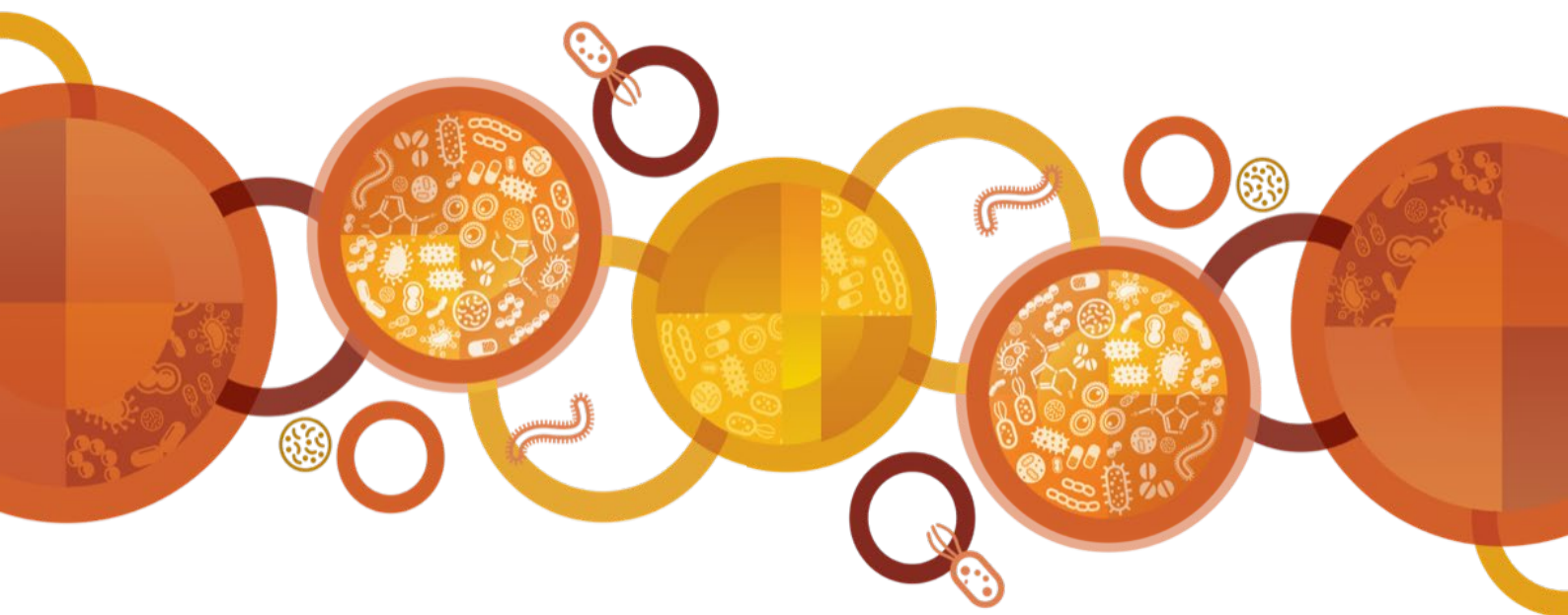


Australian Passive Antimicrobial Resistance Surveillance

Third-generation cephalosporin resistance in *Escherichia coli* and *Klebsiella pneumoniae*: prevalence of extended-spectrum β -lactamase (ESBL) phenotype

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Executive Summary

Gram-negative bacteria, such as *Escherichia coli* and *Klebsiella pneumoniae* cause a range of infections in healthcare and community settings, including urinary tract infections (UTIs), bloodstream infections, intra-abdominal infections, and wound or surgical site infections. *E. coli* is the most common cause of serious infections in hospital patients, particularly bloodstream infections; and UTIs caused by multidrug-resistant (MDR) *E. coli* are very common in community settings and in particular aged care homes. The incidence of these infections is increasing in Australia and globally.¹⁻³

Both *E. coli* and *K. pneumoniae* can become resistant to multiple antimicrobials used to treat infections with which these species are associated. These bacteria also continue to develop new ways of being resistant to antimicrobials and can pass on genetic codes that enable other bacteria to acquire resistance.

The Australian Passive Antimicrobial Resistance Surveillance (APAS) system was established by the Australian Commission on Safety and Quality in Health Care (the Commission) in 2015. In 2021, public and private pathology services across Australia contributed data to APAS on antimicrobial resistance (AMR) detected in isolates referred from public and private hospitals, aged care homes and community settings. Over 87 million records have been included in APAS covering the period 2006 to 2022.

Resistance to third-generation cephalosporins, such as ceftriaxone, is a feature of bacteria that produce extended-spectrum β -lactamases (ESBLs). ESBLs are enzymes that may be produced by a range of bacteria, including *E. coli* and *K. pneumoniae*. From 2006 to 2013, the ESBL phenotype was more common in *K. pneumoniae* than *E. coli* in data submitted to the APAS system. From 2013, it has been more common in *E. coli*. This is consistent with global trends for *E. coli*. As returned travellers are a recognised source of ESBLs, the decrease in travel to Australia due to the COVID-19 pandemic may have contributed to the small decrease in ESBLs in *E. coli* isolates in 2021. Nonetheless as ESBLs were already well-established in Australia from 2013, it is likely that other, multiple factors may also have contributed to this finding.

The COVID-19 pandemic and the related public health interventions may have affected the reporting and analysis of results of AMR data for 2020 and 2021 in different ways and to varying degrees over time. Examples of factors that changed during the COVID-19 response that have potential implications for AMR include access to community-based health care, hospital admission patterns and the range of hospital services offered such as outpatient clinics and elective surgery, antimicrobial prescribing practices, and movement of people into and within Australia.⁴

There are concerning levels of ESBLs in aged care home residents, and there was an increasing trend in this resistance in that setting from 2015 to 2021. There were state and territory differences, based on postcode of patient residence. For *E. coli*, incidences of ESBLs were generally higher in patients who resided in Victoria, New South Wales, and the Australian Capital Territory. The rate of ESBLs in *K. pneumoniae* was generally lower than in *E. coli*, although little difference was seen in these rates in Victoria, South Australia and Tasmania.

There was an increasing trend in ESBLs in all remoteness areas from 2015 to 2021; and from 2018 to 2021, ESBLs in *E. coli* was more prevalent in isolates from residents who resided in major cities and very remote areas of Australia.

The proportion of *E. coli* with ESBL phenotype was lowest among paediatric patients and highest in persons aged over 64 years. In *K. pneumoniae*, there were minimal differences in the rate of ESBL phenotype observed across age groups, although it was slightly higher in persons aged over 64 years in isolates from tissue/fluid/pus/prosthesis.

Despite increasing AMR in *E. coli* and *K. pneumoniae* in Australia up to 2019, the rates are still relatively low, compared to Asian countries and parts of Europe and the United States of America.⁵⁻⁷

Implications for patient and community safety

AMR continues to be an increasing risk to patient safety because it reduces the number of antimicrobials available to treat infections; and increases morbidity and mortality associated with infections caused by MDR organisms that therefore become more difficult to treat. AMR may also limit future capacity to perform medical procedures such as organ transplantation, cancer chemotherapy, diabetes management and major surgery, because of a lack of effective antimicrobials.

In addition, AMR contributes to increasing demand for admitted care for treatment of infections, due to limited oral antimicrobial options for treatment of infections caused by these resistant bacteria.

The level of ESBLs in isolates from aged care home residents is concerning for their health and safety, because a high proportion are vulnerable, and likely to experience increased morbidity and mortality if they were to contract an infection caused by resistant bacteria. In addition, there are flow-on implications for acute healthcare services in terms of increased demand for admitted care and infection prevention and control due to movement of residents between these settings.

What action can be taken to prevent and control increasing levels of resistance in *Escherichia coli* and *Klebsiella pneumoniae*?

Actions that the Commission will take to support prevention and control of the development and transmission of resistant *E. coli* and *K. pneumoniae* include:

- Educating clinicians and consumers regarding how resistance develops, how to prevent the spread of resistant organisms, and the importance of appropriate antimicrobial prescribing
- Promoting appropriate risk assessment and management processes for gram-negative bacteria resistance as a core part of clinical assessment of recent travellers and patients admitted to high-risk services, such as intensive care and severe burn
- Promoting appropriate protocols for assessment of all patients with infections who are admitted to health service organisations, including personal history of colonisation or infection with resistant organisms, recent travel history, and recent antimicrobial exposure
- Promoting rigorous infection prevention and control protocols, such as transmission-based precautions and patient placement in high-risk settings; and processes to detect carriage of resistance to direct appropriate antimicrobial therapies for patients at high risk of complications, such as those in intensive care or with febrile neutropenia
- Promoting comprehensive infection prevention and control programs in hospital, community and aged care settings – including hand hygiene, application of standard and transmission-based precautions, routine and targeted environmental cleaning, and waste management - to minimise environmental contamination and reservoirs
- Promoting effective antimicrobial stewardship (AMS) programs to support appropriate prescribing in hospital, community and aged care settings – reducing the inappropriate use of antimicrobials reduces selection pressure for resistance in bacteria
- Promoting antimicrobial prescribing, informed by *Therapeutic Guidelines: Antibiotic*⁸ or local health service organisation guidelines which are tailored to the local epidemiology of resistance
- Ensuring the availability of AMS and AMR data on local ESBL/gram-negative resistance profiles to hospital based AMS teams, and promoting formal arrangements for local microbiology laboratories to work with AMS leads to discuss implications for antimicrobial prescribing and formularies
- Maintaining preparedness plans for potential outbreaks of MDR organisms
- Promoting ongoing surveillance for AMR and antimicrobial use to inform AMS and infection prevention and control practices.

Introduction

Antimicrobial resistance (AMR) continues to be an increasing risk to patient safety because it reduces the number of antimicrobials available to treat infections; and increases morbidity and mortality associated with infections caused by multidrug-resistant (MDR) organisms that therefore become more difficult to treat. AMR may also limit future capacity to perform medical procedures such as organ transplantation, cancer chemotherapy, diabetes management and major surgery, because of a lack of effective antimicrobials.

This report builds on analyses presented in the series of national reports on antimicrobial use and resistance in human health prepared by the Australian Commission on Safety and Quality in Health Care (the Commission) from 2016 to 2021⁹⁻¹³, using data captured by the Antimicrobial Use and Resistance in Australia (AURA) Surveillance System.

The Australian Passive Antimicrobial Resistance Surveillance (APAS) system, which contributes data to AURA, was established by the Commission in 2015. In 2021, public and private pathology services across Australia contributed data to APAS on AMR detected in isolates referred from public and private hospitals, aged care homes and community settings. Over 87 million records have been included in APAS covering the period 2006 to 2022. Appendix 1 includes detailed information regarding APAS.

APAS is a key component of national surveillance of AMR in Australia, which provides data on rates of antimicrobial resistance, and supports development of cumulative antibiograms to inform clinical decisions regarding antimicrobial prescribing. APAS data contribute to improved patient care.

APAS data complement AMR data collected by the Australian Group on Antimicrobial Resistance (AGAR), the National Alert System for Critical Antimicrobial Resistances (CARAlert), the National Neisseria Network, the National Notifiable Diseases Surveillance System, and Sullivan Nicolaides Pathology.

This report focuses on analyses of trends for resistance to third-generation cephalosporins, such as ceftriaxone, in *Escherichia coli* and *Klebsiella pneumoniae* captured through APAS. Resistance to third-generation cephalosporins is a feature of organisms that produce extended-spectrum β -lactamases (ESBLs). Analyses of APAS data complement analyses of AGAR data on ESBLs in these bacteria.²

What are extended-spectrum β -lactamases and why are they important?

ESBLs are enzymes that may be produced by many bacteria, and primarily *E. coli* and *K. pneumoniae*. These bacteria demonstrate reduced susceptibility and resistance to ceftriaxone and a broad range of other antimicrobials including ampicillin, trimethoprim, trimethoprim–sulfamethoxazole, first- and second-generation cephalosporins (including cefalexin and cefazolin), and fluoroquinolones.

E. coli and *K. pneumoniae* are associated with a range of infections, including urinary tract infections (UTIs), biliary infections, other intra-abdominal infections (including those following surgery, and often mixed with other pathogens) and blood stream infections. *E. coli* is the most common cause of UTIs and bloodstream infections in the community and in otherwise healthy people. Less frequently, *E. coli* is a cause of bloodstream infections from intravascular lines and meningitis.

ESBLs in gram-negative bacteria have a considerable impact on resistance patterns, and limit choices for antimicrobial therapy for treatment of the infections that they cause.

How are ESBL-producing bacteria transmitted in healthcare settings?

In healthcare settings, ESBL-producing bacteria are commonly spread through person-to-person contact (for example, from patient to patient via the contaminated hands of healthcare workers).

Patients in healthcare settings also may be exposed to *K. pneumoniae* when they are ventilated or have intravenous catheters or wounds caused by injury or surgery.

These bacteria may also be spread indirectly via contaminated surfaces and equipment in the environment. These bacteria can survive for prolonged periods on wet surfaces and have been found to colonise taps and sink drains in hospitals, which have been identified as common sources for prolonged outbreaks in critical care wards.¹⁴⁻¹⁶

E. coli and *K. pneumoniae* are carried in the bowel, which means that colonised or infected patients who have diarrhoea, faecal incontinence, a colostomy or ileostomy, or whose hygiene practices may be compromised by cognitive or functional impairment, and their carers, may contaminate the surrounding environment. In critical care patients, ESBL-producing bacteria may be found colonising invasive device insertion sites, particularly tracheostomies.

What do we know about ESBL-producing bacteria in Australia?

Analyses of AGAR bacteraemia data have identified a longitudinal trend of increasing *E. coli* resistance to key anti-gram-negative antimicrobial agents, not only to antibiotics such as ceftriaxone because of ESBL production, but also to non- β -lactam antibiotics such as ciprofloxacin due to other linked, but unrelated, resistance mechanisms.² These data also show a steady rise in resistance to fluoroquinolones in hospital-onset bacteraemia, with a change from 13.7% to 21.8% between 2013 and 2020; it was 16.7% in 2021. Ceftriaxone resistance in hospital-onset bacteraemia increased from 6.8% to 12.4% between 2013 and 2020, and there was also increasing resistance to third-generation cephalosporins and fluoroquinolones in *E. coli* strains in the community.

In addition, the AGAR bacteraemia data have shown the emergence of specific types of ESBLs (CTX-M enzymes) in *E. coli* from the community, which is part of a global epidemic.¹⁷⁻¹⁹ There is also increasing recognition that ESBLs are already established in most long-term care facilities in Australia and increasing in their prevalence.²⁰

One in seven (14.7%) *E. coli* isolates reported to AGAR displayed this ESBL phenotype in 2020, although there was little change since 2018. This phenotype was significantly more common in hospital-onset compared to community-onset *E. coli* infections, with 1 in 5 (21.3%) demonstrating this pattern in hospital-onset infections compared to 13.5% for community-onset isolates. In hospital-onset *K. pneumoniae* complex isolates, this phenotype was also more common than for community-onset isolates (12.5% versus 9.1%), although the difference was not statistically significant.²

The prevalence of ESBLs also varied by state and territory. These variations were small for *E. coli*, but for *K. pneumoniae*, proportions were noticeably higher in Victoria and the Australian Capital Territory.²

Preventing and controlling resistance in *Escherichia coli* and *Klebsiella pneumoniae*

The strategies to prevent and control transmission of MDR *E. coli* and *K. pneumoniae* in healthcare settings are based on the requirements of the National Safety and Quality Health Service (NSQHS) Preventing and Controlling Infections Standard.²¹ These include:

- Surveillance of antimicrobial use and resistance
- Processes to apply standard and transmission-based precautions that are consistent with the current edition of the *Australian Guidelines for the Prevention and Control of Infection in Healthcare*²²
- A hand hygiene program
- Processes for maintaining a clean and safe environment
- Systems for the safe and appropriate prescribing and use of antimicrobials as part of an antimicrobial stewardship program.

These same strategies are also applicable in primary and community care settings and aged care homes.

Methods and considerations for interpreting the data

Data extraction

Data were extracted from the APAS system on 1 March 2022; detailed information on the attributes of the data extracted is available in the appendices.

Pathology services

At the time of data extraction, 10 large pathology services were contributing data to APAS:

- ACT Pathology (all public and some private Australian Capital Territory health services)
- Alfred Health (Victoria)
- Launceston General Hospital Pathology Service (Tasmania)
- Mater Pathology Brisbane – Queensland public and private patients
- Monash Health Service (Victoria)
- NSW Health Pathology covering the Sydney, South Western Sydney, South Eastern Sydney, Illawarra Shoalhaven, Hunter New England, Central Coast, Mid North Coast, Northern Sydney, and Northern NSW Local Health Districts and the Sydney Children’s Hospital Network (Randwick)
- Pathology Queensland (all Queensland Health public services)
- PathWest Laboratory Medicine (Western Australia)
- SA Pathology (public health catchments for South Australia)
- The Royal Hobart Hospital (Tasmania).

Historical data from 2006 were available from four of these pathology services: NSW Health Pathology (Sydney and South Western Sydney local health districts), Mater Pathology Brisbane, Pathology Queensland and SA Pathology (Table A1.1).

It is important to note that, for historical data, there may have been changes since 2006 in the number of facilities from which the pathology services have received isolates, and numbers are likely to have varied from year to year, along with laboratory criteria and methods. There have also been breakpoint changes over time.

In addition, several public laboratories have been reconfigured or renamed during the period to which the analyses relate; these changes are not addressed in detail in this report.

Sullivan Nicolaides Pathology has been an important early contributor to national passive surveillance through the provision of reports on resistance in isolates referred by hospitals, aged care homes, community and general practices in Queensland and Northern New South Wales specifically for AURA reports on antimicrobial use and resistance in human health.^{9, 10, 12, 13} Sullivan Nicolaides Pathology data are not incorporated in the analyses for this report, as the organisation does not submit data directly to APAS.

Representativeness

The distribution of the number of isolates for which data were available for all contributors (2015–2021) by state and territory was compared with the distribution of the Australian population using Australian Bureau of Statistics (ABS) Australian Demographic Statistics.²³

Jurisdictions with statewide public pathology services (Queensland, South Australia, Western Australia and the Australian Capital Territory) are most representative. Queensland is comprehensively represented due to the participation in APAS by Mater Pathology Brisbane. Data from Victoria are limited as there is only two contributing sites, and data analysed for this report are limited to Monash Health. Data are not available from the Northern Territory (Figure A1.1). New South Wales has, since APAS commenced, brought together all public laboratories as the statewide service NSW Health Pathology; the laboratory names used in this report reflect current naming conventions.

Isolates and specimen types

Data were only included where there were at least 30 isolates for each analysis. Analyses were conducted only when the proportion of isolates that were tested against a single antimicrobial was at least 75%. To minimise the impact of duplicate testing, and to avoid distortions created by testing of only selected, usually more resistant, isolates in some laboratories, only data from the first isolate, per specimen type, per patient, per year were used. Results from isolates detected in infection prevention and control and environmental sampling were excluded because they are not representative of isolates from clinical infections. Nine specimen types were defined for the purposes of analyses of APAS data (Table A1.2).

Setting

Where available, the settings from which the isolates were obtained were included in the analyses (Table A1.3). Currently, these include aged care, community, multi-purpose service, public hospital, and private hospital as assigned by the pathology service that contributed the data for the specimen. It is important to note that, for historical data, there may have been changes since 2006 in the range and acuity of services offered in some settings, particularly those currently categorised as multi-purpose services. Information about each of these changes is not routinely available.

In this report, aged care data are combined with data from settings other than hospitals or community, including multi-purpose services, in figures and tables due to a smaller sample size, limited representativeness across states and territories, and the potential impact of a change in referral patterns for one large pathology service for this setting from mid-2018.

Remoteness

The patients postcode of residence, where known, was used to stratify the data in terms of remoteness using the ABS Australian Statistical Geography Standard (ASGS).²⁴

The Remoteness Areas Structure within the ASGS divides Australia into five categories of remoteness on the basis of a measure of relative access to services. The five Remoteness Areas for Australia are major cities, inner regional, outer regional, remote and very remote.

Data characteristics

AMR surveillance involves the extraction of routine susceptibility testing results from laboratory information systems. Passive AMR surveillance differs in a number of ways from the targeted AMR surveillance conducted by AGAR for the AURA Surveillance System. These differences include:

- The range of agents tested against any given isolate tends to be smaller than with targeted AGAR surveillance
- Although there is some commonality between services, each contributor tests and reports different antimicrobials according to their local practice
- Three different susceptibility testing methods are used in clinical microbiology across Australia. These are the Clinical and Laboratory Standards Institute (CLSI)^{25, 26}, the Calibrated Dichotomous Sensitivity (CDS)²⁷ and the European Committee on Antimicrobial Susceptibility Testing (EUCAST).²⁸ Test results (categorical interpretations) are not always comparable between systems. For APAS, it is acknowledged that there are differences in the interpretation of results obtained by each method, and the Commission is working with stakeholders to promote alignment with a single method in Australia
- The results of duplicate testing are included in the data collected. Duplicate testing means that the same bacterial strain is tested and reported from repeated specimens and similar specimens from a single infection episode. This is appropriate clinical laboratory practice from a patient management perspective. The impact of these duplicates is minimised for analyses of APAS data by using algorithms based on resistance patterns and selected time periods for which duplicates are not counted. Only the first isolate for the first specimen per specimen type per year is included in the dataset for analyses. A repeat isolate from the same specimen type is not included

- Only categorical data are available through APAS, namely the reporting categories of 'susceptible', 'intermediate' and 'resistant'; these categories are defined by interpretive criteria for resistance testing that are commonly called breakpoints
- Although there is some commonality between services, each contributor tests and reports different antimicrobials according to their local practice.

ESBL phenotype

ESBL-producing isolates will be detected using the CLSI/EUCAST/CDS ceftriaxone or cefotaxime 'susceptible' breakpoint of 1 mg/L. The CLSI 'susceptible' breakpoint of 4 mg/L for ceftazidime is less reliable for ESBL detection and has not been included in these analyses.

Due to differences in testing and reporting practices across the APAS laboratories, the following antimicrobial agents were analysed:

- Ceftriaxone (non-urine isolates): ESBL phenotype defined as MIC > 1 mg/L (EUCAST and CLSI, intermediate + resistant; for CDS, resistant) for ceftriaxone or cefotaxime, if ceftriaxone not tested
- Ceftriaxone (urine isolates): due to cascade reporting rules used by several laboratories, ceftriaxone resistance is an adjusted estimate of the percentage resistant, based on the available data and that the primary susceptibility test (cefazolin) was susceptible.

Thirty-two different laboratories were identified from the 10 pathology services that contribute to APAS. Each laboratory within a group had similar reporting practices, which enabled the analyses of extracted data according to the susceptibility testing method used. The methods used by APAS contributor laboratory groups in each state and territory are currently as follows:

- Western Australia: CLSI [$n = 2$]
- Australian Capital Territory [$n = 1$], Queensland [$n = 11$], Tasmania [$n = 2$], South Australia [$n = 2$], Victoria [$n = 2$]: EUCAST
- New South Wales: EUCAST [$n = 5$], CLSI [$n = 2$], CDS [$n = 5$].

Results

Between 2006 and 2021, 1,007,638 *E. coli*, and 151,851 *K. pneumoniae* from the four long-term APAS contributor pathology services were included in the analyses. The isolates were from urine specimens (88.2% and 75.3%, for *E. coli* and *K. pneumoniae* respectively), blood culture (5.9%, 8.6% for *E. coli* and *K. pneumoniae* respectively), tissue/fluid/pus/prosthesis (4.2%, 9.0% for *E. coli* and *K. pneumoniae* respectively), respiratory specimens (0.9%, 6.0% for *E. coli* and *K. pneumoniae* respectively) and other specimen types (0.7%, 1.1% for *E. coli* and *K. pneumoniae* respectively).

It is important to note that urine and blood specimen results generally reflect resistance in isolates from community settings, whilst respiratory and tissue/fluid/pus/prosthesis specimens are more likely to have been collected in specialised hospital settings such as intensive care units (ICUs). Laboratories may also selectively test and report on respiratory and tissue/fluid/pus/prosthesis specimens for these acute admitted care settings.

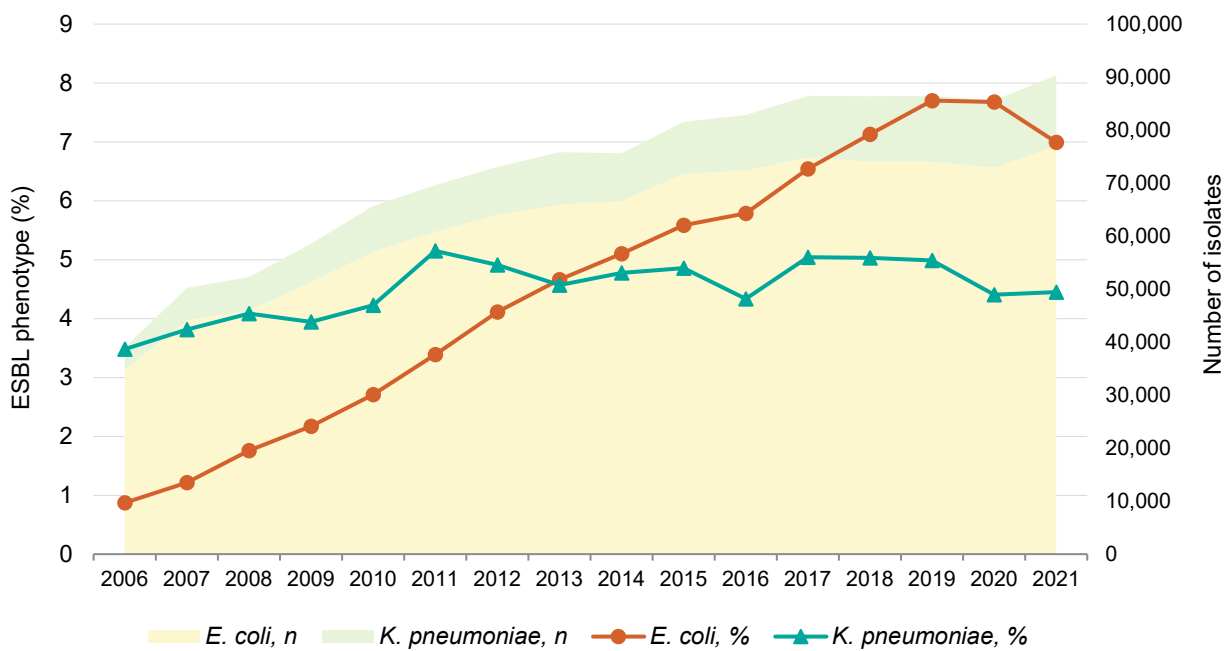
Similar distribution of specimen types was observed when the data from all APAS contributors were examined over the period 2015 to 2021. Data were available for 888,110 *E. coli* and 104,626 *K. pneumoniae* isolates for this period.

There was an increasing number of *E. coli* isolates in the four long-term APAS contributors from 2006 to 2014. Since 2015, total numbers were relatively consistent until another increase in 2021. There was a steady increase in the number of *K. pneumoniae* isolates each year from 2006, with totals generally six-fold lower than for *E. coli*. The variability may reflect expansion of the patient bases served by the contributors, changes in infection sampling practices, or both.

Figure 1 shows the 16-year trends in ESBLs in *E. coli* and *K. pneumoniae* reported by the four long-term APAS contributors.

ESBLs in *E. coli* isolates increased from 0.9% in 2006 to a peak of 7.7% in 2019 and 2020, and decreased to 7.0% in 2021. In *K. pneumoniae*, ESBLs remained stable from 2006 to 2021. The ESBL phenotype was more common in *K. pneumoniae* than *E. coli* from 2006 to 2013, and subsequently it has been more common in *E. coli*.

Figure 1: Percentage of *Escherichia coli* and *Klebsiella pneumoniae* with ESBL phenotype, long-term APAS contributors, 2006–2021



ESBL = extended-spectrum β -lactamase; *n* = denominator for total number of isolates

Notes:

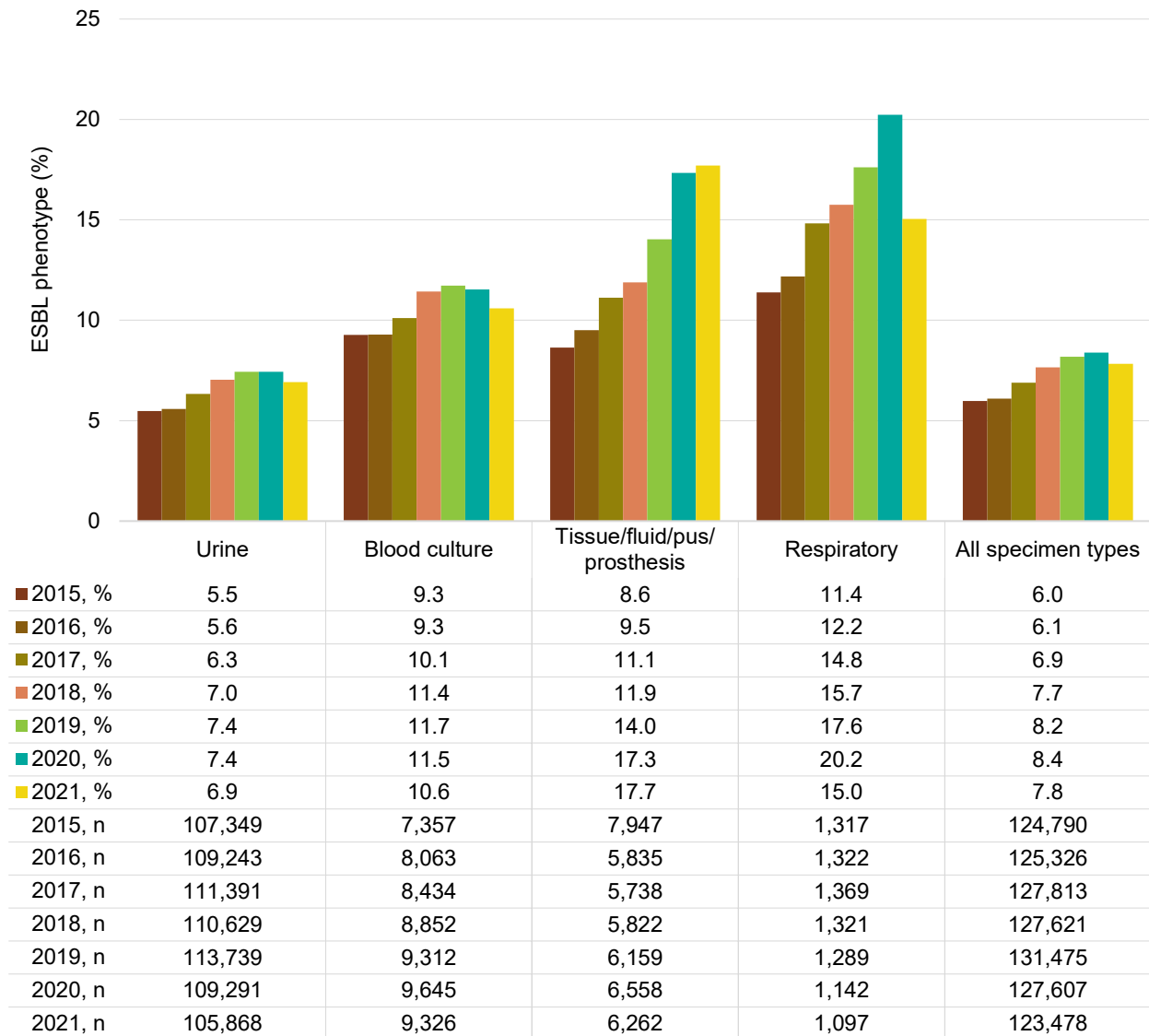
1. ESBL phenotype = ceftriaxone or cefotaxime MIC > 1 mg/L. Refer to Methods and considerations for interpreting the data.
2. The four pathology services that contributed continuously since 2006 were Mater Pathology Brisbane, NSW Health Pathology (South Western Sydney and Sydney Local Health Districts), Pathology Queensland and SA Pathology.

ESBL phenotype by specimen type

Figure 2 shows the trends in ESBL phenotype by specimen type in *E. coli*, reported from all APAS contributors from 2015 to 2021. There was an increasing percentage of ESBLs in *E. coli* isolates from tissue/fluid/pus/prosthesis and respiratory infections during that period.

The percentage of ESBLs in *K. pneumoniae* was lower than in *E. coli* across all specimen types and remained stable from 2015 to 2021 (Figure 3).

Figure 2: Percentage of *Escherichia coli* with ESBL phenotype by specimen type, APAS contributors, 2015–2021*

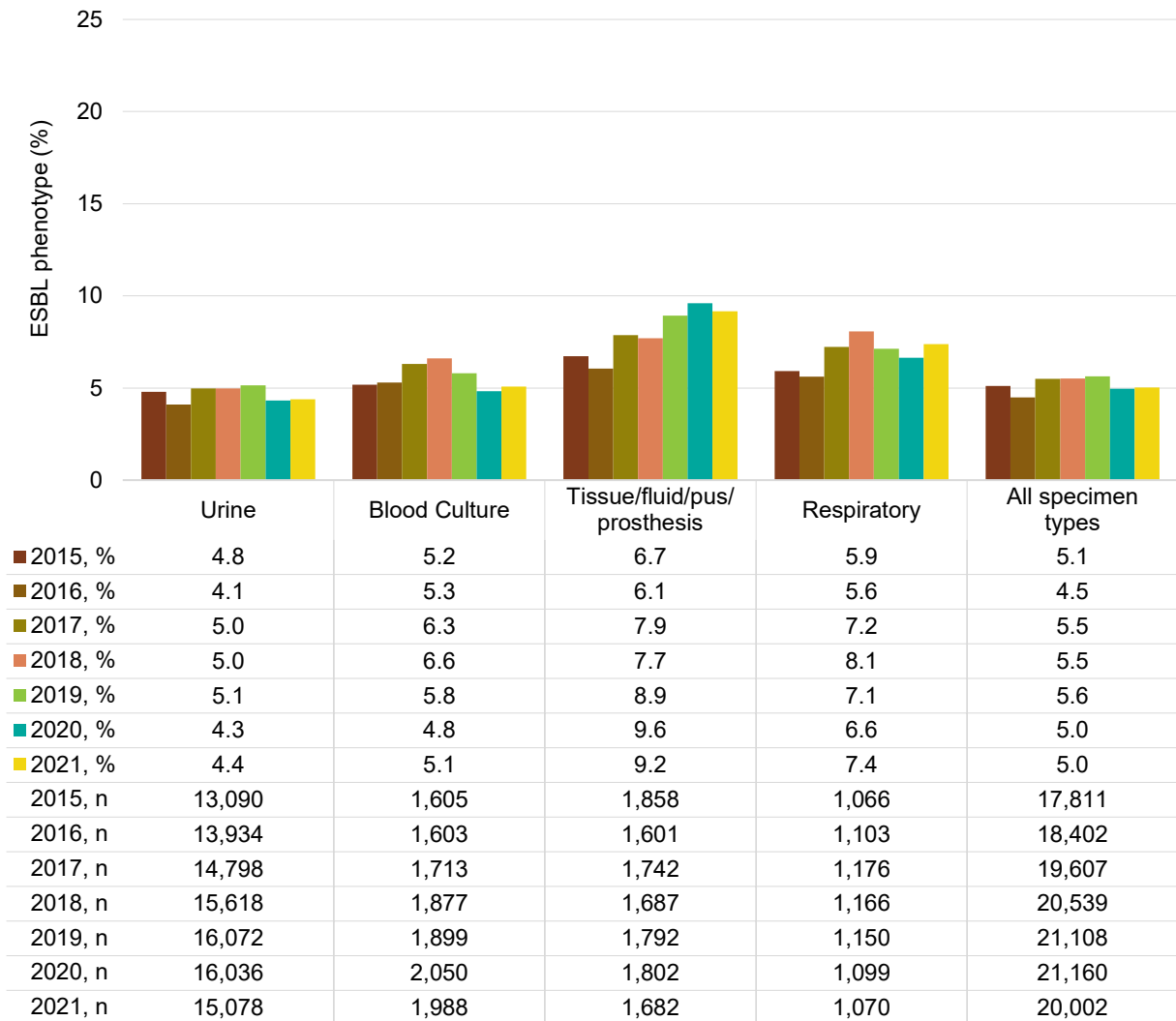


ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

* All 10 pathology service contributors to APAS (see Table A1.1)

Note: ESBL phenotype = ceftriaxone or cefotaxime MIC > 1 mg/L. Refer to Methods and considerations for interpreting the data.

Figure 3: Percentage of *Klebsiella pneumoniae* with ESBL phenotype by specimen type, APAS contributors, 2015–2021*



ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

* All 10 pathology service contributors to APAS (see Table A1.1)

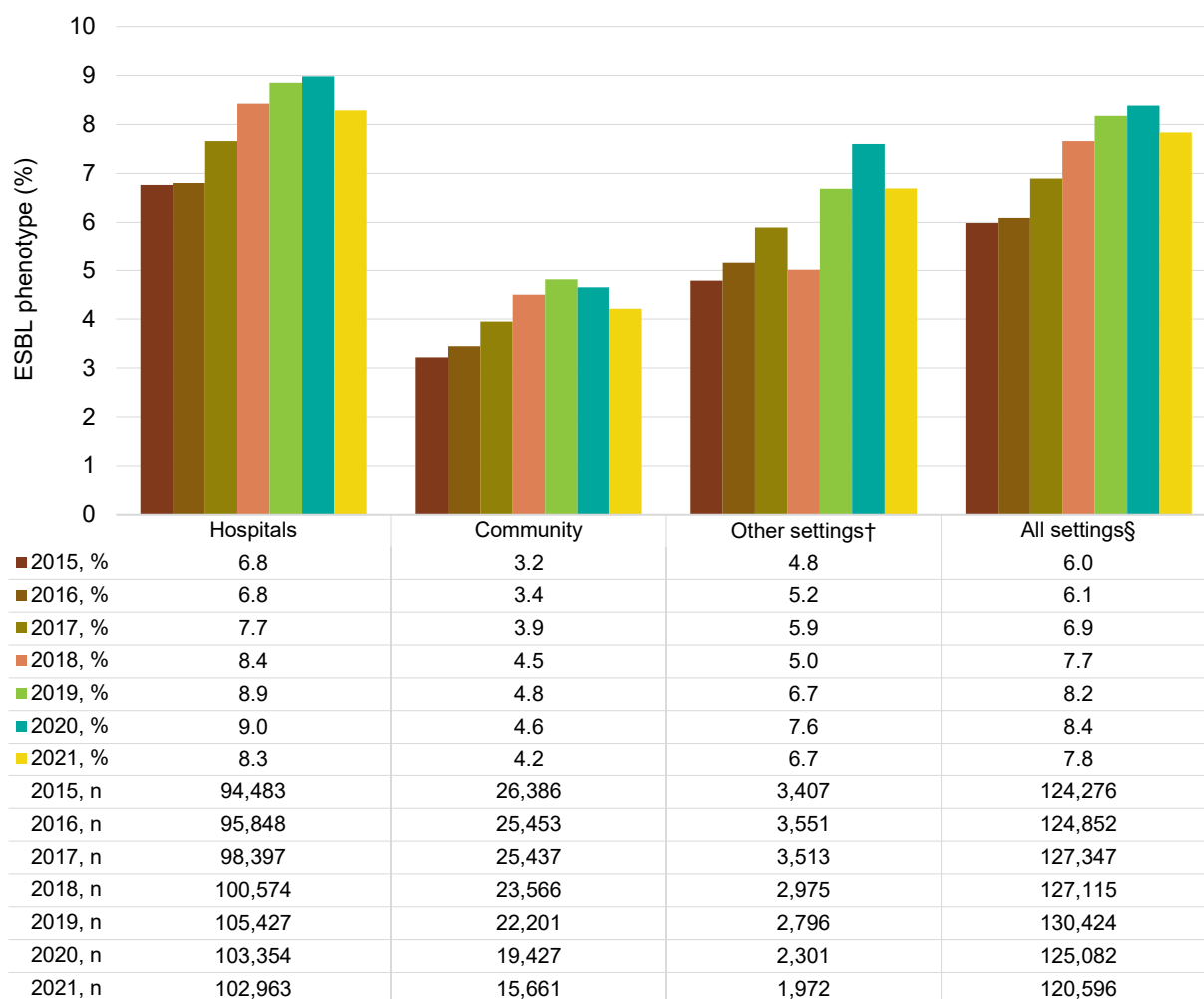
Note: ESBL phenotype = ceftriaxone or cefotaxime MIC > 1 mg/L. Refer to Methods and considerations for interpreting the data.

ESBL phenotype by setting

Settings were categorised into aged care home, community, multi-purpose service, and hospital (public and private). Of 888,110 *E. coli* isolates from APAS contributors for 2015 to 2021, 99.1% were able to be classified by setting. Of these isolates, 79.7% were from hospitals (public and private), and 18.0% from community settings (Figure 4). Data relating to aged care homes were combined with data from settings other than hospitals or community, including multi-purpose services, due to smaller numbers and limited representativeness nationally.

There was an upward trend in ESBL phenotype in *E. coli* from all settings between 2015 and 2020 (6.0%, 2015 to 8.3%, 2020), and a slight decline in 2021 (7.7%). The highest rates of the ESBL phenotype in *E. coli* was seen in isolates from patients in hospitals, followed by "other" settings, which included aged care homes (Figure 4).

Figure 4: Percentage of *Escherichia coli* with ESBL phenotype by setting, APAS contributors, 2015–2021*



ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

* All 10 pathology service contributors to APAS (see Table A1.1)

† Settings other than hospitals or community, including multi-purpose services and aged care homes

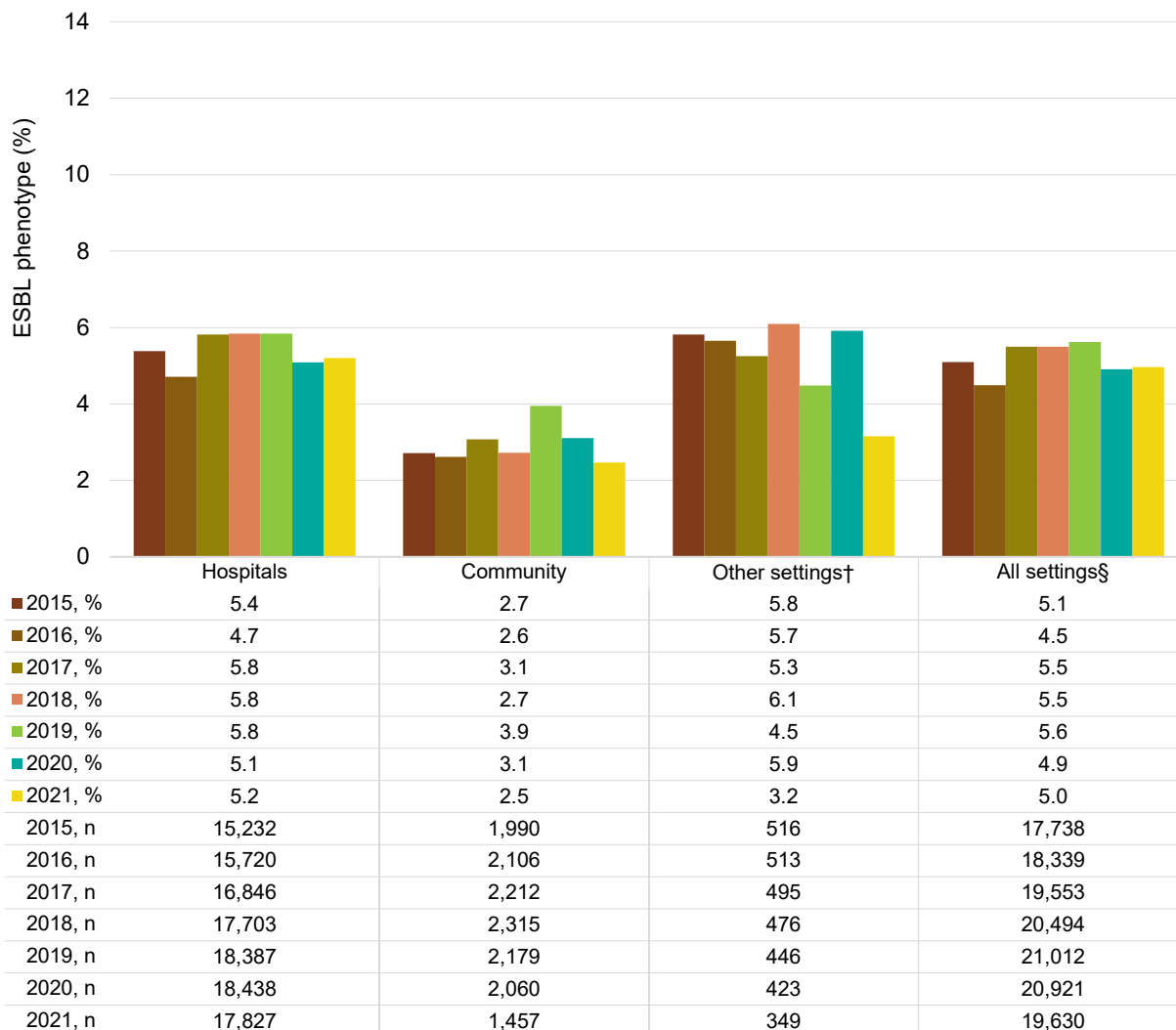
§ Where setting is known

Note: Hospitals = public and private.

Of 138,629 *K. pneumoniae* isolates, 99.3% were able to be classified by setting. Of these isolates, 87.3% were from hospitals (public and private), and 10.4% from community settings (Figure 5). The percentage of ESBL phenotype was generally lower in *K. pneumoniae* isolates compared with

E. coli isolates and remained steady throughout the seven-year period from 2015 to 2021 – the average was 5.2%, and the range was 4.5% (2016) to 5.6% (2019) for all settings (Figure 5).

Figure 5: Percentage *Klebsiella pneumoniae* with ESBL phenotype by setting, APAS contributors, 2015–2021*



ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

* All 10 pathology service contributors to APAS (see Table A1.1)

† Settings other than hospitals or community, including multi-purpose service and aged care homes

§ Where setting is known

Note: Hospitals = public and private.

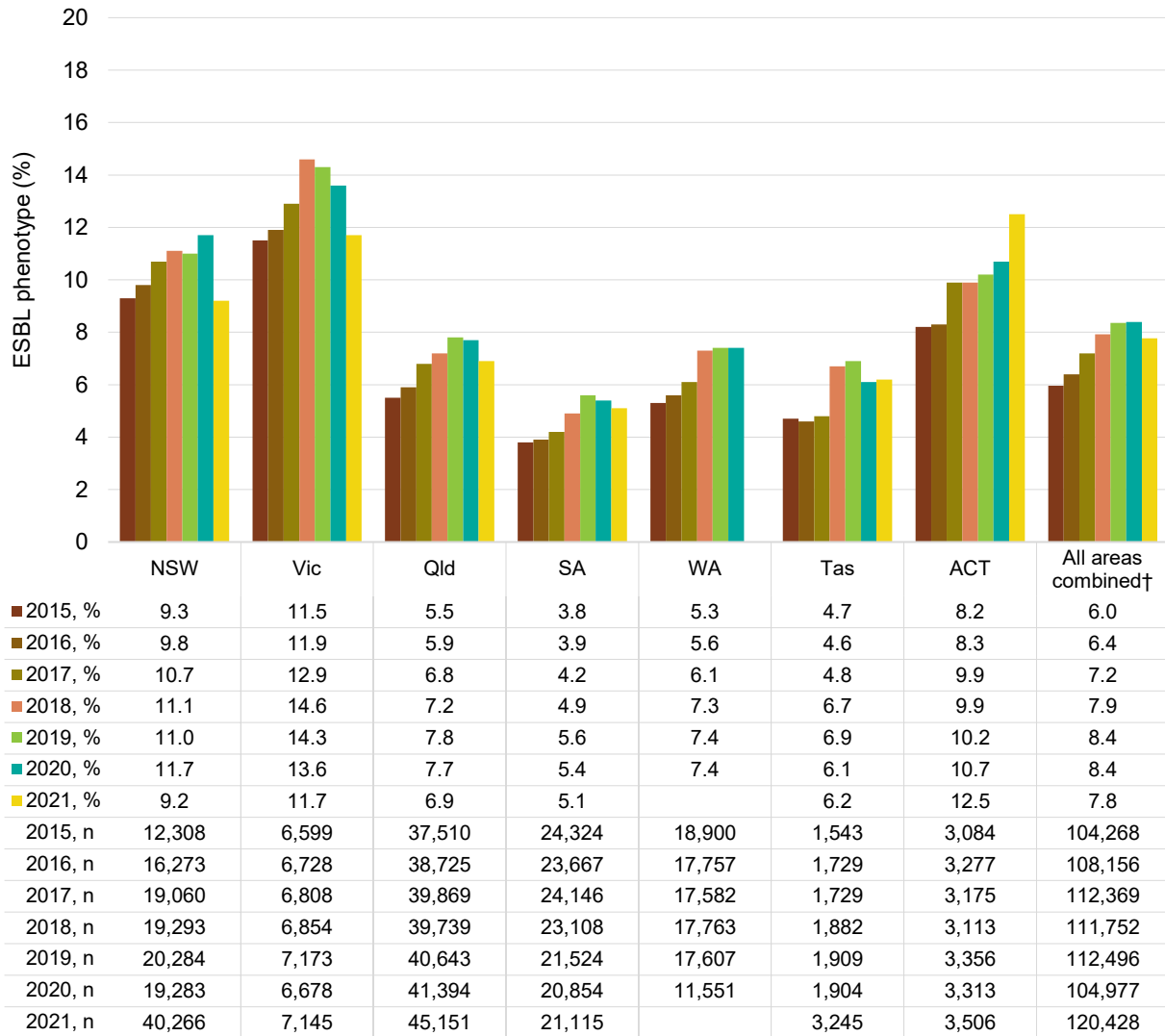
ESBL phenotype by state and territory

Data on ESBL phenotype were analysed from across the states and territories by APAS data, based on patient's postcode of residence.

For *E. coli*, ESBL phenotype was generally higher in patients who resided in Victoria, New South Wales, and the Australian Capital Territory (Figure 6). In 2021, the Australian Capital Territory was the only jurisdiction where an increased rate was observed.

In *K. pneumoniae*, the proportion with ESBL phenotype was generally lower than that seen in *E. coli*, although little difference was seen in Victoria, South Australia and Tasmania (Figure 7).

Figure 6: Percentage of *Escherichia coli* with ESBL phenotype by state and territory, APAS contributors, 2015–2021*



ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

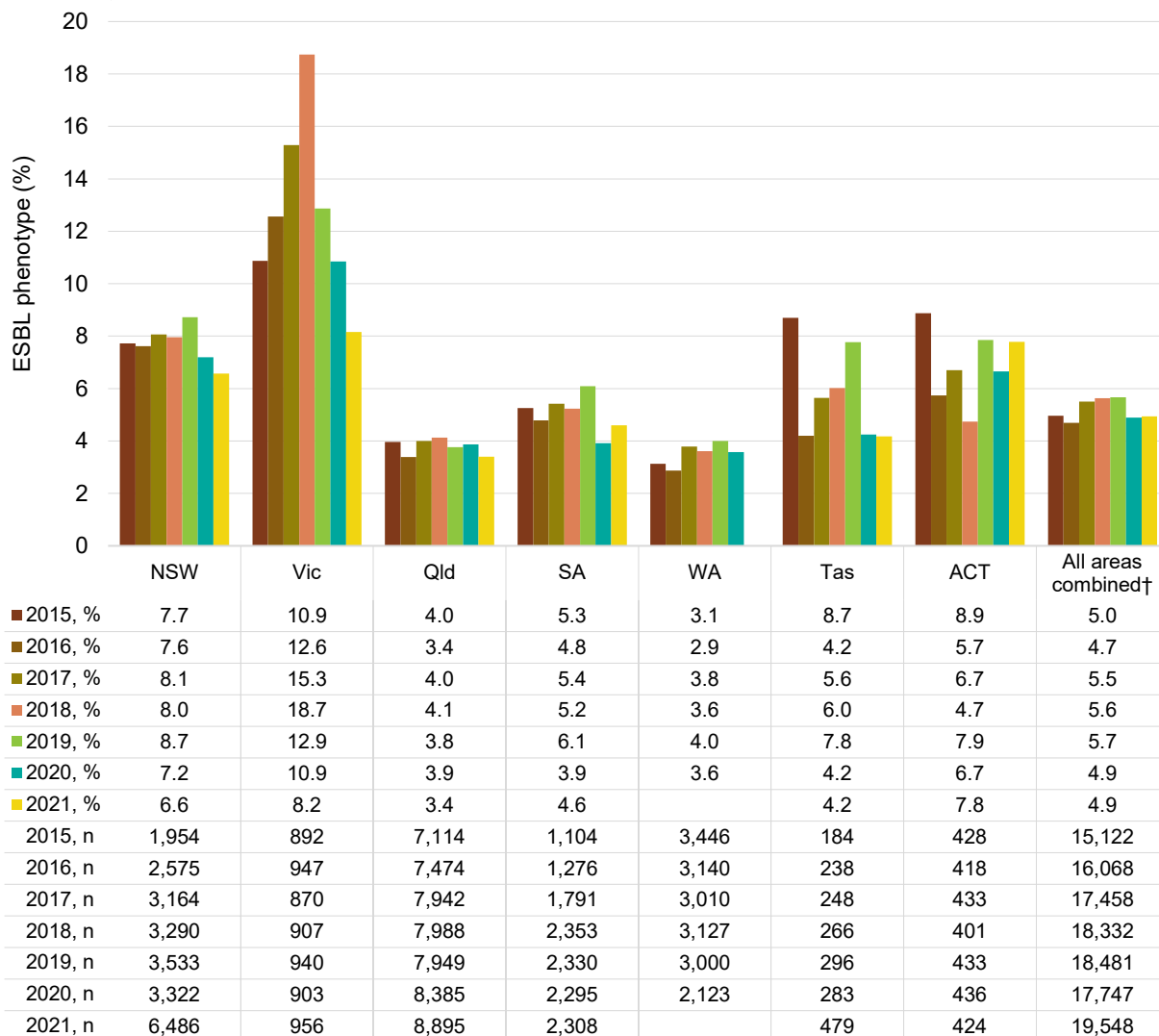
* All 10 pathology service contributors to APAS (see Table A1.1)

† Where remoteness area is known

Notes:

1. State and territory based on patient's postcode of residence. No data available from pathology services in the Northern Territory.
2. No data currently available from PathWest since mid-2020.
3. Patient's postcode of residence was only available for NSW Health Pathology North from 2021.

Figure 7: Percentage of *Klebsiella pneumoniae* with ESBL phenotype by state and territory, APAS contributors, 2015–2021*



ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

* All 10 pathology service contributors to APAS (see Table A1.1)

† Where remoteness area is known

Notes:

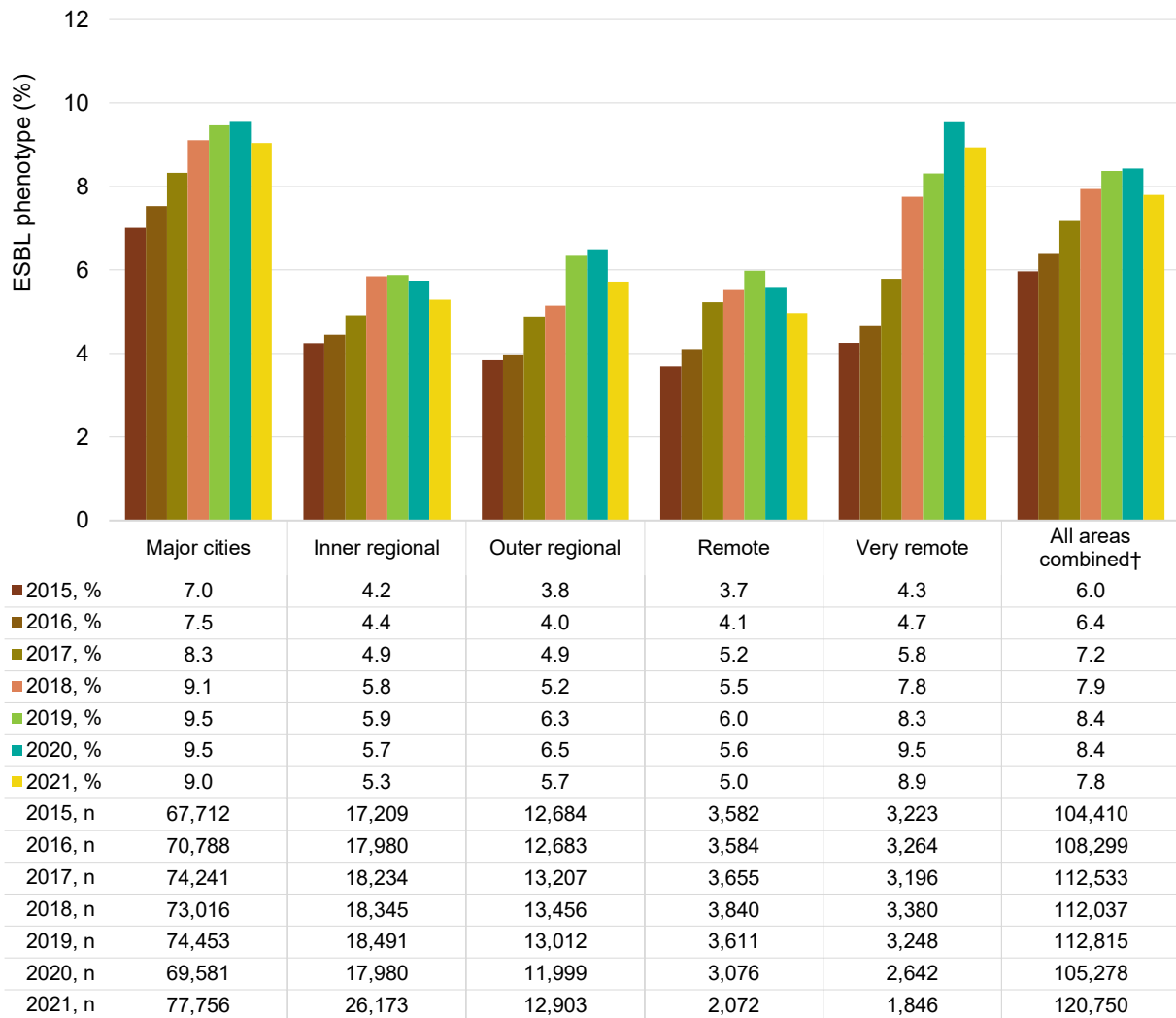
1. State and territory based on patient's postcode of residence. No data available from pathology services in the Northern Territory.
2. No data currently available from PathWest since mid-2020.
3. Patient's postcode of residence was only available for NSW Health Pathology North from 2021.

ESBL phenotype by remoteness area

Analyses of APAS data indicate that *E. coli* with ESBL phenotype are currently more prevalent in isolates from major cities and very remote areas of Australia. There was an increasing trend in ESBL phenotype across all remoteness areas from 2015 to 2020, and a slight fall in 2021 (Figure 8).

For *K. pneumoniae*, there was little difference in the proportion of ESBL phenotype from 2015 to 2021 (Figure 9).

Figure 8: Percentage of *Escherichia coli* with ESBL phenotype by remoteness area, APAS contributors, 2015–2021*



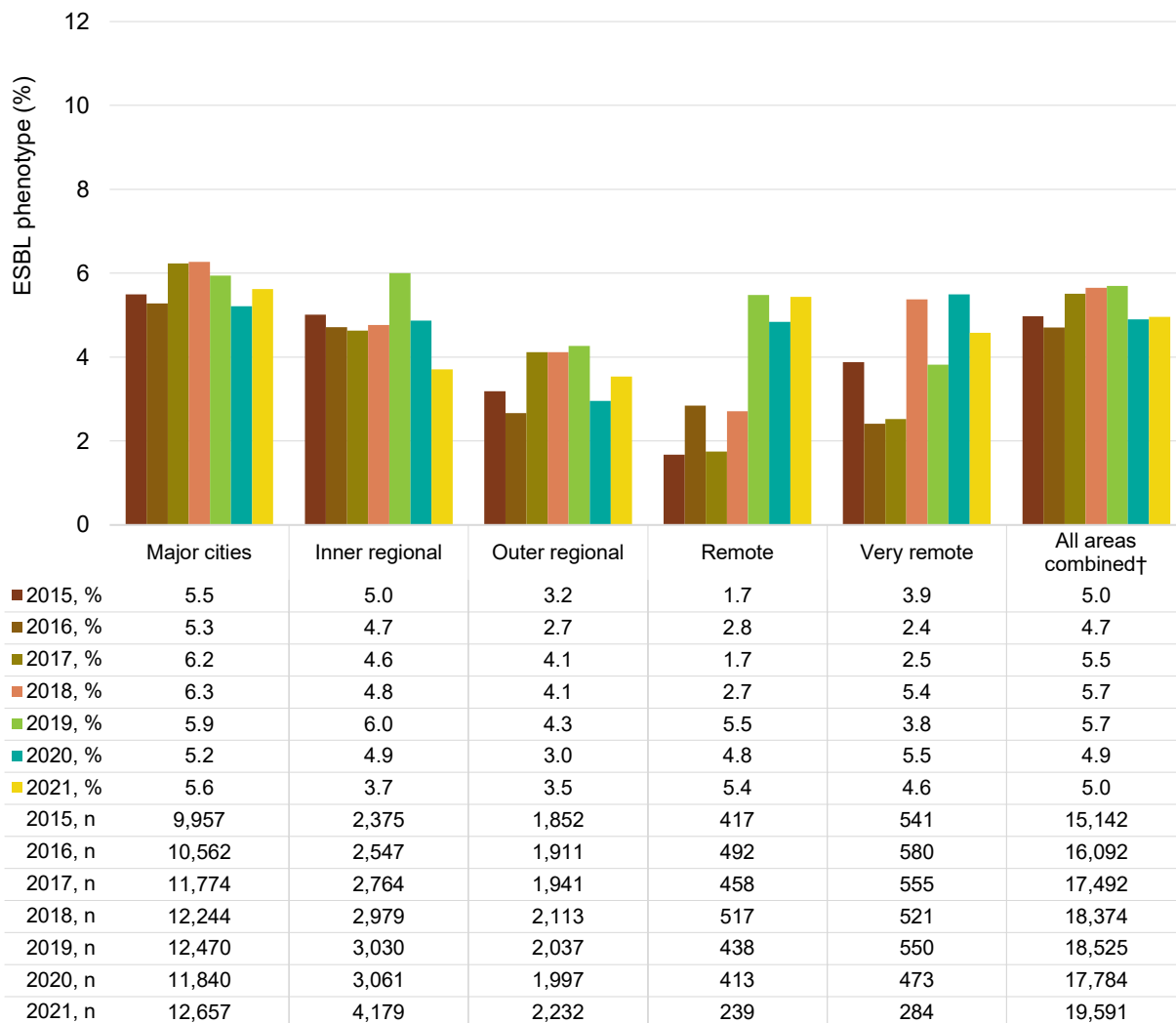
ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

* All 10 pathology service contributors to APAS (see Table A1.1)

† Where remoteness area is known

Note: Remoteness area is based on postcode of patient's place of residence.

Figure 9: Percentage of *Klebsiella pneumoniae* with ESBL phenotype by remoteness area, APAS contributors, 2015–2021*



ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates

* All 10 pathology service contributors to APAS (see Table A1.1)

† Where remoteness area is known

Note: Remoteness area is based on postcode of patient's place of residence.

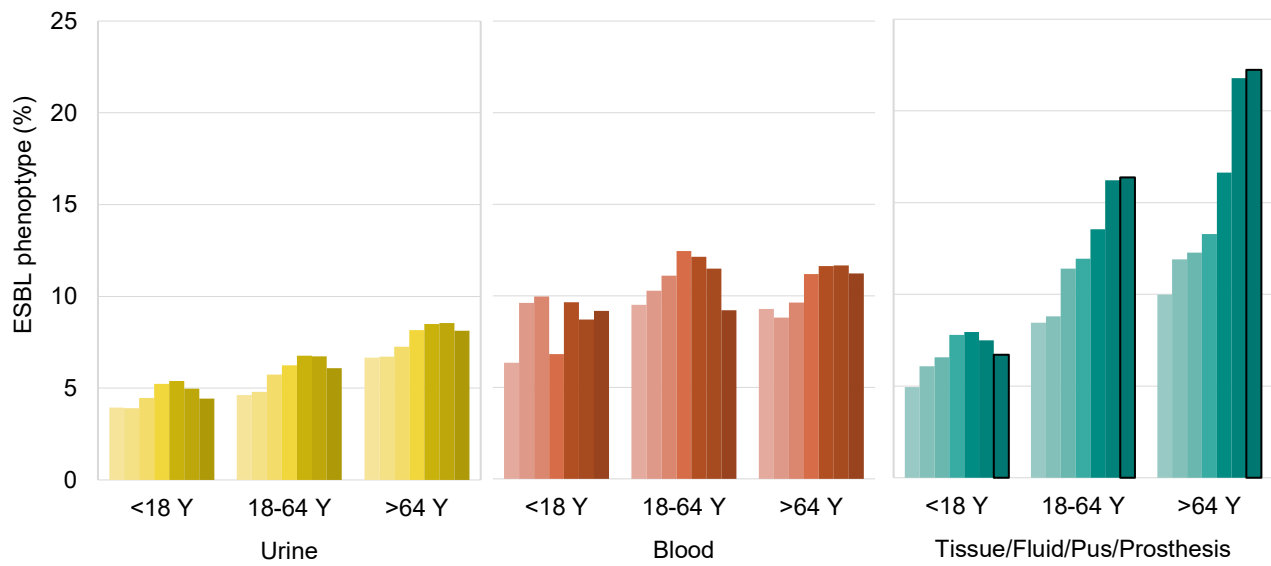
ESBL phenotype by age group

Of all *E. coli* and *K. pneumoniae* isolates from APAS contributors for 2015 to 2021, 9.4% and 5.2% respectively were from paediatric patients (less than 18 years). The proportion of *E. coli* with ESBL phenotype was lowest among paediatric patients and highest in persons aged over 64 years (Figure 10).

The highest proportion of *E. coli* with ESBL phenotype was seen in isolates from tissue/fluid/pus/prosthesis infections, which may reflect an association with health care. In 2021, the ESBL rate in *E. coli* from tissue/fluid/pus/prosthesis infections was almost 3-fold higher in persons aged 18 years or more, increasing from 2-fold higher in 2015.

In *K. pneumoniae*, there was little difference in the rate of ESBL phenotype observed in the three age groups, although it was slightly higher in persons aged over 64 years for tissue/fluid/pus/prosthesis (Figure 11).

Figure 10: Percentage of *Escherichia coli* with ESBL phenotype, by specimen type and age group, APAS contributors, 2015-2021*



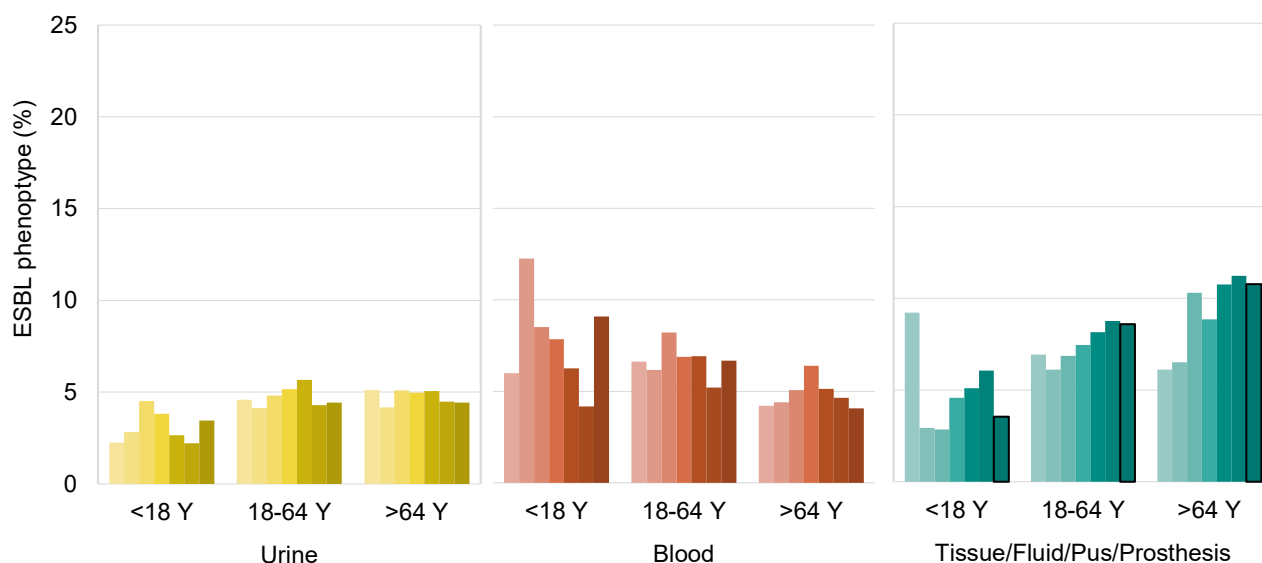
	Urine			Blood			Tissue/Fluid/Pus/Prosthesis		
	<18 Y	18-64 Y	>64 Y	<18 Y	18-64 Y	>64 Y	<18 Y	18-64 Y	>64 Y
2015, %	2.3	4.6	5.1	6.0	6.6	4.2	9.2	6.9	6.1
2016, %	2.8	4.1	4.2	12.2	6.2	4.4	2.9	6.1	6.5
2017, %	4.5	4.8	5.1	8.5	8.2	5.1	2.9	6.9	10.3
2018, %	3.8	5.2	5.0	7.8	6.9	6.4	4.6	7.5	8.9
2019, %	2.7	5.7	5.1	6.3	6.9	5.1	5.1	8.1	10.7
2020, %	2.2	4.3	4.5	4.2	5.2	4.6	6.1	8.8	11.2
2021, %	3.4	4.4	4.4	9.1	6.7	4.1	3.5	8.6	10.8
2015, n	621	4,615	7,853	50	604	951	141	880	835
2016, n	638	4,895	8,401	49	600	954	102	899	599
2017, n	707	5,124	8,966	47	621	1,045	140	919	679
2018, n	785	5,327	9,505	51	683	1,142	153	898	632
2019, n	792	5,430	9,849	32	679	1,187	137	945	707
2020, n	719	5,446	9,868	48	731	1,269	132	936	730
2021, n	754	4,970	9,352	44	689	1,253	113	873	696

ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates; Y = years of age

* All 10 pathology service contributors to APAS (see Table A1.1)

Note: There were insufficient respiratory isolates for analyses.

Figure 11: Percentage of *Klebsiella pneumoniae* complex with ESBL phenotype, by specimen type and age group, APAS contributors, 2015-2021*



	<18 Y	18-64 Y	>64 Y	<18 Y	18-64 Y	>64 Y	<18 Y	18-64 Y	>64 Y
	Urine			Blood			Tissue/Fluid/Pus/Prosthesis		
2015, %	3.9	4.6	6.7	6.3	9.5	9.3	4.9	8.5	10.0
2016, %	3.9	4.8	6.7	9.6	10.3	8.8	6.1	8.8	11.9
2017, %	4.5	5.7	7.3	10.0	11.1	9.6	6.6	11.4	12.3
2018, %	5.2	6.2	8.2	6.8	12.4	11.2	7.8	11.9	13.3
2019, %	5.4	6.8	8.5	9.6	12.1	11.6	8.0	13.5	16.6
2020, %	5.0	6.7	8.6	8.7	11.5	11.7	7.5	16.2	21.8
2021, %	4.4	6.1	8.1	9.2	9.2	11.2	6.7	16.4	22.2
2015, n	10,695	48,247	48,400	205	2,368	4,784	871	4,118	2,955
2016, n	10,600	48,830	49,810	229	2,570	5,260	707	3,167	1,957
2017, n	10,806	48,510	52,066	241	2,667	5,520	654	3,142	1,932
2018, n	10,732	48,626	51,268	264	2,723	5,860	681	3,175	1,958
2019, n	11,123	49,438	53,176	228	2,918	6,160	679	3,345	2,127
2020, n	10,573	46,655	52,054	207	2,920	6,513	667	3,508	2,378
2021, n	10,422	43,927	51,516	229	2,683	6,410	581	3,308	2,369

ESBL = extended-spectrum β -lactamase; n = denominator for total number of isolates; Y = years of age

* All 10 pathology service contributors to APAS (see Table A1.1)

Note: There were insufficient respiratory isolates for analyses.

International comparisons

Rates of ESBL production have steadily increased over the last decade for both *E. coli* and *K. pneumoniae* in the developed world.⁶ The rates of ESBL producers among *E. coli* urinary strains at hospitals in the United States increased from 7.8% in 2010 to 18.3% in 2014, but this was as high as 27.7% for strains representing hospital-acquired infection in 2014, the majority of which produced CTX-M-15.³ For *K. pneumoniae*.

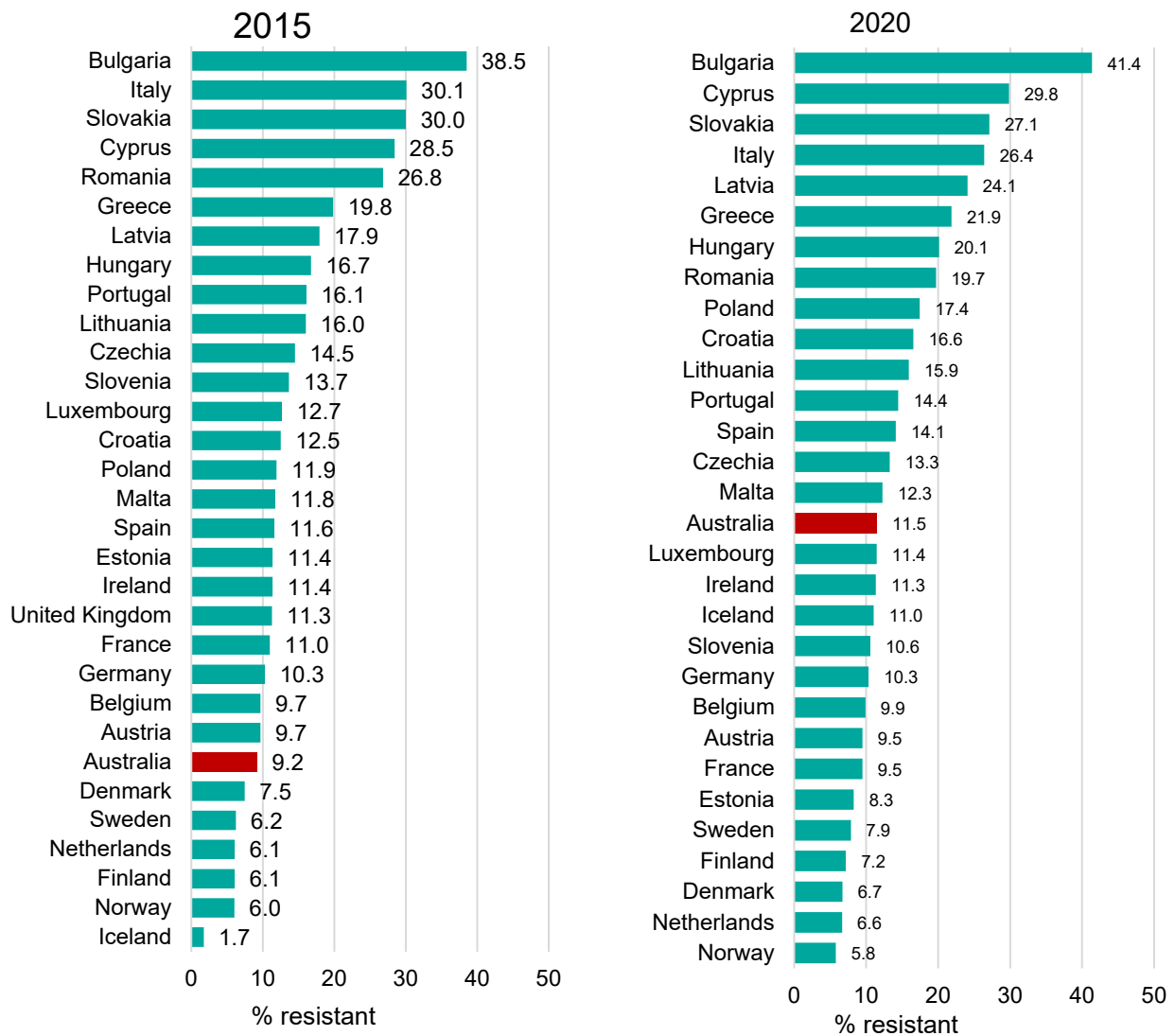
In Europe, the rates of ESBL producers differ significantly for both *E. coli* and *K. pneumoniae* depending on the regions, with very low rates observed in Northern European countries and much higher rates seen in Eastern and Southern European countries.^{29, 30} In 2016, less than 13% of *E. coli* and 14% *K. pneumoniae* produced an ESBL in Canada, but the rates appear to be increasing.^{31, 32}

In Japan, the rates of ESBL producers were around 30% *E. coli* and up to 10% in *K. pneumoniae*.⁶

Data from APAS can be compared with data from the European Antimicrobial Resistance Surveillance Network (EARs-Net) program³³, as both programs examine resistance in bacterial pathogens found in blood cultures.

In 2020, Australia ranked towards the middle in rates of resistance to third-generation cephalosporins in *E. coli*; it was ranked seventh lowest in 2015 (Figure 12). Third-generation cephalosporin resistance in *K. pneumoniae* was low by comparison (Figure 13).

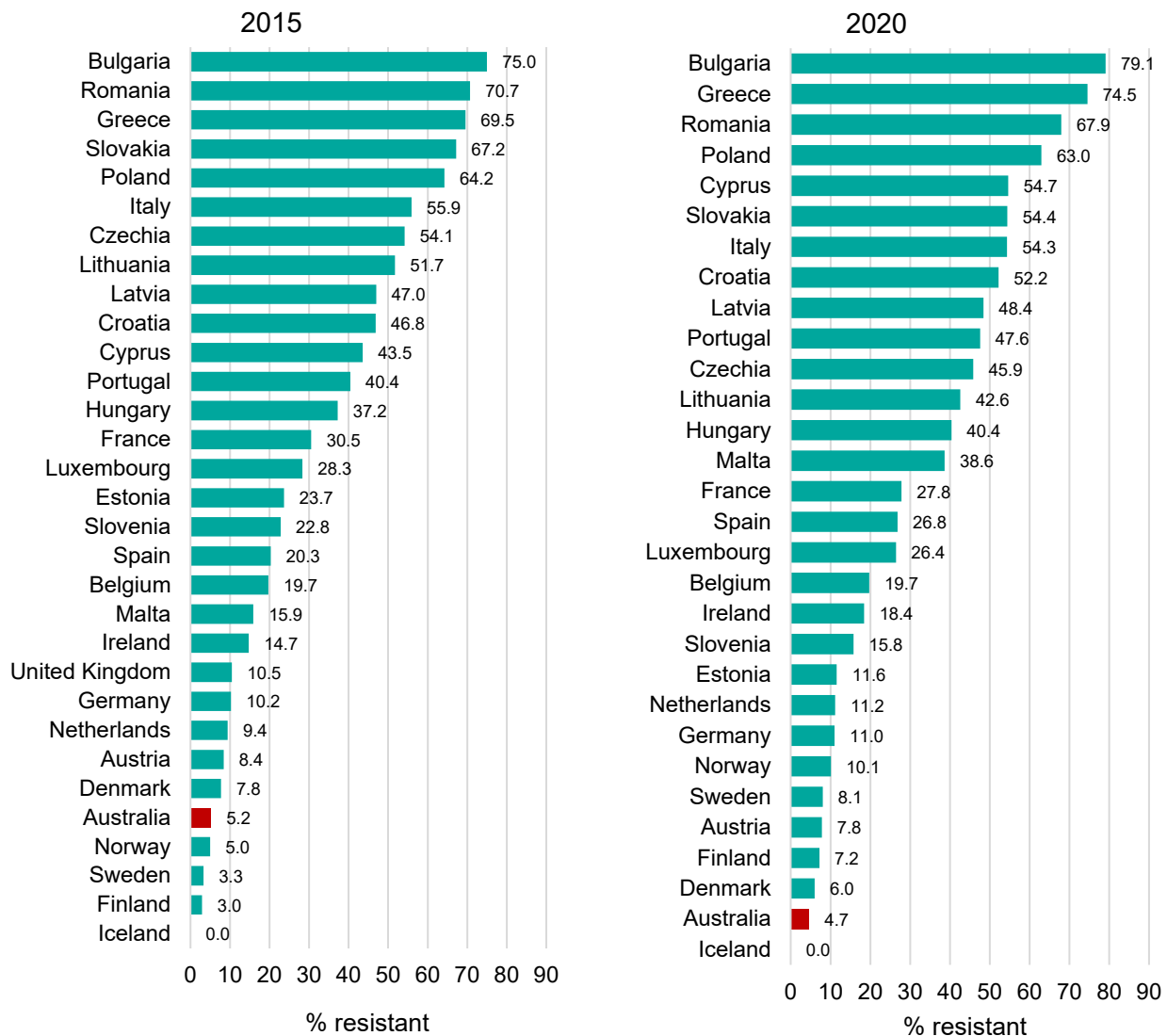
Figure 12: Comparison of *Escherichia coli* with third-generation cephalosporin resistance in Australia (APAS contributors) and European countries, blood culture isolates, APAS contributors, 2015 and 2020



Note: Excludes the United Kingdom for 2020.

Source: EARS-Net (Europe)^{29, 33}

Figure 13: Comparison of *Klebsiella pneumoniae* complex with third-generation cephalosporin resistance in Australia (APAS contributors) and European countries, blood culture isolates, APAS contributors, 2015 and 2020



Note: Excludes the United Kingdom for 2020.

Source: EARS-Net (Europe)^{29, 33}

Discussion

AMR remains a risk to patient safety because it reduces the number and effectiveness of antimicrobials available to treat infections, and potentially increases morbidity and mortality associated with infections caused by MDR organisms. Increasing resistance may limit future capacity to perform medical procedures such as organ transplantation, cancer chemotherapy, diabetes management and major surgery.

Analyses of APAS data on ESBL phenotypes in *E. coli* and *K. pneumoniae* for the period 2006 to 2021 showed increasing rates of this resistance in *E. coli* in health and community settings, and higher rates of this resistance in *E. coli*. This is consistent with global trends in this type of resistance.

The analyses also showed differences in rates of resistance in these bacteria based on remoteness, as determined by postcode of the patient's place of residence. This finding is consistent with data on other resistances, such as MDR *Staphylococcus aureus*.¹³ However, the reasons for these differences in relation to ESBL phenotype are not readily discernible. Ongoing surveillance is required to assist with improving understanding of the differences based on remoteness.

Analyses of AGAR bacteraemia data have shown that the dominance of ESBLs in *E. coli* since 2013 is due to increasing prevalence of the more virulent ST131 clone which is associated with CTX-M β -lactamases. These strains also demonstrate co-resistance to fluoroquinolones and trimethoprim–sulfamethoxazole, and as such there are limited options for treatment of these strains with oral antimicrobial agents in the community.

It is of serious concern that resistances to common antimicrobials used for treatment of infections continue to increase in *E. coli*, which is the most common cause of UTIs in community settings. Resistance was highest among people aged greater than 64 years. If people in this age group are residents of aged care homes, they often have urine specimens collected, and if *E. coli* is isolated then this is reported as a potential pathogen along with susceptibilities. Even though there are strong recommendations to not treat patients with asymptomatic bacteriuria, surveillance of antimicrobial use in aged care homes has shown that many residents are prescribed antimicrobials for this condition, and many are treated based on a laboratory report.³⁴ This results in a spiral of antimicrobial use in aged care settings and potential to maintain selective pressure on AMR development.

There are also implications for the health system, and for older people, because of the levels of AMR. For residents of aged care homes, the combination of infection prevention and control challenges, and well-documented high levels of inappropriate antimicrobial use creates the potential for ongoing transmission of resistance and spread into the community and to healthcare settings.

This situation also has a potential impact on demand for admitted care in hospital and hospital in the home settings. For example, a UTI such as cystitis or pyelonephritis in a young person may require intravenous antimicrobial treatment because of the limited availability of oral treatment options.

The primary mode of transmission of these organisms in healthcare settings is the hands of clinical staff. Patients may also spread infection by touching their own urinary catheter or wound drainage tube. As these are bowel flora, persistence of carriage can be greater than 12 to 24 months and is likely more prolonged in patients whose microbiome is disturbed by repeated courses of antimicrobials.³⁵ This is an ongoing concern in aged care homes, where the volume of inappropriate antimicrobial use is high.³⁴

Actions that the Commission will take to support prevention and control of the development and transmission of resistant *E. coli* and *K. pneumoniae* include:

- Educating clinicians and consumers regarding how resistance develops, how to prevent the spread of resistant organisms, and the importance of appropriate antimicrobial prescribing
- Promoting appropriate risk assessment and management processes for gram-negative bacteria resistance as a core part of clinical assessment of recent travellers and patients admitted to high-risk services, such as intensive care and severe burn
- Promoting appropriate protocols for assessment of all patients with infections who are admitted to health service organisations, including personal history of colonisation or infection with resistant organisms, recent travel history, and recent antimicrobial exposure
- Promoting rigorous infection prevention and control protocols, such as transmission-based precautions and patient placement in high-risk settings; and processes to detect carriage of resistance to direct appropriate antimicrobial therapies for patients at high risk of complications, such as those in intensive care or with febrile neutropenia
- Promoting comprehensive infection prevention and control programs in hospital, community and aged care settings – including hand hygiene, application of standard and transmission-based precautions, routine and targeted environmental cleaning, and waste management - to minimise environmental contamination and reservoirs
- Promoting effective antimicrobial stewardship (AMS) programs to support appropriate prescribing in hospital, community and aged care settings – reducing the inappropriate use of antimicrobials reduces selection pressure for resistance in bacteria
- Promoting antimicrobial prescribing, informed by *Therapeutic Guidelines: Antibiotic*⁸ or local health service organisation guidelines which are tailored to the local epidemiology of resistance
- Ensuring the availability of AMS and AMR data on local ESBL/gram-negative resistance profiles to hospital based AMS teams, and promoting formal arrangements for local microbiology laboratories to work with AMS leads to discuss implications for antimicrobial prescribing and formularies
- Maintaining preparedness plans for potential outbreaks of MDR organisms
- Promoting ongoing surveillance for AMR and antimicrobial use to inform AMS and infection prevention and control practices.

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Appendices

Appendix 1: About APAS

The Australian Passive Antimicrobial Resistance Surveillance (APAS) system, which contributes data to the Antimicrobial Use and Resistance in Australia (AURA) Surveillance System, was established by the Australian Commission on Safety and Quality in Health Care (the Commission) in 2015 with the support of Queensland Health, which enabled access to the OrgTRx system as the information technology infrastructure. Funding for the AURA Surveillance System provided by the Australian Government Department of Health, with further contributions from the states and territories as part of the collection and analysis of their data.

APAS collects, analyses and reports on de-identified patient-level antimicrobial resistance (AMR) data contributed by 10 public and private pathology services across Australia. These laboratories detect AMR in isolates referred from public and private hospitals, aged care homes and community settings. The APAS system includes over 83 million records from 2006 to 2021. Initially, data were captured from January 2015 from all contributing laboratories; historical data have now been incorporated from four of those laboratories.

The data captured via APAS report on AMR in the form of:

- Longitudinal datasets for specified organism-antimicrobial combinations
- Cumulative antibiograms showing rates of resistance for a range of organisms from a specified specimen type within a time period
- Tabulations showing the resistance profiles of organism strains isolated during a time period
- Reporting for individual units within hospitals or health services, or at a statewide level.

The pathology services that contributed to APAS between 2006 and 2021 are listed in Table A1.1.

Table A1.1: APAS contributors by state/territory and year for which data has been submitted

State/ Territory	Contributor	Year															
		20 06	20 07	20 08	20 09	20 10	20 11	20 12	20 13	20 14	20 15	20 16	20 17	20 18	20 19	20 20	20 21
ACT	ACT Pathology	N	N	N	N	N	N	N	N	N	Y	Y	Y	Y	Y	Y	Y
NSW	NSWHP North*	N	N	N	N	N	N	N	N	N	Y	Y	Y	Y	Y [†]	Y	Y
NSW	NSWHP South Eastern Sydney LHD and Illawarra Shoalhaven LHD	N	N	N	N	N	N	N	N	N	Y [§]	Y	Y	Y	Y	Y	Y
NSW	NSWHP South Western Sydney LHD and Sydney LHD	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
Qld	Mater Pathology Brisbane	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
Qld	Pathology Queensland	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
SA	SA Pathology Service	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
Tas	Launceston General Hospital Pathology Service	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	Y
Tas	Royal Hobart Hospital Pathology Service	N	N	N	N	N	N	N	N	N	Y	Y	Y	Y	Y	Y	Y
Vic	Alfred Health	N	N	N	N	N	N	N	N	N	Y	Y	Y	Y	Y	Y	Y
Vic	Monash Health Pathology Service	N	N	N	N	N	N	N	N	N	Y	Y	Y	Y	Y	Y	Y
WA	PathWest Pathology Service	N	N	N	N	N	N	N	N	N	Y	Y	Y	Y	Y	Y [#]	N

LHD = local health district; N = data not available; NSWHP = New South Wales Health Pathology; Y = data available

* NSWHP North provides services to Northern Sydney, Central Coast, Hunter New England, Mid North Coast and Northern NSW LHDs

† Data for Central Coast LHD from 2019 only

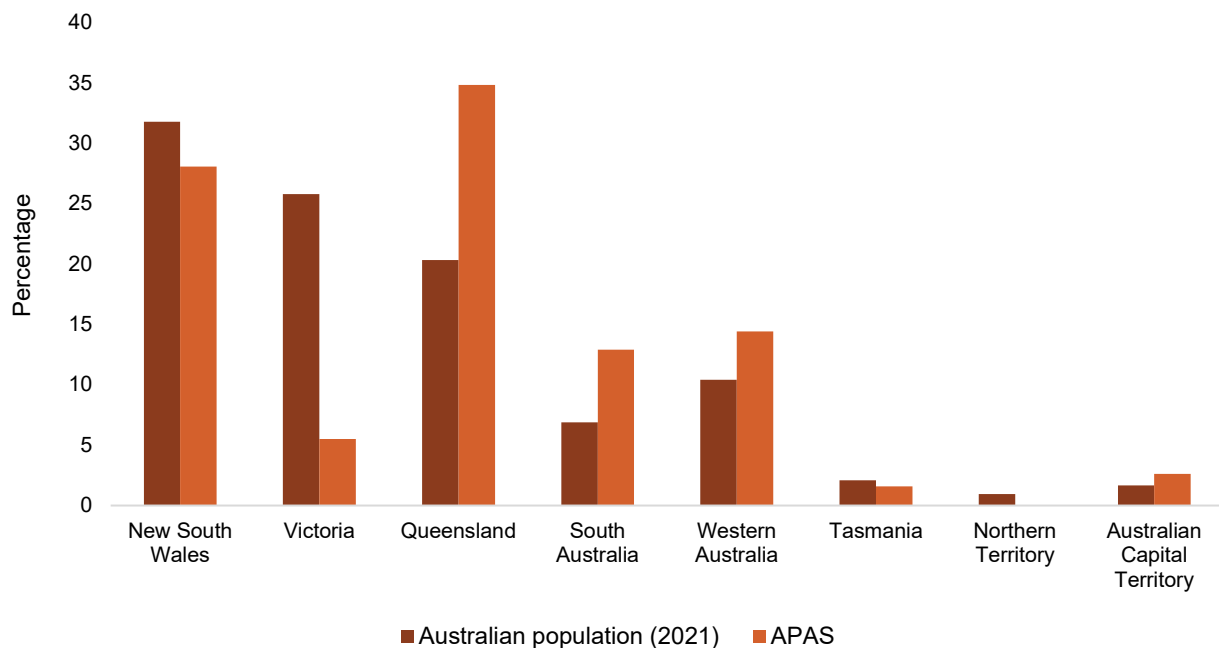
§ Data for South Eastern Sydney LHD was contributed from 2 April 2016 only

Data for PathWest Pathology Service available to August 2020 only

Note: New South Wales has, since APAS commenced, brought together all public laboratories as the state-wide service NSW Health Pathology. The pathology service names used in this report reflect 2022 naming conventions in the OrgTRx system that supports APAS.

A1.2. Representativeness

Figure A1.1: Estimated Australian population share by state and territory²³, compared with the number of isolates for which susceptibility data was available from APAS contributors, 2015–2021



A1.3. Isolates and specimen types

For the purpose of analysis, nine specimen category types, as defined in OrgTRx, were combined as indicated in Table A1.2.

Table A1.2: Classification of specimen category types for which susceptibility testing was performed

OrgTRx specimen category	APAS specimen type
Acid fast bacilli	Other*
Blood culture	Blood
Cerebrospinal fluid	Other
Ear, nose, and throat†	Other
Enteric	Other
Genital	Other
Respiratory	Respiratory
Tissue/Fluid/Pus/Prosthesis	Tissue/fluid/pus/prosthesis
Urine	Urine

AFB = acid-fast bacilli; CSF = cerebrospinal fluid; ENT = ear, nose, and throat

* Other = Other specimen types (excluding blood, urine, respiratory, tissue/fluid/pus/prosthesis)

† May occasionally include eyes

A1.4. Setting

Table A1.3: Number of facilities (by setting*) from each APAS contributor, 2015–2021

State/ Territory	Contributor	Aged Care Home	Comm unity	Multi- purpose service	Other [†]	Private hospital	Public hospital	Unknown	Total
ACT	ACT Pathology	1	31	0	4	7	11	0	54
NSW	NSWHP North [§]	29	40	17	13	17	61	1	178
NSW	NSWHP South Eastern Sydney LHD and Illawarra Shoalhaven LHD [#]	0	1	0	2	4	17	0	24
NSW	NSWHP South Western Sydney LHD and Sydney LHD	4	22	0	9	1	11	0	47
Qld	Mater Pathology Brisbane	138	16	0	4	29	3	0	190
Qld	Pathology Queensland	6	120	37	26	3	86	2	280
SA	SA Pathology Service	154	330	28	36	38	62	0	648
Tas	Launceston General Hospital Pathology Service	0	0	0	0	0	1	0	1
Tas	Royal Hobart Hospital Pathology Service	0	13	0	2	3	2	0	20
Vic	Alfred Health	0	0	0	0	0	3	0	3
Vic	Monash Health Pathology Service	0	1	0	0	0	8	1	10
WA	PathWest Pathology Service ^{**}	2	20	35	29	14	49	0	149
	Total	334	594	117	125	116	314	4	1,604

LHD = local health district; NSWHP = New South Wales Health Pathology

* Facilities from which isolates were sourced were allocated to a setting using postcode data from myagedcare.gov.au, myhospitals.gov.au, and the Australian Institute of Health and Welfare listing of public and private hospitals³⁶

† Other includes facilities that APAS contributors have categorised as correction services; the approach to use of this categorisation is not consistent across states and territories

§ NSWHP North provides services to Northern Sydney, Central Coast, Hunter New England, Mid North Coast and Northern NSW LHDs. Data for Central Coast LHD from 2019 only

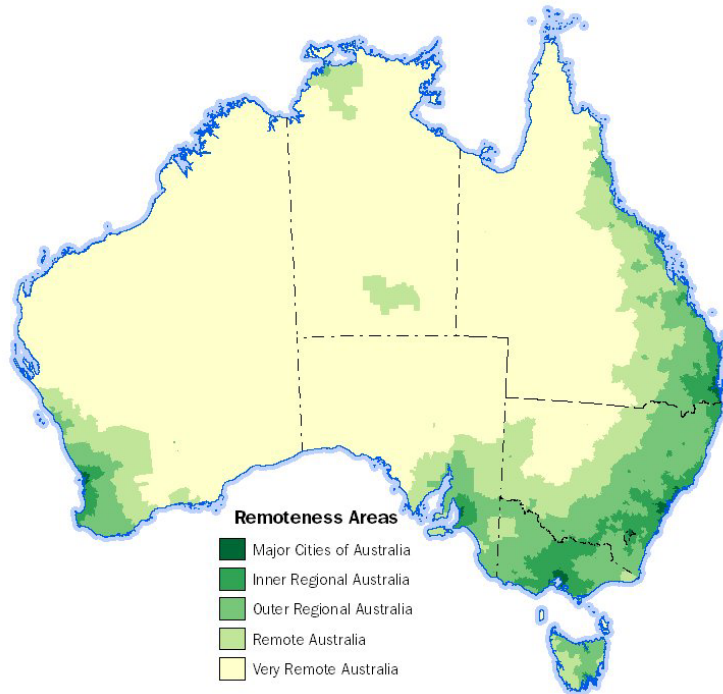
Data for South Eastern Sydney LHD was contributed from 2 April 2016 only

** Data for PathWest Pathology Service available to August 2020 only

A1.5. Remoteness

The Australian remoteness structure for 2016 as classified by the Australian Statistical Geography Standard (ASGS) ²⁴ is shown in Figure A1.2.

Figure A1.2: Map of the 2016 Remoteness Areas for Australia



Appendix 2 Terminology

A2.1 Abbreviations

Abbreviation	Definition
ABS	Australian Bureau of Statistics
ACT	Australian Capital Territory
AGAR	Australian Group on Antimicrobial Resistance
AIHW	Australian Institute of Health and Welfare
AMR	antimicrobial resistance
AMS	antimicrobial stewardship
APAS	Australian Passive AMR Surveillance
ASGS	Australian Statistical Geography Standard
AURA	Antimicrobial Use and Resistance in Australia
β -lactamase inhibitors	beta-lactamase inhibitors
CARAlert	National Alert System for Critical Antimicrobial Resistances
CDS	calibrated dichotomous sensitivity
CLSI	Clinical and Laboratory Standards Institute
Commission	Australian Commission on Safety and Quality in Health Care
EARs-Net	European Antimicrobial Resistance Surveillance Network
ESBL	extended-spectrum β -lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
ICU	intensive care unit
LHD	local health district
MDR	multidrug-resistant
MIC	minimum inhibitory concentration
NSQHS	National Safety and Quality Health Service
NSW	New South Wales
NT	Northern Territory
Qld	Queensland
SA	South Australia
Tas	Tasmania
UTI	urinary tract infection
Vic	Victoria
WA	Western Australia

A2.2 Common terms

Term	Definition
acquired resistance	Reduction in susceptibility by acquiring resistance genes from other bacteria or through mutation.
aged care home	A special-purpose facility that provides accommodation and other types of support to frail and aged residents, including assistance with day-to-day living, intensive forms of care and assistance towards independent living.
antimicrobial	Chemical substances that inhibit the growth of, or destroy, bacteria, fungi, viruses or parasites. They can be administered therapeutically to humans or animals. In this report, 'antimicrobial' is used when the surveillance data include antibiotic, antifungal, antiviral and antiparasitic agents. When the surveillance data include only antibiotics, the term 'antibiotic' is used. The terms antibacterial and antibiotic have the same meaning
antimicrobial resistance (AMR)	Failure of an antimicrobial to inhibit a microorganism at the antimicrobial concentrations usually achieved over time with standard dosing regimens.
antimicrobial stewardship (AMS)	An ongoing effort by a health service organisation to reduce the risks associated with increasing antimicrobial resistance and to extend the effectiveness of antimicrobial treatments. It may incorporate a broad range of strategies, including monitoring, reviewing and promoting appropriate antimicrobial use.
antimicrobial susceptibility test	A procedure used to determine which antimicrobials are effective at inhibiting the growth of, or destroying, an infecting microorganism.
breakpoint	The concentration of an antimicrobial used in the interpretation of susceptibility test results to define microorganisms as susceptible, intermediate or resistant.
extended-spectrum β -lactamase	An enzyme that is produced by some gram-negative bacteria. Bacteria that produce these enzymes are usually found in the bowel and urinary tract and are considered to be multidrug-resistant organisms because they are resistant to a large number of antibiotics.
hospital	All public, private, acute and psychiatric hospitals; free-standing day hospital services; and alcohol and drug treatment centres. Includes hospitals specialising in dentistry, ophthalmology and other acute medical or surgical care. It may also include hospitals run by the Australian Defence Force and corrections authorities, and those in Australia's offshore territories. It excludes outpatient clinics and emergency departments.
isolate	An organism that is grown in a laboratory culture from a patient sample.
minimum inhibitory concentration (MIC)	The lowest antimicrobial concentration at which there is no visible growth of a microorganism
multidrug-resistant organism	Microorganisms that are resistant to one or more agent in three or more antimicrobial categories.
multi-purpose service	An integrated health and aged care service in a rural or remote area.
National Safety and Quality Health Service (NSQHS) Standards	Standards developed by the Australian Commission on Safety and Quality in Health Care to drive the implementation of safety and quality systems and improve the quality of health care in Australia. The NSQHS Standards provide a nationally consistent statement about the standard of care that consumers can expect from their health service organisations.
OrgTRx	The Queensland Health information technology platform that is used for the Australian Passive AMR Surveillance system.
passive surveillance	Use of data that are already collected and designed for a broader purpose, but when a subset of the data can be used for secondary analysis. In this report, it refers to broader collections from which data on antimicrobial use and resistance can be extracted.
susceptibility	Where there is a high likelihood of therapeutic success using a standard dosing regimen of the agent, or there is a high likelihood of therapeutic success because exposure to the agent is increased by adjusting the dosing regimen or its concentration at the site of infection.

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