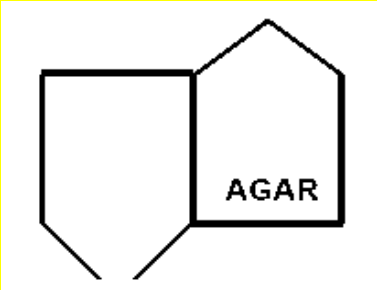

The Australian Group on Antimicrobial Resistance

Sepsis Outcome Programs

2015 Report

Prepared by

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On behalf of the Australian Group on Antimicrobial Resistance (AGAR)

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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 causing important and life threatening infections. The group commenced in 1985 and at that time involved 13 teaching hospitals. It has subsequently grown to involve 29 laboratories servicing 33 hospitals located across Australia including four private laboratories (Table 1).

Table 1 Hospitals who contributed to AGAR, by jurisdiction, 2015

Jurisdiction	Hospital
Australian Capital Territory	The Canberra Hospital
New South Wales	Concord Repatriation General Hospital John Hunter Hospital Nepean Hospital Royal North Shore Hospital Royal Prince Alfred Hospital Westmead Hospital Wollongong Hospital
Northern Territory	Alice Springs Hospital Royal Darwin Hospital
Queensland	Cairns Base Hospital Gold Coast Hospital Prince Charles Hospital * Princess Alexandra Hospital * Royal Brisbane and Women's Hospital Sullivan Nicolaides Pathology
South Australia	Flinders Medical Centre Royal Adelaide Hospital Women's and Children's Hospital †
Tasmania	Royal Hobart Hospital
Victoria	Alfred Hospital Austin Hospital [Austin Health] Monash Medical Centre [Monash Health] Royal Women's and Children's Hospital St Vincent's Hospital
Western Australia	Joondalup Hospital Fiona Stanley Hospital Sir Charles Gardnier Hospital Royal Perth Hospital ‡ Kimberley regional Hospitals (Broome, Kununurra, Derby) St John of God Murdoch Hospital

* Microbiology services provided by Pathology Queensland, Royal Brisbane and Women's Hospital
† Microbiology services provided by SA Pathology, Royal Adelaide Hospital
‡ Microbiology services provided by PathWest Laboratory Medicine-WA, Fiona Stanley Hospital

Historically, the main focus of the group has been 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. By standardised methodology AGAR has been able to collect ongoing data on what is happening in Australia over long periods of time.

AGAR now focuses on bloodstream infections and has three major programs.

1.1. Gram-negative Sepsis Outcome Programme (GNSOP)

AGAR commenced surveillance of the key gram-negative pathogens, *Escherichia coli* and *Klebsiella* species in 1992. Surveys were conducted biennially until 2008 when annual surveys commenced alternating between community– and hospital-onset infections (http://www.agargroup.org/surveys). In 2004, another genus of gram-negative pathogens in which resistance can be of clinical importance, *Enterobacter* species, was added. *E. coli* is the most common cause of community-onset urinary tract infection, while *Klebsiella* species are less common but are known to harbour important resistances. *Enterobacter* species are less common in the community, but of high importance due to 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-resistance and emerging resistance in enteric gram-negative bacilli. In 2013 AGAR commenced the ongoing Enterobacteriaceae Sepsis Outcome Programme (EnSOP) which focuses 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 name changed to the Gram-negative Sepsis Outcome Programme (GNSOP).

Resistances of particular interest include resistance to ß-lactams due to ß-lactamases, especially extended-spectrum ß-lactamases, which inactivate the third-generation cephalosporins that are normally considered reserve antimicrobials. Other resistances of interest are to agents 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.
- Examine the extent of co-resistance and multi-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 carbapenemases.
- Monitor the epidemiology of *E. coli* sequence type 131.

1.2. Australian Enterococcal Sepsis Outcome Program (AESOP)

Globally enterococci are thought to account for approximately 10% of all bacteraemias, and in North America and Europe they are the fourth and fifth leading cause of sepsis respectively.[1, 2] In the 1970s healthcare-associated enterococcal infections were primarily due to *Enterococcus faecalis*, however there has been a steadily increasing prevalence of *E. faecium* nosocomial infections.[3-5] Worldwide the increase in nosocomial *E. faecium* infections has primarily been due to the expansion of polyclonal hospital-adapted clonal complex (CC) 17 strains. While innately resistant to many classes of antibiotics, *E. faecium* has demonstrated a remarkable capacity to evolve new antimicrobial resistances. In 2009 the Infectious Diseases Society of America highlighted *E. faecium* as one of the key problem bacteria or ESKAPE (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa,* and *Enterobacter species*) pathogens requiring new therapies. [6]

AGAR commenced surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[7] In 2011 AGAR commenced the Australian Enterococcal Sepsis Outcome Programme (AESOP).[8] The objective of AESOP 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.
- Molecular epidemiology of *E. faecium*.

1.3. Australian Staphylococcal Sepsis Outcome Program (ASSOP)

Globally *Staphylococcus aureus* is one of the most frequent causes of hospital-acquired and community-acquired blood stream infections.[9] Although there is a wide variety of manifestations of serious invasive infection caused by *S. aureus*, in the great majority of these cases the organism can be detected in blood cultures. Therefore, *S. aureus* bacteraemia (SAB) is considered a very useful marker for serious invasive infection.[10]

Although prolonged antimicrobial therapy and prompt source control are used to treat SAB[11], mortality ranges from 2.5% to 40%.[12-14] Mortality rates are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[15, 16] A prospective study of SAB conducted by 27 laboratories in Australia and New Zealand found a 30-day all-cause mortality of 20.6%.[17] 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 commenced surveillance of antimicrobial resistance in *S. aureus in* 1986.[18] In 2013 AGAR commenced the Australian Staphylococcal Sepsis Outcome Programme (ASSOP).[8]

The primary objective of ASSOP 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.
- Molecular epidemiology of methicillin-resistant *S. aureus* (MRSA).

2. Methods Summary

Thirty-three hospitals from each State and mainland Territories of Australia were enrolled in the 2015 survey. The 29 AGAR laboratories collected either all or up to 200 isolates of Enterobacteriaceae, *Acinetobacter* species and *Pseudomonas aeruginosa*, and all isolates of *S. aureus* and *Enterococcus* species, from unique patient episodes of bacteraemia from 1st January to 31st December 2015. Approval to conduct the prospective collection was given by the research ethics committee 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 after admission; and as hospital-onset if collected > 48 hours after admission.

2.1. Data Fields

Laboratory data collected for each episode included an accession number, date the blood culture was collected, organism isolated (genus and species), and the antimicrobial susceptibility test results (minimum inhibitory concentrations) for each species. The patient's date of birth, gender and their postcode of residence were also provided, and if admitted, the date of admission and date of discharge. Depending on the level of participation, limited clinical and outcome data were also provided. This included the principal clinical manifestation; outcome at 30 days, and if the patient died within 30 days, the date of death; and definitive antimicrobial treatment (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, *E. 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

Testing was performed by two commercial semi-automated methods, either Vitek® 2 (bioMérieux) (n=27) or Phoenix™ (BD) (n=2), which are calibrated to the ISO reference standard method of broth microdilution. Either commercially available Vitek® 2 AST-N246, AST-N247, P612, or Phoenix™ NMIC-203 and PMIC-84 cards were utilised by all participants throughout the survey period.

The CLSI M100-A26[19] and EUCAST v6.0[20] breakpoints from January 2016 have been employed in the analysis. For analysis of cefazolin, breakpoints of ≤4 for susceptible and ≥8 for resistant were applied due to the restricted minimum inhibitory concentration (MIC) range available on the commercial cards, recognising that the January 2016 breakpoint is actually susceptible ≤2 mg/L. A list of the antimicrobials agents tested and the CLSI and EUCAST interpretative breakpoints applied in this report can be found in Appendix B.

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 USA, 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 *Pseudomonas aeruginosa* 9.0% and *Acinetobacter* species 1.4%. Of the Enterobacteriaceae, three genera, *Escherichia* spp. (61.0%), *Klebsiella* spp. (18.5%) and *Enterobacter* spp. (7.4%) contributed 86.9% of all isolates. The top ten species according to 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%), *E. aerogenes* (1.8%), *Salmonella*

species (non-typhoidal (1.6%), and *Morganella morganii* (1.1%). These ten species comprised 94.7% of all isolates (Table 2).

Of 2,398 SAB episodes 435 (18.1%, 95%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 isolates recovered by state and territory

Species	ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Total
Gram-negative species †	**280**	**1995**	**265**	**1402**	**777**	**142**	**1293**	**1176**	**7330**
Escherichia coli	149	1113	138	691	454	79	729	653	4006
Klebsiella pneumoniae	35	237	47	189	87	18	177	187	977
Pseudomonas aeruginosa	36	167	19	166	85	4	74	107	658
Enterobacter cloacae complex	10	85	9	65	13	14	80	50	326
Klebsiella oxytoca	13	76	4	45	13	8	49	30	238
Proteus mirabilis	6	66	6	45	24	3	37	36	223
Serratia marcescens	8	67	3	52	9	3	28	19	189
Enterobacter aerogenes	4	34	3	26	11	1	27	25	131
Salmonella species (non-typhoidal)	1	19	24	28	10	2	21	10	115
Morganella morganii	4	26	0 ‡	25	7	1	9	7	79
Acinetobacter baumannii complex	0	10	5	20	1	2	10	11	59
Citrobacter koseri	1	21	1	6	10	0	5	11	55
Citrobacter freundii	4	20	0	5	4	1	9	2	45
Salmonella species (typhoidal)	1	5	0	6	5	0	7	2	26
Acinetobacter species	0	3	4	3	5	0	2	3	20
Pantoea agglomerans	1	1	0	4	1	0	3	3	13
Enterobacter species	0	0	0	0	12	0	0	0	12
Raoultella ornithinolytica	2	6	0	1	0	0	1	2	12
Providencia rettgeri	0	3	0	3	2	1	0	2	11
Proteus vulgaris	1	3	0	0	3	0	1	3	11
Other species (total n=40)	4	33	2	22	21	5	24	13	124
Enterococcus species	**58**	**287**	**18**	**131**	**108**	**20**	**237**	**152**	**1011**
Enterococcus faecalis	35	150	10	96	58	12	110	91	562
Percentage vancomycin resistant	0	1.3	0	0	0	8.3	0.9	0	4
Enterococcus faecium	22	116	8	31	44	8	120	53	402
Percentage vancomycin resistant	50.0	51.7	n §	61.3	52.3	n	63.3	11.3	202
Percentage vancomycin susceptible	50.0	48.3	n	38.7	47.7	n	36.7	88.7	200
Other enterococcal species	1	21	0	4	6	0	7	8	47
Enterococcus casseliflavus	0	12	0	0	1	0	2	1	16
Enterococcus avium	1	1	0	0	3	0	2	4	11
Enterococcus raffinosus	0	1	0	2	2	0	2	0	7
Enterococcus gallinarum	0	4	0	0	0	0	0	3	7
Enterococcus hirae	0	1	0	2	0	0	1	0	4
Enterococcus durans	0	1	0	0	0	0	0	0	1
Enterococcus gilvus	0	1	0	0	0	0	0	0	1
Staphylococcus aureus	**81**	**590**	**110**	**503**	**262**	**51**	**407**	**394**	**2398**
Percentage methicillin resistant	14.8	22.9	38.2	13.5	16.4	5.9	15.5	17.5	18.1
Percentage Methicillin susceptible	85.2	77.1	61.8	86.5	83.6	94.1	84.5	82.5	81.9

ACT = Australian Capital Territory, NSW = New South Wales, NT = Northern Territory, Qld = Queensland, SA = South Australia, Tas = Tasmania, Vic = Victoria, WA = Western Australia

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

‡ No isolates

§ Insufficient numbers (< 10) to calculate

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%; and *S. aureus*, 96.5%). An episode was designated hospital-onset (HO) if the first positive blood culture was collected > 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 (CO).

Information on place of onset of bacteraemia was available for 6,928 (94.5%) gram-negative, 1,008 (99.7%) enterococcus spp., and 2397 *S. aureus* episodes (Table 3). For gram-negative species, 74.8% of all episodes were CO, although differences were observed with different species. *E. faecalis* and other *Enterococcus* spp. were predominantly CO (65.3%; 95%CI: 61.3-69.1; and 78.7%; 95%CI: 65.1-88.0) respectively however *E. faecium* was predominantly HO (72.1%; 95%CI: 67.6-76.3). The majority of *S. aureus* bacteraemia were CO (77.4%; 95%CI: 75.7-79.0).

Table 3 Organisms by place of onset

Organism	Community-onset (%)	Hospital -onset (%)	Total
Gram-negative species [a]	**5204 (75.1)**	**1724 (24.9)**	**6928**
Escherichia coli	3148 (83.6)	617 (16.4)	3765
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)**	**1008**
Enterococcus faecalis	365 (65.3)	194 (34.7)	559
vancomycin resistant	1	3	4
vancomycin susceptible	363 (65.5)	191 (34.7)	554

Organism	Community-onset (%)	Hospital -onset (%)	Total
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* spp. (n=7)	37 (78.7)	10 (21.3)	47
Staphylococcus aureus	**1855 (77.4)**	**542 (22.6)**	**2397**
methicillin resistant	313 (72.0)	122 (28.0)	435
methicillin susceptible	1542 (78.6)	420 (21.4)	1962

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

3.3. Onset versus 30-day all-cause mortality

The 30-day all-cause mortality, where place of onset was known, was available for 4586 (62.6%) gram-negative; 888 (87.8%) enterococcal; and 1986 (82.8%) *S. aureus* bacteraemia episodes. The only species where a significant difference in the 30-day all-cause mortality between CO and HO onset was seen were *E. coli*, *Proteus mirabilis*, *Salmonella* (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%) (p=0.0001). However, there was no significant difference in mortality between vancomycin-resistant and vancomycin-non-susceptible *E. faecium*.

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

Table 4 Place of onset versus 30-day all-cause mortality for the top sixteen species

Organism	Community-onset		Hospital-onset		Total		P
	N	Mortality (%)	N	Mortality (%)	N	Mortality (%)	
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
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
***Enterococcus* species**	**437**	**78 (17.8)**	**451**	**104 (23.1)**	**888**	**186 (20.9)**	
Enterococcus faecalis	311	50 (16.1)	166	25 (15.1)	477	75 (15.7)	ns

Organism	Community-onset		Hospital-onset		Total		P
	N	Mortality (%)	N	Mortality (%)	N	Mortality (%)	
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	**1511**	**242 (16.0)**	**475**	**75 (15.8)**	**1986**	**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	1264	194 (15.3)	366	55 (15.0)	1630	249 (15.3)	ns

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

‡ CA-MRSA = community-associated methicillin-resistant *S. aureus*; HA-MRSA = healthcare-associated methicillin-resistant *S. aureus*. Eight MRSA isolates were not available for typing and therefore could not be characterised as CA-MRSA or HA-MRSA strains

4. Patient demographics

4.1. 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 (Table 5). 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, with only 8.4% (gram-negative species), 8.3% (*Enterococcus* spp.), and 14.1% (*S. aureus*) of episodes in patients less than 40 years.

Table 5 Species by decade of life and gender

	Gram-negative species *			*Enterococcus* species			*Staphylococcus aureus*		
Decade	Female	Male	Total	Female	Male	Total	Female	Male	Total
1	96	128	224	15	32	47	57	68	125
2	49	39	88	4	5	9	24	64	88
3	164	115	279	16	12	28	48	77	125
4	210	128	338	15	25	40	78	108	186
5	248	229	477	33	54	87	116	173	289
6	457	498	955	59	92	151	117	221	338
7	558	766	1,324	60	136	196	125	293	418
8	634	844	1,478	70	175	245	114	264	378
9	678	739	1,417	56	99	155	123	229	352
10	267	181	448	18	32	50	38	58	96
11	3	6	9	2	1	3	0	3	3
Total	**3,364**	**3,673**	**7,037**	**348**	**663**	**1011**	**840**	**1558**	**2398**
			M/100F			M/100F			M/100F
			109			**191**			**185**

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

Figure 1 Gender versus decade of life, Gram-negative bacteraemia

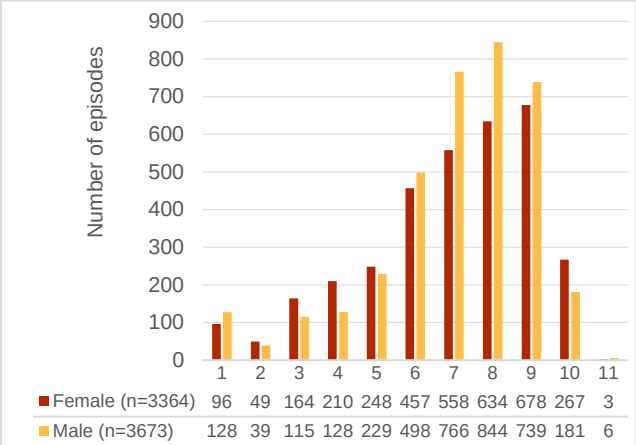


Figure 2 Gender versus decade of life, *Enterococcus* species bacteraemia

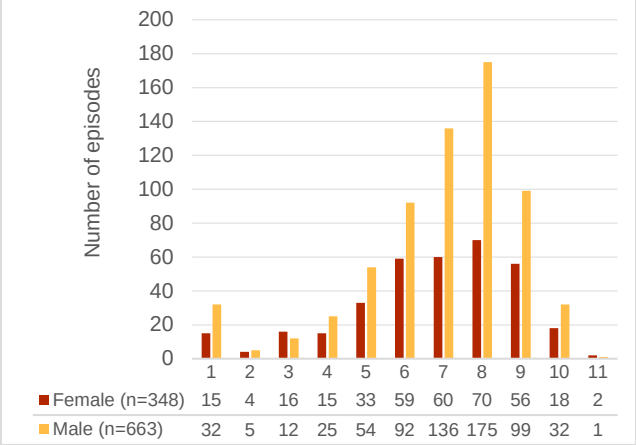
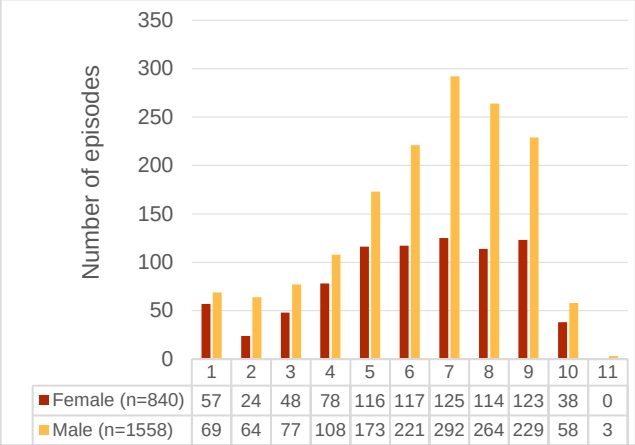


Figure 3 Gender versus decade of life for *Staphylococcus aureus* bacteraemia



4.2. Principal clinical manifestation

4.2.1. Gram-negative bacteria

The principal clinical manifestation was documented for 5,085 (69.4%) of patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations were urinary tract (43.2%), biliary tract (15.9%) and other intra-abdominal infection (10.5%) (Table 6).

Table 6 Gram-negative* bacteraemia by principal clinical manifestation and gender

Principal Clinical Manifestation	Female	Male	Total	P
Urinary tract infection	1215 (50.7)	981 (36.5)	2196 (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	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
All	**2395**	**2690**	**5085**	

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

4.2.2. *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 (17.0%), urinary tract (16.5%), and other intra-abdominal infection (14.2%) (Table 7).

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%).

Table 7 Enterococcal bacteraemia by principal clinical manifestation and gender

Principal Clinical Manifestation	Female	Male	Total	P
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	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	- †
Pneumonia/empyema	0	1	1	-
Total	**321**	**628**	**949**	

† not applicable

The principal manifestation was known for 904/972 (93.0%) of the *E. faecalis* and *E. faecium* episodes (Table 8). The most common clinical manifestation for *E. faecalis* were urinary tract infection, while 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 8 Enterococcal bacteraemia by principal clinical manifestation and *Enterococcus* species

Principal Clinical Manifestation	*E. faecalis*	*E. faecium*	P
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	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)	- †
Pneumonia/empyema	0	1 (0.3)	-
Total	**513**	**391**	

† not applicable

4.2.3. *Staphylococcus aureus*

The principal clinical manifestation was known for 2,110 (88.0%) episodes of SAB (Table 9). 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 infections (16.1%).

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

Table 9 *Staphylococcus aureus* bacteraemia by principal clinical manifestation and gender

Principal Clinical Manifestation	Female	Male	Total	P
Skin and skin structure	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)	
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	4 (0.3)	4 (0.2)	- †
Intra-abdominal infection other than biliary tract	0	1 (0.1)	1 (0.0)	-
Endocarditis-native valve, unspecified	0	1 (0.1)	1 (0.0)	-
Total	**730**	**1380**	**2110**	

* CNS = central nervous system

† not applicable

4.3. Length of stay post bacteraemic episode

Length of stay (LOS) post bacteraemia was available for 5432 (74.1%) gram-negative species, 937 (92.7%) *Enterococcus* species and 2131 (88.9%) of *S. aureus* episodes. The majority of patients (45.9%) with a gram-negative bacteraemia had a length of stay < 7 days (Table 10). Over 20.9% of patients remained in hospital >30 days after enterococcal bacteraemia (Table 11) and 27.5% after staphylococcal bacteraemia (Table 12).

Table 10 Gram-negative* bacteraemia by length of stay post bacteraemic episode and place of onset

	Length of stay post bacteraemia (days)				
Species	**< 7**	**7 - 14**	**15 – 30**	**> 30**	**Total**
Gram negative species *	**2491 (45.9)**	**1625 (29.9)**	**787 (14.5)**	**529 (9.7)**	**5432**
Enterobacteriaceae	2314 (47.4)	1438 (29.5)	689 (14.1)	439 (9.0)	4880
Escherichia coli	1582 (53.7)	838 (28.4)	340 (11.5)	186 (6.3)	2946
Community-onset	1458 (59.6)	676 (27.6)	217 (8.9)	97 (4.0)	2448
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 Enterobacteriacae (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*

There were no significant differences in LOS between *E. faecium* and *E. faecalis* episodes, or between vancomycin susceptible and non-susceptible *E. faecium* (Table 11). However, for both *E. faecalis* and *E. faecium*, patients with hospital-onset infections had a significantly longer LOS > 30 days than those with community-onset (31.8% and 26.4%, vs 14.9% and 9.4%, respectively, p<0.01).

Table 11 *Enterococcus* species bacteraemia by vancomycin-resistance, length of stay post bacteraemic episode, and place of onset

	Length of stay post bacteraemia (days)				
Species	**< 7**	**7 - 14**	**15 – 30**	**> 30**	**Total**
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

Patients with MRSA episodes had a significantly longer LOS > 30 days than those with MSSA (32.1% vs 26.1%, p=0.0284) (Table 12). For MRSA episodes, patients with hospital-onset infections had a significantly longer LOS > 30 days than those with community-onset (28.3% vs 41.1%, p=0.0129).

Table 12 *Staphylococcus aureus* bacteraemia by methicillin-susceptibility, place of onset and length of stay post bacteraemic episode

	Length of stay post bacteraemia (days)				
Species	**< 7**	**7 - 14**	**15 – 30**	**> 30**	**Total**
Staphylococcus aureus	**383 (18.0)**	**481 (22.6)**	**680 (31.9)**	**587 (27.5)**	**2131**
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)	1739
Community-onset	251 (18.6)	325 (24.1)	421 (31.2)	353 (26.1)	1350
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 Table 13. The principal antimicrobial treatment was included in the table if used for more than one bacteraemic episode for the species recovered.

Table 13 Top principal antimicrobial treatments versus onset and 30-day all-cause mortality

All episodes					Community-onset					Healthcare-onset				
Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)	
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	**2271**		**241**	**(10.6)**	**Total**	**1867**		**156**	**(8.4)**	**Total**	**404**		**85**	**(21.0)**
***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	1100	(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	**1568**		**241**	**(15.4)**	**Total**	**1215**		**188**	**(15.5)**	**Total**	**353**		**53**	**(15.0)**

All episodes					Community-onset					Healthcare-onset				
Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)	
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)
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)**
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)	Piperacillin-tazobactam	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)**

All episodes					Community-onset				Healthcare-onset			
Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)	Agent	Number (% of n)		Mortality (%)	
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)**
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)**

All episodes					Community-onset					Healthcare-onset				
Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)	
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
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)**

All episodes					Community-onset				Healthcare-onset			
Agent	Number (% of n)		Mortality (%)		Agent	Number (% of n)		Mortality (%)	Agent	Number (% of n)		Mortality (%)	
***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)**

* Insufficient numbers (< 10) to calculate

† β-lactam or β-lactam plus inhibitor, other than listed above

6. Susceptibility Testing Results

6.1. Percentages resistant/non-susceptible in indicator species (national priority)

Overall percentages of resistance or non-susceptibility, for both CLSI and EUCAST, in the indicator species of national priority are shown in Table 14. 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 resistant (R), and the term non-susceptible (NS) was used to describe these strains. Similarly, NR refers to both susceptible and intermediate.

Supplementary data of percentages susceptible, intermediate and resistant for each antibiotic and all species; and the antimicrobial profiles by state and territory can be found within the 2015 reports on the AGAR web site http://www.agargroup.org/surveys. The national reports provide summary susceptibility data (number and percent (if more than 10 isolates) using both CLSI and EUCAST interpretative guidelines for all species isolated.

Table 14 Antimicrobial resistance, number and percentage by species, CLSI and EUCAST

		CLSI		EUCAST	
Organism, antimicrobial	N	% I (*n*)	% R (*n*)	% I (*n*)	% R (*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	[a] 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	. [b]	0.0 (0)	0.2 (1)	0.0 (0)
Benzylpenicillin	547	.	2.0 (11)	– [c]	–
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)

		CLSI		EUCAST	
Organism, antimicrobial	N	% I (*n*)	% R (*n*)	% I (*n*)	% R (*n*)
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)
Tetracycline	343	0.6 (2)	57.7 (198)	–	–
Vancomycin	402	0.5 (2)	49.8 (200)	.	50.2 (202)
Escherichia coli					
Ampicillin	3992	2.1 (83)	53.1 (2118)	.	55.1 (2201)
Amoxicillin-clavulanate	3995	13.7 (546)	8.7 (349)	† [d]	†
Piperacillin-tazobactam	3974	3.5 (139)	2.8 (112)	1.0 (41)	6.3 (251)
Ceftriaxone	3994	0.1 (3)	10.5 (420)	0.1 (3)	10.5 (420)
Ceftazidime	3994	0.3 (12)	5.8 (230)	3.9 (155)	6.1 (242)
Cefepime	3994	2.0 (79)	3.7 (148)	3.9 (157)	4.8 (191)
Gentamicin	3994	0.1 (3)	7.8 (311)	0.6 (22)	7.9 (314)
Tobramycin	3982	5.1 (202)	3.7 (148)	0.7 (28)	8.8 (350)
Amikacin	3994	0.0 (1)	0.1 (4)	1.6 (62)	0.1 (5)
Ciprofloxacin	3994	0.3 (13)	12.3 (490)	1.0 (39)	12.6 (503)
Meropenem	3993	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)
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					

		CLSI		EUCAST	
Organism, antimicrobial	**N**	**% I (*n*)**	**% R (*n*)**	**% I (*n*)**	**% R (*n*)**
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	‡ [e]	1.8 (2)	‡	6.1 (7)
Meropenem	114	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin-tazobactam	142	f	f	f	f
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	2397	.	82.3 (1972)	.	82.3 (1972)
Ciprofloxacin	2398	0.4 (9)	10.2 (245)	.	10.3 (254)
Clindamycin	2398	0.0 (0)	3.3 (78)	0.2 (5)	3.3 (78)

Organism, antimicrobial	N	CLSI % I (*n*)	CLSI % R (*n*)	EUCAST % I (*n*)	EUCAST % R (*n*)
Daptomycin	2397	[g] 0.6 (6)	.	.	0.3 (6)
Erythromycin	2398	4.2 (100)	12.4 (298)	0.3 (8)	13.7 (328)
Gentamicin	2398	1.0 (24)	2.6 (62)	.	4.0 (97)
Linezolid	2397	0.0 (0)	0.0 (0)	.	0.0 (0)
Oxacillin	2396	–	17.6 (421)	.	17.6 (421)
Rifampicin	2347	0.1 (2)	0.6 (13)		[h] 0.6 (15)
Trimethoprim-sulfamethoxazole	2398	–	4.0 (96)	0.2 (5)	3.8 (91)
Teicoplanin	2398	0.0 (0)	0.0 (0)	0.0 (0)	0.1 (2)
Tetracycline	2139	0.1 (3)	5.0 (107)	0.5 (11)	5.1 (110)
Vancomycin	2397	0.0 (0)	0.0 (0)	–	0.0 (0)

[a] Includes SDD category for CLSI
[b] No category defined
[c] no guidelines for indicated species
[d] EUCAST, for susceptibility testing purposes, the concentration of clavulanate is fixed at 2 mg/L, rather than a 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
[e] Ciprofloxacin concentration range available on the cards used restricts ability to accurately determine susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species.
[f] Not indicated on susceptibility testing cards
[g] Non susceptible, resistance not defined
[h] Rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant

6.2. Antimicrobial resistance versus place of onset

Antimicrobial resistance (CLSI and EUCAST) by place of onset, where known, in indicator species are shown in Table 15.

Table 15 Resistance (CLSI and EUCAST), percentage, by place of onset

Organism	N	Community-onset I (%)	Community-onset R (%)	Hospital onset %I	Hospital onset %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	[a] 3.0 / 0.0	1.5 / 4.5	[a] 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	[a] 2.5 / 6.8	1.2 / 2.5	[a] 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

Organism	N	Community-onset I (%)	Community-onset R (%)	Hospital onset %I	Hospital onset %R
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
Enterococcus faecalis					
Community-onset, 65%; hospital-onset, 35%					
Ampicillin	558	[b] - / 0.0	0.0 / 0.0	- / 0.0	0.0 / 0.0
Benzylpenicillin	544	- / — [c]	1.1 / —	- / —	3.7 / —
Ciprofloxacin	518	2.7 / -	12.6 / 9.3	1.6 / -	19.0 / 15.2
Daptomycin	536	[d] 0.0 / —	- / —	[d] 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%					
Ampicilllin	3751	2.2 / -	50.9 / 53.1	1.5 / -	61.6 / 63.1
Amoxicllin-clavulanate	3754	12.8 / † [e]	7.7 / †	18.5 / †	13.0 / †
Piperacillin-tazobactam	3733	3.1 / 1.0	2.1 / 5.2	4.9 / 1.3	6.7 / 11.7
Ceftriaxone	3753	0.1 / 0.1	9.1 / 9.1	0.0 / 0.0	15.8 / 15.8
Ceftazidime	3753	0.3 / 3.5	5.0 / 5.3	0.5 / 5.7	8.5 / 8.9
Cefepime	3753	[a] 1.7 / 3.5	3.3 / 4.2	[a] 2.8 / 5.2	6.0 / 7.5
Gentamicin	3753	0.1 / 0.6	7.4 / 7.5	0.0 / 0.7	8.5 / 8.5
Tobramycin	3741	4.9 / 0.8	3.4 / 8.3	4.8 / 0.7	4.6 / 9.3
Amikacin	3753	0.0 / 1.3	0.0 / 0.1	0.0 / 2.6	0.3 / 0.3
Ciprofloxacin	3753	0.3 / 0.9	11.3 / 11.6	0.7 / 1.8	15.1 / 15.8
Meropenem	3752	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Klebsiella pneumoniae					
Community-onset, 70%; hospital-onset, 30%					
Amoxicllin-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	[a] 0.9 / 2.0	1.1 / 1.8	[a] 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

Organism	N	Community-onset		Hospital onset	
		I (%)	R (%)	%I	%R
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%					
Amoxicllin-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	[a] 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%					
Ampicilllin	210	0.0 / -	19.6 / 19.5	0.0 / -	7.3 / 7.3
Amoxicllin-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	[a] 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
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%					
Ampicilllin	110	0.0 / -	7.3 / 7.3	0.0 / -	21.4 / 21.4
Amoxicllin-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	[a] 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

Organism	N	Community-onset I (%)	Community-onset R (%)	Hospital onset %I	Hospital onset %R
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	‡ [f]	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%					
Ampicilllin	169	38.6 / -	34.9 / 73.5	39.5 / -	36.0 / 75.6
Amoxicllin-clavulanate	176	22.1 / -	59.3 / -	21.1 / -	65.6 / -
Piperacillin-tazobactam	132	[g]	[g]	[g]	[g]
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
Cefepime	176	[c] 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	2396	- / -	82.5 / 82.5	- / -	81.7 / 81.7
Ciprofloxacin	2397	0.3 / -	8.6 / 8.9	0.6 / -	15.9 / 16.4
Clindamycin	2397	0.0 / 0.2	2.6 / 2.6	0.0 / 0.2	5.5 / 5.5
Daptomycin	2396	[d] 0.2 / —	-/ 0.2	[d] 0.4 / —	- / 0.4
Erythromycin	2397	4.4 / 0.3	11.5. / 12.7	3.3 / 0.6	15.7 / 17.0
Gentamicin	2397	0.6 / —	1.8 / 2.8	2.4 / —	5.4 / 8.3
Linezolid	2396	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Oxacillin	2395	— / —	16.1 / 16.1	— / —	22.5 / 22.5
Rifampicin	2346	0.1 / [h]	0.3 / 0.3	0.2 / [h]	1.5 / 1.7
Trimethoprim-sulfamethoxazole	2397	— / 0.1	3.3 / 3.2	— / 0.6	6.3 / 5.7
Teicoplanin	2397	0.0 / 0.1	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Tetracycline	2138	0.1 / 0.5	3.8 / 3.9	0.2 / 0.4	9.0 / 9.2
Vancomycin	2396	0.0 /—	0.0 / 0.0	0.0 /—	0.0 / 0.0

[a] Includes SDD category for CLSI
[b] No category defined
[c] no guidelines for indicated species
[d] Non susceptible, resistance not defined
[e] EUCAST, for susceptibility testing purposes, the concentration of clavulanate is fixed at 2 mg/L, rather than a 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
[f] Ciprofloxacin concentration range available on the cards used restricts ability to accurately determine susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species.
[g] Not indicated on susceptibility testing cards
[h] Rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant

6.3. Multi-resistance

The most problematic pathogens are those with multiple acquired resistances. Although there is no agreed benchmark for the definition of multi-resistance, acquired resistance to more than three agents have been chosen to define multi-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 multi-drug resistance determination. The agents included for each species are listed in the legend after each Table. EUCAST breakpoints have been used throughout in the analysis, noting that for cefazolin the EUCAST approved Australian National Advisory Committee guidelines were used. For amoxicillin-clavulanate CLSI breakpoints were used, as both the Vitek and Phoenix cards used the CLSI formulation for this agent.

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

Multiple acquired resistance for Key species are shown in Table 16 to Table 22; for other common species of refer to Appendix D.

Table 16 *Enterobacter cloacae* complex, multiple acquired resistance

		Non-multi-resistant					Multi-resistant							
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	%
ACT	5	5	0	0	0	100.0%	0	0	0	0	0	0	0	0.0%
NSW	57	39	3	2	6	87.7%	2	1	2	2	0	0	0	12.3%
NT	9	6	1	0	1	88.9%	0	1	0	0	0	0	0	11.1%
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%
TAS	11	7	1	2	0	90.9%	0	1	0	0	0	0	0	9.1%
VIC	77	49	6	0	7	80.5%	5	3	5	2	0	0	0	19.5%
WA	41	29	0	2	4	85.4%	4	2	0	0	0	0	0	14.6%
Total	**277**	**187**	**17**	**7**	**24**	**84.8%**	**15**	**11**	**9**	**7**	**0**	**0**	**0**	**15.2%**

Antimicrobials included: piperacillin-tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table 17 *Enterococcus faecalis,* multiple acquired resistance

		Non-multi-resistant					Multi-resistant		
Region	Total	0	1	2	3	%	4	5	%
ACT	35	30	5	0	0	100.0%	0	0	0.0%
NSW	149	134	15	0	0	100.0%	0	0	0.0%
NT	10	7	3	0	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%
TAS	0 †								
VIC	109	92	16	1	0	100.0%	0	0	0.0%
WA	91	83	8	0	0	100.0%	0	0	0.0%
Total	**520**	**459**	**59**	**2**	**0**	**100.0%**	**0**	**0**	**0.0%**

Antimicrobials included: ampicillin, ciprofloxacin, nitrofurantoin, vancomycin, linezolid

† Ciprofloxacin MICs not provided

Table 18 *Enterococcus faecium,* multiple acquired resistance

Region	Total	Non-multi-resistant					Multi-resistant	
		0	1	2	3	%	4	%
ACT	22	1	0	10	11	100.0%	0	0.0%
NSW	114	16	8	48	42	100.0%	0	0.0%
NT	8	1	0	1	6	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%
TAS	1	0	0	1	0	100.0%	0	0.0%
VIC	120	12	0	32	76	100.0%	0	0.0%
WA	53	11	0	36	6	100.0%	0	0.0%
Total	**373**	**47**	**19**	**147**	**160**	**100.0%**	**0**	**0.0%**

Antimicrobials included: ampicillin, ciprofloxacin, linezolid, vancomycin

Table 19 *Escherichia coli*, multiple acquired resistance

Region	Total	Non-multi-resistant					Multi-resistant									
		0	1	2	3	%	4	5	6	7	8	9	10	11	12	13	%
ACT	146	66	23	21	14	84.9%	4	3	6	6	0	1	2	0	0	0	15.1%
NSW	1106	418	161	159	99	75.7%	59	47	30	67	23	24	10	9	0	0	24.3%
NT	137	47	26	24	13	80.3%	7	8	5	3	1	1	2	0	0	0	19.7%
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%
TAS	49	25	7	9	2	87.8%	4	1	1	0	0	0	0	0	0	0	12.2%
VIC	604	215	103	96	57	78.0%	30	33	19	26	14	7	3	1	0	0	22.0%
WA	573	216	105	86	59	81.3%	41	14	11	21	7	10	3	0	0	0	18.7%
Total	**3743**	**1497**	**580**	**561**	**358**	**80.0%**	**217**	**149**	**93**	**144**	**53**	**53**	**26**	**12**	**0**	**0**	**20.0%**

Antimicrobials included: ampicillin, amoxycillin-clavulanate [CLSI], piperacillin-tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, nitrofurantoin, trimethoprim, meropenem

Table 20 *Klebsiella pneumoniae,* multiple acquired resistance

		Non-multi-resistant					Multi-resistant								
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	%
ACT	35	20	9	3	0	91.4%	2	0	0	0	1	0	0	0	8.6%
NSW	235	170	25	14	5	91.1%	5	1	2	6	3	4	0	0	8.9%
NT	47	33	3	4	3	91.5%	3	0	0	0	0	1	0	0	8.5%
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%
TAS	9	7	1	0	1	100.0%	0	0	0	0	0	0	0	0	0.0%
VIC	150	108	12	4	2	84.0%	5	2	4	4	4	4	0	1	16.0%
WA	164	128	12	8	5	93.3%	5	1	2	1	0	2	0	0	6.7%
Total	**909**	**667**	**101**	**42**	**21**	**91.4%**	**25**	**5**	**9**	**12**	**9**	**16**	**1**	**1**	**8.6%**

Antimicrobials included: amoxycillin-clavulanate [CLSI], piperacillin-tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table 21 *Staphylococcus aureus* (methicillin-resistant), multiple acquired resistance

		Non-multi-resistant					Multi-resistant									
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	12	%
ACT	12	3	6	1		83.3%	2									16.7%
NSW	107	17	25	24	9	70.1%	20	11	1							29.9%
NT	42	23	11	1		83.3%		7								16.7%
QLD	62	33	17	9	1	96.8%	1	1								3.2%
SA	9	2	3	2	1	88.9%		1								11.1%
TAS																
VIC	63	15	23	12	6	88.9%	3	2	2							11.1%
WA	69	24	27	10	6	97.1%	2									2.9%
Total	**364**	**117**	**112**	**59**	**23**	**85.4%**	**28**	**22**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**14.6%**

Antimicrobials included: ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin [CLSI}, rifampicin, trimethoprim-sulfamethoxazole, tetracycline, vancomycin

† Nitrofurantoin and rifampicin MICs not provided

Table 22 *Staphylococcus aureus* (methicillin-susceptible), multiple acquired resistance

		Non-multi-resistant					Multi-resistant										
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	12	13	%
ACT	69	13	46	6	4	100.0%	0	0	0	0	0	0	0	0	0	0	0.0%
NSW	389	80	265	30	13	99.7%	1	0	0	0	0	0	0	0	0	0	0.3%
NT	68	10	40	16	1	98.5%	1	0	0	0	0	0	0	0	0	0	1.5%
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%
TAS	0 †																
VIC	344	86	217	33	7	99.7%	0	1	0	0	0	0	0	0	0	0	0.3%
WA	325	64	219	37	5	100.0%	0	0	0	0	0	0	0	0	0	0	0.0%
Total	**1665**	**355**	**1093**	**170**	**44**	**99.8%**	**2**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0.2%**

Antimicrobials included: benzylpenicillin, ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin [CLSI], rifampicin, trimethoprim-sulfamethoxazole, tetracycline, vancomycin

† Nitrofurantoin and rifampicin MICs not provided

6.3.1. Multidrug resistance versus onset setting and 30-day all-cause mortality

Onset setting (community or hospital) and 30-day all-cause mortality by multi-drug resistance for the most common species is shown in Table 23.

Table 23 Onset setting and 30-day all-cause mortality by multidrug resistance

Species	Category [a]	Total		Community-onset		Hospital-onset	
		n	mortality, n (%)	n	mortality, n (%)	n	mortality, n (%)
Escherichia coli	Total	2272	244 (10.7)	1880	162 (8.6)	392	82 (20.9)
	non-MDR (<=3)	1734	178 (10.3)	1475	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					
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	1697	270 (15.9)	1278	203 (15.9)	419	67 (16.0)
	non-MDR (<=3)	1562	238 (15.2)	1198	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	1398	217 (15.5)	1076	167 (15.5)	322	50 (15.5)
	non-MDR (<=3)	1390	214 (0.0)	1073	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		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)

[a] Multidrug resistance for each species was as defined in 6.3. For *P. aeruginosa*, MDR (>2 agents) was also included.

7. Trend analysis (2013-2015)

7.1. Gram-negative species

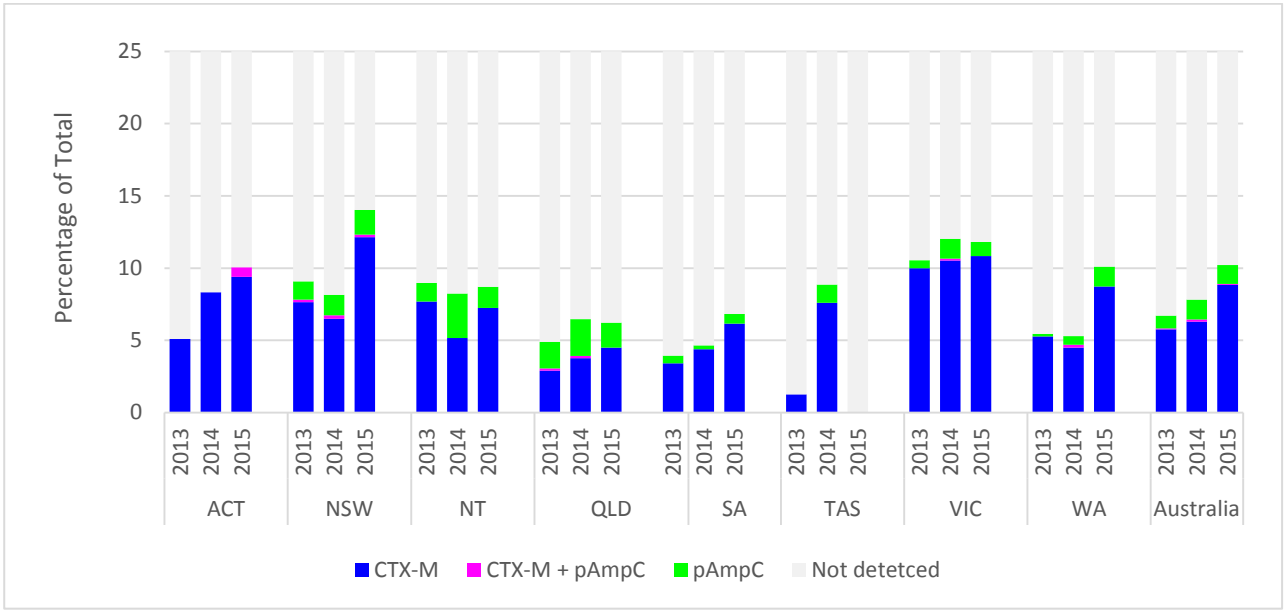
Trend data was available for Enterobacteriaceae from 2013-2015. *Acinetobacter* species and *P. aeruginosa* were introduced to the program in 2015. EUCAST interpretative criteria has been used throughout, with the notable exception of amoxicillin-clavulanate, as both the Vitek and Phoenix cards used the CLSI formulation for this agent.

7.1.1. Extended-spectrum β-lactamase

Nationally, there was a significant increase in the proportion of *E. coli* with CTX-M-types and/or plasmid-bourne AmpC β-lactamases (CTX-M-types, χ^2 for linear trend = 25.95, p<0.001); most of which was driven by the sharp increases in CTX-M types in seen in NSW and Western Australia (Figure 4). SHV or TEM types were not included in this analysis, as it was not possible to discriminate between genes that encode narrow-spectrum β-lactamases from those that encodes ESBLs.

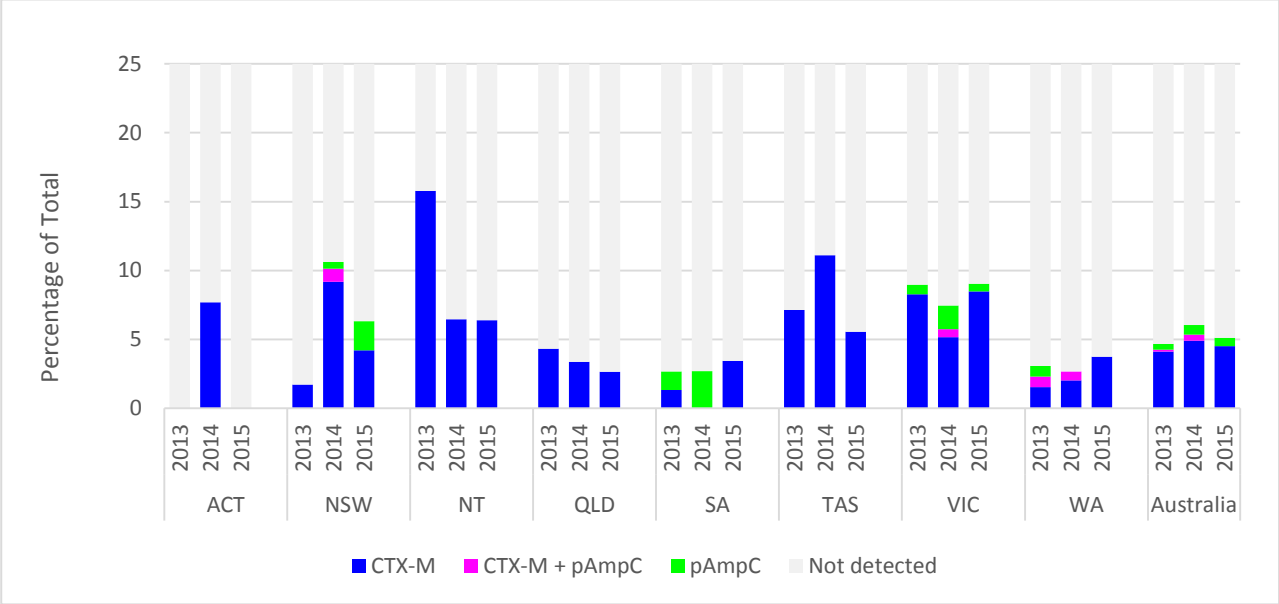
The proportion of *K. pneumoniae* with CTX-M-types or plasmid-borne AmpC β-lactamases has remained steady over the period 2013—2015, although regional variations are seen (Figure 5).

Figure 4 Proportion of CTX-M types and plasmid-borne AmpC β-lactamases in *Escherichia coli* by state and territory, 2013—2015



ACT = Australian Capital Territory, NSW = New South Wales, NT = Northern Territory, Qld = Queensland, SA = South Australia, Tas = Tasmania, Vic = Victoria, WA = Western Australia

Figure 5 Proportion of CTX-M types and plasmid-borne AmpC β-lactamases in *Klebsiella pnemoniae* by state and territory, 2013—2015

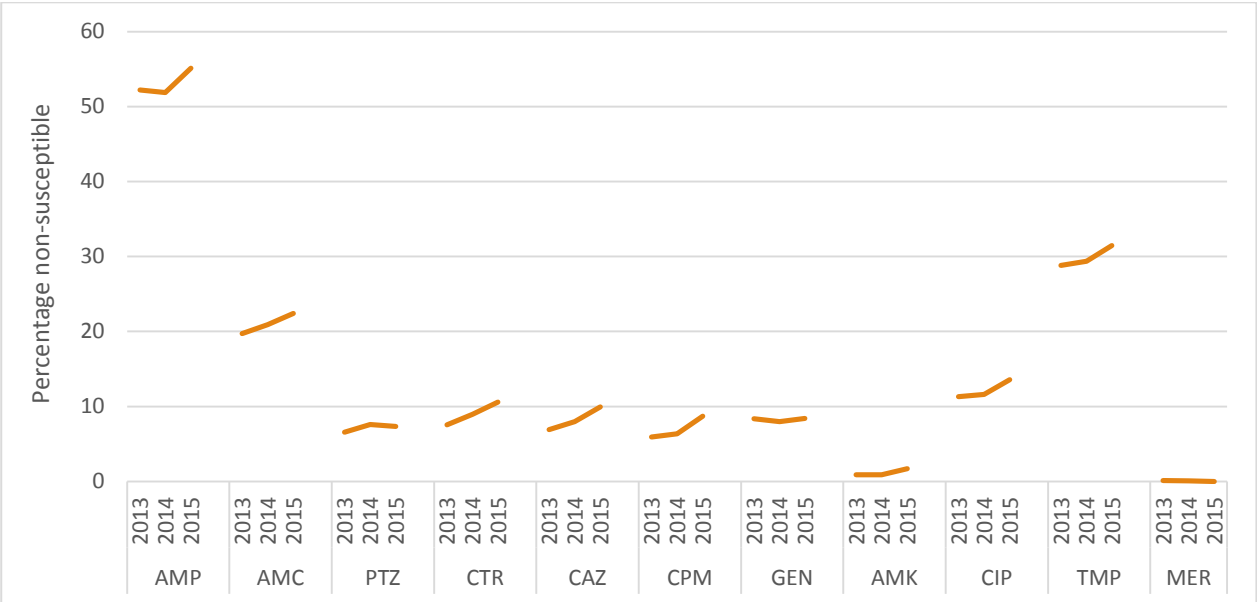


ACT = Australian Capital Territory, NSW = New South Wales, NT = Northern Territory, Qld = Queensland, SA = South Australia, Tas = Tasmania, Vic = Victoria, WA = Western Australia

7.1.2. *Escherichia coli*

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

Figure 6 *Escherichia coli* antimicrobial resistance (EUCAST), Australia, 2013-2015

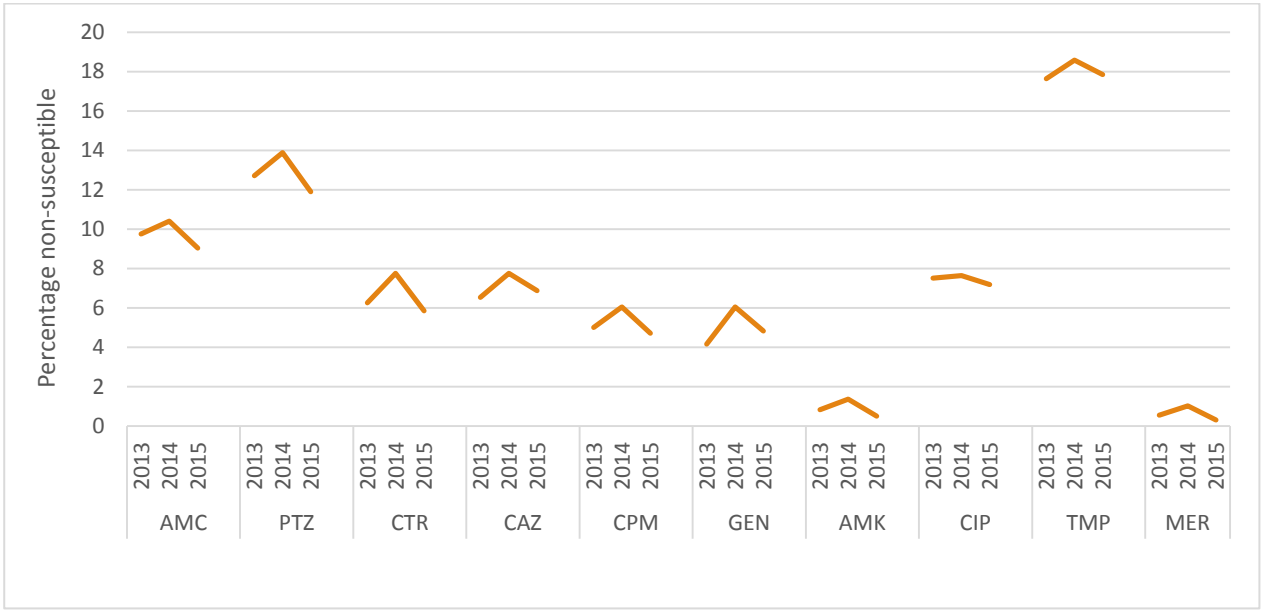


AMP = ampicillin, AMC = amoxicillin-clavulanate [2:1 ratio), PTZ = piperacillin-tazobactam, CTR = ceftriaxone, CAZ = ceftazidime, CPM = cefepime, GEN = gentamicin, AMK = amikacin, CIP = ciprofloxacin, TMP = trimethoprim, MER = meropenem

7.1.3. *Klebsiella pneumoniae*

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

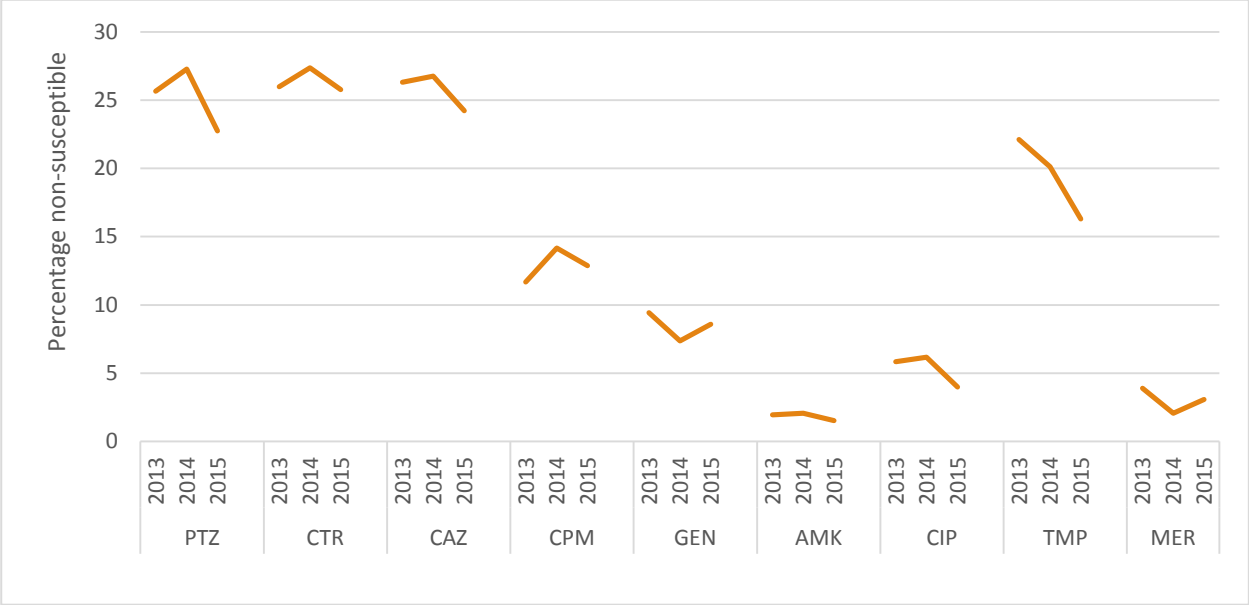
Figure 7 *Klebsiella pneumoniae* antimicrobial resistance (EUCAST), Australia, 2013-2015



AMC = amoxicillin-clavulanate [2:1 ratio), PTZ = piperacillin-tazobactam, CTR = ceftriaxone, CAZ = ceftazidime, CPM = cefepime, GEN = gentamicin, AMK = amikacin, CIP = ciprofloxacin, TMP = trimethoprim, MER = meropenem

7.1.4. *Enterobacter cloacae* complex

Figure 8 *Enterobacter cloacae* antimicrobial resistance (EUCAST), Australia, 2013-2015



PTZ = piperacillin-tazobactam, CTR = ceftriaxone, CAZ = ceftazidime, CPM = cefepime, GEN = gentamicin, AMK = amikacin, CIP = ciprofloxacin, TMP = trimethoprim, MER = meropenem

7.2. *Enterococcus* species

7.2.1. Vancomycin-resistant *Enterococcus faecium*

The proportion of vancomycin-resistant *Enterococcus faecium* (VRE) by state and territory is shown in Table 24. Although VRE were detected in both the Northern Territory and Tasmania, total numbers for each year was < 10.

Table 24 Vancomycin-resistant *Enterococcus faecium* (VRE) by state and territory, 2013-2015

State or Territory	2013		2014		2015		P *	Trend *
	Total	% R (n)	Total	% R (n)	Total	% R (n)		
ACT	18	33.3 (6)	41	24.4 (10)	22	50.0 (11)	ns	
NSW	107	43.9 (47)	104	50.0 (52)	116	51.7 (60)	ns	
NT	3	3 ‡	1	0	8	6		
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	
Tas	5	0	7	1	8	1		
Vic	80	53.8 (43)	94	66.0 (62)	120	63.3 (76)	ns	
WA	42	4.8 (2)	50	20.0 (10)	53	11.3 (6)	ns	
Australia	324	41.7 (135)	380	46.3 (176)	402	50.2 (202)	0.0213	

* χ^2 for trend

† sparkline, 2013-2015, with highest point shaded red

‡ Insufficient numbers

7.2.2. *Enterococcus faecalis*

Non-susceptibility (EUCAST) to key antimicrobial agents for *E. faecalis* by state and territory is shown in Table 25. Both ciprofloxacin non-susceptibility and high-level gentamicin resistance was lower in all states in 2015 compared to 2014; resistance to all other agents remained constant. The only significant trend over the years 2013 to 2015 was a decrease in ciprofloxacin non-susceptibility in NSW (χ^2 for trend, p=0.0410).

Table 25 *Enterococcus faecalis*, antimicrobial non-susceptibility (EUCAST), State and Territory, 2013-2015

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

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 for vancomycin (p=0.0213) and teicoplanin (p<0.0001) (Figure 9). No teicoplanin resistant strains were detected in either the NT or TAS, however, all other jurisdictions except SA and WA had a significant increase. This increase was due to the increased prevalence of in *vanA* *E. faecium* in those regions. Linezolid resistance has remained at <0.5%.

Non-susceptibility to key antimicrobial agents for *E. faecium* is shown in Table 26.

Figure 9 *Enterococcus faecium*, antimicrobial non-susceptibility (EUCAST), Australia, 2013-2015

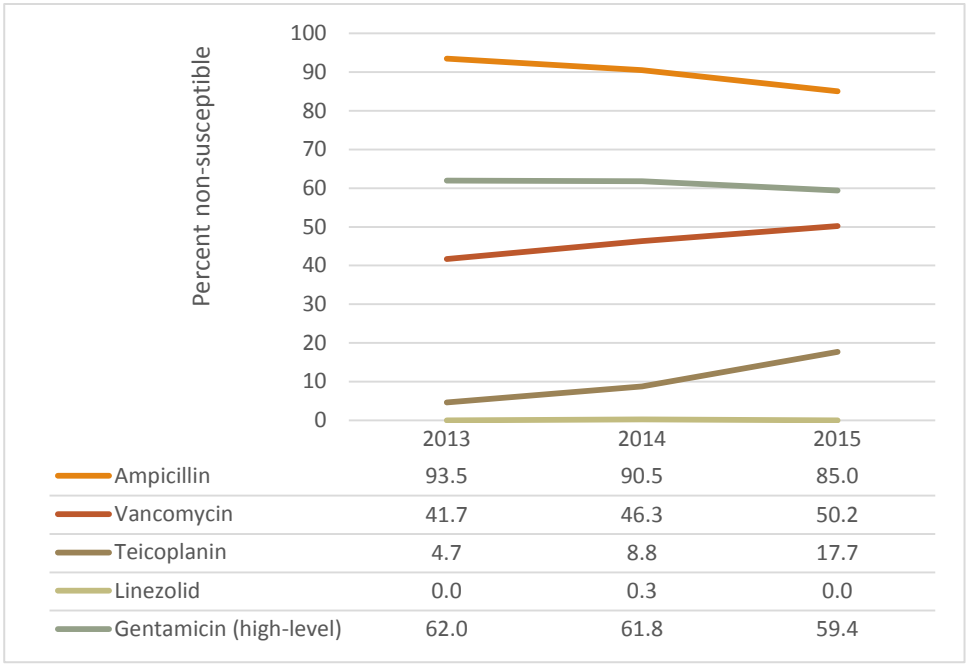


Table 26 *Enterococcus faecium*, antimicrobial non-susceptibility (EUCAST), State and Territory, 2013-2015

			State or territory, number non-susceptible (%)								
Antimicrobial	Year	Total	ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Ampicillin	2013	321	16 (100.0)	97 (90.7)	3 (100.0)	32 (88.9)	31 (96.9)	5 (100.0)	75 (93.8)	41 (97.6)	300 (93.5)
	2014	379	38 (92.7)	92 (89.3)	0	32 (86.5)	41 (89.1)	5 (71.4)	88 (93.6)	47 (94.0)	343 (90.5)
	2015	400	21 (95.5)	99 (86.1)	7 (87.5)	25 (83.3)	41 (93.2)	4 (50.0)	108 (90.0)	42 (79.2)	347 (86.8)
Vancomycin	2013	324	6 (33.3)	47 (43.9)	3 (100.0)	15 (40.5)	19 (59.4)	0	43 (53.8)	2 (4.8)	135 (41.7)
	2014	380	10 (24.4)	52 (50.0)	0	15 (40.5)	26 (56.5)	1 (14.3)	62 (66.0)	10 (20.0)	176 (46.3)
	2015	402	11 (50.0)	60 (51.7)	6 (75.0)	19 (61.3)	23 (52.3)	1 (12.5)	76 (63.3)	6 (11.3)	202 (50.2)
Teicoplanin	2013	321	0	10 (9.3)	0	2 (5.6)	1 (3.1)	0	2 (2.5)	0	15 (4.7)
	2014	377	1 (2.4)	30 (29.1)	0	0	0	0	1 (1.1)	1 (2.0)	33 (8.8)
	2015	401	7 (31.8)	39 (33.9)	0	6 (19.4)	1 (2.3)	0	15 (12.5)	3 (5.7)	71 (17.7)

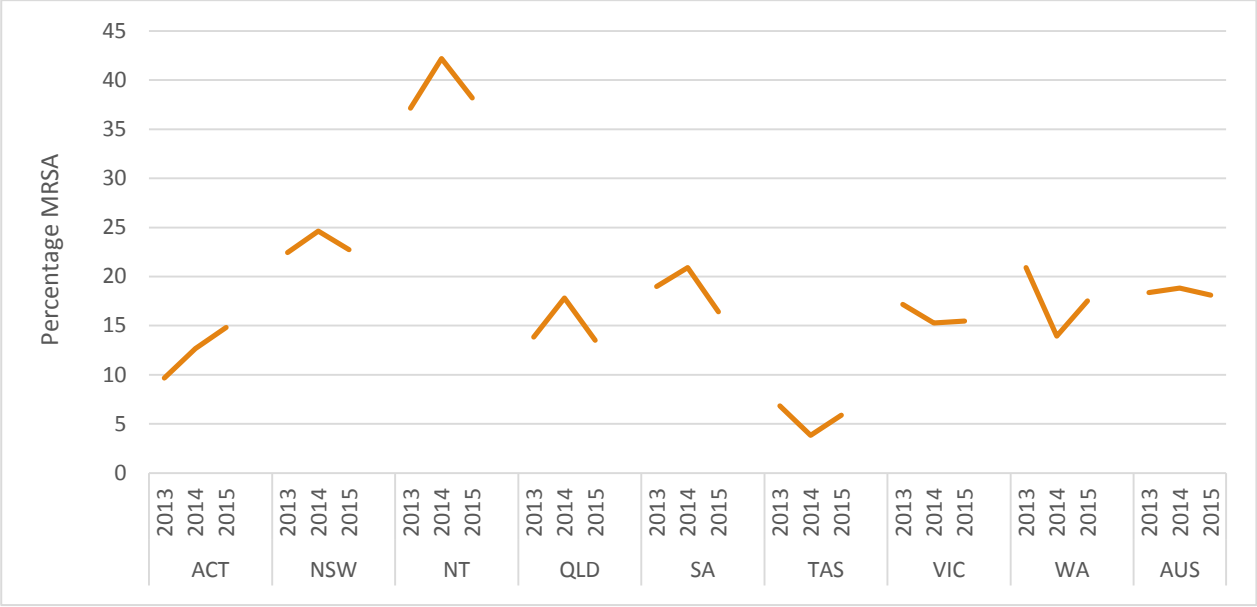
Antimicrobial	Year	Total	State or territory, number non-susceptible (%)								
			ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Gentamicin (high=level)	2013	271	14 (87.5)	64 (77.1)	3 (100.0)	28 (77.8)	2 (33.3)	3 (60.0)	41 (51.3)	13 (31.0)	168 (62.0)
	2014	377	30 (73.2)	72 (70.6)	0	25 (69.4)	31 (67.4)	1 (14.3)	54 (57.4)	20 (40.0)	233 (61.8)
	2015	387	19 (86.4)	67 (65.7)	6 (75.0)	19 (63.3)	36 (81.8)	2 (25.0)	71 (59.2)	14 (26.4)	234 (60.5)
Linezolid	2013	321	0	0	0	0	0	0	0	0	0
	2014	378	0	1 (1.0)	0	0	0	0	0	0	1 0.3
	2015	400	0	0	0	0	0	0	0	0	0

7.3. *Staphylococcus aureus*

7.3.1. *Methicillin-resistant Staphylococcus aureus (MRSA)*

The proportion of MRSA throughout Australia has remained constant over the years 2013—2015, although there were notable variations at state and territory level (Figure 10).

Figure 10 Proportion of methicillin-resistant *Staphylococcus aureus* (MRSA) by state and territory, 2013-2015

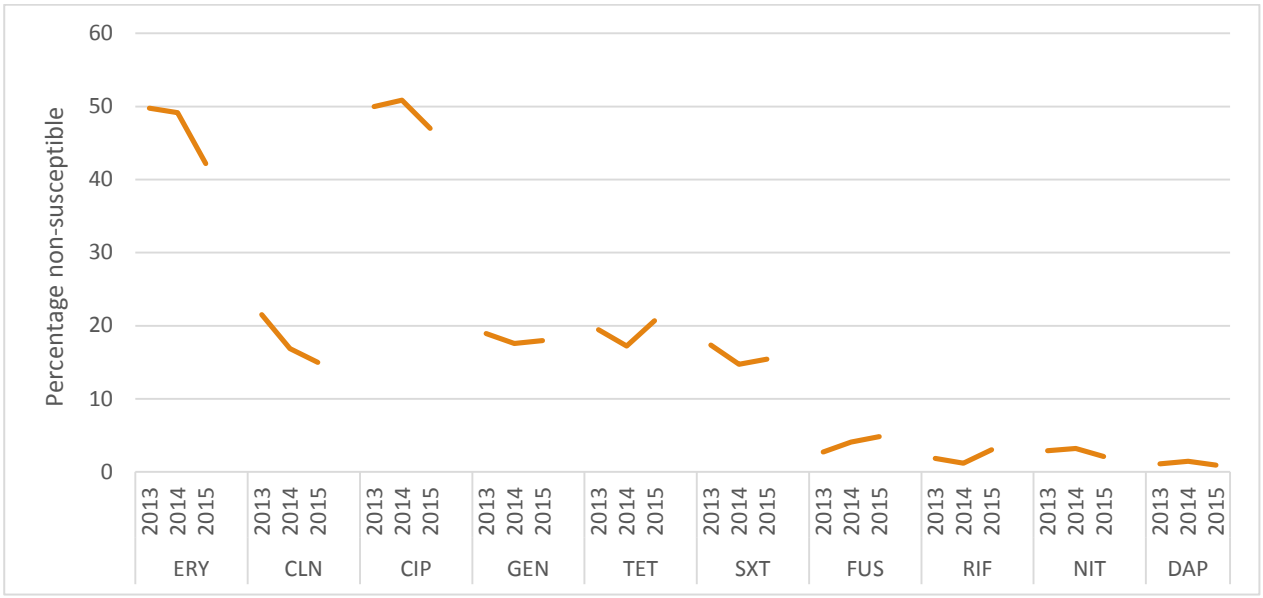


ACT = Australian Capital Territory, NSW = New South Wales, NT = Northern Territory, Qld = Queensland, SA = South Australia, Tas = Tasmania, Vic = Victoria, WA = Western Australia

7.3.2. Methicillin-resistant *Staphylococcus aureus*

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, 2013-2015 (Figure 11).

Figure 11 Methicillin-resistant *Staphylococcus aureus* by antimicrobial resistance (EUCAST), Australia, 2013—2015

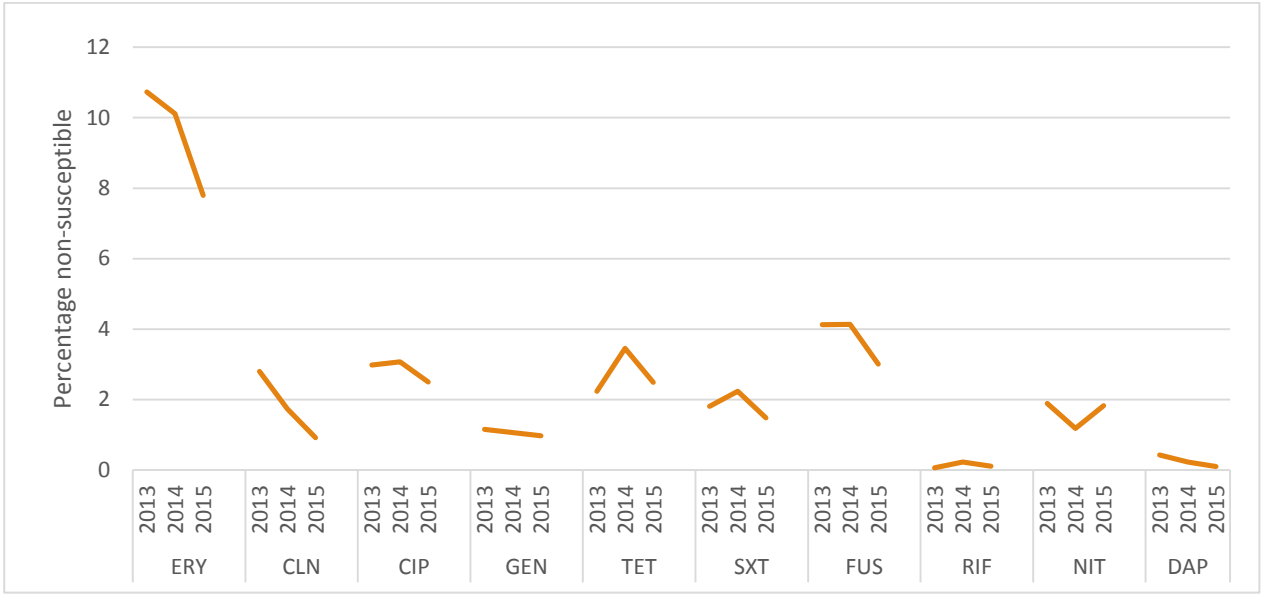


ERY = erythromycin, CLN= clindamycin, CIP = ciprofloxacin, GEN = gentamicin, TET = tetracycline,
SXT = trimethoprim/sulfamethoxazole, FUS = fusidic acid, RIF = rifampicin, NIT = nitrofurantoin [CLSI], DAP = daptomycin

7.3.3. Methicillin-susceptible *Staphylococcus aureus*

There was also 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=<0.0001) non-susceptible MRSA, 2013-2015 (Figure 12). There was also a decrease in daptomycin non-susceptibility (χ^2 for linear trend = 3.875, p=0.0490).

Figure 12 Methicillin-susceptible *Staphylococcus aureus* by antimicrobial resistance (EUCAST), Australia, 2013—2015



ERY = erythromycin, CLN= clindamycin, CIP = ciprofloxacin, GEN = gentamicin, TET = tetracycline,
SXT = trimethoprim/sulfamethoxazole, FUS = fusidic acid, RIF = rifampicin, NIT = nitrofurantoin [CLSI], DAP = daptomycin

8. Molecular studies

8.1. Gram-negative organisms

8.1.1. Extended-spectrum β-lactamases

Extended-spectrum ß-lactamases (ESBLs) are important problem resistances internationally. They have been predominantly a problem in hospital practice, and initially 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 (so-called CTX-M enzymes) in *E. coli* strains in the community. The latter is part of a global epidemic. It is unclear what is driving this community expansion of CTX-M ESBLs in Australia, as 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 of ESBLs becoming established in long-term care facilities in Australia. ESBLs are important because they compromise the efficacy of third-generation cephalosporins which have been such 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 possess co-resistance to other non β-lactam agents. This can result in delays in the use of effective empiric therapy, with a lack of available oral options for treatment resulting in excess hospitalisation, and in the setting of sepsis, increase in mortality risk.

Most ESBL-producing strains will be captured/recognised 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 > 1mg/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 that species, cefepime MICs >0.25 mg/L are suggestive that an isolate of this genus harbours an ESBL.[21] However, due to card range limitations, **isolates with a cefepime MIC > 1mg/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, from TEM genes with higher numbers that encode ESBLs. Similarly, SHV screening does not discriminate between SHV-1/11, 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/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 jurisdictions, are shown in Figure 13. The presumptive and confirmed ESBLs by state and territory are shown in Table 27.

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

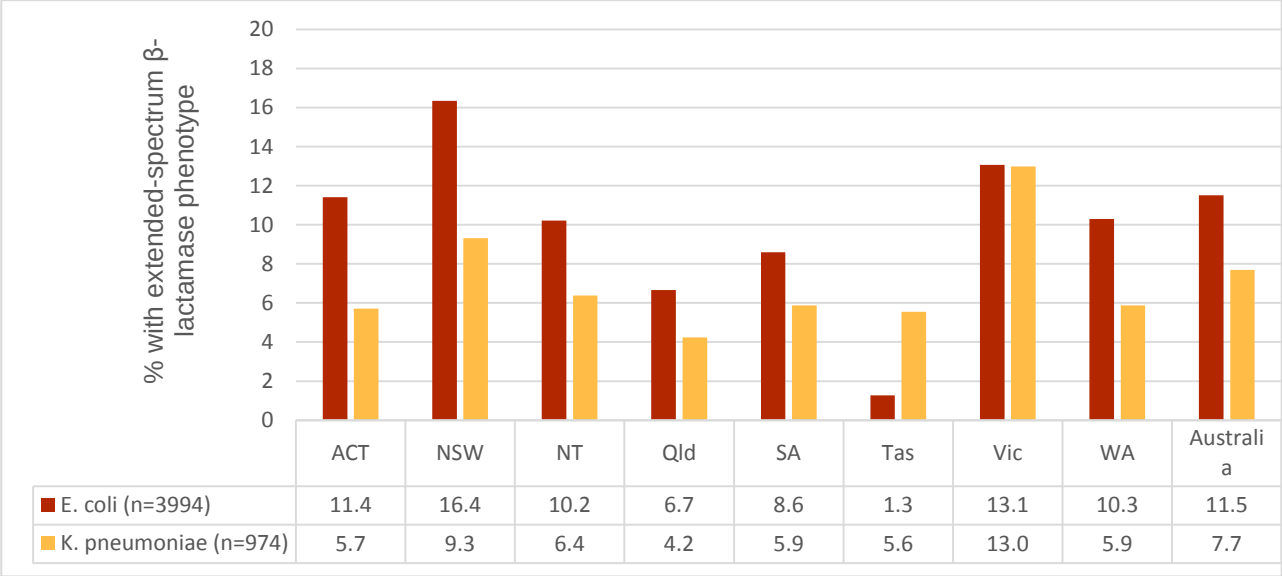


Table 27 Presumptive and confirmed extended-spectrum β-lactamase production

Species	ACT	NSW	NT	QLD	SA	TAS	VIC	WA	Australia
Escherichia coli	149	1107	137	691	454	79	727	650	3994
ESBL phenotype	17	181	14	46	39	1	95	67	460
Confirmed any ESBL* / No. received	16/17	151/162	12/14	41/45	32/38	1/1	86/92	64/66	408/435
CTX-M types	15	135	10	28	28	0	78	55	349
plasmid-borne AmpC	1	18	2	12	3	0	7	9	52
SHV	1	1	0	2	1	0	2	1	14
Klebsiella pneumoniae	35	237	47	189	87	18	177	187	977
ESBL phenotype	2	22	3	8	5	1	23	11	75
Confirmed any ESBL* / No. received	1/2	15/19	3/3	6/7	3/5	1/1	17/23	7/11	53/71
CTX-M types	0	10	3	5	3	1	15	7	44
plasmid-borne AmpC	0	4	0	0	0	0	1	0	5
TEM	1	9	2	5	1	1	13	5	37
Klebsiella oxytoca	13	76	4	45	13	8	49	30	238
ESBL phenotype	1	10		3	3		3	2	22
Confirmed any ESBL* / No. received	0/1	0/9	0/0	1/3	0/3	0/0	2/3	0/2	3/21 †
CTX-M types	0	0	0	0	0	0	1	0	1
TEM	0	0	0	1	0	0	0	0	1
SHV	0	1	0	1	0	0	1	0	2

Species	ACT	NSW	NT	QLD	SA	TAS	VIC	WA	Australia
Proteus mirabilis	6	66	6	45	24	3	37	36	223
ESBL phenotype	0	1	0	1	0	0	2	1	5
Confirmed									
any ESBL* / No. received	- ‡	1/1		1/1	-	-	1/2	1/1	4/5
CTX-M types	-	1		0	-	-	0	0	1
plasmid-borne AmpC	-	0		0	-	-	1	1	2
TEM	-	1		1	-	-	0	1	3
***Salmonella* species(non-typhoidal)**	1	19	24	28	10	2	21	10	115
ESBL phenotype	0	0	0	0	0	0	3	0	3
Confirmed									
any ESBL* / No. received	-	-	-	-	-	-	3/3	-	3/3
CTX-M types	-	-	-	-	-	-	1	-	1
plasmid-borne AmpC	-	-	-	-	-	-	2	-	2
TEM	-	-	-	-	-	-	2	-	2

* Strains may possess more than one type of ESBL gene

† See text for explanantion of low proportion of ESBL

‡ no isolates

Based on the tests performed in this study, ESBLs were more common among *E. coli* (10.2% confirmed) and *K*. *pneumoniae* (5.4% confirmed). For *Enterobacter* species with cefepime MIC > 1 mg/L, 22/42 *E. cloacae* (52%, 6.7% overall) and 2/4 *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), 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, 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.* Three hundred and forty-nine of 408 (85.5%; range 68.3%, - 93.8%) confirmed ESBLs had CTX-M types; CTX-M group 1 (n=204), CTX-M group 9 (n=142), CTX-M group 1 plus CTX-M group 9 (n=3). Among *K. pneumoniae* with confirmed ESBLs, 44/53 (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* (103/615, 16.7% vs 319/3138, 10.2%, p<0.01) and *K. pneumoniae* (32/275, 11.6% vs 40/657, 6.1%, p=<0.01) bacteraemia. No significant difference was noted among *E. cloacae* for healthcare versus community-onset.

8.1.2. Plasmid-borne AmpC β-lactamases

Plasmid-borne AmpC ß-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 into more common pathogens. There are currently six separate classes. Like ESBLs these enzymes confer resistance to the important third-generation cephalosporins such as ceftriaxone and ceftazidime. Routine phenotypic detection methods have not yet been effectively 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 *K. pneumoniae* that were available for molecular confirmation were confirmed to contain plasmid-borne AmpC (Table 28). bla_{CMY} 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 = 16 mg/L (intermediate) also contained bla_{CMY}.

Table 28 Presumptive plasmid-borne AmpC β-lactamase production

Species	ACT	NSW	NT	QLD	SA	TAS	VIC	WA	Australia
Escherichia coli	149	1113	138	691	454	79	729	653	4006
Cefoxitin ≥ 32 mg/L	2 (1.3%)	52 (4.7%)	4 (2.9%)	18 (2.6%)	12 (2.6%)	2 (2.5%)	26 (3.6%)	18 (2.8%)	134 (3.3%)
Confirmed (no. received)	0/2	18/49	2/4	10/17	3/12	0/2	6/26	8/17	47/129
bla_{CMY}	0	10	2	9	3	0	4	4	32
bla_{DHA}	0	8	0	1	0	0	2	4	15
Klebsiella pneumoniae	35	237	47	189	87	18	177	187	977
Cefoxitin ≥ 32 mg/L	2 (5.7%)	21 (8.9%)	1 (2.1%)	6 (3.2%)	2 (2.3%)	0	7 (4.0%)	8 (4.3%)	47 (4.8%)
Confirmed (no. received)	0/2	5/17	0/1	0/6	0/2	- *	1/7	0/8	6/43
bla_{DHA}	0	4	0	0	0	-	1	0	5
bla_{CMY}	0	1	0	0	0	-	0	0	1
Klebsiella oxytoca	13	76	4	45	13	8	49	30	238
Cefoxitin ≥ 32 mg/L	0 (0.0%)	4 (5.3%)	0 (0.0%)	1 (2.2%)	1 (7.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	6 (2.5%)
Confirmed (no. received)	-	0/4	-	0/1	0/1	-	-	-	0/6

* no isolates

8.1.3. Carbapenemases

Twenty-two (0.30%) isolates from 20 patients were found to harbour a carbapenemase gene (Table 29). bla_{IMP-4} was detected in 14 strains (*E. cloacae* (8, from 6 patients), *C. freundii* (2), *K. pneumoniae* (1), *K. oxytoca* (1), *R. ornithinolytica* (1), *S. marcescens* (1); bla_{OXA-48} was detected in four *K. pneumoniae* isolates (from two patients); bla_{KPC-2} was detected in one *K. pneumoniae*; bla_{GES-5} was detected in one *P. aeruginosa*; $bla_{NDM + OXA-48}$ in one *K. pneumoniae* and $bla_{IMP-4 + VIM-2}$ in one *P. aeruginosa*. Thirteen of 22 isolates with confirmed metallo-β-lactamases also contained plasmid-mediated quinolone resistance genes (*aac(6')Ib-cr* alone or with *qnrA* or *qnrB*).

Three *E. cloacae* demonstrated carbapenemase activity by the carbapenem inactivation method (CIM), but were negative for IMP, VIM, KPC, NDM, OXA-48-like, SIM, GIM, SPM, BIC, DIM, AIM, 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*$_{FRI-1}$.[22] It is possible that they contain a novel enzyme.

Overall prevalence of carbapenemase genes among *Enterobacteriaceae* was 0.30% (20/6567); and for *P. aeruginosa,* 0.30% (2/660). No carbapenemase genes were detected among 105 *Acinetobacter* species.

Table 29 Carbapenemases and associated resistance genes

Gene	State	Species	Meropenem MIC (mg/L)	ESBL Types [a]	PMQR [b]	16S rRNA methylases
bla$_{IMP-4}$ (n=14)	ACT	*K. pneumoniae* (n=1)	≥16	TEM, SHV	- c	-
	NSW	*E. cloacae* (n=1) d	≥16	TEM, SHV	aac(6')Ib-cr, qnrB	-
		E. cloacae (n=1) d	≥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	-
bla$_{IMP-4 + VIM-2}$	NSW	*P. aeruginosa* (n=1)	≥16	-	-	-
bla$_{OXA-48}$ (n=4)	QLD	*K. pneumoniae* (n=2) e	1	SHV	-	-
	VIC	*K. pneumoniae* (n=1)	1	SHV	qnrB	-
		K. pneumoniae (n=1)	0.5	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	-	-	-

[a] TEM types, SHV types, CTX-M types, pAmpC

[b] *aac(6')Ib-cr*, Qnr, efflux (*qepA*, *opxAB*)

[c] not detected

[d] *bla*$_{IMP-4}$ from same patient

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

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*, q*nrC*, *qnrD*), *aac(6')-Ib-cr*, encoding for a variant aminoglycoside acetyltransferase enzyme; or genes encoding for efflux pumps (*qepA*, *oqxAB*). Twenty-six percent of *E. coli*, 76% of *K. pneumoniae,* and 83% of *E. cloacae* with ciprofloxacin MIC > 0.25 mg/L, were confirmed to contain PMQRs (Table 30).

Table 30 Plasmid-mediated quinolone resistance

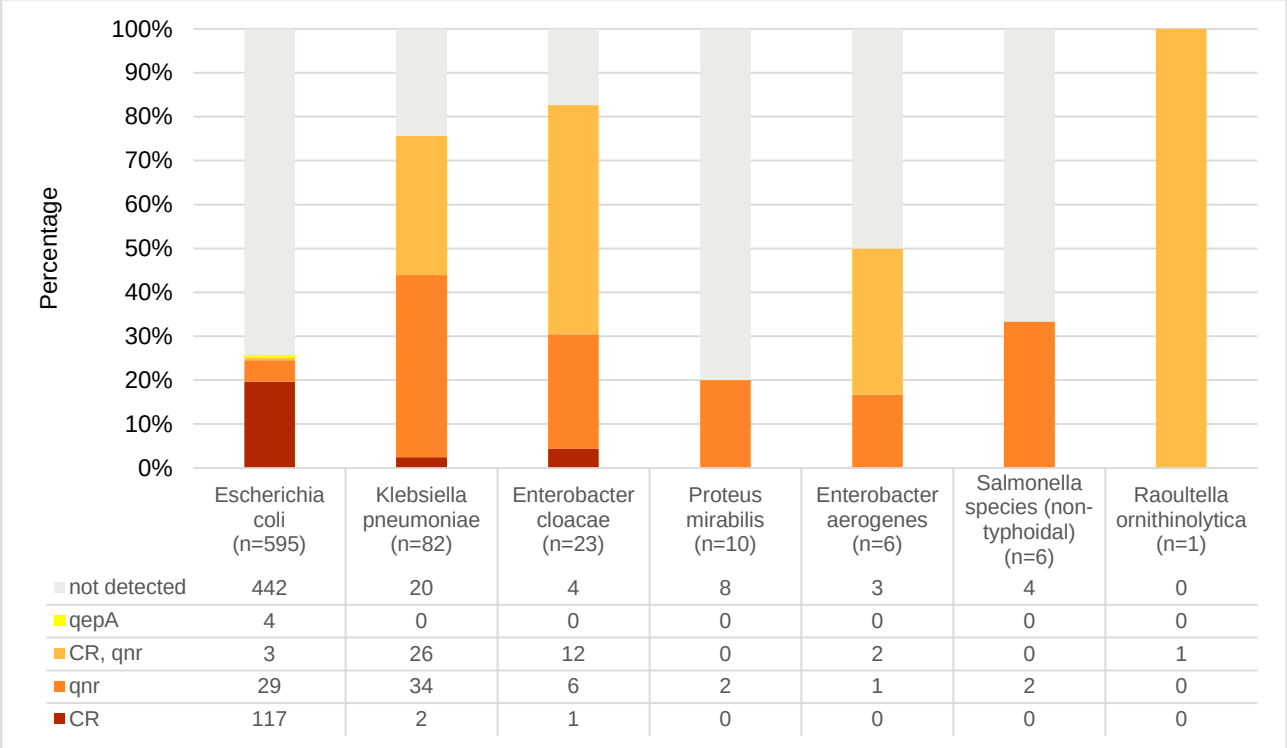
Species	ACT	NSW	NT	QLD	SA	TAS	VIC	WA	Australia
Escherichia coli	20	214	15	72	51	7	119	132	630
Ciprofloxacin > 0.25 mg/L*	13.4%	19.3%	10.9%	10.4%	11.2%	8.9%	16.4%	20.2%	15.8%
Confirmed (no. received)	5/20	48/189	4/14	14/72	10/49	0/7	41/117	31/127	153/595 [25.7%]
aac(6')-Ib-cr	2	36	4	10	9	0	33	23	117
qnrS	2	8	0	2	1	0	5	6	24
qnrB	0	3	0	1	0	0	0	1	5
aac(6')-Ib-cr + qnrB	0	0	0	1	0	0	2	0	3
qepA	1	1	0	0	0	0	1	1	4
Klebsiella pneumoniae	2	24	3	14	5	1	24	16	89
Ciprofloxacin > 0.25 mg/L	5.7%	10.2%	6.4%	7.4%	5.9%	5.6%	13.6%	8.6%	9.1%
Confirmed (no. received)	0/2	18/21	2/3	11/13	2/4	1/1	20/23	8/15	62/82 [75.6%]
aac(6')-Ib-cr	0	0	0	0	1	0	1	0	2
qnrB	0	7	1	3	0	0	8	4	23
qnrS	0	3	0	2	0	0	0	2	7
qnrA	0	1	0	2	0	0	1	0	4
aac(6')-Ib-cr + qnrB	0	7	1	4	1	1	10	2	26
Enterobacter cloacae	1	10	0	4	0	0	7	2	24
Ciprofloxacin > 0.25 mg/L	10.0%	11.8%	- †	6.2%	-	-	8.8%	4.0%	7.4%
Confirmed (no. received)	1/1	7/9	-	4/4	-	-	7/7	0/2	19/23 [82.6%]
aac(6')-Ib-cr	0	0	-	0	-	-	1	0	1
qnrA	0	0	-	0	-	-	2	0	2
qnrB	0	0	-	1	-	-	1	0	2
qnrS	1	1	-	0	-	-	0	0	2
aac(6')-Ib-cr + qnrA	0	4	-	0	-	-	3	0	7
aac(6')-Ib-cr + qnrB	0	2	-	3	-	-	0	0	5

* Concentration used to select strains for molecular testing

† no isolates

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

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



	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	442	20	4	8	3	4	0
qepA	4	0	0	0	0	0	0
CR, qnr	3	26	12	0	2	0	1
qnr	29	34	6	2	1	2	0
CR	117	2	1	0	0	0	0

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

- = no PMQR detected; resistance likely due to mutations in DNA gyrase and topoisomerase IV

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. ST131 isolates are commonly reported to produce ESBLs, such as CTX-M-15, and almost all ST-131 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 31). Sixty-six percent (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), and only 5.6% (9/160) of ciprofloxacin susceptible ESBL phenotypes. Ninety-five percent (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.[23, 24] The *H30*-Rx subclone of ST131 often carried $bla_{CTX\text{-}M\text{-}15}$ and *aac(6')-Ib-cr.* As expected, > 98% of *E. coli* isolates received that were associated with the O25b-ST131 clone belonged to phylogenetic group B2.[25]

Table 31 *Escherichia coli* with ESBL phenotype, by O25b-ST131 clone and ciprofloxacin resistance

		CTX-M-types		Other ESBL types	Ciprofloxacin MIC	
Clone /subclone	Total	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**

8.2. Molecular epidemiology of *Enterococcus faecium*

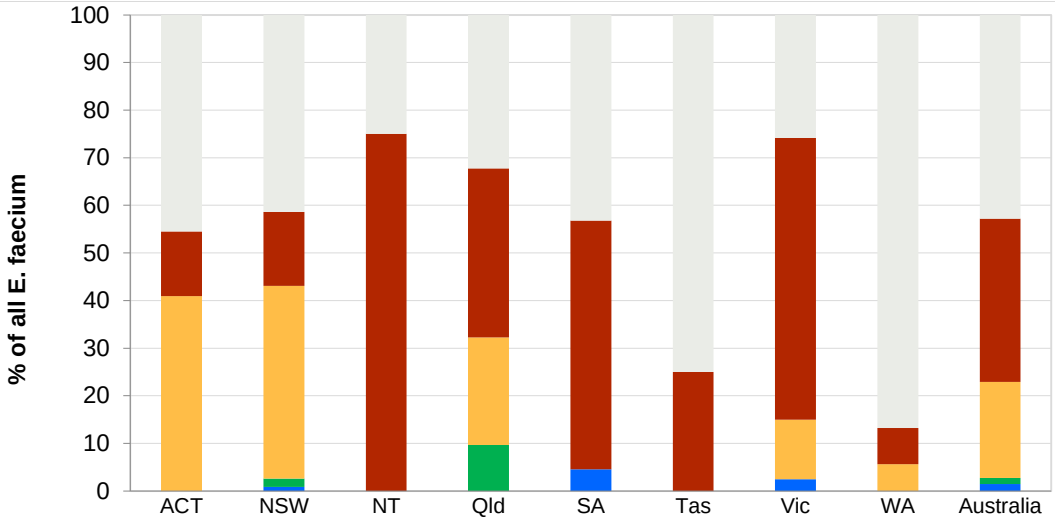
8.2.1. van *Genes*

vanA and *vanB* PCR results 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*; *vanA* in 81 (20.5%), *vanB* in 138 (34.8%), and *vanA* and *vanB* in 5 (1.3%) isolates (Figure 15).

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

van genes were detected in 25 vancomycin-susceptible *E. faecium*; 8 with *vanA*, and 17with *vanB*, in all 25 of 197 isolates (12.7%). All of these strains had vancomycin MIC ≤ 1 mg/L.

Figure 15 *Enterococcus faecium* by vancomycin genotype and state and territory



	ACT (n=22)	NSW (n=116)	NT (n=8)	Qld (n=31)	SA (n=44)	Tas (n=8)	Vic (n=120)	WA (n=53)	Australia (n=402)
not vanA or vanB (n = 172)	45.5	41.4	25.0	32.3	43.2	75.0	25.8	86.8	42.8
vanB (n = 138)	13.6	15.5	75.0	35.5	52.3	25.0	59.2	7.5	34.3
vanA (n = 81)	40.9	40.5	0.0	22.6	0.0	0.0	12.5	5.7	20.1
vanA and vanB (n=5)	0.0	1.7	0.0	9.7	0.0	0.0	0.0	0.0	1.2
Not determined (n = 6)	0.0	0.9	0.0	0.0	4.5	0.0	2.5	0.0	1.5

8.2.2. Multilocus Sequence Type (MLST)

Of the 402 *E. faecium* isolates reported, 391 (97.3%) were available for typing by whole genome sequencing (Table 32). Based on the 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 (46 isolates); ST203 (n=39) and ST78 (n=22). For the 52 non-typable MLST isolates, the *pstS* housekeeping gene was absent, however as 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.

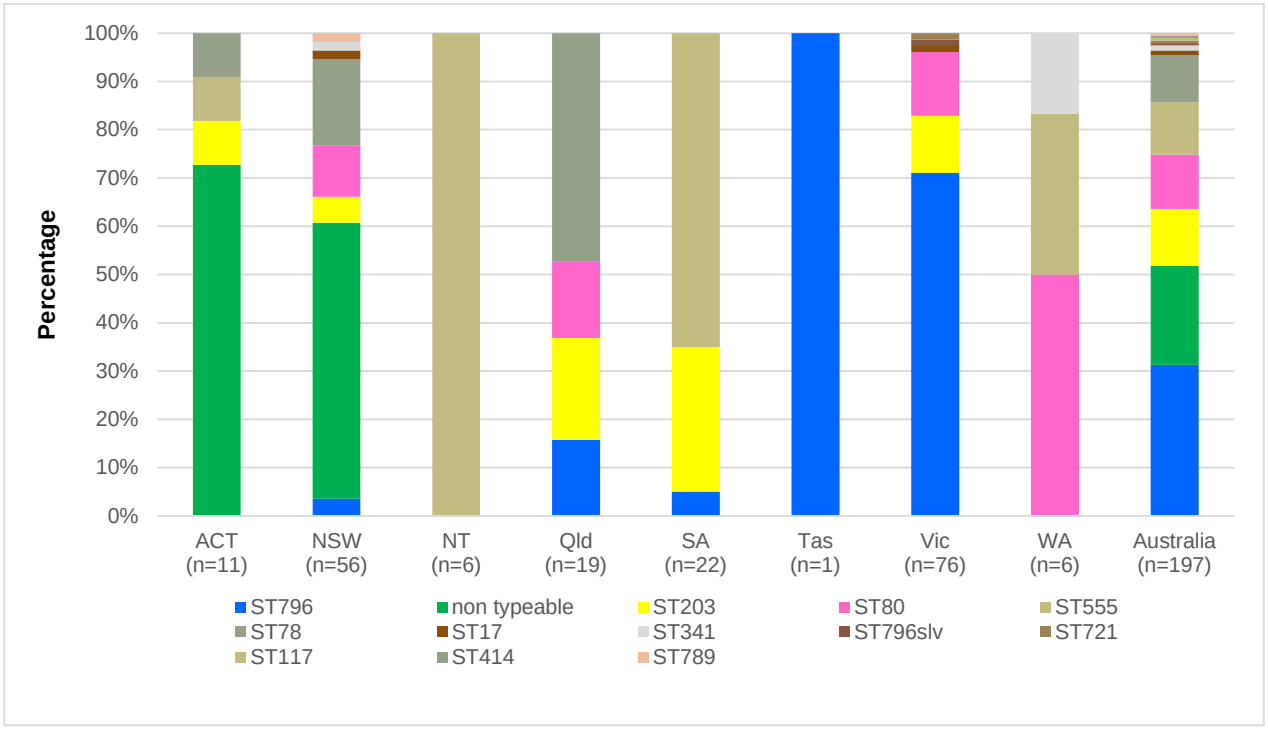
ST796 was predominant in Victoria. ST non-typable was only found in New South Wales and the Australian Capital Territory. ST555 was the predominant ST in Western Australia and South Australia.

Table 32 *Enterococcus faecium* MLST by state and territory

	Number (%) of *Enterococcus faecium* MLST by state and territory								
MLST	ACT	NSW	NT	QLD	SA	Tas	Vic	WA	Australia
796	0	2 (1.8)	0	3 (9.7)	1 (2.4)	1 (12.5)	62 (53)	0	69 (17.8)
non-typable (*pstS* gene absent)	9 (40.9)	43 (39.4)	0	0	0	0	0	0	52 (13.4)
555	0	1 (0.9)	6 (75.0)		16 (39.0)	1 (12.5)	3 (2.6)	21 (40.4)	48 (12.4)
80	6 (27.3)	15 (13.8)	1 (12.5)	3 (9.7)	1 (2.4)		14 (12)	6 (11.5)	46 (11.9)
203	4 (18.2)	6 (5.5)	0	7 (22.6)	7 (17.1)	2 (25)	10 (8.5)	3 (5.8)	39 (10.1)
78	0	12 (11.0)	0	9 (29.0)	0	0		1 (1.9)	22 (5.7)
17	0	7 (6.4)	0	1 (3.2)	0	0	2 (1.7)	9 (17.3)	19 (4.9)
262	0	0	0	0	11 (26.8)	0	1 (0.9)	0	12 (3.1)
117	1 (4.5)	5 (4.6)	0	2 (6.5)	0	0	2 (1.7)	0	10 (2.6)
Other types	2 (9.1)	18 (16.5)	1 (12.5)	6 (19.4)	5 (12.2)	4 (50.0)	23 (19.7)	12 (23.1)	71 (18.3)
Total	***22***	***109***	***8***	***31***	***41***	***8***	***117***	***52***	***388***

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

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



8.2.3. MLST and van genes

vanA 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. *vanB* was detected in 13 STs: ST796 (n = 68), ST555 (n = 23), ST203 (n = 18), ST78 (n = 15), ST17 and ST341 (n = 2 each), ST117, ST80, ST192, ST789, ST414, ST721 and ST796slv (n = 1 each) (Table 33).

Table 33 *Enterococcus faecium* MLST harbouring *vanA* and/or *vanB* genes

MLST	*vanA*	*vanB*	*vanA* and *vanB*	*vanA* or *vanB* not detected	Total
796	0 *	68 (98.6) †	1 (1.4)		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**

* No isolates

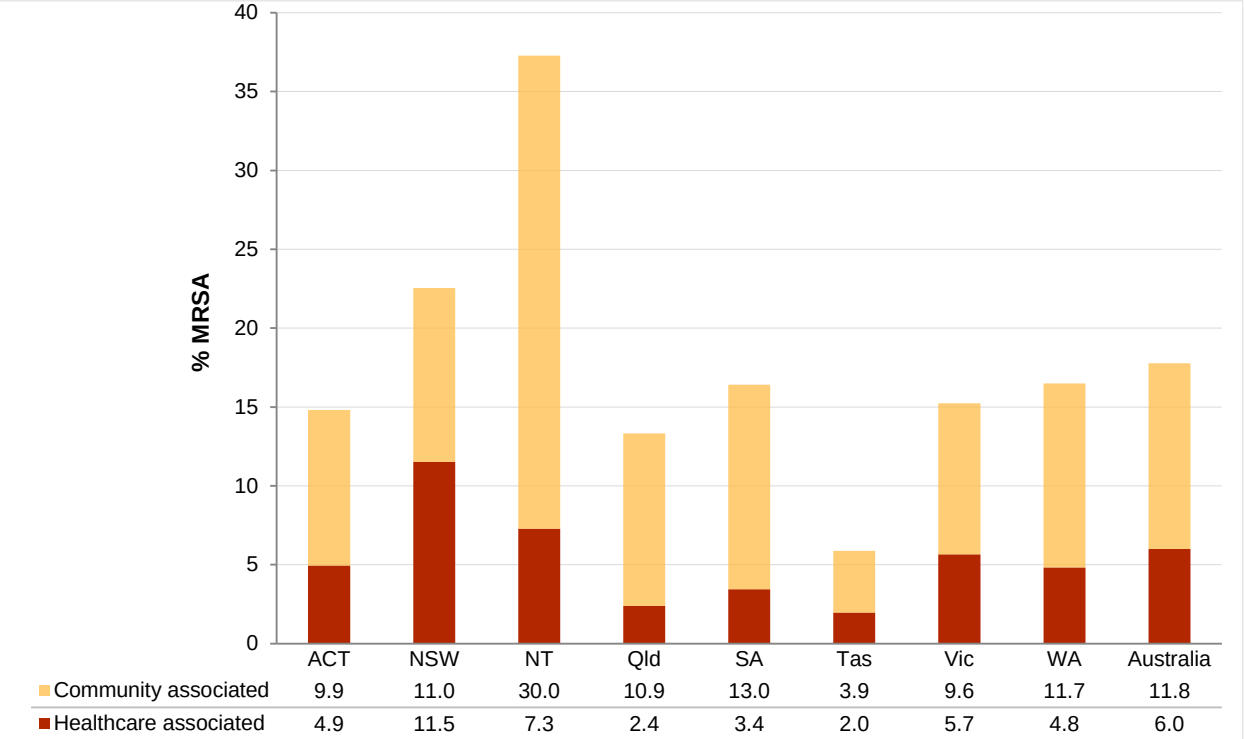
† Percentage of total with *van* genes

‡ insufficient numbers (<10) to calculate

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 (WGS). There were significant differences among the states and territories in the percentage and types of MRSA clones. Overall prevalence ranged from 5.9% in Tasmania to 38.2% in the Northern Territory (Figure 17).

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



	ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Community associated	9.9	11.0	30.0	10.9	13.0	3.9	9.6	11.7	11.8
Healthcare associated	4.9	11.5	7.3	2.4	3.4	2.0	5.7	4.8	6.0

ACT = Australian Capital Territory; MRSA = methicillin-resistant *Staphylococcus aureus*; NSW = New South Wales; NT = Northern Territory; Qld = Queensland; SA = South Australia; Tas = Tasmania; Vic = Victoria; WA = Western Australia

8.3.1. Healthcare-associated MRSA

Based on the multilocus sequence type (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 34).

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 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 Australian Capital Territory, Tasmania and Western Australia. The single isolates of ST36-II and ST225-II were identified in Western Australia (Table 35).

Table 34 Number and proportion of healthcare-associated MRSA by clone, place of onset and Panton-Valentine leucocidin (PVL) carriage

Clone	Clonal Complex	Total (%) [b]	Onset (%) [a]		PVL positive (%)
			Community	Hospital	
ST22-IV (EMRSA-15) [c]	22	108 (25.4)	74 (68.5)	34 (31.5)	2 (1.9)
ST239-III (Aus2/3 EMRSA) [d]	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)**

[a] Percentage of the clone; [b] Percentage of all MRSA; [c] Includes two isolates identified as ST22slv-IV (MLST allele submitted to MLST database curator); [d] Includes four isolates identified as ST239slv

Table 35 Healthcare-associated MRSA clones by State and Territory

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

8.3.2. Community-associated MRSA

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

The most frequently isolated CA-MRSA clone, ST93-IV (Qld CA-MRSA), was isolated in all states except Tasmania (Table 37).

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

Table 36 Number and proportion of community-associated MRSA by clone, place of onset and Panton-Valentine leucocidin carriage

Clone	Clonal Complex	Total (%) [b]	Onset (%) [a]		PVL positive (%)
			Community	Hospital	
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)**

[a] Percentage of the strain; [b] Percentage of all MRSA

Table 37 Number and proportion of the major community-associated MRSA clones (> 10 isolates) by region and Panton-Valentine leucocidin carriage

Clone	ACT	NSW	NT	QLD	SA	Tas	Vic	WA	AUS
ST93-IV (Qld CA-MRSA)	1 (12.5)	11 (16.9)	22 (66.7)	18 (32.7)	12 (35.3)	0	12 (30.8)	13 (28.3)	89 (31.6)
PVL positive	1	4	21	13	12	0	9	13	73
PVL negative	0	7	1	5	0	0	3	0	16
ST45-V (WA84 MRSA)	2 (25.0)	31 (47.0)	0	0	1 (2.9)	0	7 (17.9)	0	41 (14.5)
PVL positive	0	0	0	0	0	0	0	0	0
PVL negative	2	31	0	0	1	0	7	0	41
ST5-IV	3 (37.5)	3 (4.6)	3 (9.1)	9 (16.4)	8 (23.5)	0	1 (2.6)	7 (15.2)	34 (12.1)
PVL positive	2	1	2	1	4	0	1	7	18
PVL negative	1	2	1	8	4	0	0	0	16
ST1-IV (WA1 MRSA)	0	10 (15.4)	1 (3.0)	4 (7.3)	4 (11.8)	1 (50.0)	3 (7.7)	7 (15.2)	30 (10.6)
PVL positive	0	0	0	1	0	0	0	0	1
PVL negative	0	10	1	3	4	1	3	7	29
ST30-IV (SWP MRSA)	0	1 (1.5)	1 (3.0)	10 (18.2)	1 (2.9)	0	3 (7.7)	1 (2.2)	17 (6.0)
PVL positive	0	1	1	8	1	0	3	0	15
PVL negative	0	0	0	2	0	0	0	0	2
ST78-IV (WA2 MRSA)	1 (12.5)	2 (3.1)	0	2 (3.6)	1 (2.9)	1 (50.0)	0	5 (10.9)	12 (4.3)
PVL positive	0	1	0	0	0	0	0	0	1
PVL negative	1	1	0	2	1	1	0	5	11

Clone	ACT	NSW	NT	QLD	SA	Tas	Vic	WA	AUS
Other clones (n=30)	1 (12.5)	7 (10.8)	6 (18.2)	12 (21.8)	7 (20.6)	0	13 (33.3)	13 (28.3)	59 (20.9)
PVL positive	0	0	0	3	2	0	2	2	9
PVL negative	1	7	6	9	5	0	11	11	50
Total	**8**	**65**	**33**	**55**	**34**	**2**	**39**	**46**	**282**
PVL positive	3	7	24	26	19	0	15	23	117
PVL negative	5	58	9	29	15	2	24	23	165

9. Summary

The key points for each of the surveys for 2015 are:

9.1. Gram-negative species

1. A total of 7,330 episodes of gram-negative bacteraemia were reported. Enterobacteriaceae accounted for 89.6%, followed by *P. 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
2. 83.6% of *E. coli* bacteraemia was community-onset
3. The most frequent clinical manifestation was urinary tract infection.
4. The overall 30-day mortality was 14.1% (10.7% in *E. coli*, 18.4% in *P. aeruginosa*).
5. 47.4% of patients with bacteraemia caused by Enterobacteriaceae had a length of stay post bacteraemia less than 7 days. However, 16.3% of patients with *P. aeruginosa* bacteraemia had a length of stay > 30 days
6. ESBL phenotypes were found in 11.5% of *E. coli* and 7.7% *K. pneumoniae*. ESBL phenotypes were significantly more likely to be found among hospital- than community-onset episodes
7. 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

9.2. *Enterococcus* species

1. A total of 1,014 episodes of enterococcal bacteraemia were reported. The majority (95.3%) of enterococcal bacteraemic episodes were caused by *E. faecalis* or *E. faecium*.
2. The overall 30-day mortality was 20.2% (26.1% in E. *faecium,* 15.8% in *E. faecalis*).
3. The most frequent clinical manifestation for *E. faecalis* was urinary tract infection, and for *E. faecium*, biliary tract infection.
4. 21.1% of patients had a length of stay post enterococcal bacteraemia greater than 30 days
5. 50.1% of blood stream infections caused by *E. faecium* in Australia were phenotypically vancomycin-resistant; however, 54.2% of *E. faecium* harboured *vanA* or *vanB* genes.
6. There were 56 *E. faecium* sequence types (ST) of which ST796, ST non-typable, ST555, ST80, ST203 and ST78 were the six most frequently identified.
7. *vanA* genes were detected in five STs, and *vanB* genes in 13 STs

9.3. *Staphylococcus aureus*

1. A total of 2,398 SAB episodes were reported, of which 18.2% were methicillin-resistant.
2. 78% of SAB were community-onset.
3. There was no significant difference in mortality between community and hospital onset SAB
4. The overall thirty-day mortality was 15.9% (18.9% in MRSA and 15.2% in MSSA).
5. There was no significant difference in mortality between MRSA and MSSA.
6. Skin and soft tissue infections were the most common principle clinical manifestation.
7. 27.6% of patients had a length of stay greater than 30 days.
8. Four healthcare associated clones were identified, 1.4% of isolates harboured PVL-associated genes.
9. The dominant healthcare associated clone was ST22-IV (EMRSA-15).
10. Thirty-eight community associated clones were identified, 41.1% of isolates harboured PVL-associated genes.

11. The dominant community-associated clone was ST93-IV (Queensland clone)

10. Limitations of the Study

Although this study is comprehensive in its coverage of Australia, and the methodology follows international standards, there are a number of limitations to the data and its interpretation. These are:

- The data are not denominator controlled. 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 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, as it is not known what proportion of the population is served by these laboratories. Further, it is likely that the proportion of the population served differs across the jurisdictional groupings used in this report.
- Due to the formulation of amoxicillin-clavulanate in both the Vitex and Phoenix cards used, interpretation using EUCAST guidelines for this agent was not possible.
- Concentration range of some antimicrobial agents in both the Vitek and Phoenix cards limit the ability to accurately detect susceptibility for some antimicrobial-organism species.

11. Discussion and Conclusions

AGAR is core component of the AURA program. Because it is targeted surveillance, focussing on selected pathogens and collecting demographic, treatment and outcome data in addition to resistance rates, it allows healthcare professionals to make informed clinical decisions and to improve patient care. AGAR surveys have been conducted regularly since 1985. Since 2013, they have focussed on bacteraemia become aligned with The European surveillance (EARS-Net) which enabling benchmarking and better predictions of future trends.

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

Because of the conservative approach to quinolone use taken in community and hospital healthcare in Australia ciprofloxacin resistance in *E. coli* particularly is important. Fluoroquinolones are relied upon as 'rearguard' oral antibiotics particularly for deep-seated gram-negative infections. There is a community perception still that resistance to this class in Australia is uncommon is but this is not supported by the current AGAR data. In this context, Australia has gone over a decade from less than 1% resistance[26] to rates that are now no longer that different from some (Northern) European countries, at 12.6% overall and at 11.6% in community onset *E. coli* bacteraemias (which make up 83% 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, as described in AURA 2016[27] is driving this increase.

Fluoroquinolone resistance in *E. coli* can also be linked to the emergence of a major clone. ST131 is an international clone associated with 3rd 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 with rapid international, and now Australian emergence of clones like ST131. This shows how quickly resistance 'successes' can be undermined, but again demonstrates the value of regular surveillance in picking up rapid changes in resistance

So far carbapenemase-producing Enterobacteriaceae (CPE) remains an uncommon form of resistance. (<0.1% in *E. coli*, 0.3% in *K. pneumoniae*). Examining previous AGAR and current surveys, a majority of CREs are endemic origin (IMP).[26] The remainder are believed to be introductions of individual CPEs into individual hospitals by patients who have acquired their strains overseas but with the potential for secondary local transmission such as that which occurred recently in Victoria with KPC-producing *K. pneumoniae*.[28] The importance of infection control in limiting the transmission of CPE cannot be underestimated.[29]

ESBL phenotypes were found in 11.5% of *E. coli* and 7.7% *K. pneumoniae*. This is a continuing trend of ESBLs especially in *E.coli*, the commonest organism nationally causing bacteraemia. When ESBLs first arose they were more common in hospital-onset infections in *K. pneumoniae* (TEM, SHV) and as a result there has been a perception ever since that ESBLs are a hospital problem. This is no longer the case with 84% of *E. coli* bacteraemia being community-onset, (85.5%). The 2015 findings show that that standard therapy with 3rd generation cephalosporins may be ineffective in 11% of cases.

Although the overall rates of MRSA do not appear to be increasing (18.2%) there is an increasing rate of community-onset *S. aureus* bacteraemias that are methicillin-resistant. 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 (eg ST22) were more frequently found in community onset, this may reflect either prior hospital exposure or LTCF facility onset as the AGAR data is not able to sufficiently differentiate 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".[30]

The emergence of *E. faecium* in enterococcal bacteraemia is a worldwide phenomenon which remains unexplained, but 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 cannot be used because resistance is so high and vancomycin has had to be used for many years. Furthermore, there is a difference in the 30-day all-cause mortality between *E. faecium* (26.9%) and *E. faecalis* (15.7%) which may be consequence of underlying patient co-morbidities and/or limited therapeutic choices. Notably 54.2% of *E. faecium* harboured *vanA* or *vanB* genes in 2015. Thus, the mainstay of therapy until recently, vancomycin, cannot be used, and agents with uncertain efficacy must be used. It is striking is that in 2015 36% of VRE *E. faecium* bacteraemias nationally were caused by strains harbouring *vanA*. This type of vancomycin resistance has emerged very rapidly in the past 5 years, and particularly in NSW where this is now the dominant type. For nearly two decades, and unlike in most other countries where VRE have become a problem, vancomycin-resistant enterococci in Australia were 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 co-morbidities.

Another notable feature of the AGAR findings is the heavy dependence on broad-spectrum beta-lactam agents, in the main ceftriaxone and piperacillin-tazobactam in Gram negative sepsis. These were the dominant agents of choice for definitive treatment across the country.

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

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14. Appendices

APPENDIX A. **Study Design**

APPENDIX B. **Methods**

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APPENDIX E. **Summary reports**

The Australian Group on Antimicrobial Resistance

Sepsis Outcome Programs

2015 Report - Appendices

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On behalf of the Australian Group on Antimicrobial Resistance (AGAR)

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APPENDIX A. Study Design

Thirty-three hospitals from each state and mainland territories of Australia participated in the 2015 survey. The 29 AGAR laboratories collected either all or up to 200 isolates for GNSOP, and all isolates for ASSOP and AESOP, from different patient episodes of bacteraemia. In patients with more than one isolate, a new episode was defined as a new positive blood culture more than two weeks after the initial positive culture.

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

All laboratories obtained basic laboratory information, plus the following demographic information for each patient episode. At *Bronze* level; date of collection, date of birth, gender, postcode, admission date. Enrolment at *Silver* level participating laboratories provided discharge date, device related infection, principal clinical manifestation, ICU admission, outcome at 30 days, and date of death. Additional provision of principal antimicrobial treatment was obtained with *Gold* level enrolment.

Table A 1 Level of participation, gram-negative * bacteraemia, 2015

State	Number of Hospitals	Level of Participation		
		Bronze	*Silver*	*Gold*
Australian Capital Territory	1	1		
New South Wales	7	1		6
Northern Territory	2	1		1
Queensland	6	1	1	4
South Australia	3	2		1
Tasmania	1			1
Victoria	5	1		4
Western Australia	8	3		3
Total	**33**	**10**	**1**	**20**

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

Table A 2 Level of participation, *Staphylococcus aureus* bacteraemia, 2015

State/territory	Number of Hospitals	Level of Participation		
		Bronze	*Silver*	*Gold*
Australian Capital Territory	1			1
New South Wales	7			7
Northern Territory	2	1		1
Queensland	6	1	1	4
South Australia	3			3
Tasmania	1			1
Victoria	5	1		4
Western Australia	8	5		3
Total	**33**	**8**	**1**	**24**

Table A 3 Level of participation, enterococcal bacteraemia, 2015

State	Number of Hospitals	Level of Participation		
		Bronze	*Silver*	*Gold*
Australian Capital Territory	1			1
New South Wales	7			7
Northern Territory	2	1		1
Queensland	6		1	5
South Australia	3			3
Tasmania	1			1
Victoria	5	1		4
Western Australia	8	5		3
Total	**33**	**7**	**1**	**25**

APPENDIX B. Methods

B. 1 Species Identification

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

B. 2 Susceptibility Testing

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

The CLSI M100-A26[1] and EUCAST v6.0[2] breakpoints from January 2016 have been employed in the analysis. For analysis of cefazolin, breakpoints of ≤4 for susceptible, ≥8 for resistant were applied due to the restricted minimum inhibitory concentration (MIC) range available on the commercial cards, recognising that the January 2016 breakpoint is actually susceptible ≤2 mg/L.

B. 3 Antimicrobials Tested

Table B 1 Antimicrobials available on susceptibility testing cards and interpretative guidelines for CLSI and EUCAST

	Breakpoints (mg/L)						
	CLSI M100 [a]				EUCAST v6.0 [b]		
Antimicrobial Agent	S	SDD	I	R	S	I	R
Benzylpenicillin							
Enterococcus spp.	≤ 8		. [c]	≥ 16	— [d]	—	—
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-Clavulanic Acid							
Enterobacteriaceae	≤ 8/4		16/8	≥ 32/16	≤ 8 [e]	.	≥ 16
Enterococcus spp.	—		—	—	≤ 4	8	≥ 16
Ampicillin							
Enterobacteriaceae	≤ 8		16	≥ 32	≤ 8	—	≥ 16
Enterococcus spp.	≤ 8		.	≥ 16	≤ 4	8	≥ 16
Aztreonam *(Phoenix card only)*							
Enterobacteriaceae	≤ 4		8	≥ 16	≤ 1	2 – 4	≥ 8
Pseudomonas spp.	≤ 8		16	≥ 32	≤ 1	2 – 16	≥ 32
Cefazolin (Australian) [f]	≤ 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	—	—	—
Cephalexin	—		—	—	≤ 16	.	≥ 32

Antimicrobial Agent	Breakpoints (mg/L)						
	CLSI M100 [a]				EUCAST v6.0 [b]		
	S	SDD	I	R	S	I	R
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. [g]	≤ 0.06		0.12 - 0.5	≥ 1	≤ 0.06	.	≥ 0.12
Enterococcus spp. [h]	≤ 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
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

Antimicrobial Agent	Breakpoints (mg/L)						
	CLSI M100 [a]				EUCAST v6.0 [b]		
	S	SDD	I	R	S	I	R
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
Nitrofurantoin							
Enterobacteriaceae	≤ 32		64	≥ 128	≤ 64 [i]	.	≥ 128
Enterococcus spp.	≤ 32		64	≥ 128	≤ 64 [j]	.	≥ 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 [k]	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-Clavulanic Acid							
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
Trimethoprim							
Enterobacteriaceae	≤ 8		.	≥ 16	≤ 2	4	≥ 8
Enterococcus spp.	—		—	—	≤ 0.03	0.06 - 1	≥ 2
Staphylococcus aureus	≤ 8		.	≥ 16	≤ 2	4	≥ 8

Antimicrobial Agent	Breakpoints (mg/L)						
	CLSI M100 [a]				EUCAST v6.0 [b]		
	S	SDD	I	R	S	I	R
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.	—		—	—	[l] ≤ 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

[a] The breakpoints selected to determine resistance are described in Performance Standards for Antimicrobial Susceptibility Testing: Twenty-fifth Information Supplement, CLSI document M100-S26, January 2016

[b] The European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 6.0, 2016. http://www.eucast.org.

[c] no category defined

[d] no guidelines for indicated species

[e] EUCAST, for susceptibility testing purposes, the concentration of clavulanate is fixed at 2 mg/L, rather than a 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

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

[g] Ciprofloxacin concentration range available on the cards used restricts ability to accurately determine susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species

h Ciprofloxacin concentration range on Phoenix card restricts ability to categorize *Enterococcus* spp.

i Breakpoints apply to *E. coli* only

j Breakpoints apply to *E. faecalis* only

k Rifampicin concentration on cards restricts category interpretation to non-resistant or resistant

l Trimethoprim-sulfamethoxazole concentration on cards restricts category interpretation of non-resistant or resistant

B. 4 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 $bla_{OXA-48-like}$ genes using real-time PCR.[7, 8] Known plasmid mediated quinolone resistance (PMQR) 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 was analysed using the Nullabor platform.[14] The pipeline was used to determine the multilocus sequence type; the SCCmec type, and the presence of the Panton-Valentine-leucocidin associated genes (*S. aureus*); and van genes (*Enterococcus* species).

B. 5 Quality Control

Quality control strains utilised were those recommended by CLSI/EUCAST standards.

B. 6 Data Validation

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

1. Null values in the mandatory fields
2. Missing MIC data
3. Age ≥ 100 or < 0 years of age
4. Date of collection > discharge date
5. Discharge date < date of admission
6. Date of admission < date of birth
7. Date of admission < date of collection + two days

APPENDIX C. Susceptibility to antimicrobial agents

Overall percentages of resistance or non-susceptibility for the most common gram-negative species, *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 C 1 Susceptibility (CLSI and EUCAST) to antimicrobial agents in indicator species of national priority by state and territory

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Benzylpenicillin										
Enterococcus faecalis	n	35	149	10	94	58	0	110	91	547
	% R	2.9 / — [b]	2.0 / —	0.0 / —	2.1 / —	0.0 / —	na [c]	0.9 / —	4.4 / —	2.0 / —
Enterococcus faecium	n	22	115	8	30	44	1	118	53	391
	% R	95.5 / —	87.8 / —	na	83.3 / —	93.2 / —	na	91.5 / —	79.2 / —	88.5 / —
Staphylococcus aureus	n	81	590	110	503	261	51	407	394	2397
	% R	80.2 / 80.2	84.1 / 84.1	90.0 / 90.0	80.1 / 80.1	88.9/ 88.9	86.3 / 86.3	77.9 / 77.9	80.2 / 80.2	82.3 / 82.3
Ampicillin										
Escherichia coli	n	149	1106	137	691	453	79	727	650	3992
	% I	2.7 / —	2.2 / —	2.9 / —	1.6 / —	1.3 / —	2.5 / —	2.9 / —	1.7 / —	2.1 / —
	% R	48.3 / 51.0	55.4/ 57.6	56.9 / 59.9	51.5 / 53.1	44.2 / 45.5	43.0 / 45.6	56.9 / 59.8	54.0 / 55.7	53.1 / 55.1
Enterococcus faecalis	n	35	150	10	95	58	12	110	91	561
	% I	— / 0.0	— / 0.0	— / 0.0	— / 1.1	— / 0.0	— / 0.0	— / 0.0	— / 0.0	— / 0.2
	% R	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Enterococcus faecium	n	22	115	8	30	44	8	120	53	400
	% I	— / 0.0	— / 0.9	na	— / 0.0	— / 0.0	na	— / 1.7	— / 0.0	— / 0.8
	% R	95.5 / 95.5	85.2 / 85.2	na	83.3 / 83.3	93.2 / 93.2	na	88.3 / 88.3	79.2 / 79.2	86.0 / 86.0
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% I	na	0.0 / —	na	0.0 / —	0.0 / —	na	0.0 / —	0.0 / —	0.0 / —
	% R	na	22.7 / 22.7	na	4.5 / 4.5	12.5 / 12.5	na	18.9 / 18.9	30.6 / 30.6	17.1 / 17.1

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% I	na	0.0 / —	0.0 / —	0.0 / —	na	na	0.0 / —	0.0 / —	0.0 / —
	% R	na	5.3 / 5.3	0.0 / 0.0	10.7 / 10.7	na	na	23.8 / 23.8	0.0 / 0.0	8.8 / 8.8
Salmonella species (typhoidal)	n	1	5	0	6	4	0	7	2	25
	% I	na	na	na	na	na	na	na	na	4.0 / —
	% R	na	na	na	na	na	na	na	na	4.0 / 8.0
Amikacin										
Acinetobacter baumannii	n	0	10	5	20	1	2	10	11	59
	% R	na	0.0 / 0.0	na	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Escherichia coli	n	149	1,107	137	691	454	79	727	650	3,994
	% R	0.0 / 0.7	0.1 / 0.1	0.7 / 0.7	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.1 / 0.1	0.2 / 0.2	0.1 / 0.1
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% 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	0.6 / 0.6	0.0 / 0.0	0.1 / 0.1
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% R	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% R	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% R	na	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% R	na	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% R	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Salmonella species (typhoidal)	n	1	5	0	5	4	0	7	2	25
	% R	na	na	na	na	na	na	na	na	0.0 / 0.0
Pseudomonas aeruginosa	n	36	166	19	165	83	4	74	107	654
	% R	0.0 / 0.0	1.8 / 1.8	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	na	0.0 / 2.7	0.0 / 0.0	0.5 / 0.8
Amoxicillin-clavulanate										
Escherichia coli	n	149	1106	137	691	453	79	727	650	3992
	% I	12.8 / - [d]	14.1 / -	10.2 / -	15.2 / -	12.8 / -	10.1 / -	13.6 / -	13.4 / -	13.7 / -
	% R	3.4 / -	9.1 / -	13.1 / -	7.8 / -	6.2 / -	12.7 / -	10.6 / -	8.6 / -	8.7 / -

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% I	2.9 / -	3.8 / -	6.4 / -	4.8 / -	2.4 / -	5.6 / -	6.8 / -	5.3 / -	4.8 / -
	% R	8.6 / -	5.1 / -	4.3 / -	3.7 / -	2.4/ -	5.6 / -	5.6 / -	2.1 / -	4.2 / -
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% I	0.0 / -	3.9 / -	na	2.2 / -	7.7 / -	na	6.1 / -	0.0 / -	4.2 / -
	% R	7.7 / -	10.5 / -	na	6.7 / -	0.0 / -	na	4.1 / -	10.0 / -	7.6 / -
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% I	na	9.1 / -	na	6.8 / -	4.2 / -	na	5.4 / -	19.4 / -	8.6 / -
	% R	na	1.5 / -	na	0.0 / -	0.0 / -	na	5.4 / -	2.8 / -	1.8 / -
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% I	na	0.0 / -	0.0 / -	0.0 / -	na	na	9.5 / -	0.0 / -	1.8 / -
	% R	na	5.3 / -	0.0 / -	0.0 / -	na	na	9.5 / -	0.0 / -	2.6 / -
Salmonella species (typhoidal)	n	1	5	0	6	4	0	7	2	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	149	1107	137	691	453	49	604	574	3764
	% R	18.8 / 18.8	25.1 / 25.1	21.9 / 21.9	20.1 / 20.1	18.1 / 20.1	10.2 / 10.2	24.7 / 24.7	19.0 / 19.0	21.8 / 21.8
Klebsiella pneumoniae	n	35	236	47	189	85	9	150	165	916
	% R	8.6 / 8.6	10.6 / 10.6	17.0 / 17.0	9.0 / 9.0	8.2 / 8.2	na	16.7 / 16.7	8.5 / 8.5	10.9 / 10.9
Klebsiella oxytoca	n	13	76	4	45	13	5	41	23	220
	% R	61.5 / 61.5	63.2 / 63.2	na	62.2 / 62.2	69.2 / 69.2	na	63.4 / 63.4	47.8 / 47.8	62.3 / 62.3
Enterobacter cloacae complex	n	10	85	9	65	13	8	74	48	312
	% R	100 / 100	91.8 / 91.8	na	98.5 / 98.5	100 / 100	na	98.6 / 98.6	100 / 100	96.5 / 96.5
Enterobacter aerogenes	n	4	34	3	26	11	1	20	23	122
	% R	na	91.2 / 91.2	na	80.8 / 80.8	90.9 / 90.9	na	75.0 / 75.0	73.9 / 73.9	83.6 / 83.6
Proteus mirabilis	n	6	66	6	44	24	2	34	27	209
	% R	na	22.7 / 22.7	na	27.3 / 27.3	12.5 / 12.5	na	32.4 / 32.4	44.4 / 44.4	25.4 / 25.4
Salmonella species (non typhoidal)	n	1	19	24	28	9	0	16	9	106
	% R	na	5.3 / 5.3	0.0 / 0.0	0.0 / 0.0	na	na	12.5 / 12.5	na	2.8 / 2.8

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Salmonella species	n	1	5	0	6	4	0	7	2	25
(typhoidal)	% R	na	na	na	na	na	na	na	na	4.0 / 4.0
Cefoxitin										
Escherichia coli	n	149	1107	137	691	454	79	727	650	3994
	% R	1.3 / —	4.7 / —	2.9 / —	2.6 / —	2.6 / —	2.5 / —	3.6 / —	2.8 / —	3.4 / —
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% R	5.7 / —	8.9 / —	2.1 / —	3.2 / —	2.4 / —	0.0 / —	4.0 / —	4.3 / —	4.8 / —
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% R	0.0 / —	5.3 / —	na	2.2 / —	7.7 / —	na	0.0 / —	0.0 / —	2.5 / —
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% R	na	0.0 / —	na	0.0 / —	0.0 / —	na	0.0 / —	2.8 / —	0.5 / —
Salmonella species	n	1	19	24	28	9	2	21	10	114
(non typhoidal)	% R	na	0.0 / —	0.0 / —	0.0 / —	na	na	9.5 / —	0.0 / —	1.8 / —
Salmonella species	n	1	5	0	6	4	0	7	2	25
(typhoidal)	% R	na	na	na	na	na	na	na	na	4.0 / —
Cefepime										
Acinetobacter baumannii	n	0	10	5	20	1	0	10	11	57
	% R	na	0.0 / —	na	5.0 / —	na	na	10.0 / —	0.0 / —	3.5 / —
Escherichia coli	n	149	1107	137	691	454	79	727	650	3994
	% NS [e]	4.7 / 9.4	10.0 / 13.6	2.9 / 8.0	1.6 / 3.9	5.5 / 6.2	0.0 / 0.0	5.4 / 9.8	4.6 / 7.2	5.7 / 8.7
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% NS	0.0 / 2.9	4.2 / 5.5	2.1 / 4.3	1.6 / 2.6	3.5 / 3.5	0.0 / 5.6	3.4 / 9.0	1.1 / 2.7	2.6 / 4.7
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% NS	0.0 / 0.0	2.6 / 2.6	na	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	0.8 / 1.3
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% NS	0.0 / 0.0	9.4 / 12.9	na	4.6 / 13.8	0.0 / 0.0	0.0 / 7.1	10.0 / 18.7	0.0 / 12.0	5.8 / 12.9
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% NS	na	2.9 / 2.9	na	3.8 / 3.8	0.0 / 0.0	na	11.1 / 11.1	0.0 / 0.0	3.8 / 3.8
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% NS	na	0.0 / 0.0	na	2.3 / 2.3	0.0 / 0.0	na	2.7 / 2.7	2.8 / 2.8	1.4 / 1.4
Pseudomonas aeruginosa	n	36	166	19	165	83	4	74	107	654
	% R	5.6 / 16.7	2.4 / 6.6	0.0 / 15.8	1.8 / 5.5	2.4 / 10.8	na	4.1 / 9.5	2.8 / 6.5	2.6 / 8.0

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% NS	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Salmonella species (typhoidal)	n	1	5	0	6	4	0	7	2	25
	% NS	na	na	na	na	na	na	na	na	0.0 / 0.0
Ceftazidime										
Acinetobacter baumannii	n	0	10	5	20	1	0	10	11	57
	% NS	na	10.0 / —	na	25.0 / —	na	na	20.0 / —	0.0 / —	14.0 / —
Escherichia coli	n	149	1,107	137	691	454	79	727	650	3,994
	% NS	5.4 / 9.4	9.9 / 14.5	3.6 / 8.0	3.2 / 5.6	4.4 / 7.0	0.0 / 1.3	6.3 / 11.4	4.8 / 8.6	6.1 / 9.9
Klebsiella pneumoniae	N	35	236	47	189	85	18	177	187	974
	% NS	2.9 / 5.7	6.8 / 8.9	2.1 / 2.1	3.2 / 3.7	2.4 / 4.7	5.6 / 5.6	9.6 / 12.4	2.1 / 4.8	4.9 / 6.9
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% NS	0.0 / 0.0	0.0 / 2.6	na	2.2 / 2.2	15.4 / 15.4	na	0.0 / 0.0	0.0 / 0.0	1.3 / 2.1
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% NS	0.0 / 0.0	23.5 / 23.5	na	23.1 / 24.6	0.0 / 0.0	28.6 / 35.7	27.5 / 31.2	20.0 / 22.0	22.4 / 24.2
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% NS	na	41.2 / 47.1	na	15.4 / 19.2	27.3 / 27.3	na	55.6 / 55.6	32.0 / 32.0	37.4 / 39.7
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% NS	na	0.0 / 0.0	na	2.3 / 2.3	0.0 / 0.0	na	2.7 / 5.4	2.8 / 2.8	1.4 / 1.8
Pseudomonas aeruginosa	n	36	166	19	165	82	4	74	107	653
	% NS/R	19.4 / 19.4	12.0 / 12.0	5.3 / 5.3	7.3 / 7.3	7.3 / 7.3	na	14.9 / 14.9	10.3 / 10.3	10.4 / 10.4
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% NS	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	na	na	9.5 / 9.5	0.0 / 0.0	1.8 / 1.8
Salmonella species (typhoidal)	n	1	4	0	6	4	0	7	2	24
	% NS	na	na	na	na	na	na	na	na	0.0 / 0.0
Ceftriaxone										
Acinetobacter baumannii	n	0	10	5	20	1	0	10	11	57
	% NS	na	70.0 / —	na	85.0 / —	na	na	90.0 / —	45.5 / —	75.4 / —
Escherichia coli	n	149	1,107	137	691	454	79	727	650	3,994
	% NS	10.7 / 10.7	15.3 / 15.3	8.8 / 8.8	6.1 / 6.1	7.5 / 7.5	0.0 / 0.0	12.2 / 12.2	9.4 / 9.4	10.6 / 10.6
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% NS	2.9 / 2.9	6.8 / 6.8	6.4 / 6.4	3.7 / 3.7	3.5 / 3.5	5.6 / 5.6	10.7 / 10.7	3.7 / 3.7	5.9 / 5.9
Klebsiella oxytoca	n	13	76	4	45	13	7	49	30	237

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
	% NS	7.7 / 7.7	10.5 / 10.5	na	6.7 / 6.7	23.1 / 23.1	na	6.1 / 6.1	6.7 / 6.7	8.4 / 8.4
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% NS	10.0 / 10.0	24.7 / 24.7	na	29.2 / 29.2	0.0 / 0.0	28.6 / 28.6	32.5 / 32.5	22.0 / 22.0	25.8 / 25.8
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% NS	na	50.0 / 50.0	na	19.2 / 19.2	36.4 / 36.4	na	55.6 / 55.6	36.0 / 36.0	42.0 / 42.0
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% NS	na	1.5 / 1.5	na	2.3 / 2.3	0.0 / 0.0	na	5.4 / 5.4	2.8 / 2.8	2.3 / 2.3
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% NS	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	na	na	14.3 / 14.3	0.0 / 0.0	2.6 / 2.6
Salmonella species (typhoidal)	n	1	5	0	6	4	0	7	2	25
	% NS	na	na	na	na	na	na	na	na	4.0 / 4.0
Ciprofloxacin										
Acinetobacter baumannii	n	0	10	5	20	1	2	10	11	59
	% NS/R	na	0.0 / 0.0	na	5.0 / 5.0	na	na	10.0 / 10.0	0.0 / 0.0	3.4 / 3.4
Escherichia coli	n	149	1107	137	691	454	79	727	650	3994
	% NS	10.1 / 10.7	16.9 / 17.7	8.8 / 9.5	8.1 / 8.7	8.6 / 9.0	3.8 / 7.6	13.3 / 14.4	14.5 / 16.2	12.6 / 13.6
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% NS	5.7 / 5.7	5.1 / 7.2	2.1 / 4.3	2.6 / 6.3	2.4 / 4.7	5.6 / 5.6	5.6 / 11.9	2.7 / 5.9	3.9 / 7.2
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% NS	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	3.3 / 3.3	0.4 / 0.4
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% NS	0.0 / 0.0	5.9 / 8.2	na	3.1 / 3.1	0.0 / 0.0	0.0 / 0.0	5.0 / 5.0	0.0 / 0.0	3.4 / 4.0
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% NS	na	0.0 / 0.0	na	7.7 / 11.5	0.0 / 0.0	na	11.1 / 11.1	0.0 / 0.0	3.8 / 4.6
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% NS	na	3.0 / 3.0	na	2.3 / 4.5	8.3 / 8.3	na	2.7 / 2.7	5.6 / 5.6	4.1 / 4.5
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% R [f]	na	10.5 / -	0.0 / -	0.0 / -	na	na	0.0 / -	0.0 / -	1.8 / -
Salmonella species (typhoidal)	n	1	5	0	6	4	0	7	2	25
	%R [f]	na	na	na	na	na	na	na	na	56.0 / -
Pseudomonas aeruginosa	n	36	166	19	165	82	4	74	107	653
	% NS	8.3 / 8.6	3.6 / 3.7	5.3 / 5.6	5.5 / 5.6	9.8 / 10.5	-	10.8/ 11.3	5.6 / 5.7	6.3 / 6.5

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% NS/R	8.6 / 8.6	19.7 / 19.7	8.2 / 8.2	4.2 / 4.2	6.9 / 6.9	2.0 / 2.0	12.3 / 12.3	8.1 / 8.1	10.6 / 10.6
methicillin-resistant	n	12	135	42	68	43	3	63	69	435
	% NS/R	50.0 / 50.0	75.6 / 75.6	19.0 / 19.0	19.1 / 19.1	27.9 / 27.9	na	63.5 / 63.5	33.3 / 33.3	47.1 / 47.1
methicillin-susceptible	n	69	455	68	435	219	48	344	325	1963
	% NS/R	1.4 / 1.4	3.1 / 3.1	1.5 / 1.5	1.8 / 1.8	2.7 / 2.7	0.0 / 0.0	2.9 / 2.9	2.8 / 2.8	2.5 / 2.5
Enterococcus faecalis	n	35	149 / 140 [g]	10	83	43 / 35	0	110	91	521 / 504
	% NS/R	14.3 / 14.3	17.4 / 9.3	30.0 / 30.0	9.6 / 9.6	44.2 / 8.6	na	16.4 / 15.5	11.0 / 8.8	17.1 / 11.3
Enterococcus faecium	n	22	144 / 89	8	28	27 / 4	1	120	53	373 / 325
	% NS/R	95.5 / 95.5	92.1 / 83.1	na	85.7 / 82.1	96.3 / na	na	97.5 / 90.0	79.2 / 79.2	92.2 / 85.8
Clindamycin										
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% NS	2.5 / 2.5	5.8 / 6.3	7.3 / 7.3	2.0 / 2.0	2.7 / 3.4	2.0 / 2.0	2.9 / 2.9	1.0 / 1.0	3.3 / 3.5
methicillin-resistant	n	12	135	42	68	43	3	63	69	435
	% NS	8.3 / 8.3	19.3 / 20.7	16.7 / 16.7	13.2 / 13.2	14.0 / 16.3	na	14.3 / 14.3	5.8 / 5.8	14.3 / 14.9
methicillin-susceptible	n	69	455	68	435	219	48	344	325	1963
	% NS	1.4 / 1.4	1.8 / 2.0	1.5 / 1.5	0.2 / 0.2	0.5 / 1.0	2.1 / 2.1	0.9 / 0.9	0.0 / 0.0	0.8 / 0.9
Daptomycin										
Enterococcus faecalis	n	35	145	10	92	57	0	107	90	536
	% NS	0.0 / —	0.0 / —	0.0 / —	1.1 / —	0.0 / —	na	0.0 / —	0.0 / —	0.2 / —
Staphylococcus aureus	n	81	589	110	503	262	51	407	394	2397
	% NS/R	0.0 / 0.0	0.5 / 0.5	0.0 / 0.0	0.2 / 0.2	0.0 / 0.0	0.0 / 0.0	0.2 / 0.2	0.3 / 0.3	0.3 / 0.3
methicillin-resistant	n	12	135	42	68	43	3	63	69	435
	% NS/R	0.0 / 0.0	0.7 / 0.7	0.0 / 0.0	1.5 / 1.5	0.0 / 0.0	na	1.6 / 1.6	1.4 / 1.4	0.9 / 0.9
methicillin-susceptible	n	69	454	68	435	219	48	344	325	1962
	% NS/R	0.0 / 0.0	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	0.1 / 0.1
Erythromycin										
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% NS	11.1 / 9.9	22.9 / 20.5	26.4 / 26.4	13.5 / 9.7	11.8 / 10.7	11.8 / 3.9	15.0 / 12.0	15.0 / 12.7	16.6 / 14.0
methicillin-resistant	n	12	135	42	68	43	3	63	69	435
	% NS	25.0 / 25.0	62.5 / 61.5	31.0 / 31.0	32.4 / 29.4	27.9 / 27.9	na	46.0 / 42.9	34.8 / 34.8	43.5 / 42.1

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
methicillin-susceptible	n	69	455	68	435	219	48	344	325	1963
	% NS	8.7 / 7.2	11.2 / 8.4	23.5 / 23.5	10.6 / 6.7	8.7 / 7.3	8.3 / 2.1	9.3 / 6.4	10.8 / 8.0	10.6 / 7.8
Fusidic acid										
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% R	— / 6.2	— / 2.9	— / 4.5	— / 5.4	— / 1.9	— / 3.9	— / 2.5	— / 2.3	— / 3.3
methicillin-resistant	n	12	135	42	68	43	3	63	69	435
	% R	— / 0.0	— / 4.4	— / 7.1	— / 5.9	— / 9.3	na	— / 3.2	— / 2.9	— / 4.8
methicillin-susceptible	n	69	455	68	435	219	48	344	325	1963
	% R	— / 7.2	— / 2.4	— / 2.9	— / 5.3	— / 0.5	— / 4.2	— / 2.3	— / 2.2	— / 3.0
Gentamicin										
Acinetobacter baumannii	n	0	10	5	20	1	2	10	11	59
	% R	na	0.0 / 0.0	na	5.0 / 5.0	na	na	10.0 / 10.0	0.0 / 0.0	3.4 / 3.4
Escherichia coli	n	149	1,107	137	691	454	79	727	650	3,994
	% R	4.0 / 4.7	9.3 / 9.4	8.8 / 8.8	6.5 / 6.7	7.3 / 7.3	2.5 / 2.5	6.9 / 6.9	9.2 / 9.2	7.8 / 7.9
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% R	2.9 / 2.9	5.5 / 5.9	10.6 / 10.6	3.2 / 3.2	4.7 / 5.9	5.6 / 5.6	3.4 / 4.0	2.7 / 2.7	4.2 / 4.5
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% R	0.0 / 0.0	0.0 / 0.0	na	2.2 / 2.2	0.0 / 0.0	na	0.0 / 2.0	3.3 / 3.3	0.8 / 1.3
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% R	0.0 / 0.0	12.9 / 12.9	na	9.2 / 10.8	0.0 / 0.0	7.1 / 7.1	3.8 / 5.0	0.0 / 0.0	6.7 / 7.4
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% R	na	2.9 / 2.9	na	3.8 / 3.8	0.0 / 0.0	na	7.4 / 7.4	0.0 / 0.0	3.1 / 3.1
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% R	na	1.5 / 3.0	na	0.0 / 2.3	0.0 / 0.0	na	0.0 / 2.7	0.0 / 0.0	0.5 / 1.8
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% R	na	5.3 / 5.3	0.0 / 0.0	0.0 / 0.0	na	na	4.8 / 4.8	0.0 / 0.0	1.8 / 1.8
Salmonella species (typhoidal)	n	1	5	0	5	4	0	7	2	25
	% R	na	na	na	na	na	na	na	na	0.0 / 0.0
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% R	0.0 / 2.5	5.4 / 9.7	7.3 / 7.3	0.8 / 1.4	3.1 / 3.1	0.0 / 0.0	2.0 / 3.2	0.5 / 0.5	2.6 / 4.0
methicillin-resistant	n	12	135	42	68	43	3	63	69	435
	% R	0.0 / 8.3	21.5 / 39.3	16.7 / 16.7	1.5 / 2.9	9.3 / 9.3	na	11.1 / 14.3	2.9 / 2.9	11.5 / 17.9

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
methicillin-susceptible	n	69	455	68	435	219	48	344	325	1963
	% R	0.0 / 1.4	0.7 / 0.9	1.5 / 1.5	0.7 / 1.1	1.8 / 1.8	0.0 / 0.0	0.3 / 1.2	0.0 / 0.0	0.6 / 1.0
Pseudomonas aeruginosa	n	36	166	19	165	83	4	74	107	654
	% R	0.0 / 0.0	4.8 / 5.4	0.0 / 5.3	0.6 / 1.8	2.4 / 2.4	na	4.1 / 6.8	1.9 / 1.9	2.4 / 3.4
Linezolid										
Enterococcus faecalis	n	35	150	10	95	58	12	110	91	561
	% NS/R	0.0 / 0.0	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	0.2 / 0.2
Enterococcus faecium	n	22	115	8	30	44	8	120	53	400
	% NS/R	0.0 / 0.0	3.5 / 0.0	na	0.0 / 0.0	2.3 / 0.0	na	5.0 / 0.0	3.8 / 0.0	3.3 / 0.0
Staphylococcus aureus	n	81	589	110	503	262	51	407	394	2397
	% 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	12	135	42	68	43	3	63	69	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	69	454	68	435	219	48	344	325	1962
	% 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	0	10	5	20	1	2	10	11	59
	% NS	na	0.0 / 0.0	na	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Escherichia coli	n	149	1,107	137	691	453	79	727	650	3,993
	% NS	0.0 / 0.6	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	<0.1 / 0.0
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% NS	2.9 / 2.9	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	1.2 / 1.2	0.0 / 0.0	0.6 / 0.6	0.0 / 0.0	0.3 / 0.3
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% NS	0.0 / 0.0	0.0 / 0.0	na	2.2 / 2.2	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	0.4 / 0.4
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% NS	0.0 / 0.0	7.1 / 5.9	na	4.6 / 4.6	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	4.0 / 4.0	3.4 / 3.1
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% NS	na	2.9 / 2.9	na	0.0 / 0.0	0.0 / 0.0	na	3.7 / 3.7	0.0 / 0.0	1.5 / 1.5
Proteus mirabilis	n	6	66	6	44	24	3	37	35	221
	% NS	na	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Salmonella species	n	1	19	24	28	9	2	21	10	114
(non typhoidal)	% NS	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Salmonella species (typhoidal)	n	1	5	0	6	4	0	7	2	25
	% NS	na	na	na	na	na	na	na	na	0.0 / 0.0
Pseudomonas aeruginosa	n	36	166	19	165	82	4	74	107	653
	% NS	2.8 / 2.8	9.0 / 9.0	15.8 / 15.8	9.7 / 9.7	7.3 / 7.3	-	9.5 / 9.5	3.7 / 3.7	8.1 / 8.1
Nitrofurantoin										
Escherichia coli	n	149	1,107	137	691	454	79	727	650	3,994
	% R	1.3 / 1.3	1.0 / 1.0	0.0 / 0.0	0.7 / 0.7	1.3 / 1.3	0.0 / 0.0	2.2 / 2.2	1.5 / 1.5	1.3 / 1.3
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% R	37.1 / —	30.9 / —	38.3 / —	20.6 / —	35.3 / —	22.2 / —	44.1 / —	32.6 / —	32.4 / —
Klebsiella oxytoca	n	13	76	4	45	13	8	49	30	238
	% R	0.0 / —	0.0 / —	na	2.2 / —	23.1 / —	na	0.0 / —	0.0 / —	2.1 / —
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% R	10.0 / —	16.5 / —	na	15.4 / —	46.2 / —	21.4 / —	25.0 / —	20.0 / —	20.6 / —
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% R	na	47.1 / —	na	46.2 / —	27.3 / —	na	51.9 / —	32.0 / —	43.5 / —
Proteus mirabilis	n	6	66	6	44	24	3	37	36	222
	% R	na	92.4 / —	na	100 / —	91.7 / —	na	94.6 / —	91.7 / —	94.6 / —
Salmonella species (non typhoidal)	n	1	19	24	28	9	2	21	10	114
	% R	na	5.3 / —	0.0 / —	7.1 / —	na	na	9.5 / —	40.0 / —	8.8 / —
Salmonella species (typhoidal)	n	1	5	0	6	4	0	7	2	25
	%R	na	na	na	na	na	na	na	na	4.0 / —
Staphylococcus aureus	n	81	589	110	448	262	0	407	394	2291
	% R	0.0 / —	0.3 / —	0.0 / —	0.0 / —	0.0 / —	na	0.0 / —	0.0 / —	0.1 / —
methicillin-resistant	n	12	135	42	68	43	0	63	69	426
	% R	0.0 / —	0.7 / —	0.0 / —	0.0 / —	0.0 / —	na	0.0 / —	0.0 / —	0.2 / —
methicillin-susceptible	n	69	454	68	386	219	0	344	325	1865
	% R	0.0 / —	0.2 / —	0.0 / —	0.0 / —	0.0 / —	na	0.0 / —	0.0 / —	0.1 / —
Enterococcus faecalis	n	35	149	10	95	57	12	109	91	558
	% R	0.0 / 0.0	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	0.2 / 0.2
Enterococcus faecium	n	22	115	8	30	44	8	120	53	400
	% R	81.8 / —	53.0 / —	na	40.0 / —	40.9 / —	na	20.0 / —	28.3 / —	38.3 / —

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Oxacillin										
Staphylococcus aureus	n	81	587	110	503	262	51	407	394	2395
	% R	14.8 / 14.8	22.5 / 22.5	37.3 / 37.3	13.3 / 13.3	15.3 / 15.3	3.9 / 3.9	14.7 / 14.7	16.8 / 16.8	17.5 / 17.5
Piperacillin-Tazobactam										
Acinetobacter baumannii	n	0	10	1	8	1	0	8	7	35
	% R	na	0.0 / —	na	na	na	na	na	na	2.9 / —
Escherichia coli	n	146	1107	137	676	454	79	726	649	3974
	% R	1.4 / 3.4	3.4 / 6.3	2.9 / 6.6	3.3 / 7.5	2.0 / 4.6	2.5 / 5.1	3.2 / 7.4	1.8 / 5.7	2.8 / 6.3
Klebsiella pneumoniae	n	35	235	47	184	85	18	176	186	966
	% R	5.7 / 5.7	4.3 / 6.4	2.1 / 12.8	3.8 / 7.1	2.4 / 4.7	0.0 / 5.6	4.0 / 7.4	2.7 / 4.3	3.5 / 6.4
Klebsiella oxytoca	n	13	76	4	43	13	8	49	30	236
	% R	7.7 / 7.7	13.2 / 14.5	na	7.0 / 7.0	7.7 / 15.4	na	6.1 / 6.1	10.0 / 10.0	8.9 / 10.2
Enterobacter cloacae complex	n	5	57	9	64	13	11	77	41	277
	% R	na	5.3 / 14.0	na	14.1 / 18.8	0.0 / 7.7	9.1 / 18.2	26.0 / 27.3	24.4 / 26.8	15.9 / 20.6
Enterobacter aerogenes	n	4	34	3	25	11	1	27	25	130
	% R	na	17.6 / 38.2	na	16.0 / 24.0	18.2 / 27.3	na	44.4 / 55.6	28.0 / 40.0	27.7 / 40.0
Proteus mirabilis	n	6	65	6	42	24	3	37	36	219
	% R	na	0.0 / 1.5	na	0.0 / 0.0	0.0 / 0.0	na	2.7 / 2.7	0.0 / 0.0	0.5 / 0.9
Pseudomonas aeruginosa	n	35	166	19	159	83	4	74	107	647
	% R	20.0 / 20.0	7.8 / 15.7	5.3 / 10.5	6.3 / 15.1	6.0 / 10.8	na	5.4 / 14.9	5.6 / 10.3	7.1 / 13.9
Salmonella species	n	1	19	24	28	9	2	21	10	114
(non typhoidal)	% R	na	5.3 / 5.3	0.0 / 0.0	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.9 / 0.9
Salmonella species	n	1	5	0	5	4	0	6	1	22
(typhoidal)	% R	na	na	na	na	na	na	na	na	0.0 / 0.0
Rifampicin										
Staphylococcus aureus	n	81	590	110	503	262	0	407	394	2347
	% R	0.0 / 0.0	1.5 / 1.7	0.0 / 0.0	0.2 / 0.2	0.0 / 0.0	na	0.0 / 0.2	0.8 / 0.8	0.6 / 0.6
methicillin-resistant	n	12	135	42	68	43	0	63	69	432
	% R	0.0 / 0.0	5.9 / 5.9	0.0 / 0.0	1.5 / 1.5	0.0 / 0.0	na	0.0 / 1.6	4.3 / 4.3	2.8 / 3.0
methicillin-susceptible	n	69	455	68	435	219	0	344	325	1915
	% R	0.0 / 0.0	0.2 / 0.4	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

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Teicoplanin										
Enterococcus faecalis	n	35	149	10	95	57	12	109	91	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	22	115	8	31	44	8	120	53	401
	% NS/R	31.8 / 31.8	33.0 / 33.9	na	19.4 / 19.4	2.3 / 2.3	na	12.5 / 12.5	5.7 / 5.7	17.5 / 17.7
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% NS/R	0.0 / 0.0	0.0 / 0.2	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.3	0.0 / 0.1
Tetracycline										
Enterococcus faecalis	n	35	120	10	95	28	0	110	91	489
	% R	80.0 / —	75.0 / —	90.0 / —	80.0 / —	92.9.0 / —	na	82.7 / —	69.2 / —	78.3 / —
Enterococcus faecium	n	22	89	8	30	20	1	120	53	343
	% R	36.4 / —	34.8 / —	na	70.0 / —	90.0 / —	na	77.5 / —	37.7 / —	57.5 / —
Staphylococcus aureus	n	81	499	110	503	94	51	407	394	2139
	% NS	4.9 / 6.2	9.6 / 10.0	6.4 / 6.4	3.2 / 4.4	3.2 / 3.2	2.0 / 2.0	4.2 / 4.4	3.6 / 3.8	5.1 / 5.7
methicillin-resistant	n	12	107	42	68	9	3	63	69	373
	% NS	8.3 / 16.7	38.3 / 38.3	16.7 / 16.7	14.7 / 16.2	na	na	17.5 / 17.5	2.9 / 2.9	20.1 / 20.6
methicillin-susceptible	n	69	392	68	435	85	48	344	325	1766
	% NS	4.3 / 4.3	1.8 / 2.3	0.0 / 0.0	1.4 / 2.5	0.0 / 0.0	2.1 / 2.1	1.7 / 2.0	3.7 / 4.0	2.0 / 2.5
Ticarcillin-clavulanate										
Acinetobacter baumannii	n	0	10	5	20	1	0	10	11	57
	% R	na	0.0 / —	na	0.0 / —	na	na	0.0 / —	0.0 / —	0.0 / —
Escherichia coli	n	149	985	137	691	454	79	726	650	3871
	% R	6.7 / 14.1	10.4 / 25.3	13.1 / 19.7	10.6 / 19.4	7.9 / 20.9	6.3 / 13.9	10.2 / 22.2	9.2 / 18.0	9.8 / 21.1
Klebsiella pneumoniae	n	35	213	47	189	85	18	177	187	951
	% R	8.6 / 11.4	7.0 / 10.8	4.3 / 8.5	6.3 / 7.9	4.7 / 10.6	5.6 / 11.1	10.7 / 13.0	3.2 / 8.0	6.5 / 10.0
Klebsiella oxytoca	n	13	66	4	45	13	8	49	30	228
	% R	7.7 / 7.7	12.1 / 15.2	na	8.9 / 8.9	7.7 / 7.7	na	6.1 / 10.0	10.0 / 10.0	9.2 / 11.4
Enterobacter cloacae complex	n	10	74	9	65	13	14	80	50	315
	% R	0.0 /	16.2 / 23.0	na	21.5 / 26.2	0.0 / 0.0	14.3 / 21.4	31.3 / 31.3	22.0 / 22.0	21.0 / 23.8
Enterobacter aerogenes	n	4	33	3	26	11	1	27	25	130
	% R	na	30.3 / 45.5	na	15.4 / 15.4	18.2 / 36.4	na	40.7 / 55.6	24.0 / 36.0	28.5 / 40.0

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Proteus mirabilis	n	6	51	6	44	24	3	37	36	207
	% R	na	0.0 / 0.0	na	0.0 / 0.0	0.0 / 0.0	na	2.7 / 2.7	0.0 / 0.0	0.5 / 0.5
Pseudomonas aeruginosa	n	36	166	19	163	83	4	74	107	652
	% R	22.2 / 38.9	16.3 / 53.6	26.3 / 47.4	16.6 / 50.9	13.3 / 48.2	na	21.6 / 52.7	11.2 / 45.8	16.3 / 50.0
Salmonella species	n	1	17	24	28	9	2	21	10	112
(non typhoidal)	% R	na	5.9 / 5.9	0.0 / 0.0	0.0 / 0.0	na	na	9.5 / 14.3	0.0 / 0.0	2.7 / 3.6
Salmonella species	n	1	5	0	6	4	0	7	2	25
(typhoidal)	% R	na	na	na	na	na	na	na	na	0.0 / 8.0
Tobramycin										
Acinetobacter baumannii	n	0	10	5	20	1	2	10	11	59
	% R	na	0.0 / 0.0	na	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0
Escherichia coli	n	149	1107	137	679	454	79	727	650	3982
	% R	1.3 / 4.0	4.7 / 10.2	5.1 / 11.7	2.1 / 6.8	3.7 / 7.5	0.0 / 2.5	4.4 / 9.2	3.7 / 10.2	3.7 / 8.8
Klebsiella pneumoniae	n	35	236	47	184	85	18	177	187	969
	% R	0.0 / 2.9	3.0 / 6.8	2.1 / 10.6	2.2 / 3.8	1.2 / 5.9	5.6 / 5.6	3.4 / 6.8	1.6 / 3.2	2.4 / 5.5
Klebsiella oxytoca	n	13	76	4	43	13	8	49	30	236
	% R	0.0 / 0.0	0.0 / 0.0	na	0.0 / 2.3	0.0 / 0.0	na	0.0 / 2.0	0.0 / 3.3	0.0 / 1.3
Enterobacter cloacae complex	n	10	85	9	64	13	14	80	50	325
	% R	0.0 / 0.0	7.1 / 14.1	na	4.7 / 12.5	0.0 / 0.0	0.0 / 7.1	2.5 / 10.0	0.0 / 0.0	3.4 / 9.2
Enterobacter aerogenes	n	4	34	3	25	11	1	27	25	130
	% R	na	0.0 / 2.9	na	4.0 / 4.0	0.0 / 0.0	na	7.4 / 11.1	0.0 / 0.0	2.3 / 3.8
Proteus mirabilis	n	6	66	6	43	24	3	37	36	221
	% R	na	0.0 / 3.0	na	2.3 / 2.3	0.0 / 0.0	na	2.7 / 2.7	0.0 / 0.0	0.9 / 1.8
Salmonella species	n	1	19	24	28	9	2	21	10	114
(non typhoidal)	% R	na	5.3 / 5.3	0.0 / 0.0	0.0 / 0.0	na	na	0.0 / 0.0	0.0 / 0.0	0.9 / 0.9
Salmonella species	n	1	5	0	5	4	0	7	2	24
(typhoidal)	% R	na	na	na	na	na	na	na	na	0.0 / 0.0
Pseudomonas aeruginosa	n	36	166	19	160	83	4	74	107	649
	% R	0.0 / 0.0	4.2 / 4.2	0.0 / 0.0	0.6 / 1.3	2.4 / 2.4	na	4.1 / 4.1	0.9 / 0.9	2.2 / 2.3

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Trimethoprim										
Escherichia coli	n	149	1107	137	679	454	79	727	650	3982
	% R	30.2 / 30.9	34.7 / 34.8	35.0 / 35.0	30.2 / 30.2	24.0 / 24.4	15.2 / 15.2	32.2 / 33.0	30.3 / 30.6	31.0 / 31.3
Klebsiella pneumoniae	n	35	236	47	184	85	18	177	187	969
	% R	31.4 / 31.4	14.8 / 15.3	17.0 / 17.0	15.2 / 15.2	12.9 / 14.1	22.2 / 22.2	18.6 / 19.8	10.2 / 11.8	15.4 / 16.1
Klebsiella oxytoca	n	13	76	4	43	13	8	49	30	236
	% R	0.0 / 0.0	3.9 / 3.9	na	2.3 / 2.3	0.0 / 0.0	na	4.1 / 4.1	6.7 / 6.7	3.4 / 3.4
Enterobacter cloacae complex	n	10	85	9	64	13	14	80	50	325
	% R	20.0 / 20.0	16.5 / 16.5	na	18.8 / 18.8	15.4 / 15.4	21.4 / 21.4	20.0 / 20.0	2.0 / 2.0	16.0 / 16.0
Enterobacter aerogenes	n	4	34	3	25	11	1	27	25	130
	% R	na	8.8 / 8.8	na	8.0 / 8.0	0.0 / 0.0	na	11.1 / 11.1	0.0 / 0.0	6.2 / 6.2
Proteus mirabilis	n	6	66	6	43	24	3	37	36	221
	% R	na	25.8 / 25.8	na	9.3 / 11.6	20.8 / 20.8	na	13.5 / 16.2	22.2 / 22.2	18.1 / 19.0
Salmonella species	n	1	19	24	28	9	2	21	10	114
(non typhoidal)	% R	na	5.3 / 5.3	0.0 / 0.0	3.6 / 3.6	na	na	9.5 / 9.5	0.0 / 0.0	4.4 / 4.4
Salmonella species	n	1	5	0	5	4	0	7	2	24
(typhoidal)	%R	na	na	na	na	na	na	na	na	4.2 / 4.2
Trimethoprim-Sulfamethoxazole										
Acinetobacter baumannii	n	0	10	5	20	1	2	10	11	59
	% R	na	0.0 / 0.0	na	5.0 / 5.0	na	na	0.0 / 0.0	0.0 / 0.0	3.4 / 3.4
Escherichia coli	n	149	1107	137	691	452	79	727	648	3990
	% R	30.2 / 30.2	33.1 / 33.0	32.8 / 32.8	28.8 / 28.5	23.2 / 23.0	15.2 / 15.2	30.9 / 30.9	26.5 / 26.5	29.3 / 29.2
Klebsiella pneumoniae	n	35	236	47	189	85	18	177	187	974
	% R	28.6 / 28.6	12.7 / 12.3	17.0 / 14.9	14.8 / 14.8	10.6 / 9.4	16.7 / 16.7	16.9 / 16.4	6.4 / 6.4	13.3 / 12.9
Klebsiella oxytoca	n	13	76	4	45	13	8	48	30	237
	% R	0.0 / 0.0	2.6 / 1.3	na	2.2 / 2.2	0.0 / 0.0	na	4.2 / 4.2	6.7 / 6.7	3.0 / 2.5
Enterobacter cloacae complex	n	10	85	9	65	13	14	80	50	326
	% R	20.0 / 20.0	16.5 / 16.5	na	18.5 / 18.5	15.4 / 15.4	21.4 / 21.4	18.8 / 18.8	2.0 / 2.0	15.6 / 15.6
Enterobacter aerogenes	n	4	34	3	26	11	1	27	25	131
	% R	na	2.9 / 2.9	na	3.8 / 3.8	0.0 / 0.0	na	11.1 / 11.1	0.0 / 0.0	3.8 / 3.8
Enterococcus faecalis	n	35	149	10	95	58	0	66	91	504
	% R	— / 22.9	— / 16.8	— / 50.0	— / 24.2	— / 20.7	na	— / 21.2	— / 15.4	— / 20.0

Species	Category [a]	CLSI / EUCAST percentage susceptibility at indicated category								
		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Australia
Enterococcus faecium	n	22	113	8	30	44	1	55	53	326
	% R	— / 59.1	— / 47.8	na	— / 70.0	— / 45.5	na	— / 83.6	— / 62.3	— / 59.5
Proteus mirabilis	n	6	66	6	43	24	3	37	36	221
	% R	na	19.7 / 19.7	na	6.8 / 6.8	20.8 / 20.8	na	8.1 / 8.1	20.0 / 20.0	14.0 / 14.0
Salmonella species	n	1	19	24	28	9	2	21	10	114
(non typhoidal)	% R	na	5.3 / 5.3	0.0 / 0.0	3.6 / 3.6	na	na	9.5 / 9.5	0.0 / 0.0	4.4 / 4.4
Salmonella species	n	1	5	0	6	4	0	7	2	25
(typhoidal)	%R	na	na	na	na	na	na	na	na	4.0 / 4.0
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% R	3.7 / 3.7	4.9 / 4.7	10.0 / 6.4	1.4 / 1.4	7.3 / 7.3	0.0 / 0.0	2.5 / 2.5	4.3 / 4.3	4.0 / 3.8
methicillin-resistant	n	12	135	42	68	43	3	63	69	435
	% R	25.0 / 25.0	16.3 / 15.6	23.8 / 14.3	1.5 / 1.5	23.3 / 23.3	na	12.7 / 12.7	18.8 / 18.8	15.4 / 14.3
methicillin-susceptible	n	69	455	68	435	219	48	344	325	1963
	% R	0.0 / 0.0	1.5 / 1.5	1.5 / 1.5	1.4 / 1.4	4.1 / 4.1	0.0 / 0.0	0.6 / 0.6	1.2 / 1.2	1.5 / 1.5
Vancomycin										
Enterococcus faecalis	n	35	149	10	95	57	12	109	91	558
	% NS	0.0 / 0.0	1.3 / 1.3	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	8.3 / 8.3	0.9 / 0.9	0.0 / 0.0	0.7 / 0.7
Enterococcus faecium	n	22	116	8	31	44	8	120	53	402
	% NS	50.0 / 50.0	51.7 / 51.7	na	58.1 / 61.3	52.3 / 52.3	na	62.5 / 63.3	11.3 / 11.3	49.8 / 50.2
Staphylococcus aureus	n	81	590	110	503	262	51	407	394	2398
	% NS	0.0 / 0.0	0.0 / 0.2	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.0	0.0 / 0.3	0.0 / 0.1

[a] Category analyzed for each organism. If different for CLSI and EUCAST they are separated by /. Abbreviations: R = resistant, I = intermediate, NS = sensitive dose dependent (SDD) or intermediate plus resistant, NR = susceptible plus intermediate (concentration range limitation)

[b] No breakpoints defined

[c] Insufficient numbers (< 10) to calculate

[d] EUCAST, for susceptibility testing purposes, the concentration of clavulanate is fixed at 2 mg/L, rather than a 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

[e] NS category for cefepime included includes CLSI SDD for Enterobacteriaceae

[f] Ciprofloxacin concentration range available on the cards used restricts ability to accurately determine susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species

[g] Concentration range on Phoenix card prohibits interpretation for *Enterococcus* species. Figures reflect number of isolates that can be interpreted using CLSI and EUCAST respectively

APPENDIX D. Multiple acquired resistance by species and region

The most problematic pathogens are those with multiple acquired resistances. Although there is no agreed benchmark for the definition of multi-resistance, acquired resistance to more than three agents have been chosen to define multi-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 multi-drug resistance determination. The agents included for each species are listed in the legend after each Table. EUCAST breakpoints have been used throughout in the analysis, noting that for cefazolin the EUCAST approved Australian National Advisory Committee guidelines were used. For amoxicillin-clavulanate CLSI breakpoints were used, as both the Vitek and Phoenix cards used the CLSI formulation for this agent.

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

Table D-1 *Citrobacter koseri*, multiple acquired resistance

		Non-multi-resistant					Multi-resistant								
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	%
ACT	1	1	0	0	0	100.0%	0	0	0	0	0	0	0	0	0.0%
NSW	20	16	2	0	1	95.0%	0	1	0	0	0	0	0	0	5.0%
NT	1	0	0	0	0	0.0%	0	0	0	1	0	0	0	0	100.0%
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%
TAS	0														
VIC	4	4	0	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%
Total	**52**	**43**	**6**	**0**	**1**	**96.2%**	**0**	**1**	**0**	**1**	**0**	**0**	**0**	**0**	**3.8%**

Antimicrobials included: amoxycillin-clavulanate [CLSI], piperacillin-tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table D 2 *Citrobacter freundii*, multiple acquired resistance

		Non-multi-resistant					Multi-resistant							
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	%
ACT	4	3	0	0	1	100.0%	0	0	0	0	0	0	0	0.0%
NSW	19	8	0	2	5	78.9%	2	1	1	0	0	0	0	21.1%
NT	0													
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%
TAS	1	0	1	0	0	100.0%	0	0	0	0	0	0	0	0.0%
VIC	9	8	0	0	0	88.9%	0	1	0	0	0	0	0	11.1%
WA	2	1	0	1	0	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%**

Antimicrobials included: piperacillin-tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table D-3 *Enterobacter aerogenes,* multiple acquired resistance

Region	Total	Non-multi-resistant					Multi-resistant							
		0	1	2	3	%	4	5	6	7	8	9	10	%
ACT	4	1	0	0	3	100.0%	0	0	0	0	0	0	0	0.0%
NSW	34	15	2	1	14	94.1%	1	1	0	0	0	0	0	5.9%
NT	3	2	0	0	1	100.0%	0	0	0	0	0	0	0	0.0%
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%
TAS	1	0	0	0	1	100.0%	0	0	0	0	0	0	0	0.0%
VIC	27	12	0	0	10	81.5%	1	1	1	2	0	0	0	18.5%
WA	25	14	2	0	9	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%**

Antimicrobials included: piperacillin-tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table A-4 *Enterococcus faecium* (vancomycin-resistant), multiple acquired resistance

Region	Total	0	1	2	3	%
ACT	11	0	0	11	0	100.0%
NSW	58	0	16	42	0	100.0%
NT	6	0	0	6	0	100.0%
QLD	18	0	0	18	0	100.0%
SA	13	0	12	1	0	100.0%
TAS	0 †					
VIC	76	0	0	76	0	100.0%
WA	6	0	0	6	0	100.0%
Total	**188**	**0**	**28**	**160**	**0**	**100.0%**

Antimicrobials included: ampicillin, ciprofloxacin, linezolid

† Ciprofloxacin MICs not provided

Table D-5 *Enterococcus faecium* (vancomycin-susceptible), multiple acquired resistance

Region	Total	0	1	2	3	%
ACT	11	1	0	10	0	100.0%
NSW	56	16	8	32	0	100.0%
NT	2	1	0	1	0	100.0%
QLD	10	5	0	5	0	100.0%
SA	14	1	11	2	0	100.0%
TAS	1	0	0	1	0	100.0%
VIC	44	12	0	32	0	100.0%
WA	47	11	0	36	0	100.0%
Total	**185**	**47**	**19**	**119**	**0**	**100.0%**

Antimicrobials included: ampicillin, ciprofloxacin, linezolid

Table D 6 *Klebsiella oxytoca*, multiple acquired resistance

Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	%
ACT	13	5	7	0	0	92.3%	1	0	0	0	0	0	0	0	7.7%
NSW	76	23	36	3	8	92.1%	6	0	0	0	0	0	0	0	7.9%
NT	4	1	3	0	0	100.0%	0	0	0	0	0	0	0	0	0.0%
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%
TAS	4	1	2	1	0	100.0%	0	0	0	0	0	0	0	0	0.0%
VIC	41	15	22	0	1	92.7%	2	1	0	0	0	0	0	0	7.3%
WA	23	9	10	0	2	91.3%	1	1	0	0	0	0	0	0	8.7%
Total	**217**	**72**	**111**	**4**	**12**	**91.7%**	**15**	**2**	**0**	**1**	**0**	**0**	**0**	**0**	**8.3%**

Antimicrobials included: amoxycillin-clavulanate [CLSI], piperacillin-tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table D 7 *Morganella morganii*, multiple acquired resistance

		Non-multi-resistant					Multi-resistant							
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	%
ACT	4	4	0	0	0	100.0%	0	0	0	0	0	0	0	0.0%
NSW	26	17	5	3	1	100.0%	0	0	0	0	0	0	0	0.0%
NT	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%
TAS	1	0	1	0	0	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%
WA	7	6	0	0	0	85.7%	0	1	0	0	0	0	0	14.3%
Total	**79**	**59**	**10**	**6**	**1**	**96.2%**	**0**	**2**	**1**	**0**	**0**	**0**	**0**	**3.8%**

Antimicrobials included: piperacillin-tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table D 8 *Proteus mirabilis*, multiple acquired resistance

		Non-multi-resistant					Multi-resistant								
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	12	%
ACT	6	6	0	0	0	100.0%	0	0	0	0	0	0	0	0	0	0.0%
NSW	65	34	15	5	4	89.2%	5	1	1	0	0	0	0	0	0	10.8%
NT	6	4	2	0	0	100.0%	0	0	0	0	0	0	0	0	0	0.0%
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%
TAS	2	2	0	0	0	100.0%	0	0	0	0	0	0	0	0	0	0.0%
VIC	34	19	8	2	1	88.2%	2	1	0	0	0	1	0	0	0	11.8%
WA	26	14	5	0	5	92.3%	1	1	0	0	0	0	0	0	0	7.7%
Total	**205**	**109**	**56**	**11**	**14**	**92.7%**	**9**	**3**	**1**	**0**	**0**	**2**	**0**	**0**	**0**	**7.3%**

Antimicrobials included: ampicillin, amoxycillin-clavulanate [CLSI], piperacillin-tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table D 9 *Pseudomonas aeruginosa*, multiple acquired resistance

		Non-multi-resistant					Multi-resistant		
Region	Total	0	1	2	3	%	4	5	%
ACT	34	24	4	6	0	100.0%	0	0	0.0%
NSW	162	128	13	13	2	96.3%	2	2	2.5%
NT	18	15	1	1	1	100.0%	0	0	0.0%
QLD	155	125	12	11	5	98.7%	2	0	1.3%
SA	75	61	7	4	1	97.3%	2	0	2.7%
TAS	4	3	1	0	0	100.0%	0	0	0.0%
VIC	71	55	5	7	0	94.4%	4	0	5.6%
WA	106	87	7	10	2	100.0%	0	0	0.0%
Total	**625**	**498**	**50**	**52**	**11**	**97.8%**	**10**	**2**	**1.9%**

Antimicrobials included: ceftazidime, ciprofloxacin, piperacillin-tazobactam, tobramycin, meropenem

Table D 10 *Salmonella* species (non typhoidal), multiple acquired resistance

		Non-multi-resistant					Multi-resistant									
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	12	%
ACT	1	1	0	0	0	100.0%	0	0	0	0	0	0	0	0	0	0.0%
NSW	19	17	1	0	0	94.7%	0	0	1	0	0	0	0	0	0	5.3%
NT	24	24	0	0	0	100.0%	0	0	0	0	0	0	0	0	0	0.0%
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%
TAS	0 †															
VIC	16	12	2	0	1	93.8%	0	0	1	0	0	0	0	0	0	6.3%
WA	9	9	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%**

Antimicrobials included: ampicillin, amoxycillin-clavulanate [CLSI], piperacillin-tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

† Cefazolin MICs not provided

Table D 11 *Salmonella* species (typhoidal), multiple acquired resistance

		Non-multi-resistant					Multi-resistant									
Region	Total	0	1	2	3	%	4	5	6	7	8	9	10	11	12	%
ACT	1	1	0	0	0	100.0%	0	0	0	0	0	0	0	0	0	0.0%
NSW	4	4	0	0	0	100.0%	0	0	0	0	0	0	0	0	0	0.0%
NT	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%
TAS	0															
VIC	6	6	0	0	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%
Total	**21**	**19**	**0**	**1**	**1**	**100.0%**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0.0%**

Antimicrobials included: ampicillin, amoxycillin-clavulanate [CLSI], piperacillin-tazobactam, cefazolin, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

Table D 12 *Serratia marcescens*, multiple acquired resistance

Region	Total	Non-multi-resistant					Multi-resistant							
		0	1	2	3	%	4	5	6	7	8	9	10	%
ACT	0 †													
NSW	59	52	2	2	2	98.3%	0	1	0	0	0	0	0	1.7%
NT	3	2	0	1	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%
TAS	3	3	0	0	0	100.0%	0	0	0	0	0	0	0	0.0%
VIC	19	15	4	0	0	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%
Total	**142**	**127**	**6**	**4**	**3**	**98.6%**	**1**	**1**	**0**	**0**	**0**	**0**	**0**	**1.4%**

Antimicrobials included: piperacillin-tazobactam, ceftriaxone, ceftazidime, cefepime, gentamicin, amikacin, ciprofloxacin, trimethoprim, meropenem

† Piperacillin-tazobactam MICs not provided

Table D 13 *Staphylococcus aureus*, multiple acquired resistance

Region	Total	Non-multi-resistant					Multi-resistant										
		0	1	2	3	%	4	5	6	7	8	9	10	11	12	13	14	%
ACT	81	13	46	9	10	96.3%	1	0	2	0	0	0	0	0	0	0	0	3.7%
NSW	496	80	263	50	36	86.5%	26	12	17	11	1	0	0	0	0	0	0	13.5%
NT	110	10	41	38	12	91.8%	2	0	0	7	0	0	0	0	0	0	0	8.2%
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%
TAS	0 †																	
VIC	407	86	217	50	28	93.6%	14	5	3	2	2	0	0	0	0	0	0	6.4%
WA	394	64	219	61	33	95.7%	11	4	2	0	0	0	0	0	0	0	0	4.3%
Total	**2029**	**355**	**1093**	**291**	**153**	**93.2%**	**64**	**23**	**25**	**22**	**3**	**0**	**0**	**0**	**0**	**0**	**0**	**6.8%**

Antimicrobials included: benzylpenicillin, ciprofloxacin, daptomycin, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin (high level), nitrofurantoin [CLSI], oxacillin, rifampicin, trimethoprim-sulfamethoxazole, tetracycline, vancomycin

† Nitrofurantoin and rifampicin MICs not provided

APPENDIX E. Summary Reports

E. 1 Susceptibility Results

National reports provide summary susceptibility data (number and percent (if more than 10 isolates) using both CLSI and EUCAST interpretative guidelines for all species isolated. They can be assessed through the AGAR web site http://www.agargroup.org/surveys

E. 2 Antimicrobial Resistance Profiles by Frequency

Only isolates where the full range of antimicrobial agents was tested are included in the profiles. The regional antibiotic profiles for the top 12 species can be accessed by following the hyperlinks. Profiles are generated using EUCAST guidelines. Reports are available on the AGAR web site http://www.agargroup.org/surveys