistance in *Proteus mirabilis*, by state and territory, 2015

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	65	34	15	5	4	89.2	5	1	1	0	0	0	0	0	0	10.8
Vic	34	19	8	2	1	88.2	2	1	0	0	0	1	0	0	0	11.8
Qld	42	24	14	1	2	97.6	0	0	0	0	0	1	0	0	0	2.4
SA	24	6	12	3	2	95.8	1	0	0	0	0	0	0	0	0	4.2
WA	26	14	5	0	5	92.3	1	1	0	0	0	0	0	0	0	7.7
Tas	2	2	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
NT	6	4	2	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
ACT	6	6	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
Total	205	109	56	11	14	92.7	9	3	1	0	0	2	0	0	0	7.3

MDR = multi-drug resistant

Note: Antimicrobials were ampicillin, amoxicillin–clavulanate (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D9: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, 2015

State or territory	Total	Number of drug resistances (non-MDR)					Number of drug resistances (MDR)		
		0	1	2	3	%	4	5	%
NSW	162	128	13	13	2	96.3	2	2	2.5
Vic	71	55	5	7	0	94.4	4	0	5.6
Qld	155	125	12	11	5	98.7	2	0	1.3
SA	75	61	7	4	1	97.3	2	0	2.7
WA	106	87	7	10	2	100.0	0	0	0.0
Tas	4	3	1	0	0	100.0	0	0	0.0
NT	18	15	1	1	1	100.0	0	0	0.0
ACT	34	24	4	6	0	100.0	0	0	0.0
Total	625	498	50	52	11	97.8	10	2	1.9

MDR = multi-drug resistant

Note: Antimicrobials were ceftazidime, ciprofloxacin, piperacillin–tazobactam, tobramycin, meropenem.

Table D10: Multiple acquired resistance in *Salmonella* species (non-typhoidal), by state and territory, 2015

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	19	17	1	0	0	94.7	0	0	1	0	0	0	0	0	0	5.3
Vic	16	12	2	0	1	93.8	0	0	1	0	0	0	0	0	0	6.3
Qld	28	25	2	1	0	100.0	0	0	0	0	0	0	0	0	0	0.0
SA	9	9	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
WA	9	9	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
Tas	0*	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na
NT	24	24	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
ACT	1	1	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
Total	106	97	5	1	1	98.1	0	0	2	0	0	0	0	0	0	1.9

MDR = multi-drug resistant; na = not applicable (no isolates)

* Cefazolin minimum inhibitory concentrations not provided

Note: Antimicrobials were ampicillin, amoxicillin–clavulanate (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D11: Multiple acquired resistance in *Salmonella* species (typhoidal), by state and territory, 2015

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	4	4	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
Vic	6	6	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
Qld	5	4	0	0	1	100.0	0	0	0	0	0	0	0	0	0	0.0
SA	4	3	0	1	0	100.0	0	0	0	0	0	0	0	0	0	0.0
WA	1	1	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
Tas	0	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na
NT	0	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na
ACT	1	1	0	0	0	100.0	0	0	0	0	0	0	0	0	0	0.0
Total	21	19	0	1	1	100.0	0	0	0	0	0	0	0	0	0	0.0

MDR = multi-drug resistant; na = not applicable (no isolates)

Note: Antimicrobials were ampicillin, amoxicillin–clavulanate (CLSI), piperacillin–tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

Table D12: Multiple acquired resistance in *Serratia marcescens*, by state and territory, 2015

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	%
NSW	59	52	2	2	2	98.3	0	1	0	0	0	0	0	1.7
Vic	19	15	4	0	0	100.0	0	0	0	0	0	0	0	0.0
Qld	42	40	0	1	0	97.6	1	0	0	0	0	0	0	2.4
SA	9	8	0	0	1	100.0	0	0	0	0	0	0	0	0.0
WA	7	7	0	0	0	100.0	0	0	0	0	0	0	0	0.0
Tas	3	3	0	0	0	100.0	0	0	0	0	0	0	0	0.0
NT	3	2	0	1	0	100.0	0	0	0	0	0	0	0	0.0
ACT	0*	na	na	na	na	na	na	na	na	na	na	na	na	na
Total	142	127	6	4	3	98.6	1	1	0	0	0	0	0	1.4

MDR = multi-drug resistant; na = not applicable (no isolates)

* Piperacillin–tazobactam minimum inhibitory concentrations not provided

Note: Antimicrobials were piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem.

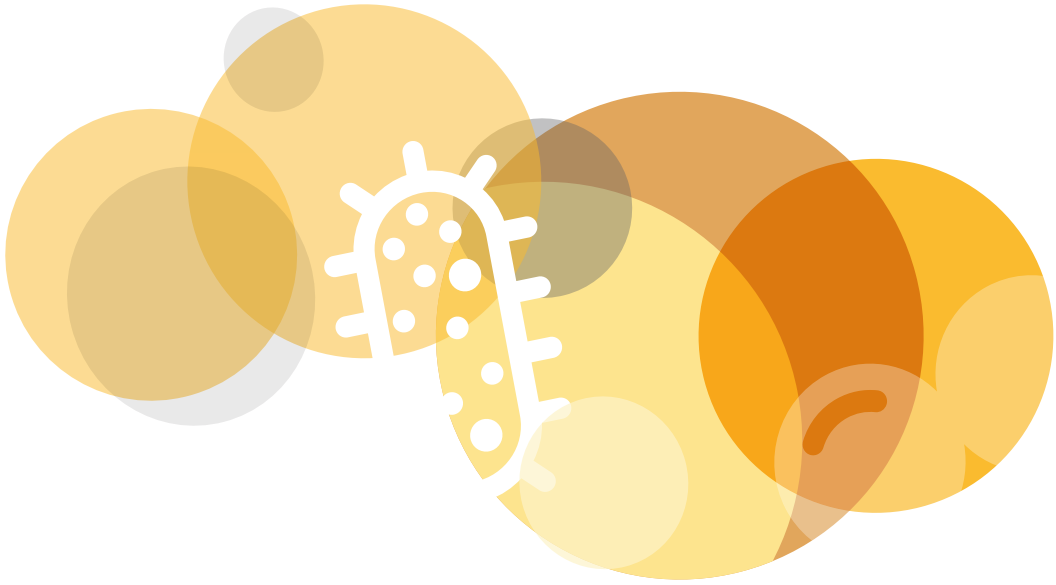
Table D13: Multiple acquired resistance in *Staphylococcus aureus*, by state and territory, 2015

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	496	80	263	50	36	86.5	26	12	17	11	1	0	0	0	0	0	0	13.5
Vic	407	86	217	50	28	93.6	14	5	3	2	2	0	0	0	0	0	0	6.4
Qld	447	81	248	76	31	97.5	8	1	1	1	0	0	0	0	0	0	0	2.5
SA	94	21	59	7	3	95.7	2	1	0	1	0	0	0	0	0	0	0	4.3
WA	394	64	219	61	33	95.7	11	4	2	0	0	0	0	0	0	0	0	4.3
Tas	0*	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na	na
NT	110	10	41	38	12	91.8	2	0	0	7	0	0	0	0	0	0	0	8.2
ACT	81	13	46	9	10	96.3	1	0	2	0	0	0	0	0	0	0	0	3.7
Total	2,029	355	1,093	291	153	93.2	64	23	25	22	3	0	0	0	0	0	0	6.8

MDR = multi-drug resistant; na = not applicable (no isolates)

* Nitrofurantoin and rifampicin minimum inhibitory concentrations not provided

Note: Antimicrobials were benzylpenicillin, ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin (CLSI), oxacillin, rifampicin, trimethoprim–sulfamethoxazole, tetracycline, vancomycin.



APPENDIX E

Summary reports

Susceptibility results

National reports provide summary susceptibility data (number, and percentage if more than 10 isolates) using both CLSI and EUCAST interpretive guidelines for all species isolated. They can be accessed through the AGAR website.*

Antimicrobial resistance profiles by frequency

Only isolates for which the full range of antimicrobial agents was tested are included in the profiles. The regional antibiotic profiles for the top 12 species are available on the AGAR website.* Profiles are generated using EUCAST guidelines.

* http://www.agargroup.org/surveys

References

1. Australian Government Department of Health and Department of Agriculture. Responding to the threat of antimicrobial resistance: Australia's first National Antimicrobial Resistance Strategy 2015-2019. Canberra: Australian Government Department of Health and Department of Agriculture; 2015.
2. Deshpande LM, Fritsche TR, Moet GJ, Biedenbach DJ, Jones RN. Antimicrobial resistance and molecular epidemiology of vancomycin-resistant enterococci from North America and Europe: a report from the SENTRY antimicrobial surveillance program. Diagn Microbiol Infect Dis 2007;58:163-70.
3. Pinholt M, Ostergaard C, Arpi M, Bruun NE, Schønheyder HC, Gradel KO, et al. Incidence, clinical characteristics and 30-day mortality of enterococcal bacteraemia in Denmark 2006-2009: a population-based cohort study. Clin Microbiol Infect 2014;20:145-51.
4. Murray BE. The life and times of the *Enterococcus*. Clin Microbiol Rev 1990;3:46-65.
5. Simonsen GS, Småbrekke L, Monnet DL, Sørensen TL, Møller JK, Kristinsson KG, et al. Prevalence of resistance to ampicillin, gentamicin and vancomycin in *Enterococcus faecalis* and *Enterococcus faecium* isolates from clinical specimens and use of antimicrobials in five Nordic hospitals. J Antimicrob Chemother 2003;51:323-31.
6. Treitman AN, Yarnold PR, Warren J, Noskin GA. Emerging incidence of *Enterococcus faecium* among hospital isolates (1993 to 2002). J Clin Microbiol 2005;43:462-3.
7. Boucher HW, Talbot GH, Bradley JS, Edwards JE, Gilbert D, Rice LB, et al. Bad bugs, no drugs: no ESKAPE! An update from the Infectious Diseases Society of America. Clin Infect Dis 2009;48:1-12.
8. Christiansen KJ, Turnidge JD, Bell JM, George NM, Pearson JC. Prevalence of antimicrobial resistance in *Enterococcus* isolates in Australia, 2005: report from the Australian Group on Antimicrobial Resistance. Commun Dis Intell 2007;31:392-7.
9. Coombs GW, Nimmo GR, Daley DA, Le TT, Pearson JC, Tan H-L, et al. Australian *Staphylococcus aureus* Sepsis Outcome Programme annual report, 2013. Commun Dis Intell 2014;38:E309-19.
10. Laupland KB. Incidence of bloodstream infection: a review of population-based studies. Clin Microbiol Infect 2013;19:492-500.
11. Johnson AP, Pearson A, Duckworth G. Surveillance and epidemiology of MRSA bacteraemia in the UK. J Antimicrob Chemother 2005;56:455-62.
12. Thwaites GE, Edgeworth JD, Gkrania-Klotsas E, Kirby A, Tilley R, Török ME, et al. Clinical management of *Staphylococcus aureus* bacteraemia. Lancet Infect Dis 2011;11:208-22.
13. Benfield T, Espersen F, Frimodt-Møller N, Jensen AG, Larsen AR, Pallesen LV, et al. Increasing incidence but decreasing in-hospital mortality of adult *Staphylococcus aureus* bacteraemia between 1981 and 2000. Clin Microbiol Infect 2007;13:257-63.
14. Collignon P, Nimmo GR, Gottlieb T, Gosbell IB. *Staphylococcus aureus* bacteremia, Australia. Emerg Infect Dis 2005;11:554-61.
15. Frederiksen MS, Espersen F, Frimodt-Møller N, Jensen AG, Larsen AR, Pallesen LV, et al. Changing epidemiology of pediatric *Staphylococcus aureus* bacteremia in Denmark from 1971 through 2000. Pediatr Infect Dis J 2007;26:398-405.
16. Kaasch AJ, Barlow G, Edgeworth JD, Fowler VG Jr, Hellmich M, Hopkins S, et al. *Staphylococcus aureus* bloodstream infection: a pooled analysis of five prospective, observational studies. J Infect 2014;68:242-51.
17. van Hal SJ, Jensen SO, Vaska VL, Espedido BA, Paterson DL, Gosbell IB. Predictors of mortality in *Staphylococcus aureus* bacteremia. Clin Microbiol Rev 2012;25:362-86.

18. Turnidge JD, Kotsanas D, Munckhof W, Roberts S, Bennett CM, Nimmo GR, et al. *Staphylococcus aureus* bacteraemia: a major cause of mortality in Australia and New Zealand. Med J Aust 2009;191:368–73.

19. Nimmo GR, Bell JM, Collignon PJ, Australian Group for Antimicrobial Resistance. Fifteen years of surveillance by the Australian Group for Antimicrobial Resistance (AGAR). Commun Dis Intell Q Rep 2003;27 Suppl:S47–54.

20. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. CLSI document M100S. Wayne, PA: Clinical and Laboratory Standards Institute; 2016.

21. European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 6.0, valid from 2016-01-01. Available from: http://www.eucast.org

22. Bell JM, Turnidge JD, Jones RN, SENTRY Asia-Pacific participants. Prevalence of extended-spectrum beta-lactamase-producing *Enterobacter cloacae* in the Asia-Pacific region: results from the SENTRY Antimicrobial Surveillance Program, 1998 to 2001. Antimicrob Agents Chemother 2003;47:3989–93.

23. Dortet L, Poirel L, Abbas S, Ouestlati S, Nordmann P. Genetic and biochemical characterization of FRI-1, a carbapenem-hydrolyzing class A β-lactamase from *Enterobacter cloacae*. Antimicrob Agents Chemother 2015;59:7420–5.

24. Banerjee R, Robicsek A, Kuskowski MA, Porter S, Johnston BD, Sokurenko E, et al. Molecular epidemiology of *Escherichia coli* sequence type 131 and its *H30* and *H30*-Rx subclones among extended-spectrum-β-lactamase-positive and -negative *E. coli* clinical isolates from the Chicago region, 2007 to 2010. Antimicrob Agents Chemother 2013;57:6385–8.

25. Colpan A, Johnston B, Porter S, Clabots C, Anway R, Thao L, et al. *Escherichia coli* sequence type 131 (ST131) subclone *H30* as an emergent multidrug-resistant pathogen among US veterans. Clin Infect Dis 2013;57:1256–65.

26. Johnson JR, Johnston B, Clabots C, Kuskowski MA, Castanheira M. *Escherichia coli* sequence type ST131 as the major cause of serious multidrug-resistant *E. coli* infections in the United States. Clin Infect Dis 2010;51:286–94.

27. Australian Group on Antimicrobial Resistance. The evolution of carbapenemases in major gram-negative bacteria in Australia 2015. Available from: http://www.agargroup.org/surveys

28. Australian Commission on Safety and Quality in Health Care. AURA 2016: first Australian report on antimicrobial use and resistance in human health. Sydney: ACSQHC; 2016. Available from: https://www.safetyandquality.gov.au/publications/aura-2016-first-australian-report-on-antimicroibal-use-and-resistance-in-human-health

29. Chang LW, Buising KL, Jeremiah CJ, Cronin K, Poy Lorenzo YS, Howden BP, et al. Managing a nosocomial outbreak of carbapenem-resistant *Klebsiella pneumoniae*: an early Australian hospital experience. Intern Med J 2015;45:1037–43.

30. Australian Commission on Safety and Quality in Health Care. Recommendations for the control of multi-drug resistant gram-negatives: carbapenem resistant Enterobacteriaceae. Sydney: ACSQHC; 2013. Available from: https://www.safetyandquality.gov.au/publications/mrgn-guidelines-enterobacteriacea

31. Australian Commission on Safety and Quality in Health Care. MRSA: a tale of three types – 15 years of survey data from AGAR. Sydney: ACSQHC; 2016.

AUSTRALIAN COMMISSION
ON SAFETY AND QUALITY IN HEALTH CARE

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

Phone: (02) 9126 3600
Fax: (02) 9126 3613

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