The Molecular Epidemiology of Penicillin-Susceptible *Staphylococcus aureus* Bacteraemia in Australia and the Reliability of Diagnostic Phenotypic Susceptibility Method to Detect Penicillin Susceptibility

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Declaration

I declare that this thesis is my own account of my research and contains as its main content work which has not previously been submitted for a degree at any tertiary education institution.

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Table of Contents

1. Introduction

1.1. History

Staphylococcus was first identified by Sir Alexander Ogston in 1881 when he was investigating the cause of suppurative inflammation in post-operative human patients. Using a light microscope, Ogston observed the spherical nature of the bacterium arranged in clusters in pus collected from an abscess. He was able to demonstrate the bacterium was the cause of the abscess by injecting healthy guinea pigs with pus, which resulted in septicaemia with the presence of the bacterium in blood (1). Conceived by Ogston, the term '*Staphylococcus'* is from the Greek words "staphyle" (σταφύλια) meaning grapes, and "kokkos" (κόκκος) meaning berry (2). The species name of *Staphylococcus aureus,* derived from the Latin word "aurum" for gold, was subsequently coined by Friedrich Julius Rosenbach due to the distinct golden yellow pigmented colonies produced by the bacterium (3).

1.2. *Staphylococcus aureus*

1.2.1. Microbiological Characteristics

S. aureus is a gram-positive, opportunistic pathogen which commonly resides in the human nose and axillae (4). A non-spore forming facultative anaerobe, the bacterium is 0.5 – 1 μm in diameter and grows at an optimal temperature range of 18 – 40ºC (5). All staphylococci produce catalase which serves as a defence mechanism against reactive oxygen species in oxygen metabolism (6). In addition to catalase, *S. aureus* produces coagulase, which is responsible for the coagulative conversion of fibrinogen to fibrin in the bloodstream (7). Various growth media are used to culture *S. aureus*. On 5% sheep blood agar, *S. aureus* often produces a clear zone around each bacterial colony, known as β-haemolysis – the β-hemolysin produced by *S. aureus* breaks down the red blood cells and haemoglobin in the media (8). Recent studies suggest evidence of passive motility by comet formation and spreading, even though *S. aureus* has long been regarded as non-motile. In 2015, using a

modified motility assay, Pollitt *et al.* observed aggregates of cells which moved separately from the main colony, leaving a "comet" trail of cells in its path (9). Phenol soluble modulins, cell surfactants produced by *S. aureus* whenever there is sufficient cell density in a colony, help reduce surface tension and spread cells outwards as the colony grows denser (10).

1.2.2. Genomics

S. aureus has an approximate genome size of 2.8 Mbp, encoding an average of 2,800 genes (11, 12). The genome has a mean GC content of 32.7% (12). *S. aureus* can be effectively described by its pan-genome (or total composite genome) which consists of the core and accessory genomes. The core genome accounts for approximately 80% of the pan-genome, and includes genes responsible for metabolic functions, transcription, translation, and replication in *S. aureus* (11). The accessory genome includes mobile genetic elements (MGEs) such as transposable elements, bacteriophages, plasmids, and genomic islands. MGEs are fragments of deoxyribonucleic acid (DNA) which may encode resistance and virulence determinants. Transferring genetic information among bacterial species is crucial for bacterial adaptive response (13). Transposable elements are repetitive DNA sequences that are located throughout the genome, either on the chromosome or on plasmids in numerous copies. Although some transposable elements do not carry any genetic information required for transposition, they help stabilize resistance genes by regulating gene transcription. Most *S. aureus* isolates harbour at least one plasmid, which may vary from 1 to 60 kb in size. Plasmids may carry a combination of resistance and virulence genes, transposons, and insertion sequences. Resistance and virulence determinants in plasmids can be transferred from one bacterium to another via horizontal gene transfer (14). Prophages, which are bacteriophages integrated within the genome of *S. aureus*, may be present (13). Some prophages (phage genome) confer antimicrobial resistance to and increase the virulence of the bacterium, depending on the genes they carry. Genomic islands such as the vSaα, vSaβ, and staphylococcal chromosomal cassette *mec* (SCC*mec*) are MGEs which encode resistance genes, virulence factors, and an integrase (15). Apart from SCC*mec*, the acquisition of which

is unclear, genomic islands traverse the host chromosome using site-specific recombinases (13).

1.2.3. Nomenclature

S. aureus can be classified into methicillin-resistant *S. aureus* (MRSA), or methicillin-susceptible *S. aureus* (MSSA). MRSA, which harbours either a *mecA* or *mecC* gene located on the SCC*mec* genetic element (16), is typically resistant to all β-lactam antibiotics including the penicillinase-resistant semisynthetic penicillins (PRSPs) such as flucloxacillin, oxacillin and methicillin (17). Conversely, MSSA does not harbour a *mec* gene, and is typically susceptible to the PRSPs. Based on their susceptibility to penicillin, MSSA can be classified as penicillin-resistant *S. aureus* (PRSA), or penicillin-susceptible *S. aureus* (PSSA).

1.2.4. Typing Methods

1.2.4.1. Staphylococcal protein A (Spa) Typing

Staphylococcal protein A (Spa) typing is a single locus genotyping method of the *spa* gene repeat region. Polymorphic short sequence repeats located in the 3' coding region of the *spa* gene are assessed for nucleotide differences. Different short sequence repeats are given a unique repeat code which are combined into a *spa* type, starting with the letter "t" (18). The *spa* type of a *S. aureus* isolate can be determined by pulse-field gel electrophoresis or by sequencing the *spa* gene. Software algorithms such as BURP (based on repeat pattern) uses the *spa* nucleotide sequence to classify *S. aureus* isolates into a *spa* types (19, 20).

1.2.4.2. Multi-locus Sequence Typing (MLST)

Multi-locus sequence typing (MLST) is a genotyping method used to characterise microbial species. The MLST scheme for *S. aureus* involves sequencing internal fragments of seven housekeeping genes (Table 1) (21).

Table 1. Housekeeping genes used in *S. aureus* MLST (22).

Housekeeping genes	Gene product	Sequence length (bp)	Number of alleles
arcC	Carbamate kinase	456	893
aroE	Shikimate dehydrogenase	456	1068
glpF	Glycerol kinase	465	933
gmk	Guanylate kinase	417	586
pta	Phosphate acetyltransferase	474	904
tpi	Triosephosphate isomerase	402	826
yqiL	Acetyl coenzyme A acetyltransferase	516	1002

The differentiation of bacterial clones by MLST is based on the DNA sequence variations within the seven housekeeping genes. Prior to whole genome sequencing, the technique involved PCR amplification followed by DNA Sanger sequencing. For each housekeeping gene, different sequences are given a unique allele integer. The combination of seven integers (one for each locus) generates an allelic profile and is assigned a sequence type (ST). Isolates with the same ST are the same clone. Isolates with the same allelic profile in five of seven housekeeping genes are deemed to be closely related and are grouped into a CC (23).

1.2.4.3. Capsule typing

S. aureus can be characterised based on their capsule serotype. The *S. aureus* capsule is made up of polysaccharides and offers protection from environmental pressures and host immune response. Although 11 capsule serotypes have been identified to date, clinical *S. aureus* strains primarily produce capsule serotype five (cap5) or eight (cap8) (24, 25).

1.3. Clinical Manifestations of *S. aureus* Infections

1.3.1. Pathogenesis of Virulence Factors

S. aureus can produce multiple virulence factors which may assist its ability to colonise human hosts. Clinically significant virulence factors include the exotoxins and the immune evasion cluster (IEC) (7, 23, 26). Panton-Valentine leukocidin (PVL) toxin, enterotoxins, exfoliative toxins, epidermal cell differentiation inhibitor (EDIN) toxin, and toxic shock syndrome toxin are

five significant exotoxins produced by *S. aureus*. PVL is a two component, hetero-oligomeric β-pore-forming toxin, which is responsible for the lysis of leukocytes (27). Enterotoxins (encoded by *sea, seb, sed, see, seg, seh, sei, ser, selk, selq, selo, selm, seln, selw, selx*) produced by *S. aureus* assist the bacterium to colonise the human gut, serving as a reservoir for the distribution of the bacterium to other epithelial sites (28). The enterotoxin gene cluster (egc), made up of five enterotoxin genes (*selo, selm, sei, seln, seg*), is located on the vSaβ genomic island. Serological distinct exfoliative toxins (encoded by *eta, etb, etc, etd, ete*) exert their effect by diffusing through the dermal capillaries, hydrolysing the peptide bond of desmoglein-1 cell adhesion molecule and cause dissociation of keratinocytes (29, 30). EDIN toxins (encoded by *edinA, edinB*, or *edinC*) inhibit keratinocyte differentiation and trigger transcellular tunnels in endothelial cells, breaching physical barriers of the host for the bacterium allowing entry into the bloodstream (31, 32). Toxic shock syndrome toxin (TSST-1, encoded by *tst*) has been associated with toxic shock syndrome, binding to major histocompatibility complex (MHC) class II to stimulate cytokine production and sustain the release of tumour necrosis factor (8). Important immune modulatory factors are encoded by IEC genes located on the 3' end of βC-Φ phage in *S. aureus*. A total of seven different IEC variants consisting of five genes have been identified, including IEC type A (*sea-sak-chp-scn*), B (*sak-chp-scn*), C (*chp-scn*), D (*sea-sak-scn*), E (*sak-scn*), F (*sep-sak-chp-scn*), and G (*sep-sak-scn*). These genes affect the innate immune system through a variety of mechanisms, such as the modulation of specific chemokine receptors, inhibiting specific molecules like α-defensins and C3 convertase (33).

S. aureus virulence factors are coordinated by two-component regulatory systems. The most extensively studied regulatory system is the accessory gene regulator (*agr*) system (26, 34, 35). The *agr* is a prokaryotic quorum sensor which regulates gene expression in response to cell population density (36). The polycistronic *agr* locus encodes a four gene operon, *agrBDCA*, and contains two divergent promoters that can be induced by the expression of RNA polymerase III (37). Depending on the number of bases within the variable region in the operon,

strains can be classified into four respective types: *agr* types I, II, III, and IV (38). Expression of virulence factors is selectively coordinated during different growth phases. For instance, the expression of exotoxins predominates from exponential to post-exponential phase, while other factors like capsule polysaccharides are downregulated during those phases of growth (39, 40). Differential expression of virulence factors has been observed in multiple studies during each phase of bacterial growth, signifying the role *agr* plays in regulation of virulence factors (40, 41).

1.3.2. *S. aureus* Bacteraemia

S. aureus bacteraemia (SAB) is characterised by the presence of viable *S. aureus* in the bloodstream. Bloodstream infections can occur in three different groups of people: (i) immunological normal hosts; (ii) patients with impaired immunological defences due to their physiological condition (i.e., infants, children, and elderly); and (iii) patients with debilitating conditions (42). SAB continues to be a burden in today's healthcare system, primarily due to an increase in community-onset infections (43). In a multinational study performed by Laupland *et al.*, paediatric and geriatric patients were reported to have the highest incidence of SAB, and notably there was a higher proportion of males than females (44). Despite the use of antimicrobial therapy and prompt source control, SAB mortality can still be high, varying from 2.3% to 51.7% when caused by MSSA, and up to 83.3% when caused by MRSA (45, 46).

1.3.3. Hospital- and Community- Onset Infections

A SAB episode is classified as a hospital-onset if the first positive blood culture is collected 48 hours post hospital admission, or as community-onset if the first blood culture was collected within 48 hours of hospital admission (47). In Australia, 79.7% (n=2,180/2,734) of SAB reported in the Australian Group on Antimicrobial Resistance (AGAR) 2020 Australian

Staphylococcal Sepsis Outcome Program (ASSOP) were community-onset (47). Community infections have a higher disease burden especially in patients older than 70 years (48).

1.3.4. Treatment for *S. aureus* Bacteraemia

In Australia, vancomycin is the preferred antimicrobial for MRSA bacteraemia. The Antibiotic Therapeutic Guidelines recommend flucloxacillin or cefazolin be used for patients with MSSA bacteraemia. In patients with MSSA bacteraemia who display immediate severe or delayed hypersensitivity to penicillins, cefazolin is recommended (49). Although benzylpenicillin is the ideal antibiotic for the treatment of PSSA infections, optimal treatment remains unknown since clinical practice has not altered (50). Flucloxacillin treatment on PSSA bacteraemia patients however does have consequences. A comparative study of PSSA bacteraemia patients in Australia and New Zealand showed a decreased 30-day mortality rate and better pharmacological profiles when benzylpenicillin was administered, as opposed to flucloxacillin (51). Furthermore, benzylpenicillin has been shown to display better short-term outcome than third generation cephalosporin cefuroxime in PSSA bacteraemia patients (52).

1.4. Penicillin

1.4.1. Historical Introduction of Penicillin and its Structure

Penicillin, a β-lactam antibiotic produced by the *Penicillium rubens* (previously known as *Penicillium notatum*) mould, was identified by Sir Alexander Fleming in 1929 (53). Fleming observed the inhibition of *P. rubens* on an agar plate growing staphylococci. Fleming's colleague, Craddock, extracted the inhibiting compound from the contaminated culture. The compound, penicillin, was soluble in organic solvents and was purified via evaporation. *In vitro* staphylococcal culture, and *in vivo* experiments in rabbits with diluted titres of the crude penicillin extract demonstrated the compound's potential as a therapeutic drug for sepsis. Implementing penicillin as a treatment began soon after its discovery. Although treating patients with nasal sinus or rheumatoid arthritis was futile, a medical student with persisting

pneumococcal conjunctivitis was successfully treated with penicillin. Wide variations in penicillin titres, instability of penicillin extract, and limited patients for treatment were challenges Fleming faced at the time. The pH-sensitive penicillin extracts were not standardized to have the same titre after each extraction, and efficacy was lost after a fortnight (54). Howard Florey and Ernst Chain saw massive potential in Fleming's work and after a decade from the discovery of penicillin, they began to mass-produce sufficient penicillin for research. To demonstrate penicillin's bacteriostatic potential, they optimised the growth of *P. rubens* and increased the production of purified penicillin. The purified penicillin was approximately 1000 times more potent and stable compared to the crude extracts made by Fleming. The bacteriostatic nature of penicillin was validated on 32 different species of bacteria. A therapeutic trial with ten human participants was subsequently performed after pharmacokinetic studies were performed *in vivo* in cats, rabbits, and humans. Using an intravenous injection containing 200 mg of penicillin, favourable responses were observed without adverse effects, demonstrating the possibility of maintaining the bacteriostatic concentration of penicillin in humans (55). *Penicillium chrysogenum*, an alternative penicillium mould which provides higher yields of penicillin, was subsequently used by Florey and his team to meet the demand during World War II (56). The chemical formula of their original penicillin extract was 2-pentenylpenicillin (penicillin F), while the extract produced by *Penicillium chrysogenum* was benzylpenicillin (penicillin G) (57). As benzylpenicillin is hydrophobic, its sodium or potassium salt is used to treat a variety of bacterial infections (58).

The molecular structure of penicillin, particularly the β-lactam ring has been extensively studied. The structure of penicillin was first described in 1949 by Dorothy Hodgkin (59). The penicillin structure consists of a 'R' variable side chain and 6-aminopenicillanic acid (6-APA), made up of a β-lactam and a thiazolidine ring (Figure 1A) (60). β-lactam is a cyclic amide with a nitrogen atom paired covalently to the β-carbonyl (61). Benzylpenicillin, a penicillin β-lactam derivative, was synthesised with the addition of phenylacetic acid to the penicillin ether extract (Figure 1B) (62). Through the synthesis of another derivative, phenoxymethylpenicillin

(penicillin V), Sheehan *et al.* discovered that 6-APA was an essential structure in β-lactam derivatives (Figure 1C) (63). Phenoxymethylpenicillin resist gastric acid inactivation and is better absorbed from the gastrointestinal tract than benzylpenicillin (64).

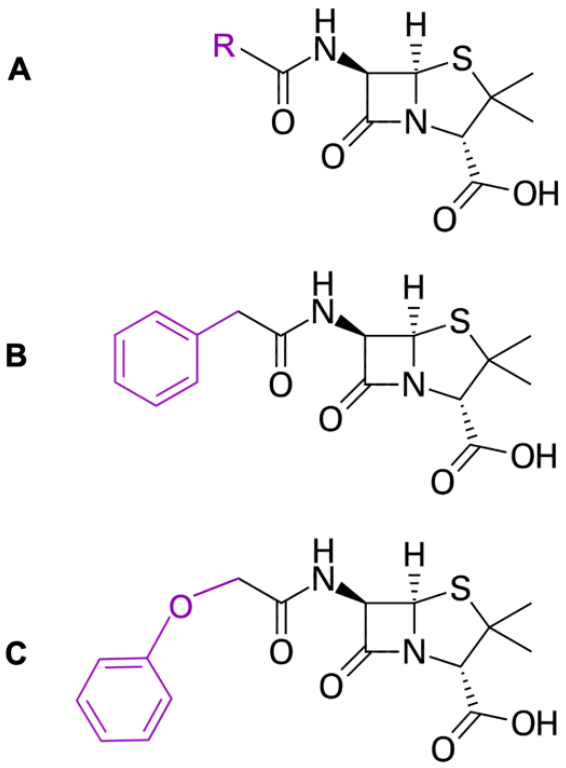

Figure 1. Structure of penicillins. (A) The penicillin structure is made up of a 6-aminopenicillanic acid (6-APA) and a 'R' variable side chain (60). (B) Benzylpenicillin contains a benzyl group as the side chain (58). (C) Phenoxymethylpenicillin contains a phenoxymethyl group as the side chain.

1.4.2. Mechanism of Action

Penicillin binds irreversibly to a group of bacterial enzymes commonly known as the penicillin binding proteins (PBPs). In *S. aureus*, there are at least four PBPs (PBP1, PBP2, PBP3 and PBP4) (65).PBPs have transpeptidase activity and catalyse the cross-linking of peptidoglycan during bacterial cell wall biosynthesis (66). PBPs are responsible for transpeptidation of tetrapeptide and pentapeptide chains, by crosslinking amino polysaccharides *N*-acetylglucosamine and *N*-acetylmuramic acid in an alternating pattern. Penicillin interacts with

the active serine site in the PBPs and form an acyl-enzyme complex, rendering PBPs inactive (Figure 2) (66). Disrupting synthesis of the peptidoglycan cell wall results in the loss of structural integrity, causing lysis and subsequent death of the bacterium (67).

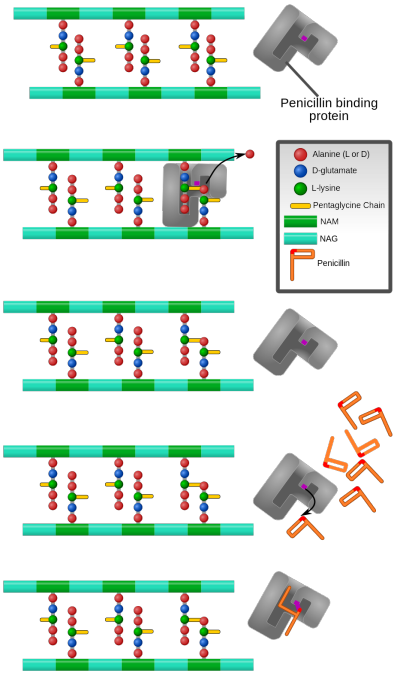

Figure 2. Mechanism of action of penicillin (68). A stable penicilloyl enzyme is formed from the penicillin binding protein due to its interaction with penicillin.

Interference of prokaryotic cell division by penicillin was first identified by Gardner in 1940. He observed changes in the morphological structure of bacteria, particularly gram-positive bacteria, at low concentrations of penicillin. Spherical enlargement and imperfect cellular fission were observed in staphylococci (69). When Duguid *et al.* assessed the integrity of the cell wall at increasing inhibitory concentrations of penicillin, he also observed congruent signs of swollen, oval morphology with incomplete fission in *S. aureus* isolated from septicaemic wounds (70). Research investigating the penicillin binding site was undertaken in an attempt to understand penicillin's mechanism of action, and the penicillin binding protein was discovered by Rowley and Cooper (71).

1.4.3. Penicillin Resistance

Penicillinase (also known as β-lactamase) production was first identified in the 1940s by Sir Edward Abraham when he added penicillin to a bacterial suspension of *S. aureus* and observed no lytic effect on agar plates (72). Kirby validated Abraham's findings and he concluded that the penicillin was destroyed by the penicillinase, as the microbial growth was equivalent with the growth control (73). In *S. aureus*, penicillin resistance can occur by the production of low affinity penicillin binding protein variants due to polymorphisms (74), the expression of altered penicillin-binding protein 2a (PBP2a) encoded by *mecA* and *mecC* in MRSA (16, 75), or the production of β-lactamase encoded by the *blaZ* gene, which cleaves the β-lactam ring of penicillin via hydrolysis (76).

The prevalence of penicillin resistance in *S. aureus* surged in the 1940s. Penicillin resistance in London increased from 14.1% in 1946 to 38% in 1947, and 59% in 1948 after penicillin was administered to patients suffering from sepsis (77). Furthermore, resistance to other antibiotics such as streptomycin and tetracycline were also observed in *S. aureus* (78). Within two decades of penicillin use, approximately 25% of community-acquired SAB were penicillin resistant (79). In 1959, methicillin, a disubstituted methoxy group of benzylpenicillin which is resistant to β-lactamase hydrolysis, was synthesized. Flucloxacillin, an isoxazole PRSP, was synthesized in 1970 following the increase in MRSA incidence (80).

More than 300 types of β-lactamases have been identified to date (81). Multiple functional and biochemical classification schemes have been previously developed to classify β-lactamases. The current classification, the Ambler classification, classifies β-lactamases into four distinct groups (A to D) based on their amino acid at positions 128 and 216 (Table 2): the Class A active site serine β-lactamases or penicillinase, the Class B Zn^{2+} metallo-β-lactamase, the Class C cephalosporinases, and the Class D oxacillin-hydrolysing β-lactamases (82-86). Genes encoding the class A, C, and D β-lactamases are typically located on plasmids, while the class B β-lactamases gene is typically located on the chromosome (87).

Table 2. Amino acid in respective positions of the *blaZ* sequences in different β-lactamase class (85, 86).

Amino acid positions	β-lactamase class			
	A	B	C	D
128	Thr (T)	Lys (K)	Thr (T)	Ala (A)
216	Ser (S)	Asn (N)	Asn (N)	Ser (S)

1.4.4. The *bla* Operon and Induction of β-lactamase

The *bla* operon consists of a structural *blaZ* gene, an operator region, and the *blaR1* and *blaI* adjacent regulatory genes (Figure 3). Transcription of β-lactamase is negatively regulated in *S. aureus*. Repressor of the *bla* operon, BlaI (encoded by *blaI*) binds to the R1 dyad and Z dyad regions on the operator to regulate gene transcription of *blaZ*, *blaR1*, and *blaI* in the absence of penicillin (76). BlaR1 (encoded by *blaR1*) is a proteolytic transmembrane transducer which consists of a C-terminal sensor domain, a four α-helical transmembrane domain and a cytoplasmic N-terminal Zn^{2+} metalloprotease. The zinc protease domain of BlaR1 is an inducer for transcription to occur (Figure 4 [Step III]) (88).

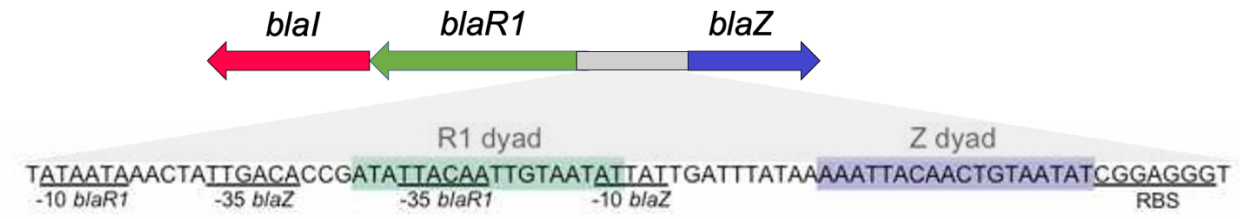

Figure 3. Diagram of the *bla* operon (89). The *blaZ* and *blaR1* promoter regions reside in between both genes and contain dyads. Upstream of the *blaZ* coding region consists of the promoter regions, *blaR1* and *blaI* coding region.

In the presence of penicillin, BlaR1 is acylated when penicillin interacts with its penicillin-binding sensor domain (Figure 4 [Step II]). BlaR1 zinc protease domain is cleaved from its extracellular domain upon acylation, and it interacts with the repressor, causing it to dissociate

from the operator (Figure 4 [Step IV]). Divergent transcription of *blaZ*, *blaR1,* and *blaI* occurs. Transcription and translation of *blaZ* produces BlaZ, the β-lactamase which hydrolyses the β-lactam ring of penicillin, inactivating the antibiotic. BlaR1 replaces the signal transducer domain which can only transduce once. Expression of β-lactamase continues until the β-lactam antibiotic concentration diminishes, and the synthesized BlaI binds to the operator region to suppress *blaZ* transcription (88).

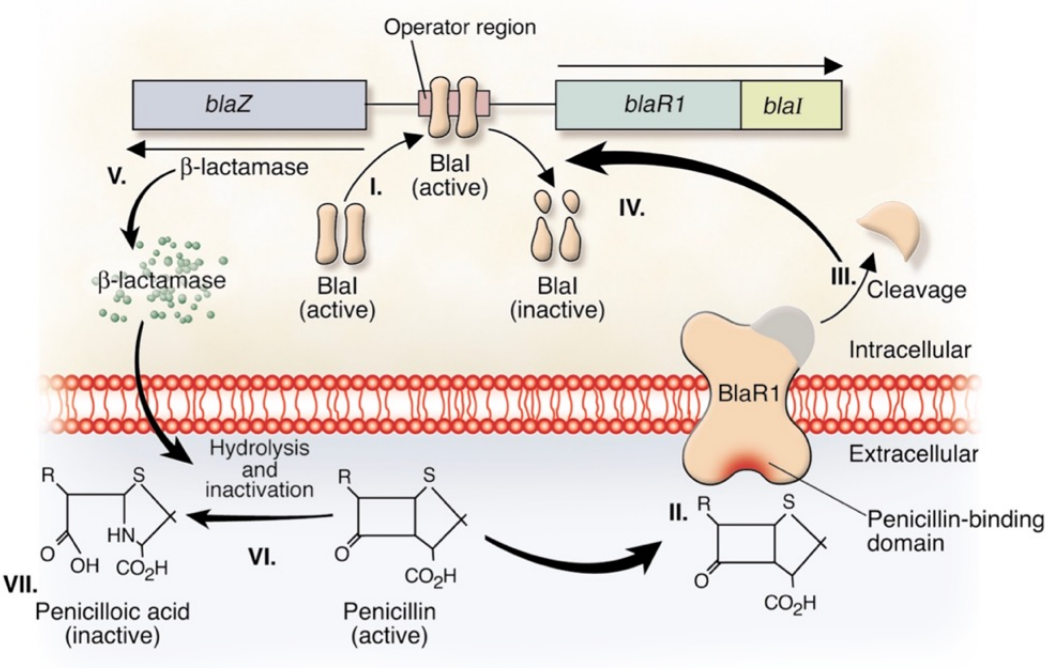

Figure 4. Induction of β-lactamase synthesis in *S. aureus* (90). Expression of β-lactamase is regulated by the negative inducible *bla* operon.

1.5. Detection of Penicillin Resistance in MSSA

1.5.1. *blaZ* Polymerase Chain Reaction (PCR)

In MSSA, penicillin resistance is primarily due to the *blaZ*-mediated production of β-lactamase. Penicillin resistance in *S. aureus* can be determined using PCR, via the detection of the *blaZ* gene. Genomic investigation of the *blaZ* gene is not only helpful in understanding penicillin resistance in staphylococci, but it can also be utilized to elucidate diversity and evolutionary history of the *bla* operon. Using PCR, Olsen *et al.* demonstrated separate evolution for plasmid-encoded and chromosomally encoded *blaZ*. Although most isolates harbour one copy

of *blaZ*, some isolates may harbour a plasmid-encoded and a chromosomally encoded *blaZ* (87). *blaZ* PCR is the golden method for the detection of PRSA, since it has superior sensitivity and specificity compared to most phenotypic tests. In 2011 the Clinical and Laboratory Standards Institute (CLSI) recommended diagnostic laboratories to employ *blaZ* PCR on MSSA with a penicillin MIC ≤0.125 mg/L or disc diffusion zone ≥29 mm (91). *blaZ* PCR can be replaced with whole genome sequencing, which provides a higher resolution of the bacterial genome, identifying genes and capturing polymorphisms which may be overlooked (92). Genomic data generated also allows for re-interrogation as new polymorphisms, mutations and resistance genes are identified. However, whole genome sequencing is more costly compared to *blaZ* PCR.

1.5.2. β-lactamase Tests

There are three different methods for the detection of β-lactamases: (i) the nitrocefin test; (ii) the starch-plate test; and (iii) the acidimetric method. The nitrocefin test uses a chromogenic cephalosporin that undergoes a distinctive colour change in the presence of β-lactamases.

A moistened nitrocefin disc is inoculated with bacteria near the edge of the zone of inhibition produced by a penicillin disc. When β-lactamase is present, the amide bond in the cephalosporin β-lactam ring is hydrolysed and is converted into cephalosporanoic acid, turning the yellow disc into a red-pink colour after one hour of incubation. The colour intensity is directly proportional to the amount of β-lactamase present (93). Nitrocefin test is available in the form of a disc, solution, or an assay kit. The starch-plate test is an iodometric method that demonstrates β-lactamase production via discolouration of the dark blue starch-iodine complex in the presence of penicilloic acid, a by-product of β-lactamase activity on penicillin (94). An isolate is inoculated onto nutrient agar containing 0.2% (w/v) soluble starch and incubated overnight. The plate is then flooded with a pH 6.4 adjusted solution containing benzylpenicillin, iodine and potassium iodide. After 30 minutes, the plate is assessed for decolourisation (95). The acidimetric test uses the pH indicator phenol red, to detect the presence of β-lactamase. An isolate is added to the penicillin-phenol red reagent mixture, and

after 15 minutes of incubation the mixture is examined for colour change. A change in colour from red to yellow occurs when penicilloic acid is generated from the hydrolysis of penicillin due to the presence of β-lactamase (96).

Comparative studies of the nitrocefin, starch-plate, and acidimetric tests have reported a range of sensitivities. The nitrocefin test has a sensitivity ranging from 35.7% to 98.3% (96, 97); and the starch-iodine test from 42.9% to 98.4% (97). The acidimetric method has a sensitivity of 97.3% (96). Although the starch-iodine test has a comparable sensitivity to the chromogenic nitrocefin test, the former method is very laborious and requires additional preparation of reagents.

1.6. Phenotypic Penicillin Susceptibility Testing

1.6.1. Penicillin Susceptibility

Antimicrobial susceptibilities are standardized by two standard organisations: the Clinical and Laboratory Standards Institute (CLSI), and the European Committee on Antimicrobial Susceptibility Testing (EUCAST). Penicillin susceptibility of an isolate is determined if the minimum inhibitory concentration (MIC), defined as the minimum concentration of antimicrobial required to inhibit bacterial growth, is above or below the penicillin breakpoint. According to both CLSI and EUCAST guidelines, the penicillin breakpoints for *S. aureus* are 0.125 mg/L. Penicillin susceptibility can also be determined with zone of inhibition of two antibiotic discs, penicillin 1U and 10U, by measuring the zone diameter and assessing the zone edge. Penicillin susceptibility can be defined with an MIC value of <0.125 mg/L, zone diameter inhibition of ≥26 mm for penicillin 1U and zone diameter of ≥29 mm for penicillin 10U, and a penicillin fuzzy zone edge. Penicillin zone edge is an interpretive criterion that should not be used solely for the determination of penicillin resistance. Zone diameter of inhibition should also be reported, even though an isolate with a susceptible zone diameter of inhibition

will be considered resistant if a sharp zone edge is observed with the penicillin disc tested (98, 99).

1.6.2. Conventional Antimicrobial Susceptibility Tests for Penicillin

The conventional antimicrobial susceptibility tests (ASTs) for penicillin include the broth microdilution (BMD) method, the E-test® method and the disc-diffusion method. The BMD method which reports a MIC value, uses a diluted standardised inoculum of 0.5 McFarland, containing approximately 5×10^5 CFU/mL of bacteria (98). In the BMD assay, two-fold serial dilution of the antibiotic is performed in each column of the 96-well microtiter plate, prior to addition of the bacterial suspension. Isolates need to be tested in duplicates to ensure the MIC determination is robust. After adding the bacterial suspension, the plates are incubated for a minimum 16 hours. After incubation, the plate/glass tubes are inspected visually for the presence of bacterial growth. The MIC of penicillin for the test isolate is determined as the lowest concentration of penicillin that showed absence of growth in the microtiter well or tube (Figure 5A).

MIC can also be determined using the Etest® method. The Etest® is a pre-prepared non-porous plastic strip with a predefined gradient of antibiotic, covering a continuous concentration range of the antibiotic. The strip is applied to the surface of an agar plate inoculated with the test isolate. A release of the antimicrobial from the strip to the agar occurs, forming a stable and continuous gradient surrounding the strip. The antibiotic gradient remains stable for at least 18 to 24 hours; that is, a period that covers the critical times of many species of fastidious and non-fastidious organisms (100). Bacterial growth is visible as a symmetrical inhibition ellipse centred along the strip after incubation. The MIC value is determined by reading the pre-printed scale (in mg/L) on the strip, where the ellipse edge intersects with the side of the Etest® strip (Figure 5B). The MIC endpoints are usually well defined, although different growth and inhibition patterns may occur depending on the antimicrobial used. The MIC value should not be recorded if the lawn of growth on the plate appears to be very light

or heavy. This may occur when the bacterial suspension is not standardised appropriately to 0.5 McFarland (98).

The disc diffusion method, like the Etest®, determines antimicrobial susceptibility via the zone of bacterial inhibition. A paper disc impregnated with an antibiotic containing a standardised concentration, is placed on the agar plate after a bacterial lawn has been performed (Figure 5C) (101). Incubation times vary depending on the type of agar plate and the bacterium that is being tested. After incubation, bacterial growth is visible as a circular clear zone of inhibition surrounding the antibiotic disc. Plates should be read from the back with reflected light and the plate held above a dark background. For penicillin susceptibility testing of *S. aureus*, the zone edge is examined closely from the front of the plate, and held up to light (102). The diameter of the zone of inhibition is measured using a ruler or a vernier calliper. Interpretation for penicillin resistance using penicillin 1U or penicillin 10U is based on the EUCAST and CLSI guidelines, respectively (98, 103).

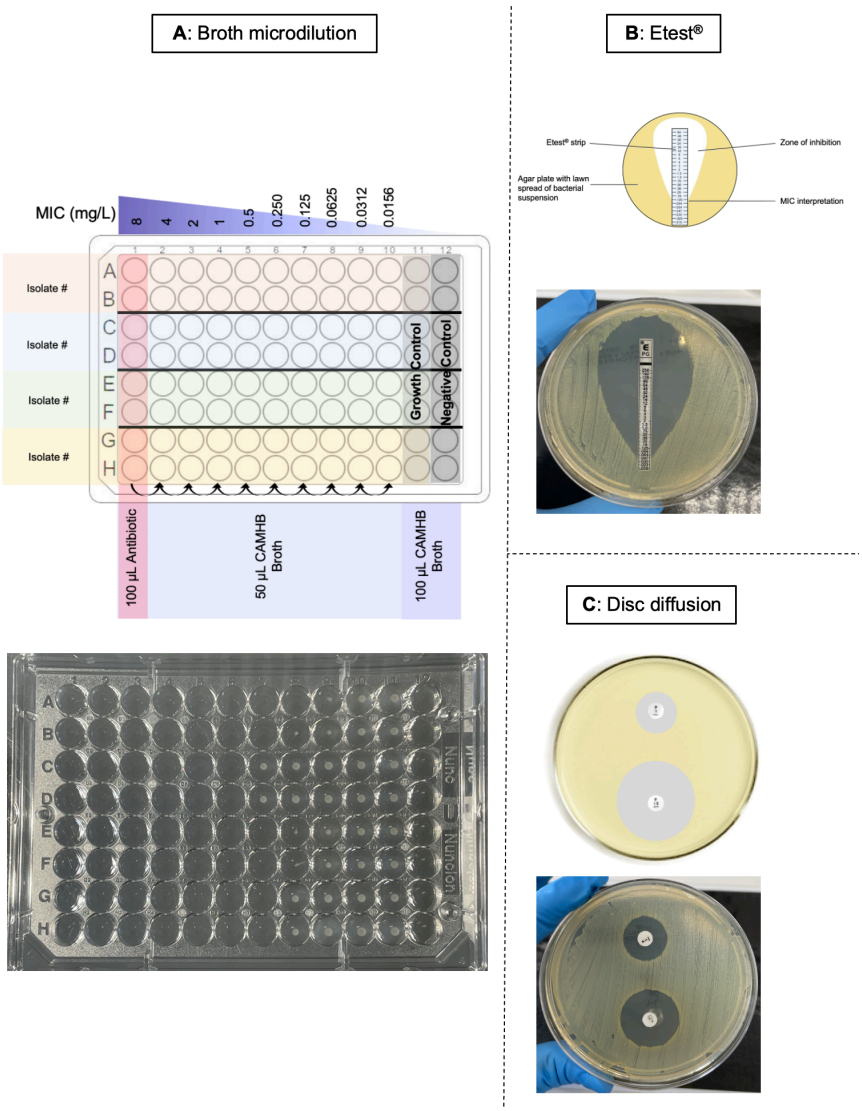

Figure 5. Summary of conventional ASTs and their expected results. (A) Growth of inhibition seen in the respective wells at different antibiotic concentrations in BMD. (B) Zone of inhibition seen in Etest®. (C) Zone of inhibition seen with two penicillin discs in disc diffusion.

1.6.3. Automated Antimicrobial Susceptibility Tests for Penicillin

In the diagnostic microbiology laboratory, susceptibility testing is often performed using an automated system such as the Vitek® 2 or the BD Phoenix™. In addition to penicillin, the automated systems provide susceptibility results for a wide range of antimicrobials tested within a short turnaround time. The commercially prepared Vitek® 2 AST card provides comprehensive testing on a range of antimicrobials within five to eight hours (104). Homogenous bacterial suspension of 0.5 McFarland is prepared in a clear polystyrene tube,

which is placed on a card rack. The Vitek® 2 AST card has an L-shaped transfer tube, which goes into the clear tube, with the card also placed on the rack. The rack is then loaded into the first compartment of the Vitek® 2 automated system, where the bacterial suspension is aspirated into the Vitek® 2 AST card. Once aspiration is complete, the rack is removed and loaded onto the load/unload station, where incubation of isolates and reading of susceptibility results occurs. The BD Phoenix™ automated identification and susceptibility testing system consists of the AP Instrument, M50 Instrument, panels, reagents, and broths. AST reagents are added into the AST tube containing 0.5 McFarland standard of bacterial suspension. Once the mixture is prepared, it is poured into the AST panel, the panel is incubated and the MIC is interpreted by the automated system within a few hours (105).

1.6.4. Limitations of Current Laboratory Susceptibility Methods

A major concern when phenotypic assays are performed to determine penicillin susceptibility in *S. aureus* is that the β-lactamase may not be constitutively expressed. Consequently, flucloxacillin has remained the preferred treatment option for PSSA bacteraemia. Several studies have questioned the reliability of phenotypic susceptibility testing methods. In 2015, Baddour *et al.* cited unreliable laboratory screening procedures for detecting PSSA in patients with infective endocarditis (106). Even when coupled with a negative nitrocefin reaction, disc diffusion and MIC detection methods may misclassify approximately 2% of *blaZ*-positive *S. aureus* as PSSA (107, 108).

The BMD method is considered the gold standard for phenotypic susceptibility testing; however, this method is laborious and requires preparation and serial dilution of the antibiotic. The Etest® method is easier to perform and allows determination of the MIC of at most two antimicrobials on a single 90 mm agar plate. The disc diffusion method also offers a more practical approach in a diagnostic laboratory setting as it is relatively easy to perform and provides qualitative susceptibility results for up to six antimicrobials on one 90 mm agar plate. However, unlike the Etest®, the disc diffusion method does not provide an MIC value (in mg/L)

but a zone of inhibition (diameter measured in mm). Although the penicillin disc diffusion test may predict penicillin susceptibility reliably in the routine microbiology diagnostic laboratory, the method relies on the subjective determination of the zone edge appearance, which makes the test less reproducible. According to the CLSI guidelines, a sharp zone edge with a zone diameter ≥26 mm radiating from the penicillin disc is reported as penicillin-resistant, while a fuzzy zone of inhibition with the same zone diameter is reported as penicillin-susceptible (Figure 6) (98). Discrepancies between the automated ASTs and conventional phenotypic ASTs have been observed in AGAR laboratories. As *blaZ* is not always constitutively expressed, isolates deemed susceptible by the automated ASTs may display resistance when tested by conventional ASTs (109).

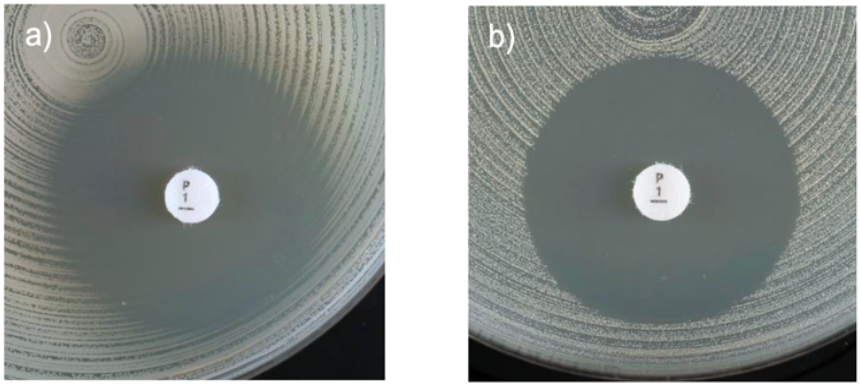

Figure 6. Fuzzy and sharp zone edges produced by β-lactamase negative (a), and positive (b) *S. aureus* isolates respectively (98).

1.7. Prevalence of Penicillin-Susceptible *Staphylococcus aureus* in Australia

1.7.1. PSSA Incidence

Despite the use of non-penicillin β-lactams over many decades, the proportion of SAB that are penicillin-susceptible has increased worldwide. A cross-sectional study of MSSA isolates in the United States reported a 19.2% increase in PSSA SAB infections over a ten-year period (2003 – 2012), and a study in Canada reported 28% (n=90/324) of MSSA SAB infections as penicillin-susceptible over a five-year period (2010 – 2015) (110, 111). In Australia, the AGAR ASSOPs have reported an overall increase in *S. aureus* penicillin susceptibility, with 17.5%

and 19.5% of all SAB infections reported as penicillin-susceptible in 2013 and 2020, respectively (47, 112). In addition, the quarterly mean penicillin MIC in *S. aureus* reported in North America has also decreased over a decade (50). With data suggesting a period of renaissance for *S. aureus* penicillin susceptibility, the increase in PSSA incidence offers an opportunity for a change in antimicrobial stewardship to investigate the re-introduction of penicillin as the preferred treatment option for PSSA infections.

1.7.2. Molecular Characterisation of PSSA Population Structure

Information on the population structure of PSSA is limited, as STs and CCs have only been characterised in three PSSA bacteraemia studies. The Resman *et al.* study conducted in Sweden in 2014 observed penicillin susceptibility in 33.1% (n=85/257) of SAB isolates with the use of three phenotypic screening tests – disc diffusion, Etest® and nitrocefin test. Using *spa* typing and BURP algorithm, the predominant *spa* types were t002 (associated with CC5) and t015 (associated with CC45), and the corresponding CC5 and CC45 are the predominant clonal lineages. In addition, five (5.9%) *blaZ*-positive PSSA isolates were identified in the study, with uncharacterised *blaZ* allotypes (113).

The Mama *et al.* multi-centre study conducted across 16 hospitals in Spain between 2018 – 2019 identified 156 MSSA bacteraemia isolates determined to be penicillin-susceptible by the Vitek® 2 system. The predominant clonal lineages in these isolates were CC5 (23.2%), CC398 (16.6%) and CC45 (15.9%). Predominant *spa* types were t002 (associated with CC5) and t571 (associated with CC398). There were six different IEC types identified in 72.4% (n=113) of isolates. Predominant IEC type was IEC type B (n=47), and the predominant IEC type in various clonal lineages were IEC type F in CC5, IEC type C in CC398 and IEC type B in CC45. Pan-susceptibility was observed in 77.5% of *blaZ*-negative PSSA isolates, whilst the remaining *blaZ*-negative isolates had phenotypic antimicrobial resistance (AMR) to erythromycin, clindamycin, tobramycin, ciprofloxacin, fusidic acid, mupirocin, and tetracycline. Genomic sequences of AMR genes associated with aminoglycosides (*ant(4')-Ia*),

lincosamides (*lnuA*), macrolides (*ermA, ermC*), macrolide-lincosamide-streptogramin B (*ermT*), streptogramin A (*vgaA*), and tetracycline (*tetK*) were also detected in isolates belonging to the same group. There were five (3.2%) *blaZ*-positive isolates, three isolates harboured *blaZ* allotype C, while one isolate harboured the *blaZ* allotype A and B, respectively (114).

Recently, a multi-centre retrospective study conducted across 55 hospitals in China investigated SAB isolates collected between 2014 – 2019, and identified predominant clonal lineages CC188 (17.1%), CC5 (15.7%), and CC398 (15.7%) in 140 PSSA isolates. Predominant *spa* types were t189 (associated with CC188), t571 (associated with CC398), and t548 (associated with CC5). There were five different IEC types identified in 82.1% (n=115) of isolates, and the predominant IEC type was IEC type E (n=53). Genomic sequences of AMR genes associated with aminoglycosides [*aac(6')-aph(2"), aph(2")-Ia*], lincosamides (*lnuA, lnuG*), macrolides (*ermB, ermC*), macrolide-lincosamide-streptogramin B (*ermT*), phenicol (*cat*), trimethoprim (*drfG*) and tetracycline (*tetK*) were detected in PSSA isolates. Phenotypic AMR to erythromycin, clindamycin, ciprofloxacin, levofloxacin, moxifloxacin, tetracycline, gentamicin, fusidic acid was detected in 41.9% (n=54) of *blaZ*-negative PSSA isolates. There were 11 (7.8%) *blaZ*-positive isolates, ten isolates harboured *blaZ* allotype C, while one isolate harboured *blaZ* allotype A. Most of the *blaZ* allotype C isolates belonged to CC188 clonal lineage. *blaZ* allotype C isolates were phenotypically pan-susceptible, while the isolate harbouring *blaZ* allotype A displayed multi-drug resistance to rifampicin, moxifloxacin, and levofloxacin. (115).

The population structure of PSSA isolates in Australia is not known. Characterisation of the Australian PSSA isolates is vital as it may provide important information on the genetic evolution of PSSA, and determine the effectiveness of penicillin in treating serious *S. aureus* infections.

1.8. Summary

S. aureus is an opportunistic pathogen which is responsible for hospital-acquired and community-acquired infections worldwide. SAB is characterised by the presence of viable *S. aureus* within the bloodstream, and individuals can be infected with either methicillin-resistant or -susceptible strains. Benzylpenicillin, a β-lactam antibiotic synthesized in the 1940s following the discovery of penicillin, is currently not recommended in patients with PSSA bacteraemia though it has been shown to have significantly lower 30-day mortality rate and lesser adverse effects compared to flucloxacillin, the current treatment of choice. Clinicians refrain from administering benzylpenicillin to PSSA patients due to the unreliability of ASTs. Although penicillin resistance has been an ongoing problem since the last century, an increase in PSSA prevalence has been observed worldwide over the past decade. Little is known about the population structure of PSSA causing bacteraemia globally, including in Australia. Elucidating the population structure of PSSA isolates in Australia will provide information on the recent increase in PSSA prevalence. Performing ASTs and β-lactamase confirmatory assay on whole genome sequenced isolates will evaluate the performance of these tests.

1.9. Project Aims

The aims of the Honours project are:

1. To use whole genome sequencing to determine the population structure of PSSA causing bacteraemia in Australia in 2020

   Whole genome sequencing will be performed on AGAR ASSOP 2020 SAB isolates classified as penicillin-susceptible by the Vitek® 2 automated systems. Genomic DNA will be extracted using the MagMAX™ Express automated platform and QIAGEN DNA DNeasy DNA Extraction Kit, and quantified using the Qubit™ 1X dsDNA HS Assay Kit. DNA Libraries will be prepared using the Illumina Nextera® XT DNA Library Preparation Kit, and short read sequencing will be performed using 150 bp paired-end chemistry on the NextSeq® Illumina platform. Raw reads will be assembled using the SPAdes Genome Assembler. Bioinformatics pipelines will be used to assess the population structure and the distribution of antimicrobial resistance and virulence genes.

2. To evaluate the phenotypic ASTs for detecting penicillin resistance in *S. aureus*

   Antimicrobial susceptibility testing will be performed to determine the MIC values of all *blaZ*-positive SAB isolates identified by whole genome sequencing. CLSI broth microdilution, disc diffusion, Etest®, and nitrocefin β-lactamase test will be performed. CLSI and EUCAST guidelines and zone edge interpretive criteria will be used (98, 103).

3. To characterise the *blaZ* alleles harboured by the PRSA previously classified as PSSA by the automated ASTs

   The *blaZ* alleles in the *blaZ*-positive isolates classified as penicillin-susceptible by the Vitek® 2 will be characterised based on their phylogeny and assessed for mutations.

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Declaration

I declare that this scientific manuscript is my own account of my research and contains as its main content work which has not previously been submitted for a degree at any tertiary education institution.

Nicholas Wei Tek Yee

The Molecular Epidemiology of Penicillin-Susceptible *Staphylococcus aureus* Bacteraemia in Australia and the Reliability of Diagnostic Phenotypic Susceptibility Method to Detect Penicillin Susceptibility

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Abstract

Staphylococcus aureus (*S. aureus*) penicillin susceptibility may be in a period of renaissance, yet the population structure of penicillin-susceptible *S. aureus* (PSSA) is inadequately defined, and penicillinase detection remains difficult. PSSA isolates across Australia in 2020 were sequenced to determine the population structure, presence of antimicrobial genes and virulence factors. Phenotypic assays were performed on *blaZ*-positive isolates. The predominant sequence types (STs) in this study included ST5 (27.2%, n=128/470), ST97 (7.2%, n=34/470), and ST45 (6.4%, n=30/470). The predominant clonal complexes (CCs) included CC5 (31.9%, n=150/470), CC97 (10.3%, n=48/470), CC45 (10%, n=47/470), and CC15 (8.7%, n=41/470). Of the PSSA isolates, 9.6% (n=45/470) were *blaZ*-positive. Several virulence factors and antimicrobial resistance genes were identified, and 97.2% (n=457) of the isolates present an immune evasion cluster (IEC) type. Detection of penicillin resistance in *blaZ*-positive isolates varied with different assays. Using the broth microdilution method, Etest®, P1 and P10 disc diffusion, 13 (28.8%) isolates, 12 (26.7%) isolates, 37 (82.2%) isolates and 26 (57.8%) isolates were classified as resistant, respectively. All *blaZ*-positive isolates displayed sharp zone edge with P1 and P10 antibiotic discs. A positive reaction to nitrocefin was observed in 22 (48.9%) isolates. This study demonstrated vast genetic diversity of PSSA isolates from multiple lineages causing bacteraemia in Australia in 2020. Although the disc diffusion test is strongly recommended, a combination of genotypic and phenotypic laboratory methods should be considered in routine testing.

Introduction

Staphylococcus aureus is a common pathogen that causes a wide variety of infections. *S. aureus* infections may be relatively minor, such as boils, moderate, such as cellulitis, or serious, such as septicaemia (1). Globally *S. aureus* is one of the most frequent causes of hospital-onset and community-onset bacteraemia (2). Despite advances in the treatment of bacterial infections, *S. aureus* bacteraemia (SAB), characterised by viable *S. aureus* in the bloodstream, is associated with frequent complications such as endocarditis and osteomyelitis, and has significant morbidity and mortality (2, 3). Increasing prevalence of penicillin-susceptible *S. aureus* (PSSA) causing bacteraemia has been reported globally in recent years (4-7).

Appropriate antimicrobial treatment is necessary to capitalise on the resurgence of PSSA (6, 8). Although penicillin (benzylpenicillin) is the ideal antibiotic for treating PSSA, the optimal treatment remains unknown for PSSA bacteraemia; flucloxacillin or cefazolin use in treatment has not been altered despite the increase in PSSA infections (9). Compared to flucloxacillin, penicillin has been associated with improved treatment outcomes. In the largest retrospective study comparing 915 patients with PSSA, Australian investigators found a significantly higher association between 30-day mortality rate (OR 1.06, 95% CI 1.01 to 1.1; p=0.03) and flucloxacillin, when compared to penicillin (10). Despite improved treatment outcomes, there remains scepticism towards the use of penicillin for the treatment of serious PSSA infections, owing to the clinical laboratory's inability to reliably detect penicillinase-producing strains by traditional phenotypic methods.

The use of penicillin as a treatment option in the 1940s led to the prevalence of penicillin-resistant *S. aureus* (PRSA) (11). Over the following decades, penicillin resistance increased worldwide to approximately 85% among *S. aureus* isolates causing community- and hospital-acquired infections (12). Consequently, some countries discontinued routine testing for penicillin susceptibility (13). The β-lactam antibiotics of penicillins produce a bactericidal effect by interacting with the active serine site of the penicillin binding protein, rendering its transpeptidase activity ineffective for the biosynthesis of peptidoglycan (14). PRSA produces an inducible extracellular β-lactamase, which inactivates the antibiotic by hydrolysing the β-lactam ring (15). Although the β-lactamase-encoding structural gene, *blaZ*, is typically carried on plasmids, it can also be located on the chromosome (16).

It is vital to have a reliable β-lactamase detection method prior to prescribing penicillin for the treatment of PSSA bacteraemia. However, the phenotypic detection for penicillin resistance remains difficult, as β-lactamase may not be constitutively expressed. Consequently, different studies questioned the reliability of phenotypic susceptibility testing. Even when coupled with

a negative nitrocefin reaction, the disc diffusion and minimum inhibitory concentration (MIC) detection methods may misclassify approximately 2% of *blaZ*-positive *S. aureus* as penicillin-susceptible (17). Although the penicillin disc diffusion test seems to predict penicillin susceptibility well in the routine microbiology diagnostic laboratory, it includes a step of subjective determination of zone edge appearance, which potentially makes the test less reproducible (9).

It is crucial to investigate the population structure and clonal distribution of PSSA to uncover reasons for its resurgence. There is a paucity of information on PSSA, since many whole genome sequencing (WGS) population structure studies have been centred on MRSA. In the peer-reviewed literature only a handful of studies can be cited (13, 18, 19). There is no study, however, that elucidates the population structure of PSSA in Australia. The aims of this study was firstly to determine the genomic diversity of PSSA causing bacteraemia and secondly, to evaluate the phenotypic antimicrobial susceptibility methods for the detection of PSSA.

Materials and Methods

2.1. Isolate collection

As part of the 2020 Australian Group on Antimicrobial Resistance (AGAR) Australian *Staphylococcus aureus* Sepsis Outcome Programme (ASSOP), SAB isolates collected by 49 participating AGAR institutions across Australia were referred to the Antimicrobial Resistance and Infectious Diseases (AMRID) reference laboratory at Murdoch University. *S. aureus* was confirmed by matrix-assisted laser desorption (MALDI) using either the Vitek® MS (bioMérieux, France) or the MALDI Biotyper® system (Bruker, Germany). AGAR laboratories performed antimicrobial susceptibility testing using the Vitek® 2 (bioMérieux, France, AST-P612 susceptibility panel, software v.7.01) or BD Phoenix™ (Becton Dickinson, USA, PMIC-84 susceptibility panel, software v.1.1.20.0) automated microbiology system. The susceptibility raw data, patient metadata and isolates were referred to the AMRID reference laboratory. All isolates were stored as frozen glycerol stocks at -80°C. Vitek® 2 antimicrobial susceptibility testing was subsequently performed on isolates previously classified as penicillin-susceptible by the BD Phoenix™ automated microbiology system. *S. aureus* isolates identified as penicillin-susceptible by the Vitek® 2, either by participating laboratory or by AMRID, were included in the study.

2.2. Whole genome sequencing

Genomic DNA was extracted using the MagMAX™-96 DNA Multi-Sample Kit (Life Technologies, 4413021) and/or the DNeasy® Blood & Tissue Kit (QIAGEN, USA, 69506) according to manufacturers' instructions. DNA quantification was performed using the Qubit™ 1X dsDNA HS Assay Kit (Thermo Fisher Scientific, Q33232). Sequencing libraries were prepared using the Illumina Nextera® XT DNA Library Preparation Kit (Illumina, USA, FC-131-1096) and sequenced on the NextSeq 500 platform (Illumina, USA) with 150 bp paired-end chemistry as previously described (20).

2.3. Genomic assembly and alignment

Genomes were *de novo* assembled using SPAdes v.3.15.4 (21). The contiguous sequences were annotated using Prokka v.1.14 (22). The Roary v3.11.2 pipeline was used to create an alignment of all protein-encoding genes (23).

2.4. Bioinformatics analyses

In silico multi-locus sequence typing (MLST) was performed on *de novo* assemblies using mlst v2.19.0 (24, 25) to assign a sequence type (ST) and a clonal complex (CC) to each isolate. Undefined sequence types (STs) were submitted to the PubMLST database for ST assignment (25). Typing methods such as *agr* typing and *spa* typing were also performed on *de novo* assemblies using BLAST and SPAtyper v0.3.1, respectively (26, 27). The ABRicate tool (28) was used to identify antimicrobial resistance genes using the Resfinder database (29). *blaZ* allotypes (A-D) are determined based on the amino acid located at positions 128 and 216 of *blaZ* (30). The collection was also screened for PVL-encoding genes (*lukF-PV, lukS-PV*), immune evasion cluster (IEC) genes (*sea*, *sep*, *chp*, *sak*, *scn*), epidermal cell differentiation inhibitor (*edinA, edinB, edinC*), toxins (*eta*, *etb, etd, and tst*), staphylococcal enterotoxins and staphylococcal enterotoxin-like genes (*selo, sele, sei, seu, seln, seg, seb, sec, sell, sed, sej, ser, see, seh, selk, selq, selw,* and *selx*) using BLAST (26). Mutations in *blaZ* were identified using the *S. aureus* β-lactamase reference sequence (NCBI accession no. M25252.1). The Geneious Prime R11 (31) software was used to visualise the *blaZ* sequence. A MLST minimal spanning tree was constructed using Grapetree (32).

2.5. Phylogenetic analyses

A phylogenetic tree was constructed using the neighbour-joining algorithm with 200 bootstrap replicates in MEGA v.11 (33). The phylogenetic tree was annotated and visualised on the integrative Tree of Life (iTOL) website (34).

2.6. β-lactamase detection

β-lactamase activity was detected using the BD BBL™ Cefinase™ nitrocefin paper discs (Becton Dickinson, USA, 231650) according to the manufacturer's instructions. A change in colour from yellow to red, after one hour incubation at room temperature was recorded as a positive reaction (35). *S. aureus* ATCC® 29213 and ATCC® 25923 were used as quality control strains as an indicator for positive and negative β-lactamase activity, respectively (36).

2.7. Penicillin susceptibility testing

Penicillin susceptibility tests performed on the *blaZ*-positive isolates included disc diffusion, broth microdilution (BMD), and Etest®. Oxoid™ penicillin 1U (P1) and penicillin 10U (P10) antibiotic discs were used for the disc diffusion assay (Thermo Fisher Scientific, CT0152B and CT0043B). Zone diameter and zone edge of penicillin 1U and 10U were interpreted according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) (37) and the Clinical and Laboratory Standards Institute (CLSI) guidelines (36), respectively. Penicillin solution used for BMD was prepared using penicillin powder dissolved in distilled water, as recommended by the manufacturer (Sigma Aldrich, 13752). The penicillin Etest® strip was used as recommended by the manufacturer (bioMérieux, 412262). MIC values determined using BMD and Etest® were interpreted using both the CLSI and EUCAST guidelines. *S. aureus* ATCC® 29213 and ATCC® 25923 were used as quality control isolates in BMD and disc diffusion assays, respectively (36).

Results

3.1. Penicillin-susceptible SAB episodes in Australia in 2020

Of the 2,734 SAB episodes reported in the AGAR 2020 ASSOP, 530 (19.4%) isolates were classified as PSSA (MIC ≤0.125 mg/L) by the Vitek® 2. Overall, 479 (90.4%) of the 530 PSSA were referred to the AMRID Research Laboratory. Following WGS, nine isolates were identified as *Staphylococcus argenteus* and excluded from the study. Among the remaining 470 Vitek® 2 penicillin-susceptible SAB episodes, 83.4% (n=392) were classified as community-onset. The majority of the 470 isolates in this study were from New South Wales (31.7%, n=149), Victoria (19.6%, n=92) and Western Australia (16.2%, n=76) (Supplementary Table 1).

3.2. Genetic diversity of PSSA causing bacteraemia in Australia in 2020

Among the 470 PSSA isolates, 86 STs belonging to 22 different clonal complexes (CCs) were identified, including 38 novel STs. The predominant STs in this study were ST5 (27.2%, n=128), ST97 (7.2%, n=34), and ST45 (6.4%, n=30). The predominant CCs were CC5 (31.9%,

n=150), CC97 (10.2%, n=48), CC45 (10%, n=47), and CC15 (8.7%, n=41) (Figure 1). Each CC had its *agr* type and capsule serotype characterised in Supplementary Table 2. Five STs (ST425, ST573, ST2867, ST5491, ST7270) consisting of seven isolates were considered singletons (Figure 1) (Supplementary Tables 2 and 3). Predominant *spa* types in PSSA were t002 and t1265 (associated with CC5), t267 (associated with CC97), and t189 (associated with CC188) (Supplementary Table 1). The core genome phylogeny showed clustering of isolates that were congruent with CCs. Close relationship between CC59 and ST425 was observed from the earliest branch point. CC30, CC291 and CC398 shared a common ancestral node, and high divergence was observed between these three CCs and CC45. CC22 shared a common ancestral node with the remaining CCs (Figure 2).

3.4 Analysis of virulence genes

PVL-encoding genes were identified in three (0.64%) isolates which belonged to ST1 (CC1), ST30 (CC30) and ST88 (CC88). The toxic shock syndrome toxin gene was found in 23 (4.9%) isolates, that belonged to CC5, CC22, CC30, CC45 and CC97 (Figure 2). The epidermal cell differentiation inhibitor gene *edinB* was identified in nine (1.9%) isolates and was primarily associated with CC291 and ST2867. Single isolates of ST25 and ST80 also harboured *edinB*. The exfoliative toxin A gene *eta* was identified in four (0.84%) isolates that belonged to CC15, and single isolates of ST1 and ST9. A total of 457 (97.2%) isolates harboured the IEC cluster genes. Seven IEC types were identified, and IEC Type B (*sak*, *chp* and *scn*) and type E (*sak*, and *scn*) were the predominant IEC types, identified in 169 (36.0%) and 127 (27.0%) of isolates, respectively. The remaining IEC types were type C (*chp* and *scn*, n=59), F (*sep, sak, chp,* and *scn*, n=39), D (*sea, sak,* and *scn*, n=32), G (*sep, sak,* and *scn*, n=26), and A (*sea, sak, chp,* and *scn*, n=5). There were 13 isolates with unassigned IEC type, including seven ST5 isolates and single isolates of ST1, ST20, ST78, ST573, ST582, ST2867 (Figure 2) (Supplementary Table 2).

Most PSSA isolates harboured staphylococcal enterotoxins (*se*) or staphylococcal enterotoxin-like (*sel*) genes. The *selw* and *selx* genes were identified in 99.8% and 94.0% of isolates, respectively. The *egc-cluster* (*seg*, *sei*, *sem*, *sen*, *seo*, and *seu*) was identified in 47.0% (n=220) of isolates, was restricted to eight CCs including all CC5, CC9, CC20, CC22 and CC361 isolates, and in 98% (n=46) of CC45 isolates. The *sea* gene, which was identified in 6 CCs, predominated in CC6 (93.8%) and CC1 (52.9%); *seb* which was identified in 13 CCs, predominated in CC12 (62.5%) and CC59 (55.5%); *sec*+*sel* which were identified in 11 CCs, predominated in CC45 (59.6%); and *sel*+*sek* which were identified in four CCs, predominated in CC1 (82.3%) and CC59 (55.5%) (Supplementary Table 2).

3.3. Analysis of antimicrobial resistance genes

A total of 56 (11.9%) PSSA isolates harbour one or more antimicrobial resistance (AMR) genes. The *blaZ* gene was detected in 45 (9.6%) isolates. A total of 18 AMR genes associated with aminoglycosides [*aadD, ant(4')-Ia, ant(9)-Ia, aph(3')-IIIa*], β-lactams (*blaZ*), fusidic acid (*fusC*), macrolides (*ermA, ermB, ermC, mphC*), macrolide-lincosamide-streptogramin B (*ermT*), lincosamides (*lnuA, lsaA*), phenicol (*fexA*), trimethoprim (*drfG*), tetracycline (*tetK, tetM*), and multi-drug resistance (*mdfA*) were detected in 56 (11.9%) isolates. The *fusC* gene was found in 13 isolates which were primarily CC1 isolates (n=12, 70.6% of CC1), the *ermT* gene found in 75.0% of isolates in CC398 (Supplementary Table 3).

3.5. Characterisation of PSSA blaZ-positive isolates

The 45 *blaZ*-positive isolates belonged to 22 different STs, across 13 different CCs. All isolates from the following STs harboured the *blaZ* gene: ST582, ST3911, ST5059, ST7273, ST7283, ST7251, ST7255, ST7262, ST7276, ST25, and ST9. The remaining *blaZ*-positive isolates belonged to ST34, ST30, ST20, ST22, ST3628, ST101, ST8, ST5, ST6, ST15, ST188, and ST45, and accounted for 75%, 50%, 33.3%, 16.7%, 16.7%, 8.3%, 7.7%, 6.3%, 6.3%, 5.3% 4.8%, and 3.3% of isolates belonging to the ST, respectively. Most *blaZ*-positive isolates belonged to CC15 (n=20, 48.8% of CC15) and CC5 (n=10, 6.7% of CC5) (Table 1). In addition to *blaZ*, three isolates harboured other antimicrobial resistance genes: two isolates each harboured *ermC* and *fusC*, and one isolate harboured *ant(9)-Ia, ermA, ermC, and tetK.* Among the *blaZ*-positive isolates, eight (17.7%) harboured virulence genes: four (10.4%) isolates, three (6.25%) isolates, and one (2.2%) isolate each harboured only *tst*, *eta*, and *edinB*, respectively. None of the *blaZ*-positive isolates were PVL-positive. IEC type C and B were the predominant IEC types, identified in 20 isolates, and 16 isolates, respectively. Whilst all IEC type C isolates belong to a single CC15 (n=20), IEC type B comprised of isolates belonging to eight CCs: CC5 (n=6), CC30 (n=3), CC45 (n=2), and singletons of CC8, CC9, CC20, CC22, and CC25. There were four (8.8%) isolates and two (4.4%) isolates that harboured IEC type F and E, respectively. Singletons were observed in IEC type D and G respectively, and one (2.2%) *blaZ*-positive isolate was IEC-negative.

3.6. Nitrocefin test

The nitrocefin test had a sensitivity rate of 48.9%. Of the 45 *blaZ*-positive isolates, 22 (48.9%) had a positive reaction to nitrocefin colour change, whilst 23 (51.1%) isolates had a negative reaction to colour change of the nitrocefin disc (Table 2). Control strain *S. aureus* ATCC® 29213 and ATCC® 25923 had positive and negative reaction, respectively, in all experiments.

3.7. BMD and Etest®

Isolates classified as penicillin-resistant based on the MIC values from BMD and Etest® are listed in Table 2. Sensitivity rate of 28.8% and 26.7% were observed for BMD and Etest®, respectively. Using a MIC breakpoint of >0.125 mg/L, only 13 (28.8%) and 12 (26.7%) isolates were classified as resistant by BMD and Etest®, respectively. Twelve isolates were classified as resistant using both BMD and Etest®. MIC values determined in BMD from control strain *S. aureus* ATCC® 29213 were >0.125 mg/L in all experiments.

3.8. Disc diffusion

Results of the disc diffusion tests performed on the *blaZ*-positive isolates are summarised in Table 2. Sensitivity rate of the P1, P10, and zone edge interpretation of both discs were 82.2%, 57.8%, and 100%, respectively. Using the P1 disc, 37 (82.2%) isolates were classified as resistant (resistant, <26 mm) according to the EUCAST interpretive criteria. Using the P10 disc, 26 (57.8%) isolates were classified as resistant (resistant, ≤28 mm) according to the CLSI interpretive criteria. All isolates produced a sharp zone edge (sharp, resistant) when either disc was used, hence all *blaZ*-positive isolates were classified as resistant using P1 and P10 antibiotic discs since zone edge was considered for penicillin resistance (Table 2). Zone diameters from the control strain *S. aureus* ATCC® 25923 were in concordance with susceptible results in all experiments.

3.9. Analysis of blaZ alleles

A total of 17 different *blaZ* alleles were characterised from 45 *blaZ*-positive isolates based on their phylogenetic relationship. Three *blaZ* allotypes were identified in *blaZ*-positive isolates: *blaZ* allotype A, comprised of 25 (55.6%) isolates, allotype C, comprised of eight (17.8%) isolates, and allotype B, comprised of two (4.4%) isolates. There were 10 (22.2%) isolates with undetermined *blaZ* allotype because the *blaZ* gene harboured a stop codon polymorphism, resulting in a nonsense mutation. Although most alleles were phylogenetically distinct, four clades (1-4), shaded green containing identical sequences were observed within the population. Whilst isolates from multiple clonal lineages were present in clades 1 and 2, only isolates within the same clonal lineage were present in clades 3 and 4 (Figure 3). One isolate (ISTOP-53) with a *blaZ* allotype C harboured a 36 bp in-frame deletion within the *blaZ* coding sequence (Figure 3). Further investigation of conserved amino acid residues important for the catalytic activity (Ser70, Lys73, Ser130, Asp131, Asn132) and structural integrity (Glu166, Ile167, Arg164, Asn169) of the β-lactamase protein showed presence of all residues in the translated sequence encoded by the 34 intact *blaZ* and the truncated *blaZ* harboured by ISTOP-53.

Discussion

This study demonstrated high genetic diversity among PSSA isolates causing bacteraemia in Australia in 2020 with the use of WGS, and the limitations of diagnostic laboratory methods. Multiple clonal lineages present in the collection of PSSA isolates have been characterised. Polyclonal distribution of virulence factors and AMR genes were observed, and there is no correlation between clonal lineages and virulence factors. Presence of the *blaZ* gene in approximately half of the isolates in CC15 suggest that penicillin resistance may be driven by a single clone. Identifying the population structure of PSSA causing bacteraemia across Australia is an accomplishment, since there were no prior studies in Australia that shed light on the epidemiological diversity of PSSA. Predominant clonal lineages identified in this study were congruent to studies reported in other geographical regions, such as CC5 and CC45 lineages in Sweden and Spain (13, 18), CC15, CC188, and CC398 clonal lineages in China (19), suggesting that the movement of strains is likely a result of international travel. These lineages may be present in other countries; however, they have been uncharacterised to date. Despite having congruent clonal lineages with other studies, PSSA strains characterised in this study cannot be compared with studies from Sweden and Spain, since the clonal lineages of the isolates in both studies were determined from BURP (Based on Repeat Pattern) algorithm analysis of *spa* types. Sequence types determined from this study are only concordant with the study by Jin *et al.*, since most sequence types identified in China were also identified in this study, due to WGS (19). Although overseas travel can introduce strains of PSSA into Australia, it is interesting that there are also novel STs identified which are unique to Australia. Whilst the reasons for the resurgence of PSSA remain unknown, some possible inference could be made. Firstly, phenotypic reversion of penicillin resistance can occur, due to the use of broad-spectrum antimicrobials (i.e., vancomycin, cefazolin) for the treatment of SAB. Secondly, the emergence of novel STs identified in the study might suggest genetic evolution within isolates, in the selection of fitter clones.

The ideal method for β-lactamase detection in clinical isolates remains a contemporary challenge. Penicillin susceptibility testing using the Vitek® 2 automated system is not sufficient in classifying PSSA isolates, since the Vitek® 2 system fail to detect *blaZ*-positive isolates despite having a low error rate. Disc diffusion is the most reliable phenotypic test, as the zone diameter criteria with the P1 and P10 disc had greater sensitivity rate compared to BMD and Etest®. Although the zone diameter criterion with P10 disc only detected approximately half of the *blaZ*-positive isolates, sharp penicillin zone edge observed in all disc diffusion isolates suggest that the zone edge interpretive criterion is accurate and reliable. Hence the combination of both antibiotic discs is strongly recommended for β-lactamase detection. In a situation where a laboratory has limited resources and can only use one antibiotic disc for disc

diffusion, the P1 disc interpreted by the EUCAST guidelines is recommended, since it has superior performance compared to the P10 disc. The BMD method had unacceptable inferior performance despite it being considered the gold standard for phenotypic susceptibility testing (38). In addition, the Etest® performed similarly to BMD, hence BMD and Etest® are not recommended for β-lactamase detection. The β-lactamase nitrocefin test fared average, hence it should only be used as a confirmatory test with disc diffusion. Variation in the detection of penicillin resistance between phenotypic tests might suggest heteroresistance in this study; that is, the presence of a heterogenous population of bacteria with increased AMR in a subpopulation. To reliably confirm for the presence of heteroresistance, population analysis profile must be performed on *blaZ*-positive isolates. Disc diffusion, BMD, and Etest® performed in this study cannot provide any information on the frequency and MIC of the resistant subpopulation (39). With that said, phenotypic tests may also be influenced by additional factors other than the expression of *blaZ* – mutations present within the coding sequence of the BlaR1 (signal transducer) and BlaI (*blaZ* repressor), presence of insertion sequences, and/or physical characteristics such as the thickness of bacterial cell wall, presence of more efflux pumps, which are not investigated in this study.

Molecular genotypic techniques such as WGS or polymerase chain reaction for the detection of *blaZ*, should be also performed in tandem to determine penicillin susceptibility in PSSA isolates. However, according to CLSI guidelines, it is mentioned that the PCR testing for the *blaZ* gene in isolates may be considered (36). In addition, there is no recommendation on the specific assay and reagents used, making it obscure and challenging for diagnostic laboratories to select a superior method for the detection of β-lactamase. A study conducted by Gordon *et al.* found WGS to have a discrepancy rate of only 1.2%, when they predicted phenotypic antimicrobial susceptibility in isolates only using genomic data (40). This emphasises the need for a combination of genotypic and phenotypic testing in the laboratory. To ensure that the implementation of various screening methods is worthwhile, assessing the use of penicillin in clinical practice for patients with PSSA bacteraemia should be warranted first.

Genetically diverse PSSA isolates also harboured genetically diverse *blaZ* alleles, although four identical alleles were observed in four clades. Horizontal gene transfer is a likely reason for the presence of isolates from multiple lineages harbouring identical alleles in Clade 1 and 2. Horizontal gene transfer can occur via three mechanisms: the exchange of identical *blaZ* allele in plasmids during conjugation, the integration of identical *blaZ* allele into the bacterium during transformation, and the integration of bacteriophages harbouring the same *blaZ* allele, known as transduction. Presence of *blaZ*-positive isolates from a single lineage in Clade 3 and

4 suggest that the identical *blaZ* allele may have resided on the chromosome and is restricted within the lineage. Penicillin resistance may have been driven by CC15 clonal lineage, since the isolates in Clade 4, comprised approximately half of the lineage within the collection, had identical *blaZ* allele and *blaZ* allotype. It is unclear if the expression of β-lactamase may occur in isolates with truncated *blaZ* alleles since the point mutations may be detected and corrected by the DNA mismatch repair system after DNA replication and recombination.

There are several limitations in this study. Firstly, these isolates were only collected from a single year period. Sequencing PSSA isolates prior and beyond 2020 will provide a greater longitudinal scale of data, providing information if one or more clones are responsible for the resurgence of PSSA isolates. The evolution of sequence types that are locus variants apart, and the presence of more *blaZ*-positive CC15 isolates, may also be observed. Secondly, genetic diversity of carriage isolates is not known, since these isolates were clinical PSSA isolates causing bacteraemia. Thirdly, I could not determine if the isolates carrying AMR genes and virulence factors have been driven by plasmids and phages, since they were not investigated in the study. Fourthly, antimicrobial susceptibility tests were not performed on *blaZ*-negative isolates. Not only the specificity of various tests cannot be determined, but it is also unsure if there are *blaZ*-negative isolates that may display phenotypic penicillin resistance. Finally, limitations of diagnostic laboratory methods made an impact in gathering phenotypic data. For instance, the nitrocefin disc can be hard to interpret when detecting for β-lactamase in weak β-lactamase producing isolates. Hues of pink colour on nitrocefin disc which is still considered a positive reaction according to manufacturer's protocol, can be observed. Misclassification of *S. argenteus* identified through WGS, and not Vitek® MS or the MALDI Biotyper® microbial identification system, also present a flaw in current diagnostic laboratory technique.

Conclusions

In conclusion, this study has illustrated vast genomic diversity of PSSA causing bacteraemia in Australia in 2020. Multiple clones were identified and characterised in the collection, and disc diffusion has been shown to be a reliable phenotypic test. Although the P1 disc diffusion has superior performance and is strongly recommended as a phenotypic test, a combination of genotypic and phenotypic methods is still necessary in diagnostic laboratories, after the efficacy of penicillin treatment for PSSA bacteraemia have been evaluated. Longitudinal population study of PSSA should be conducted in the future to provide better epidemiological understanding of PSSA, which may confirm the presence of one or more clones responsible for its resurgence. Evaluating phenotypic expression of *blaZ*-negative isolates should be

performed to confirm their penicillin susceptibility and determine specificity of phenotypic tests. Population analysis profile can be performed to confirm heteroresistance in PSSA isolates. Further investigation into the sequences of BlaR1 and BlaI in isolates should be performed to uncover presence of mutations that may impact penicillin susceptibility. Mutations discovered can be validated with molecular knockout experiments. Epidemiological data and characteristics of PSSA isolates elucidated in this study have provided valuable genomic and bioinformatic information for a global context, and thus create better opportunities for antimicrobial stewardship.

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Figures and Figure legends

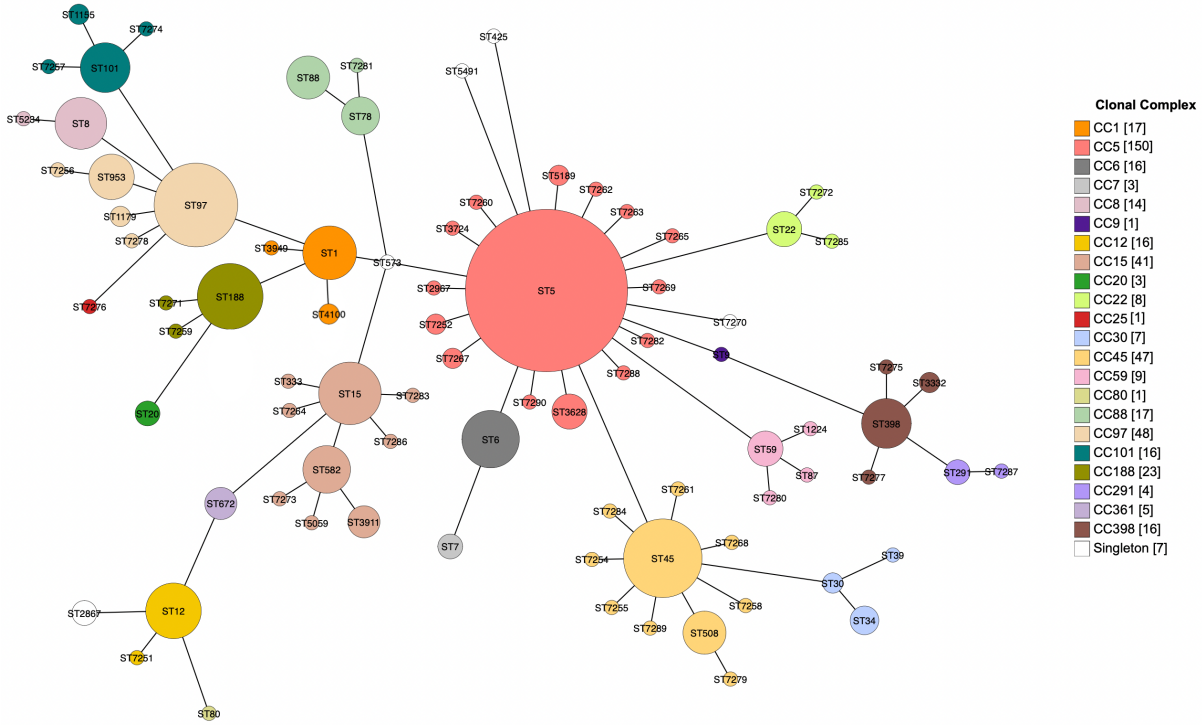

Figure 1. Minimal spanning tree of the sequence type (ST) of PSSA isolates. Each ST is represented by a circle, and the size of the circle is directly proportional to the number of isolates in a particular ST. The length of the line joining two circles is directly proportional to the number of allelic differences between the two STs. The circles are coloured by clonal complex (CC) and the number of isolates in each CC is shown in the colour legend.

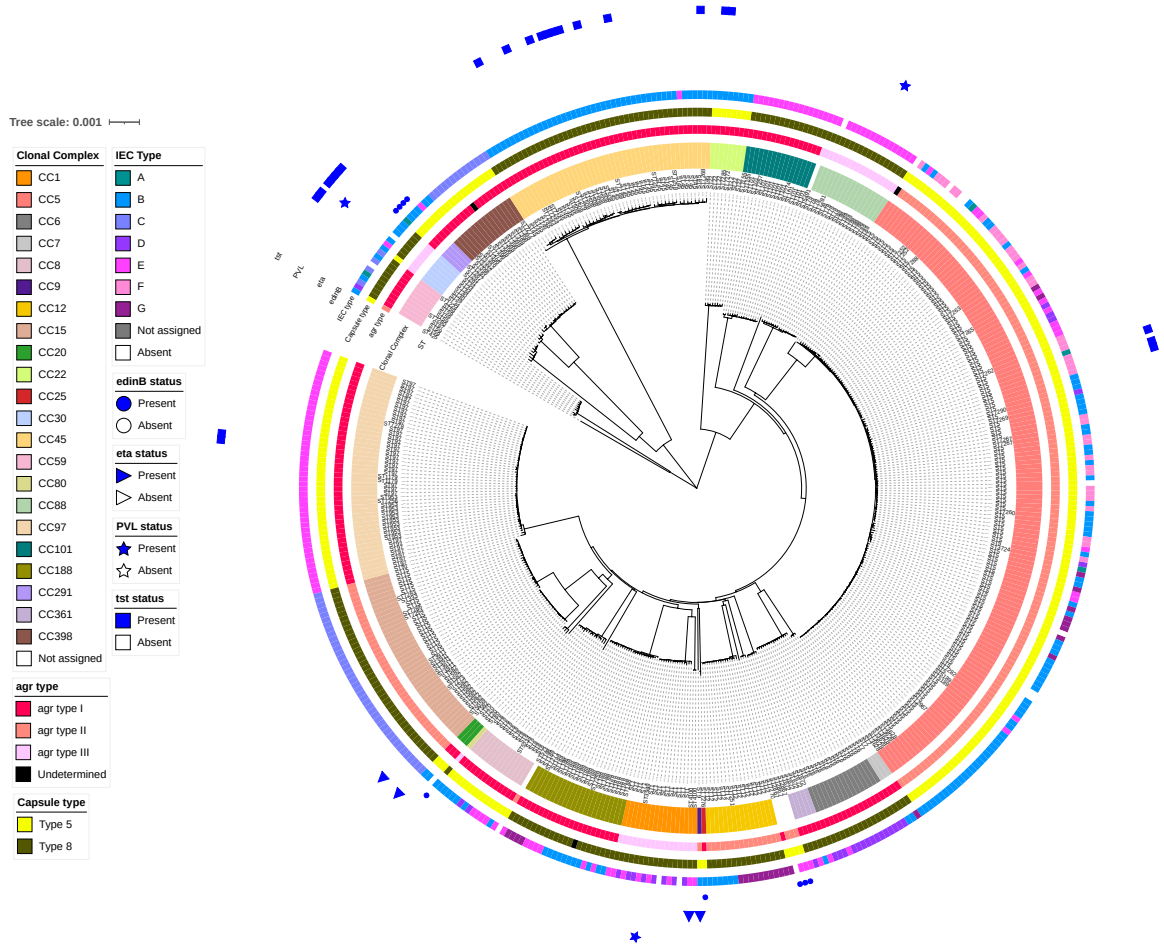

Figure 2. Rooted core genome neighbour-joining phylogenetic tree of 470 PSSA isolates. The branch labels represent the sequence type (ST) of each isolate. The clonal complex (CC), *agr* type, capsule type and immune evasion cluster (IEC) type are shown by different colours in each ring (from inner ring to outer ring). The presence of virulence genes including *edinB* (circle), *eta* (triangle) and *tst* (square) is shown in blue. PVL-positive isolates are shown with a blue star.

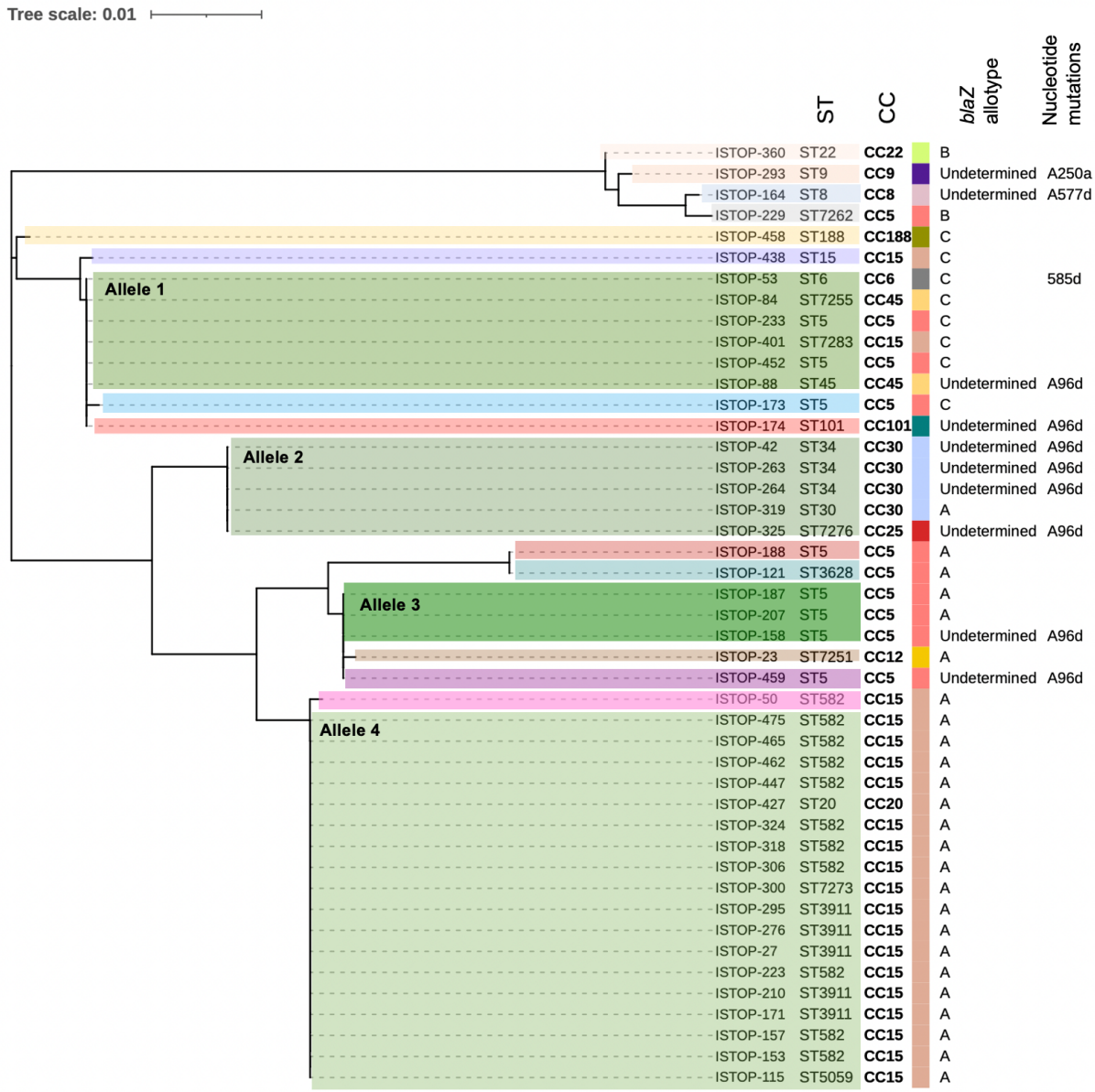

Figure 3. Neighbour-joining phylogenetic tree of 45 *blaZ*-positive isolates. The sequence type (ST), clonal complex (CC), *blaZ* allotype (A-D), and presence of nucleotide mutations identified are shown for each isolate. Different *blaZ* alleles were coloured from their branch lengths. Four clades identified, labelled Alleles 1-4, were shaded green.

Tables

Table 1. Distribution of 45 *blaZ*-positive isolates in each clonal complex

CC	No. (%) of *blaZ*-positive isolates in each CC	ST(s) of *blaZ*-positive isolates
CC1	-	
CC5	10 (6.7)	ST5 (n=8) ST3628 (n=1) ST7262 (n=1)
CC6	1 (6.3)	ST6 (n=1)
CC7	-	
CC8	1 (7.1)	ST8 (n=1)
CC9	1 (100)	ST9 (n=1)
CC12	1 (6.3)	ST7251 (n=1)
CC15	20 (48.8)	ST582 (n=11) ST3911 (n=5) ST15 (n=1) ST5059 (n=1) ST7273 (n=1) ST7283 (n=1)
CC20	1 (33.3)	ST20 (n=1)
CC22	1 (12.5)	ST22 (n=1)
CC25	1 (100)	ST7276 (n=1)
CC30	4 (57.1)	ST34 (n=3) ST30 (n=1)
CC45	2 (4.3)	ST45 (n=1) ST7255 (n=1)
CC59	-	
CC80	-	
CC88	-	
CC97	-	
CC101	1 (6.3)	ST101 (n=1)
CC188	1 (4.3)	ST188 (n=1)
CC291	-	
CC361	-	
CC398	-	
Singletons	-	

CC, clonal complex; ST, sequence type.

Table 2. Summary of phenotypic antimicrobial susceptibility testing of 45 *blaZ*-positive isolates

Antimicrobial susceptibility tests and nitrocefin test	Interpretive Guidelines	No. (%) of isolates				Sensitivity
		Resistant	Susceptible	Positive β-lactamase reaction	Negative β-lactamase reaction	
BMD [a]	CLSI, EUCAST	13 (28.8)	32 (71.1)			28.8%
Etest® [a]	CLSI, EUCAST	12 (26.7)	33 (73.3)			26.7%
Disc Diffusion						
Zone diameter, P1 [b]	EUCAST	37 (82.2)	8 (17.8)			82.2%
Zone diameter, P10 [c]	CLSI	26 (57.8)	19 (42.2)			57.8%
Zone Edge, P1 [d]	EUCAST	45 (100)	0			100.0%
Zone Edge, P10 [d]	CLSI	45 (100)	0			100.0%
Nitrocefin test	-	-	-	22 (48.9)	23 (51.1)	48.9%

BMD, brothmicrodilution; CLSI, Clinical and Laboratory Standards Institute; EUCAST, European Committee on Antimicrobial Susceptibility Testing

[a] Resistant, >0.125 mg/L; Susceptible, ≤0.125 mg/L

[b] Resistant, <26 mm; Susceptible, ≥26 mm

[c] Resistant, ≤28 mm; Susceptible, ≥29 mm

[d] Resistant, sharp zone edge; Susceptible, fuzzy zone edge

Supplementary Information

Supplementary Table 1. Typing results for the Vitek® 2 penicillin-susceptible *Staphylococcus aureus* isolates identified in the Australian Group on Antimicrobial Resistance's 2020 Australian *Staphylococcus aureus* Sepsis Outcome Programme

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-1	NSW	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25	t304	0.06	-
ISTOP-2	NSW	Hospital	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-3	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-4	WA	Hospital	1-4-374-4-12-1-10	ST2967	5	26-23-17-12-12-16	t1345	≤0.03	-
ISTOP-5	WA	Community	144-1-1-1-1-5-3	ST1179	97	07-34-34-33-34	t237	0.12	-
ISTOP-6	WA	Community	3-779-1-1-4-4-3	ST5234	8	11-19-12-21-17-34-24-34-22-33-25	t955	0.06	-
ISTOP-7	WA	Hospital	13-13-1-1-12-11-13	ST15	15	07-23	t605	0.06	-
ISTOP-8	WA	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17-21-17-34-34-34-33-34	UD	0.12	-
ISTOP-9	WA	Community	1-4-1-4-12-1-10	ST5	5	26-17-20-17-12-17-17	t1227	≤0.03	-
ISTOP-10	WA	Community	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-11	WA	Community	3-35-19-2-20-26-29	ST398	398	08-12-16-34-24-25	t2928	0.06	-
ISTOP-12	WA	Community	1-3-1-8-11-5-11	ST12	12	07-23-24-33-22-22-17	UD	≤0.03	-
ISTOP-13	WA	Community	1-4-463-4-12-1-10	ST3628	5	26-23-17-34-17-12-16	t5259	0.06	-
ISTOP-14	WA	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-17	t160	0.06	-
ISTOP-15	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-17-16	t1560	0.06	-
ISTOP-16	VIC	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	0.06	-
ISTOP-17	VIC	Community	3-3-1-1-4-4-3	ST8	8	11-12-21-17-34-24-34-22-25	t024	0.12	-
ISTOP-18	VIC	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-19	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-17-16	t306	0.12	-
ISTOP-20	VIC	Community	44-13-1-1-12-11-13	ST333	15	07-23-13-34-12-12-23-02-12-23	UD	0.06	-
ISTOP-21	VIC	Community	100-1-1-8-1-1-1	ST4100	1	07-23-12-21-17-34-16-23-23	UD	≤0.03	-
ISTOP-22	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	≤0.03	-
ISTOP-23	VIC	Hospital	1-3-1-8-859-5-11	ST7251	12	07-23-21-24-33-22-17	t160	0.12	**DETECTED**
ISTOP-24	VIC	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-25	NSW	Hospital	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	≤0.03	-
ISTOP-26	NSW	Community	10-40-8-6-10-3-2	ST508	45	08-16-xx-16-34-76	UD	≤0.03	-
ISTOP-27	VIC	Community	13-13-1-1-12-10-530	ST3911	15	07-23-12-34-34-12-12-16-23-02-12-23	t2859	0.06	**DETECTED**
ISTOP-28	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-29	QLD	Hospital	1-3-1-8-11-5-11	ST12	12	15-22-17	t336	≤0.03	-
ISTOP-30	QLD	Community	1-3-1-8-11-5-11	ST12	12	07-23-24-33-22-22-17	UD	0.06	-
ISTOP-31	QLD	Hospital	10-14-8-6-10-3-2	ST45	45	08-16-34	t026	0.06	-
ISTOP-32	QLD	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-33	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-34	NSW	Community	1-4-463-4-12-1-10	ST3628	5	26-23-17-34-17-20-17-12-12-12-16	t1265	≤0.03	-
ISTOP-35	NSW	Community	10-40-8-6-10-3-2	ST508	45	08-16-02-16-34-13-17-34-16-34	t015	0.12	-
ISTOP-36	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-17-16	t2049	0.06	-
ISTOP-37	NSW	Community	3-1-1-1-1-5-3	ST97	97	26-23-21-17-34-34-34-33-34	t9432	0.06	-
ISTOP-38	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-39	TAS	Community	1-4-463-4-12-1-10	ST3628	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.12	-
ISTOP-40	TAS	Community	1-3-1-8-11-5-11	ST12	12	07-23-12-33-17	t909	0.12	-
ISTOP-41	VIC	Community	1-311-1-4-12-1-10	ST7252	5	26-23-17-34-17-20-17-12-17-17	t686	0.12	-
ISTOP-42	VIC	Hospital	8-2-2-2-6-3-2	ST34	30	04-24-33-31-12-16-12-33-34	UD	0.06	**DETECTED**
ISTOP-44	NSW	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	-
ISTOP-45	NSW	Hospital	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-33-34	t359	0.06	-
ISTOP-46	NSW	Hospital	13-13-1-1-12-11-13	ST15	15	07-23-02-12-23	t803	0.12	-
ISTOP-47	NSW	Community	22-1-14-23-12-53-31	ST78	88	07-12-21-17-34-34-34-33-34	t1814	0.12	-
ISTOP-48	NSW	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	0.12	-
ISTOP-49	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-16	t548	≤0.03	-
ISTOP-50	NSW	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-34-12-23-02-12-23	t085	0.12	**DETECTED**
ISTOP-51	NSW	Hospital	1-3-1-8-11-5-11	ST12	12	07-23-24-33-22-22-17	UD	0.06	-
ISTOP-52	NSW	Community	3-1-1-8-1-1-1	ST188	188	07-23-21-17-34	t2883	0.12	-
ISTOP-53	NSW	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	0.12	**DETECTED**
ISTOP-54	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-55	NSW	Community	3-37-19-2-20-26-32	ST291	291	08-16-34-24-34-17-17-17	t3096	0.12	-
ISTOP-56	NSW	Community	3-1-1-8-1-1-1	ST188	1	07-23-12-21-17-34	t189	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-57	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-33-34	t359	0.06	-
ISTOP-58	NSW	Community	3-1-122-1-1-5-3	ST953	97	07-33-34	t1109	0.12	-
ISTOP-59	NSW	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-12-23-02-12-23	t085	0.06	-
ISTOP-60	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-61	VIC	Community	1-311-1-4-12-1-10	ST7252	5	26-23-17-34-17-20-17-12-17-17	t686	0.06	-
ISTOP-62	VIC	Hospital	1-4-1-4-12-577-10	ST5189	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-63	VIC	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-64	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-65	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-13-34-33-34	t14122	0.12	-
ISTOP-66	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-67	WA	Hospital	19-23-15-2-19-20-15	ST59	59	04-20-17-20-17-25-34	t437	0.12	-
ISTOP-68	WA	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34	t230	0.06	-
ISTOP-69	NSW	Community	100-1-1-8-1-1-1	ST4100	1	Not Determined	-	0.06	-
ISTOP-70	NSW	Community	10-14-8-6-10-3-2	ST45	45	09-34-34-17-34-16-34	t563	0.06	-
ISTOP-71	NSW	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17-13-34-34-33-34	t4013	0.06	-
ISTOP-72	QLD	Community	69-1-14-15-11-19-3	ST1155	101	04-13-21-12-17-17	t4171	0.12	-
ISTOP-73	NSW	Hospital	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-74	NSW	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-22-17	t771	0.06	-
ISTOP-75	NSW	Community	10-14-8-6-10-3-964	ST7254	45	09-34-16-34	t132	≤0.03	-
ISTOP-76	ACT	Community	22-1-14-23-12-53-31	ST78	88	08-21-17-13-34-34	UD	0.12	-
ISTOP-77	ACT	Community	19-23-15-2-19-20-15	ST59	59	04-20-17-20-17-31-16-34	t216	0.06	-
ISTOP-78	ACT	Community	3-3-1-1-4-4-3	ST8	8	11-19-12-21-17-34-24-34-22-25	t008	0.06	-
ISTOP-79	ACT	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.06	-
ISTOP-80	NSW	Hospital	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-33-34	t359	0.12	-
ISTOP-81	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-xx-17-12-17-16	UD	0.12	-
ISTOP-82	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-83	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-84	TAS	Community	10-14-8-6-10-3-26	ST7255	45	08-16-02-16-34	t230	0.12	**DETECTED**
ISTOP-85	TAS	Community	4-9-1-8-1-10-8	ST20	20	07-17-21-34-34-22-34	t3277	0.12	-
ISTOP-86	TAS	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-22-17	t771	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-87	TAS	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	≤0.03	-
ISTOP-88	TAS	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-16-34	t015	0.12	**DETECTED**
ISTOP-89	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-90	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16-16	t214	0.12	-
ISTOP-91	SA	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25	t304	0.12	-
ISTOP-92	SA	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-93	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-94	SA	Community	10-14-8-6-10-3-2	ST45	45	09-02-16-34-16-34	t371	0.12	-
ISTOP-95	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-96	VIC	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	≤0.03	-
ISTOP-97	VIC	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	≤0.03	-
ISTOP-98	VIC	Community	3-35-19-2-402-26-29	ST3332	398	08-16-02-25-34-24-25	t011	≤0.03	-
ISTOP-99	VIC	Community	3-1-122-1-1-5-925	ST7256	97	07-23-12-21-17-34-34-33-34	t359	0.06	-
ISTOP-100	VIC	Community	3-35-19-2-402-26-29	ST3332	398	08-16-02-25-34-24-25	t011	≤0.03	-
ISTOP-101	VIC	Community	8-2-2-2-6-3-2	ST34	30	04-44-33-31-12-16-34-12-33-34	t1670	≤0.03	-
ISTOP-102	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-12-12-17-16	t3597	≤0.03	-
ISTOP-103	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-13-16	t9394	0.06	-
ISTOP-104	SA	Community	1-4-166-4-12-1-10	ST3724	5	26-23-17-34-17-16	t688	0.06	-
ISTOP-105	NSW	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	0.12	-
ISTOP-106	NSW	Community	1-4-1-4-12-1-10	ST5	5	35-17-34-17-20-17-12-16	t2958	0.06	-
ISTOP-107	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-108	QLD	Community	4-3-1-1-11-72-11	ST672	361	26-22-17-20-17-12-17-16-16	t3841	≤0.03	-
ISTOP-109	QLD	Community	13-13-1-1-12-11-13	ST15	15	07-23-02-12-23	t803	0.12	-
ISTOP-110	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-111	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-16	t111	0.06	-
ISTOP-112	NSW	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-113	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	≤0.03	-
ISTOP-114	NSW	Hospital	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	0.12	-
ISTOP-115	NSW	Hospital	13-13-1-212-12-10-13	ST5059	15	07-23-12-34-23-02-12-23	t4714	0.12	**DETECTED**
ISTOP-116	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-117	WA	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-17	t160	0.06	-
ISTOP-118	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-119	WA	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	-
ISTOP-120	WA	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17-21-17-34-34-34-33-34	UD	0.12	-
ISTOP-121	WA	Community	1-4-463-4-12-1-10	ST3628	5	26-23-17-34-17-20-17-12-12-16	t179	0.12	**DETECTED**
ISTOP-122	WA	Community	10-14-8-6-10-3-2	ST45	45	09-34-13-17-34-16-34	t130	0.06	-
ISTOP-123	SA	Hospital	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-13-16-34	t302	0.12	-
ISTOP-124	SA	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-125	SA	Community	5-4-1-4-4-6-3	ST7	7	07-23-21-17-34-12-23-02-20	t7234	0.12	-
ISTOP-126	SA	Community	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-127	SA	Hospital	1-1-1-1-1-1-1	ST1	1	26-23-21-16-34-33-13	t177	0.12	-
ISTOP-128	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-129	NSW	Hospital	13-13-1-1-12-11-13	ST15	15	07-23-34-34-12-23-02-12-23	t2216	0.06	-
ISTOP-130	NSW	Hospital	1-606-1-1-1-1-1	ST3949	1	07-33-13	t2207	0.12	-
ISTOP-131	NSW	Community	4-3-1-1-11-72-11	ST672	361	26-17	t2379	0.06	-
ISTOP-132	NSW	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-02-25-25	t1170	0.12	-
ISTOP-133	NSW	Community	3-1-14-15-860-19-3	ST7257	101	04-13-21-12-297-20-17-12-17-17	UD	0.06	-
ISTOP-134	NSW	Hospital	13-13-1-1-12-11-13	ST15	15	08-34-34-12-34-12-12-23-02-12-23	t14014	0.12	-
ISTOP-135	NSW	Community	22-1-14-23-12-4-31	ST88	88	07-12-21-17-13-13-13-34-34-33-34	t2649	0.12	-
ISTOP-136	TAS	Community	3-1-14-15-11-19-3	ST101	101	4	t528	0.06	-
ISTOP-137	VIC	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-12-12-23	t1877	0.06	-
ISTOP-138	VIC	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.06	-
ISTOP-139	VIC	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-02-16-34	t10588	≤0.03	-
ISTOP-140	VIC	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-17	t160	0.12	-
ISTOP-141	VIC	Community	1-1-1-1-1-1-1	ST1	1	07-33-13	t2207	≤0.03	-
ISTOP-142	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-16	t688	0.06	-
ISTOP-143	SA	Community	3-3-1-1-4-4-3	ST8	8	11-12-21-17-34-24-34-22-25	t024	≤0.03	-
ISTOP-144	ACT	Community	3-3-1-1-4-4-3	ST8	8	563-19-12-21-17-34-24-34-22-25	ND	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-145	ACT	Community	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-17-16	t17058	0.06	-
ISTOP-146	ACT	Community	18-33-6-20-7-50-48	ST425	Singleton	14-44-12-17-23	UD	0.06	-
ISTOP-147	ACT	Community	850-14-8-6-10-3-965	ST7258	45	08-16-02-16-34-34-17-13-13-17-34-16-13	UD	0.06	-
ISTOP-148	ACT	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-16-17-20-17-12-17-16	t8241	0.06	-
ISTOP-149	ACT	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-16-34	t015	0.06	-
ISTOP-150	ACT	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-17	t160	0.06	-
ISTOP-151	ACT	Community	4-3-1-1-11-72-11	ST672	361	26-22-17-20-17-17-16-16	t14090	0.12	-
ISTOP-152	TAS	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	≤0.03	-
ISTOP-153	TAS	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	**DETECTED**
ISTOP-154	TAS	Community	10-40-8-6-10-3-2	ST508	45	08-16-02-16-13-17-34-16-34	t073	≤0.03	-
ISTOP-155	TAS	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	-
ISTOP-156	NSW	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-157	NSW	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-12-12-12-23-02-12-23	t393	0.12	**DETECTED**
ISTOP-158	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	≤0.03	**DETECTED**
ISTOP-159	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-12-12-12-16	t7186	0.06	-
ISTOP-160	NSW	Community	10-14-8-6-10-3-2	ST45	45	08-16-34-16-34	t728	0.06	-
ISTOP-161	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-162	NSW	Community	1-152-1-8-1-5-11	ST2867	Singleton	07-23-12-21-12-41-20-17-12-12-17	t2016	0.12	-
ISTOP-163	NSW	Community	10-40-8-6-10-3-2	ST508	45	08-16-02-16-34-13-17-34-16-34	t015	0.06	-
ISTOP-164	NSW	Community	3-3-1-1-4-4-3	ST8	8	11-19-12-21-17-34-24-34-22-25	t008	0.06	**DETECTED**
ISTOP-165	NSW	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	-
ISTOP-166	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20	t2595	0.12	-
ISTOP-167	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-168	WA	Community	69-1-14-15-11-19-3	ST1155	101	04-21-12-17-17	UD	0.06	-
ISTOP-169	WA	Community	10-40-8-6-10-3-2	ST508	45	08-16-02-16-34-13-17-34-16-34	t015	0.06	-
ISTOP-170	WA	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-34-13-17-34-16	t8453	≤0.03	-
ISTOP-171	WA	Community	13-13-1-1-12-10-530	ST3911	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	**DETECTED**
ISTOP-172	VIC	Community	3-1-1-1-1-5-3	ST97	97	07-34-33-34	t1028	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-173	VIC	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	**DETECTED**
ISTOP-174	VIC	Hospital	3-1-14-15-11-19-3	ST1155	101	04-13-21-12-17-20-17-12-17-17	t2078	0.12	**DETECTED**
ISTOP-175	VIC	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17	UD	0.06	-
ISTOP-176	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-178	VIC	Community	1-4-1-4-12-1-10	ST5	5	35-17-34-17-20-17-12-17-16	t442	0.06	-
ISTOP-179	VIC	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-180	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-12-17-16	t062	0.12	-
ISTOP-181	VIC	Community	3-3-1-1-4-4-3	ST8	8	11-19-12-21-17-34-24-34-22-25	t008	0.06	-
ISTOP-182	VIC	Community	22-1-14-23-12-53-31	ST78	88	07-12-21-17-13-34-34-33-34	t786	0.12	-
ISTOP-184	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	≤0.03	-
ISTOP-185	NSW	Community	3-1-1-8-1-803-1	ST7259	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-186	NSW	Community	19-23-15-2-19-20-136	ST1224	59	04-02-17-20-17-31-16-34	t471	≤0.03	-
ISTOP-187	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-12-17-16	t010	0.12	**DETECTED**
ISTOP-188	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	**DETECTED**
ISTOP-189	NSW	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-13-17-13-16-34	t10421	0.06	-
ISTOP-190	VIC	Community	1-49-60-15-28-38-145	ST5491	Singleton	15-34-16-17-17-23-75	t5925	≤0.03	-
ISTOP-191	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-192	VIC	Community	3-1-14-15-11-19-3	ST101	101	04-21-12-17	t643	0.12	-
ISTOP-193	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-195	SA	Community	851-4-1-4-12-1-10	ST7260	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-198	SA	Community	3-1-1-1-1-5-3	ST97	97	26-23-12-21-17-34-34-34-33-34	t1236	0.12	-
ISTOP-199	VIC	Community	1-3-1-14-11-51-10	ST80	80	26-23-12-34-34-33-34	t042	0.12	-
ISTOP-200	VIC	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-201	VIC	Community	1-4-1-4-12-1-10	ST5	5	35-17-34-17-20-17-12-17-16	t442	0.06	-
ISTOP-203	SA	Community	852-14-8-6-10-3-2	ST7261	45	164-34-16-34	t2726	≤0.03	-
ISTOP-204	SA	Hospital	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	0.12	-
ISTOP-205	NSW	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	-
ISTOP-206	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-207	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-273-17-34-17-20-17-12-12-12-16	UD	0.12	**DETECTED**
ISTOP-208	QLD	Community	1-152-1-8-1-5-11	ST2867	Singleton	07-23-12-21-12-41-20-17-12-12-12-17	UD	0.12	-
ISTOP-209	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-210	QLD	Community	13-13-1-1-12-10-530	ST3911	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.06	**DETECTED**
ISTOP-211	QLD	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-02-34	t231	0.06	-
ISTOP-212	QLD	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	0.06	-
ISTOP-213	VIC	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	0.12	-
ISTOP-214	VIC	Community	3-35-19-2-20-26-29	ST398	398	Not Determined	-	0.06	-
ISTOP-215	VIC	Community	3-3-1-1-4-4-3	ST8	8	11-10-21-21-17-34-24-34-22-25	t10888	0.12	-
ISTOP-216	TAS	Community	10-14-8-6-10-3-2	ST45	45	09-34	t362	0.06	-
ISTOP-217	TAS	Community	22-1-14-23-12-53-31	ST78	88	07-12-12-21-17-13-13-34-34-33-34	t2311	0.06	-
ISTOP-218	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-12-17-16	t010	0.12	-
ISTOP-219	TAS	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	0.06	-
ISTOP-220	TAS	Community	5-4-1-4-4-6-3	ST7	7	07-23-21-17-34-12-23-02-20	t7234	0.06	-
ISTOP-221	TAS	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-12-12-23-02-12-23	t346	≤0.03	-
ISTOP-222	WA	Community	4-3-1-1-11-72-11	ST672	361	26-22-17-20-17-12-17-17-16-16	t1309	0.06	-
ISTOP-223	WA	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-34-12-23-02-12-23	t085	0.06	**DETECTED**
ISTOP-224	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-225	WA	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	-
ISTOP-226	WA	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	0.06	-
ISTOP-227	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-228	WA	Community	1-4-1-4-12-577-10	ST5189	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-229	WA	Community	1-4-1-4-12-1-966	ST7262	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	**DETECTED**
ISTOP-230	WA	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34	t230	0.06	-
ISTOP-231	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-232	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-12-17-16	t5081	0.12	-
ISTOP-233	WA	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-16	t179	0.12	**DETECTED**
ISTOP-234	WA	Community	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-34-33-34	t267	≤0.03	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-235	WA	Hospital	13-13-1-1-12-11-13	ST15	15	07-23-12-34-12-12-23-02-12-23	t346	0.06	-
ISTOP-236	WA	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-12-23-02-12-23	t085	0.12	-
ISTOP-237	WA	Community	3-1-122-1-1-5-3	ST953	97	07-23-21-17-34-34-33-34	t2802	0.12	-
ISTOP-238	WA	Community	1-4-1-4-861-1-10	ST7263	5	26-17-20-17-12-17-16	t045	0.12	-
ISTOP-239	SA	Community	3-3-1-1-4-4-3	ST8	8	11-10-12-21-17-21-17-34-24-34-22-16	UD	0.06	-
ISTOP-240	SA	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-02-02-25-34-25	t6605	0.06	-
ISTOP-241	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-242	SA	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-243	SA	Community	853-13-1-1-12-11-13	ST7264	15	07-23-12-34-34-12-23-02-12-23	t085	0.06	-
ISTOP-244	SA	Hospital	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	0.06	-
ISTOP-245	WA	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-33-34	t359	0.12	-
ISTOP-246	WA	Hospital	1-4-1-566-12-1-967	ST7265	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-248	WA	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25	t304	0.12	-
ISTOP-249	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-17-16	t088	0.06	-
ISTOP-250	WA	Community	3-1-1-1-1-5-3	ST97	97	07-23-21-17-34-34-33-34	t3380	0.12	-
ISTOP-251	WA	Community	1-4-1-4-12-1-968	ST7267	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-252	WA	Community	1-4-1-4-12-1-10	ST5	5	26-17-20-17-12-17-16	t045	0.12	-
ISTOP-253	WA	Hospital	10-40-8-6-10-3-2	ST508	45	08-16-02-16-34-13-17-34-16-34	t015	0.12	-
ISTOP-254	WA	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-17	t160	0.06	-
ISTOP-255	NSW	Community	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-33-34	t359	0.06	-
ISTOP-256	WA	Community	19-23-15-2-41-20-15	ST87	59	04-20-17-31-16-34	t316	0.12	-
ISTOP-257	WA	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25	t304	0.06	-
ISTOP-259	ACT	Community	3-3-1-1-4-4-3	ST8	8	11-19-12-21-17-34-24-34-22-25	t008	≤0.03	-
ISTOP-260	ACT	Hospital	10-14-8-6-10-3-2	ST45	45	09-02-16-34-17-34-16-34	t706	0.06	-
ISTOP-261	ACT	Community	22-1-14-23-12-53-31	ST78	88	07-12-21-17-13-34-13-34-33-34	t2177	0.06	-
ISTOP-262	ACT	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-263	ACT	Hospital	8-2-2-2-6-3-2	ST34	30	04-33-31-12-16-34-16-12-33-34	t089	0.06	**DETECTED**
ISTOP-264	ACT	Hospital	8-2-2-2-6-3-2	ST34	30	04-33-31-12-16-34-16-12-33-34	t089	0.06	**DETECTED**
ISTOP-265	ACT	Community	1-4-1-4-12-1-10	ST5	5	07-23-17-34-17-20-17-12-17-16	t570	0.12	-
ISTOP-266	ACT	Community	7-6-1-5-8-8-6	ST22	22	26-23-13-23-31-05-17-25-16-28	t474	0.06	-
ISTOP-267	ACT	Community	1-4-1-4-12-1-10	ST5	5	35-17-12-16	t3660	0.06	-
ISTOP-268	NSW	Community	854-14-8-6-10-3-2	ST7268	45	08-16-02-16-34-13-17-34-16-34	t015	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-269	NSW	Community	10-40-8-6-10-3-2	ST508	45	08-16-34	t026	0.06	-
ISTOP-270	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-271	NSW	Hospital	1-4-903-4-12-1-10	ST7269	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-272	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-273	TAS	Community	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-274	TAS	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-17	t160	0.06	-
ISTOP-275	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-17-16	t306	≤0.03	-
ISTOP-276	NSW	Community	13-13-1-1-12-10-530	ST3911	15	07-23-12-34-34-34-12-12-23-02-12-23	t279	0.12	**DETECTED**
ISTOP-277	NSW	Community	1-61-904-8-12-4-20	ST7270	Singleton	11-19-17-20-17-12-17-17-16	UD	0.06	-
ISTOP-278	NSW	Community	7-6-1-5-8-8-6	ST22	22	07-23-13-23-31-05-17-25-17-25-16-28	t852	0.12	-
ISTOP-279	NSW	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-16-34	t015	0.12	-
ISTOP-280	NSW	Hospital	3-1-1-1-1-5-3	ST97	97	26-23-12-21-17-34-34	t7753	0.12	-
ISTOP-281	NSW	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	0.06	-
ISTOP-282	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.12	-
ISTOP-283	NSW	Community	10-14-8-6-10-3-2	ST45	45	09-34-34-17-16-34	t10771	0.06	-
ISTOP-284	NSW	Hospital	3-1-14-15-11-19-3	ST101	101	4	t528	0.12	-
ISTOP-285	NSW	Hospital	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-22-25	t4407	0.12	-
ISTOP-286	NSW	Hospital	3-3-1-1-4-4-3	ST8	8	11-19-12-21-17-34-24-34-22-25	t008	0.06	-
ISTOP-287	NSW	Community	3-1033-1-8-1-1-1	ST7271	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-288	NSW	Community	1-152-1-8-1-5-11	ST2867	Singleton	07-23-12-21-12-17-20-17-12-12-17	t148	0.06	-
ISTOP-289	NSW	Hospital	3-1-14-15-11-19-3	ST101	101	4	t528	0.06	-
ISTOP-290	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-291	QLD	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.06	-
ISTOP-292	QLD	Community	7-1034-1-5-8-8-6	ST7272	22	26-23-13-23-31-05-17-25-17-25-16-28	t005	≤0.03	-
ISTOP-293	VIC	Hospital	3-3-1-1-1-1-10	ST9	9	07-16-12-23-02-34	t4812	0.12	**DETECTED**
ISTOP-294	VIC	Community	3-1-14-15-11-19-3	ST101	101	4	t528	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-295	VIC	Community	13-13-1-1-12-10-530	ST3911	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	**DETECTED**
ISTOP-296	VIC	Community	2-2-2-2-2-2-2	ST39	30	15-12-16-16-02-25-17-24	t1504	≤0.03	-
ISTOP-298	VIC	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-13-34-33-34	t224	0.12	-
ISTOP-299	VIC	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	-
ISTOP-300	QLD	Community	13-13-91-1-12-10-13	ST7273	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	**DETECTED**
ISTOP-301	QLD	Hospital	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-12-17-16	t010	0.06	-
ISTOP-302	QLD	Community	4-3-1-1-11-72-11	ST672	361	26-22-17-20-17-12-17-17-16-16	t1309	0.06	-
ISTOP-303	QLD	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-304	QLD	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	0.12	-
ISTOP-305	QLD	Community	3-1-14-15-11-19-53	ST7274	101	4	t528	0.06	-
ISTOP-306	QLD	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	**DETECTED**
ISTOP-307	VIC	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-13-34-33-34	t224	≤0.03	-
ISTOP-308	VIC	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17-13-34-34-34-33-34	t3341	0.12	-
ISTOP-309	VIC	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	-
ISTOP-310	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-311	VIC	Community	2-2-2-2-6-3-2	ST30	30	15-12-12-16-02-16-02-25-17-24	t3037	0.06	-
ISTOP-312	NSW	Community	22-1-14-23-12-53-31	ST78	88	07-12-34-33-34	t2191	0.06	-
ISTOP-313	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-16	t179	0.06	-
ISTOP-315	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-17-20-17-12-17-16	t045	0.06	-
ISTOP-316	VIC	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-16	t179	0.12	-
ISTOP-317	VIC	Hospital	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	-
ISTOP-318	VIC	Hospital	13-13-1-1-12-10-13	ST582	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	**DETECTED**
ISTOP-319	VIC	Community	2-2-2-2-6-3-2	ST30	30	15-12-16-02-16-02-25-17-24-24	t012	0.12	**DETECTED**
ISTOP-320	VIC	Community	3-1-1-1-1-5-3	ST97	97	07-23-21-17-34-34-33-34	t2734	0.12	-
ISTOP-321	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-322	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-323	NSW	Community	3-1035-19-2-20-26-39	ST7275	398	08-16-02-25-02-02-31-25-34-25	UD	0.12	-
ISTOP-324	VIC	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.06	**DETECTED**
ISTOP-325	VIC	Community	855-1-4-1-5-5-4	ST7276	25	04-21-12-41-20-17-12-12-12-17	t258	≤0.03	**DETECTED**
ISTOP-326	VIC	Community	3-37-19-2-20-26-32	ST291	291	08-16-34-24-34-34-17-17	t937	≤0.03	-
ISTOP-327	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-12-17-16	t010	≤0.03	-
ISTOP-328	NSW	Community	3-1036-19-2-20-26-39	ST7277	398	08-16-02-25-34-25	t1451	0.06	-
ISTOP-329	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-330	NSW	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	≤0.03	-
ISTOP-331	NSW	Hospital	3-3-1-1-4-4-3	ST8	8	11-19-12-17-34-24-34-22-25	t1171	0.06	-
ISTOP-332	NSW	Community	3-1-14-15-11-19-3	ST101	101	4	t528	0.06	-
ISTOP-333	NSW	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17-21-17-13-34-34-33-34	t6928	0.12	-
ISTOP-334	SA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-335	SA	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	≤0.03	-
ISTOP-336	SA	Community	10-40-8-6-10-3-2	ST508	45	08-16-02-16-34-34-17-34-16-34	t050	0.06	-
ISTOP-337	WA	Community	10-14-8-6-10-3-2	ST45	45	08-23-16-34-13-293-34-16-34	UD	0.06	-
ISTOP-338	WA	Community	1-4-463-4-12-1-10	ST3628	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-339	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-340	NSW	Community	3-1-14-15-11-19-3	ST101	101	4	t528	0.12	-
ISTOP-342	TAS	Community	4-9-1-8-1-10-8	ST20	20	26-06-17-21-34-34-34-22-34	t2919	0.12	-
ISTOP-343	TAS	Community	19-23-25-2-19-20-15	ST59	59	07-23-21-17-34-12-23-02-12-23	t471	0.06	-
ISTOP-344	TAS	Community	3-1037-1-1-1-5-3	ST7278	97	07-23-12-21-17-34-34-33-34	t359	0.12	-
ISTOP-345	VIC	Community	5-4-1-4-4-6-3	ST7	7	07-23-21-17-34-12-23-02-12-23	t091	0.06	-
ISTOP-346	VIC	Community	10-40-8-19-10-3-2	ST7279	45	08-16-02-16-34-34-17-34-16-34	t050	0.06	-
ISTOP-347	WA	Community	7-6-1-5-8-8-6	ST22	22	26-23-13-23-05-17-25-16-28	t3243	0.12	-
ISTOP-348	WA	Community	13-13-1-1-12-11-13	ST15	15	26-23-12-34-34-12-12-23-02-12-23	t491	0.06	-
ISTOP-349	WA	Community	1-4-463-4-12-1-10	ST3628	5	26-17-20-17-12-12-12-16	t7026	0.12	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-350	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-351	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-16	t179	0.12	-
ISTOP-352	WA	Community	3-1-1-1-1-5-3	ST97	97	7	t693	0.12	-
ISTOP-353	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-354	WA	Community	19-23-15-2-19-20-969	ST7280	59	08-16-02-25-34-25	t216	0.06	-
ISTOP-355	WA	Community	22-1-14-567-12-53-31	ST7281	88	07-34-34-34-33-34	t730	≤0.03	-
ISTOP-356	WA	Community	13-13-1-1-12-11-13	ST15	15	07-23	t605	0.06	-
ISTOP-357	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16-16	t10218	0.06	-
ISTOP-358	WA	Community	3-1-1-1-1-5-3	ST97	97	07-23-20-12-21-17-34-34-34-33-34	t10212	0.06	-
ISTOP-359	WA	Hospital	3-1-1-1-1-5-3	ST97	97	23-34-33-34	UD	≤0.03	-
ISTOP-360	WA	Hospital	7-6-1-5-8-8-6	ST22	22	26-23-13-23-31-29-17-31-12-25-17-25-16-28	UD	0.06	**DETECTED**
ISTOP-361	NSW	Community	3-1-14-15-11-19-3	ST101	101	4	t528	0.12	-
ISTOP-362	NSW	Hospital	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	≤0.03	-
ISTOP-363	NSW	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	0.06	-
ISTOP-364	NSW	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	0.12	-
ISTOP-365	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-17-16	t17484	0.12	-
ISTOP-366	NSW	Community	10-14-8-6-10-3-2	ST45	45	09-34	t362	0.06	-
ISTOP-367	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-368	NSW	Community	19-23-15-2-19-20-15	ST59	59	04-20-17-31-16-34	t316	0.12	-
ISTOP-369	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-17-16	t088	0.12	-
ISTOP-370	NSW	Community	1-1038-1-4-12-1-10	ST7282	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-372	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-17-34-17-20-17-12-12-12-16	t7186	0.06	-
ISTOP-373	VIC	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-16-34	t015	0.06	-
ISTOP-374	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-375	VIC	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25	t304	0.06	-
ISTOP-376	WA	Hospital	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-16-34	t015	0.06	-
ISTOP-377	NSW	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-22-17	t771	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-378	ACT	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16-17-16	t494	0.12	-
ISTOP-379	ACT	Community	13-13-1-1-12-11-13	ST15	15	07-23-12-34-34-23	t5393	0.06	-
ISTOP-380	ACT	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-16	t179	0.06	-
ISTOP-381	ACT	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-382	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-383	VIC	Hospital	7-6-1-5-8-8-6	ST22	22	26-23-13-23-05-17-25-17-25-16-16-28	t2933	0.12	-
ISTOP-384	VIC	Hospital	7-6-1-5-8-8-6	ST22	22	26-17-25-16-28	t1328	≤0.03	-
ISTOP-385	QLD	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.06	-
ISTOP-386	QLD	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-13-16-34	t302	0.06	-
ISTOP-388	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-17-20-17-12-17-16	t045	0.06	-
ISTOP-389	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-390	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-17-16	t105	0.06	-
ISTOP-391	VIC	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-12-17-16	t062	0.06	-
ISTOP-392	NSW	Community	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-34-33-34	t267	≤0.03	-
ISTOP-393	NSW	Community	3-1-14-15-11-19-3	ST101	101	4	t528	≤0.03	-
ISTOP-394	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-13-17-20-17-12-17-16	t242	≤0.03	-
ISTOP-395	WA	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-396	WA	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	0.12	-
ISTOP-397	WA	Community	3-3-1-1-4-4-3	ST8	8	11-19-12-21-17-34-24-34-22-25	t008	0.06	-
ISTOP-398	WA	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-399	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.12	-
ISTOP-400	WA	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-16-16	t6071	0.12	-
ISTOP-401	VIC	Community	13-13-1-1-12-11-970	ST7283	15	07-23-12-23-02-12-23	t547	0.12	**DETECTED**
ISTOP-402	VIC	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	0.06	-
ISTOP-403	VIC	Community	19-23-15-2-19-20-15	ST59	59	07-06-17-21-34-34-22-34	t437	0.12	-
ISTOP-404	VIC	Community	144-1-1-1-1-5-3	ST1179	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-405	VIC	Community	3-3-1-1-4-4-3	ST8	8	11-19-12-21-17-34-24-34-22-25	t008	0.12	-
ISTOP-406	VIC	Community	1-3-1-8-11-5-11	ST12	12	07-23-21-24-33-22-17	t160	0.06	-
ISTOP-407	VIC	Hospital	1-1-1-1-1-1-1	ST1	1	14-21-16-34-33-13	t174	0.12	-
ISTOP-408	VIC	Community	10-40-8-6-10-3-2	ST508	45	08-16-02-16-34-13-17-34-16-34	t015	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-409	NSW	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	0.06	-
ISTOP-410	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-411	NSW	Community	3-1-14-15-11-19-3	ST101	101	04-13-21-12-17-20-17-12-17-17	t2078	0.06	-
ISTOP-412	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20	t2595	0.06	-
ISTOP-413	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-414	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-33-34	t359	0.06	-
ISTOP-415	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-16	t179	0.06	-
ISTOP-416	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-34-33-34	t1028	0.12	-
ISTOP-417	NSW	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	≤0.03	-
ISTOP-418	NSW	Community	3-37-19-2-20-26-32	ST291	291	08-16-34-34-34-17-17	t16932	0.06	-
ISTOP-419	NSW	Community	10-1039-8-6-10-3-2	ST7284	45	09-02-16-34-13-17-34	t715	0.12	-
ISTOP-420	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-421	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-422	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-423	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-12-16	t5349	0.12	-
ISTOP-424	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.06	-
ISTOP-425	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.12	-
ISTOP-426	SA	Hospital	10-14-8-6-10-3-2	ST45	45	09-02-16-34-16-34	t371	0.06	-
ISTOP-427	SA	Hospital	4-9-1-8-1-10-8	ST20	20	07-06-17-21-34-34-22-34	t164	0.12	**DETECTED**
ISTOP-428	VIC	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	≤0.03	-
ISTOP-429	VIC	Community	12-4-1-4-12-1-3	ST6	6	11-10-12-34-24-34-22-25	t4298	0.06	-
ISTOP-430	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-431	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-16	t548	≤0.03	-
ISTOP-432	TAS	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12	t6181	0.06	-
ISTOP-433	TAS	Community	1-1-1-1-1-1-1	ST1	1	07-23-23-16-34-33-13	t1909	0.06	-
ISTOP-434	TAS	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-02-34	t231	0.12	-
ISTOP-435	TAS	Community	7-6-83-5-8-8-6	ST7285	22	26-17-25-16-28	UD	0.06	-
ISTOP-436	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-437	NSW	Community	19-23-15-2-19-20-15	ST59	59	04-20-17-02-17-31-16-34	t1293	0.06	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-438	NSW	Community	13-13-1-1-12-11-13	ST15	15	07-23-13-34-34-12-12-23-02-12-23	t11928	0.12	**DETECTED**
ISTOP-439	NT	Community	10-14-8-6-10-3-2	ST45	45	09-02-16-34-16-34	t371	0.12	-
ISTOP-440	NT	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	-
ISTOP-441	NT	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17-13-34-34-33-34	t4013	0.12	-
ISTOP-442	NT	Community	1-1-1-1-1-1-1	ST1	1	07-23-21-16-34-33-13	t127	≤0.03	-
ISTOP-443	NT	Community	3-1-122-1-1-5-3	ST953	97	07-23-12-21-17-34-34-34-33-34	t267	≤0.03	-
ISTOP-444	NT	Community	22-1-14-23-12-4-31	ST88	88	26-12-21-17-21-17-34-34-34-33-34	UD	≤0.03	-
ISTOP-445	NSW	Community	13-13-1-1-12-11-971	ST7286	15	07-23-12-34-34-12-12-23-02-02-12-23	t144	≤0.03	-
ISTOP-446	NSW	Hospital	3-1-1-8-1-1-1	ST188	188	07-20-12-21-17-34	UD	0.06	-
ISTOP-447	NSW	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-23	t1509	0.06	**DETECTED**
ISTOP-448	NSW	Community	3-35-19-2-20-26-29	ST398	398	08-16-02-25-34-25	t1451	≤0.03	-
ISTOP-449	NSW	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.12	-
ISTOP-450	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	≤0.03	-
ISTOP-451	NSW	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-
ISTOP-452	NSW	Hospital	1-4-1-4-12-1-10	ST5	5	Not Determined	-	0.06	**DETECTED**
ISTOP-453	NSW	Community	3-37-19-2-862-26-32	ST7287	291	08-16-34-24-34-34-17-17	t937	0.12	-
ISTOP-454	NSW	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-16-13	t1510	0.06	-
ISTOP-455	NSW	Hospital	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-16-13	t1510	0.06	-
ISTOP-456	NSW	Community	10-14-8-6-10-3-2	ST45	45	08-16-34	t026	≤0.03	-
ISTOP-457	NSW	Community	1-1040-1-4-12-1-10	ST7288	5	26-23-17-34-17-16	t688	0.06	-
ISTOP-458	QLD	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.12	**DETECTED**
ISTOP-459	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-17-20-17-12-17-16	t579	0.12	**DETECTED**
ISTOP-460	QLD	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-461	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-12-12-16	t1531	0.06	-
ISTOP-462	QLD	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-12-12-12-23-02-12-23	t393	0.12	**DETECTED**
ISTOP-463	QLD	Community	10-14-901-6-10-3-2	ST7289	45	08-16-34	t026	0.12	-
ISTOP-464	QLD	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-34	t416	0.06	-
ISTOP-465	QLD	Community	13-13-1-1-12-10-13	ST582	15	07-23-12-34-12-12-12-23-02-12-23	t393	0.12	**DETECTED**
ISTOP-466	QLD	Community	1-4-1-4-863-1-10	ST7290	5	26-23-17-34-17-20-17-12-17-16	t002	0.12	-

Isolate	State [a]	ONSET	MLST	ST	CC	*spa* repeats	*spa* Type [b]	Vitek® 2 Pen (mg/L) [c]	*blaZ*
ISTOP-467	QLD	Community	3-1-1-8-1-1-1	ST188	188	07-23-12-02-17-34	UD	0.06	-
ISTOP-468	QLD	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-34-13-17-34-16-34	t589	≤0.03	-
ISTOP-469	QLD	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.06	-
ISTOP-470	QLD	Community	10-14-8-6-10-3-2	ST45	45	08-16-02-16-34-13-17-34-34	t1078	0.06	-
ISTOP-471	QLD	Community	22-1-14-23-12-53-31	ST78	88	07-12-21-17-13-13-34-34-33-34	t186	0.06	-
ISTOP-472	QLD	Hospital	3-1-1-8-1-1-1	ST188	188	07-23-12-21-17-34	t189	0.06	-
ISTOP-473	QLD	Hospital	10-14-8-6-10-3-2	ST45	45	08-16-34	t026	≤0.03	-
ISTOP-474	QLD	Community	3-1-1-1-1-5-3	ST97	97	07-23-12-21-17-34-34-34-33-34	t267	0.06	-
ISTOP-475	QLD	Hospital	13-13-1-1-12-10-13	ST582	15	07-23-12-34-34-12-12-23-02-12-23	t084	0.12	**DETECTED**
ISTOP-476	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-02-17-12-12-12-16	t5150	≤0.03	-
ISTOP-477	QLD	Community	3-1-1-1-1-5-3	ST97	97	07-16-21-17-34-34-34	UD	0.06	-
ISTOP-478	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-17-20-17-12-17-16	t045	0.06	-
ISTOP-479	QLD	Community	12-4-1-4-12-1-3	ST6	6	11-10-21-17-34-24-34-22-25-25	t701	0.06	-
ISTOP-480	QLD	Community	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-20-17-12-12-12-16	t1265	0.06	-
ISTOP-481	QLD	Hospital	1-4-1-4-12-1-10	ST5	5	26-23-17-34-17-12-12-17-16	t2666	0.12	-
ISTOP-482	QLD	Community	1-4-1-4-12-1-968	ST7267	5	07-23-17-34-17-20-17-12-17-16	t570	0.06	-
ISTOP-483	QLD	Community	1-1-1-1-12-1-1	ST573	Singleton	26-23-13-21-17-34-34-34-33-34	t1839	0.12	-
ISTOP-484	QLD	Hospital	3-1-14-15-11-19-3	ST101	101	04-20-12-17-20-17-12-17-17	t056	0.12	-

MLST, multi-locus sequence typing; ST, sequence type; CC, clonal complex; *spa*, staphylococcal protein A; Pen, penicillin

[a] ACT, Australian Capital Territory; NSW, New South Wales; QLD, Queensland; SA, South Australia; TAS, Tasmania; VIC, Victoria; WA, Western Australia

[b] UD, undetermined *spa* type

[c] Penicillin-resistant, >0.125 mg/L; penicillin-susceptible, <0.125 mg/L

Supplementary Table 2. Virulence factors identified in 470 penicillin-susceptible *Staphylococcus aureus* isolates

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
Clonal Complex 1 (n=17)										
ISTOP-48	ST1	NSW	0.12	-	III	8	t127	*seh, sek+seq, selx*	-	*sak, scn* (E)
ISTOP-127	ST1	SA	0.12	-	III	8	t177	*sea*, *seh, sek+seq, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-141	ST1	VIC	≤0.03	-	III	8	t2207	*seh, sek+seq, selx*	-	*sak, scn* (E)
ISTOP-152	ST1	TAS	≤0.03	-	III	8	t127	*seh, selx*	-	-
ISTOP-212	ST1	QLD	0.06	-	III	8	t127	*seh, sek+seq, selx*	-	*sak, scn* (E)
ISTOP-219	ST1	TAS	0.06	-	III	8	t127	*sea, seh, sek+seq, selx*	-	*sea, sak, scn* (D)
ISTOP-281	ST1	NSW	0.06	-	III	8	t127	*sea*, *seh, sek+seq, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-330	ST1	NSW	≤0.03	-	III	8	t127	*seh, sek+seq, selx*	-	*sak, scn* (E)
ISTOP-364	ST1	NSW	0.12	-	III	8	t127	*seh, sek+seq, selx*	-	*sak, scn* (E)
ISTOP-396	ST1	WA	0.12	-	III	8	t127	*sea*, *seb*, *seh, sek+seq, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-407	ST1	VIC	0.12	-	III	8	t174	*sea*, *seh, sek+seq, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-409	ST1	NSW	0.06	-	III	8	t127	*sea*, *seh, sek+seq, selx*	*lukF/S-PVL*	*sea*, *sak*, *scn* (D)
ISTOP-433	ST1	TAS	0.06	-	III	8	t1909	*sea*, *seh, sek+seq, selx*	--	*sea*, *sak*, *scn* (D)
ISTOP-442	ST1	NT	≤0.03	-	III	8	t127	*sea*, *seh, sek+sel, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-130	ST3949	NSW	0.12	-	III	8	t2207	*sea, sec+sel, seh, sek+seq, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-21	ST4100	VIC	≤0.03	-	III	8	UD	*selx*	*eta*	*sak, scn* (E)
ISTOP-69	ST4100	NSW	0.06		III	8	UD	*selx*	-	*sak, scn* (E)
Clonal Complex 5 (n=150)										
ISTOP-3	ST5	WA	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-9	ST5	WA	≤0.03	-	II	5	t1227	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-15	ST5	VIC	0.06	-	II	5	t1560	*seb, sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-18	ST5	VIC	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-19	ST5	VIC	0.12	-	II	5	t306	*egc-cluster (seg+sei+sem+sen+seo+selw),*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
								selx		
ISTOP-22	ST5	VIC	≤0.03	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	-
ISTOP-28	ST5	VIC	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-32	ST5	QLD	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-33	ST5	NSW	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-36	ST5	NSW	0.06	-	II	5	t2049	*sea, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-38	ST5	TAS	0.12	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-49	ST5	NSW	≤0.03	-	II	5	t548	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-60	ST5	VIC	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-63	ST5	VIC	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-64	ST5	NSW	0.12	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-66	ST5	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-81	ST5	NSW	0.12	-	II	5	UD	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	-
ISTOP-82	ST5	TAS	≤0.03	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-83	ST5	TAS	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-89	ST5	TAS	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-90	ST5	SA	0.12	-	II	5	t214	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-93	ST5	SA	0.12	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-95	ST5	SA	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-102	ST5	VIC	≤0.03	-	II	5	t3597	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-103	ST5	SA	0.06	-	II	5	t9394	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-106	ST5	NSW	0.06	-	II	5	t2958	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-107	ST5	NSW	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-110	ST5	QLD	≤0.03	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-111	ST5	QLD	0.06	-	II	5	t111	*sea, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sea, sak, chp, scn* (A)
ISTOP-113	ST5	NSW	≤0.03	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-116	ST5	SA	0.12	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-118	ST5	WA	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	-
ISTOP-124	ST5	SA	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-128	ST5	SA	0.12	-	II	5	t002	*sep, egc-cluster*	-	*sep, sak, chp, scn* (F)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
								(seg+sei+sem+sen+seo+selw), selx		
ISTOP-142	ST5	SA	0.06	-	II	5	t688	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-145	ST5	ACT	0.06	-	II	5	t17058	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-148	ST5	ACT	0.06	-	II	5	t8241	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-158	ST5	NSW	≤0.03	**DETECTED**	II	5	t1265	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-159	ST5	NSW	0.06	-	II	5	t7186	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-161	ST5	NSW	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-166	ST5	NSW	0.12	-	II	5	t2595	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-167	ST5	NSW	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-173	ST5	VIC	0.12	**DETECTED**	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-176	ST5	VIC	0.12	-	II	5	t002	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-178	ST5	VIC	0.06	-	II	5	t442	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-179	ST5	VIC	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-180	ST5	VIC	0.12	-	II	5	t062	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-184	ST5	NSW	≤0.03	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-187	ST5	NSW	0.12	**DETECTED**	II	5	t010	*sed+selj+ser, sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-188	ST5	NSW	0.06	**DETECTED**	II	5	t1265	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-191	ST5	VIC	0.12	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-193	ST5	SA	0.06	-	II	5	t002	*sea, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-200	ST5	VIC	0.12	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sep, sak, chp, scn* (F)
ISTOP-201	ST5	VIC	0.06	-	II	5	t442	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-206	ST5	NSW	0.06	-	II	5	t002	*sed+selj+ser, sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-207	ST5	QLD	0.12	**DETECTED**	II	5	UD	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-209	ST5	QLD	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-218	ST5	TAS	0.12	-	II	5	t010	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-224	ST5	WA	0.12	-	II	5	t002	*sea, sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-227	ST5	WA	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-231	ST5	WA	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-232	ST5	WA	0.12	-	II	5	t5081	*sed+selj+ser, sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-233	ST5	WA	0.12	**DETECTED**	II	5	t179	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-241	ST5	SA	≤0.03	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-249	ST5	WA	0.06	-	II	5	t088	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-252	ST5	WA	0.12	-	II	5	t045	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-262	ST5	ACT	≤0.03	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-265	ST5	ACT	0.12	-	II	5	t570	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-267	ST5	ACT	0.06	-	II	5	t3660	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-270	ST5	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-272	ST5	TAS	≤0.03	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sep, sak, chp, scn* (F)
ISTOP-275	ST5	TAS	≤0.03	-	II	5	t3065	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-282	ST5	NSW	0.12	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-290	ST5	NSW	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-301	ST5	QLD	0.06	-	II	5	t010	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-303	ST5	QLD	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-310	ST5	VIC	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-313	ST5	NSW	0.06	-	II	5	t179	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-315	ST5	VIC	0.06	-	II	5	t045	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-316	ST5	VIC	0.12	-	II	5	t179	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-321	ST5	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-322	ST5	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-327	ST5	VIC	≤0.03	-	II	5	t010	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-329	ST5	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-334	ST5	SA	0.06	-	II	5	t1265	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-339	ST5	NSW	0.06	-	II	5	t1265	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-350	ST5	WA	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-351	ST5	WA	0.12	-	II	5	t179	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-353	ST5	WA	≤0.03	-	II	5	t002	*sea, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sea, sak, chp, scn* (A)
ISTOP-357	ST5	WA	0.06	-	II	5	t10218	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-365	ST5	NSW	0.12	-	II	5	t17484	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-369	ST5	NSW	0.12	-	II	5	t088	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-372	ST5	QLD	0.06	-	II	5	t7186	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-374	ST5	VIC	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-378	ST5	ACT	0.12	-	II	5	t494	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-380	ST5	ACT	0.06	-	II	5	t179	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-381	ST5	ACT	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-382	ST5	VIC	≤0.03	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-388	ST5	VIC	0.06	-	II	5	t045	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-389	ST5	VIC	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-390	ST5	VIC	0.06	-	II	5	t105	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-391	ST5	VIC	0.06	-	II	5	t062	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-394	ST5	WA	≤0.03	-	II	5	t242	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sep, sak, chp, scn* (F)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-395	ST5	WA	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-398	ST5	WA	0.06	-	II	5	t1265	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-399	ST5	WA	0.12	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-400	ST5	WA	0.12	-	II	5	t6071	*sea, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sea, sak, chp, scn* (A)
ISTOP-410	ST5	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-412	ST5	NSW	0.06	-	II	5	t2595	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	-
ISTOP-413	ST5	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-415	ST5	NSW	0.06	-	II	5	t179	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-421	ST5	NSW	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-423	ST5	NSW	0.12	-	II	5	t5349	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-424	ST5	NSW	0.06	-	II	5	t002	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-425	ST5	NSW	0.12	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-430	ST5	TAS	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw),*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
								selx		
ISTOP-431	ST5	TAS	≤0.03	-	II	5	t548	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	-
ISTOP-432	ST5	TAS	0.06	-	II	5	t6181	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-436	ST5	NSW	0.12	-	II	5	t002	*sed+selj+ser, sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-450	ST5	NSW	≤0.03	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	-
ISTOP-451	ST5	NSW	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	-
ISTOP-452	ST5	NSW	0.06	**DETECTED**	II	5	UD	*sec2+sel, sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx, sel31, sel32*	-	*sep, sak, chp, scn* (F)
ISTOP-459	ST5	QLD	0.12	**DETECTED**	II	5	t579	*sed+selj+ser, sep, egc-cluster (seg+sen+seo+sev+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-461	ST5	QLD	0.06	-	II	5	t1531	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn (*E*)*
ISTOP-476	ST5	QLD	≤0.03	-	II	5	t5150	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, scn* (G)
ISTOP-478	ST5	QLD	0.06	-	II	5	t045	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-480	ST5	QLD	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-481	ST5	QLD	0.12	-	II	5	t2666	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-4	ST2967	WA	≤0.03	-	II	5	t1345	*egc-cluster (seg+sei+sem+sen+seo+selw),*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
								selx		
ISTOP-13	ST3628	WA	0.06	-	II	5	t5259	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-34	ST3628	NSW	≤0.03	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-39	ST3628	TAS	0.12	-	II	5	t7026	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-121	ST3628	WA	0.12	**DETECTED**	II	5	t179	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-338	ST3628	WA	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-349	ST3628	WA	0.12	-	II	5	t7026	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-104	ST3724	SA	0.06	-	II	5	t688	*sea, egc-cluster (seg+sei+sem+sen+seo+selw), selx*		*sea*, *sak*, *scn* (D)
ISTOP-62	ST5189	VIC	0.06	-	II	5	t1265	*sed+selj+ser, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-228	ST5189	WA	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-41	ST7252	VIC	0.12	-	II	5	t686	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-61	ST7252	VIC	0.06	-	II	5	t686	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-195	ST7260	SA	≤0.03	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-229	ST7262	WA	0.12	**DETECTED**	II	5	t002	*sec2+sel, sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)
ISTOP-238	ST7263	WA	0.12	-	II	5	t045	*sep, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sep, sak, chp, scn* (F)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-246	ST7265	WA	≤0.03	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-251	ST7267	WA	0.12	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-482	ST7267	QLD	0.06	-	II	5	t570	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-271	ST7269	NSW	0.06	-	II	5	t002	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-370	ST7282	NSW	0.06	-	II	5	t1265	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-457	ST7288	NSW	0.06	-	II	5	t688	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-466	ST7290	QLD	0.12	-	II	5	t002	*sea, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sea*, *sak*, *scn* (D)
Clonal Complex 6 (n=16)										
ISTOP-1	ST6	NSW	0.06	-	I	8	t304	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-53	ST6	NSW	0.12	**DETECTED**	I	8	t701	*sea, seb, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-87	ST6	TAS	≤0.03	-	I	8	t701	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-91	ST6	SA	0.12	-	I	8	t304	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-105	ST6	NSW	0.12	-	I	8	t701	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-114	ST6	NSW	0.12	-	I	8	t701	*selx*	-	*sak, scn* (E)
ISTOP-204	ST6	SA	0.12	-	I	8	t701	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-244	ST6	SA	0.06	-	I	8	t701	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-248	ST6	WA	0.12	-	I	8	t304	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-257	ST6	WA	0.06	-	I	8	t304	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-285	ST6	NSW	0.12	-	I	8	t4407	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-375	ST6	VIC	0.06	-	I	8	t304	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-402	ST6	VIC	0.06	-	I	8	t701	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-428	ST6	VIC	≤0.03	-	I	8	t701	*sea, seb, selx*	-	*sea*, *sak*, *scn* (D)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-429	ST6	VIC	0.06	-	I	8	t4298	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-479	ST6	QLD	0.06	-	I	8	t701	*sea, seb, selx*	-	*sea*, *sak*, *scn* (D)
Clonal Complex 7 (n=3)										
ISTOP-125	ST7	SA	0.12	-	I	8	t7234	*selx*	-	*sak, chp, scn* (B)
ISTOP-220	ST7	TAS	0.06	-	I	8	t7234	*selx*	-	*sak, chp, scn* (B)
ISTOP-345	ST7	VIC	0.06	-	I	8	t091	*sep, selx*		*sep, sak, scn* (G)
Clonal Complex 8 (n=14)										
ISTOP-17	ST8	VIC	0.12	-	I	5	t024	*sea, sec2+ sel, sek+selq, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-78	ST8	ACT	0.06	-	I	5	t008	*sed+selj+ser, selx*	-	*sak, scn* (E)
ISTOP-143	ST8	SA	≤0.03	-	I	5	t024	*selx*	-	*sak, chp, scn* (B)
ISTOP-144	ST8	ACT	0.06	-	I	5	UD	*selx*	-	*sak, chp, scn* (B)
ISTOP-164	ST8	NSW	0.06	**DETECTED**	I	5	t008	*sek+seq, selx*	-	*sak, chp, scn* (B)
ISTOP-181	ST8	VIC	0.06	-	I	5	t008	*selx*	-	*sak, scn* (E)
ISTOP-215	ST8	VIC	0.12	-	I	5	t10888	*selx*	-	*sak, chp, scn* (B)
ISTOP-239	ST8	SA	0.06	-	I	5	UD	*selx*	-	*sak, scn* (E)
ISTOP-259	ST8	ACT	≤0.03	-	I	5	t008	*sek+seq, selx*	-	*sak, chp, scn* (B)
ISTOP-286	ST8	NSW	0.06	-	I	5	t008	*sea, selx*	-	*sea*, *sak*, *scn* (D)
ISTOP-331	ST8	NSW	0.06	-	I	5	t1171	*selx*	-	*sak, scn* (E)
ISTOP-397	ST8	WA	0.06	-	I	5	t008	*selx*	-	*sak, chp, scn* (B)
ISTOP-405	ST8	VIC	0.12	-	I	5	t008	*selx*	-	*sak, chp, scn* (B)
ISTOP-6	ST5234	WA	0.06	-	I	5	t955	*seb, sek+seq, selx*	-	*sak, scn* (E)
Clonal Complex 9 (n=1)										
ISTOP-293	ST9	VIC	0.12	**DETECTED**	II	5	t4812	*egc-cluster (seg+sei+sem+sen+seo+selw), selx, sely, sel27, sel28*	*eta*	*sak, chp, scn* (B)
Clonal Complex 12 (n=16)										
ISTOP-12	ST12	WA	≤0.03	-	II	8	UD	*seb, selx, selz*	-	*sak, chp, scn* (B)
ISTOP-14	ST12	WA	0.06	-	II	8	t160	*sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-29	ST12	QLD	≤0.03	-	II	8	t336	*sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-30	ST12	QLD	0.06	-	II	8	UD	*seb, selx, selz*	-	*sak, chp, scn* (B)
ISTOP-40	ST12	TAS	0.12	-	II	8	t909	*sec2+sel, sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-51	ST12	NSW	0.06	-	II	8	UD	*seb, selx, selz*	-	*sak, chp, scn* (B)
ISTOP-74	ST12	NSW	0.06	-	II	8	t771	*seb, selx, selz*	-	*sak, chp, scn* (B)
ISTOP-86	ST12	TAS	0.06	-	II	8	t771	*seb, selx, selz*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-117	ST12	WA	0.06	-	II	8	t160	*seb, sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-140	ST12	VIC	0.12	-	II	8	t160	*sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-150	ST12	ACT	0.06	-	II	8	t160	*seb, sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-254	ST12	WA	0.06	-	II	8	t160	*sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-274	ST12	TAS	0.06	-	II	8	t160	*seb, sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-377	ST12	NSW	0.06	-	II	8	t771	*seb, selx, selz*	-	*sak, chp, scn* (B)
ISTOP-406	ST12	VIC	0.06	-	II	8	t160	*seb, sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-23	ST7251	VIC	0.06	**DETECTED**	II	8	t160	*seb, sep, selx, selz*	-	*sep, sak, scn* (G)
Clonal Complex 15 (n=41)										
ISTOP-7	ST15	WA	0.06	-	II	8	t605	*selx*	-	*chp, scn* (C)
ISTOP-46	ST15	NSW	0.12	-	II	8	t803	*selx*	-	*chp, scn* (C)
ISTOP-59	ST15	NSW	0.06	-	II	8	t085	*selx*	-	*chp, scn* (C)
ISTOP-79	ST15	ACT	0.06	-	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-109	ST15	QLD	0.12	-	II	8	t803	*selx*	-	*chp, scn* (C)
ISTOP-119	ST15	WA	0.12	-	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-129	ST15	NSW	0.06	-	II	8	t2216	*selx*	-	*chp, scn* (C)
ISTOP-134	ST15	NSW	0.12	-	II	8	t14014	*selx*	-	*chp, scn* (C)
ISTOP-137	ST15	VIC	0.06	-	II	8	t877	*selx*	-	*chp, scn* (C)
ISTOP-221	ST15	TAS	≤0.03	-	II	8	t346	*selx*	-	*chp, scn* (C)
ISTOP-225	ST15	WA	0.12	-	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-235	ST15	WA	0.06	-	II	8	t346		-	*chp, scn* (C)
ISTOP-236	ST15	WA	0.12	-	II	8	t085	*selx*	-	*chp, scn* (C)
ISTOP-299	ST15	VIC	0.12	-	II	8	t084	*seb, selx*	-	*chp, scn* (C)
ISTOP-309	ST15	VIC	0.12	-	II	8	t084	*seb, selx*	-	*chp, scn* (C)
ISTOP-348	ST15	WA	0.06	-	II	8	t491	*selx*	-	*chp, scn* (C)
ISTOP-356	ST15	WA	0.06	-	II	8	t605	*selx*	-	*chp, scn* (C)
ISTOP-379	ST15	ACT	0.06	-	II	8	t5393	*selx*	-	*chp, scn* (C)
ISTOP-438	ST15	NSW	0.12	**DETECTED**	II	8	t11928	*selx*	-	*chp, scn* (C)
ISTOP-20	ST333	VIC	0.06	-	II	8	UD	*selx*	-	*chp, scn* (C)
ISTOP-50	ST582	NSW	0.12	**DETECTED**	II	8	t085	*selx*	-	*chp, scn* (C)
ISTOP-153	ST582	TAS	0.12	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-157	ST582	NSW	0.12	**DETECTED**	II	8	t393	*selx*	-	*chp, scn* (C)
ISTOP-223	ST582	WA	0.06	**DETECTED**	II	8	t085	*selx*	*eta*	*chp, scn* (C)
ISTOP-306	ST582	Qld	0.12	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-318	ST582	VIC	0.12	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-324	ST582	VIC	0.06	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-447	ST582	NSW	0.06	**DETECTED**	II	8	t1509	*selx*	-	*chp, scn* (C)
ISTOP-462	ST582	QLD	0.12	**DETECTED**	II	8	t393	*selx*	-	*chp, scn* (C)
ISTOP-465	ST582	QLD	0.12	**DETECTED**	II	8	t393	*selx*	*eta*	*chp, scn* (C)
ISTOP-475	ST582	QLD	0.12	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-27	ST3911	VIC	0.06	**DETECTED**	II	8	t2859	*selx*	-	*chp, scn* (C)
ISTOP-171	ST3911	WA	0.12	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-210	ST3911	QLD	0.06	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-276	ST3911	NSW	0.12	**DETECTED**	II	8	t279	*selx*	-	*chp, scn* (C)
ISTOP-295	ST3911	VIC	0.12	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-115	ST5059	NSW	0.12	**DETECTED**	II	8	t4714	*selx*	-	*chp, scn* (C)
ISTOP-243	ST7264	SA	0.06	-	II	8	t085	*selx*	-	*chp, scn* (C)
ISTOP-300	ST7273	QLD	0.12	**DETECTED**	II	8	t084	*selx*	-	*chp, scn* (C)
ISTOP-401	ST7283	VIC	0.12	**DETECTED**	II	8	t547	*selx*	-	*chp, scn* (C)
ISTOP-445	ST7286	NSW	≤0.03	-	II	8	t144	*selx*	-	*chp, scn* (C)
Clonal Complex 20 (n=3)										
ISTOP-85	ST20	TAS	0.12	-	I	5	t3277	*egc-cluster (seg+sei+sem+sen+seo+selw), selx, sely*	-	*sak, chp, scn* (B)
ISTOP-342	ST20	TAS	0.12	-	I	5	t2919	*egc-cluster (seg+sei+sem+sen+seo+selw), selx, sely*	-	-
ISTOP-427	ST20	SA	0.12	**DETECTED**	I	5	t164	*seb, egc-cluster (seg+sei+sem+sen+seo+selw), selx, sely*	-	*sak, chp, scn* (B)
Clonal Complex 22 (n=8)										
ISTOP-266	ST22	ACT	0.06	-	I	5	t474	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-278	ST22	NSW	0.12	-	I	5	t852	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-347	ST22	WA	0.12	-	I	5	t3243	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-360	ST22	WA	0.06	**DETECTED**	I	5	UD	*sec1+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-383	ST22	VIC	0.12	-	I	5	t2933	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-384	ST22	VIC	≤0.03	-	I	5	t1328	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-292	ST7272	QLD	≤0.03	-	I	5	t005	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-435	ST7285	TAS	0.06	-	I	5	UD	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
Clonal Complex 25 (n=1)										
ISTOP-325	ST7276	VIC	≤0.03	**DETECTED**	I	5	-	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*edinB*	*sak, chp, scn* (B)
Clonal Complex 30 (n=7)										
ISTOP-311	ST30	VIC	0.06	-	III	8	t3037	*egc-cluster (seg+sei+sem+sen+seo+selw)*	*lukF/S-PVL*	*sak, chp, scn* (B)
ISTOP-319	ST30	VIC	0.12	**DETECTED**	III	8	t012	*egc-cluster (seg+sei+sem+sen+seo+selw)*	*tst*	-
ISTOP-42	ST34	VIC	0.06	**DETECTED**	III	8	UD	*seh, egc-cluster (seg+sei+sem+sen+seo+selw)*	*tst*	*sak, chp, scn* (B)
ISTOP-101	ST34	VIC	≤0.03	-	III	5	t1670	*seb, seh, sel, egc-cluster (seg+sei+sem+sen+seo+selw)*	*tst*	*sak, chp, scn* (B)
ISTOP-263	ST34	ACT	0.06	**DETECTED**	III	8	t089	*seh, egc-cluster (seg+sei+sem+sen+seo+selw)*	*tst*	*sak, chp, scn* (B)
ISTOP-264	ST34	ACT	0.06	**DETECTED**	III	8	t089	*seh, egc-cluster (seg+sei+sem+sen+seo+selw)*	*tst*	*sak, chp, scn* (B)
ISTOP-296	ST39	VIC	≤0.03	-	III	8	t1504	*sec3+sel, selo*	*tst*	*sak, scn* (E)
Clonal Complex 45 (n=47)										
ISTOP-31	ST45	QLD	0.06	-	I	8	t026	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-68	ST45	WA	0.06	-	I	8	t230	*sec2+sel, egc-cluster*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
								(seg+sei+sem+sen+seo+selw), selx		
ISTOP-70	ST45	NSW	0.06	-	I	8	t563	*seb, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-88	ST45	TAS	0.12	**DETECTED**	I	8	t015	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-94	ST45	SA	0.12	-	I	8	t371	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-122	ST45	WA	0.06	-	I	8	t130	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*chp, scn* (C)
ISTOP-123	ST45	SA	0.12	-	I	8	t302	*sec2+sel, selx*	-	*sak, chp, scn* (B)
ISTOP-139	ST45	VIC	≤0.03	-	I	8	t10588	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-149	ST45	ACT	0.06	-	I	8	t015	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-160	ST45	NSW	0.06	-	I	8	t728	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-170	ST45	WA	≤0.03	-	I	8	t8453	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-189	ST45	NSW	0.06	-	I	8	t10421	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-216	ST45	TAS	0.06	-	I	8	t362	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-230	ST45	WA	0.06	-	I	8	t230	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-260	ST45	ACT	0.06	-	I	8	t706	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-279	ST45	NSW	0.12	-	I	8	t015	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-283	ST45	NSW	0.06	-	I	8	t10771	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-337	ST45	WA	0.06	-	I	8	UD	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-366	ST45	NSW	0.06	-	I	8	t362	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-373	ST45	VIC	0.06	-	I	8	t015	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-376	ST45	WA	0.06	-	I	8	t015	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-386	ST45	QLD	0.06	-	I	8	t302	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-426	ST45	SA	0.06	-	I	8	t371	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-439	ST45	NT	0.12	-	I	8	t371	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-454	ST45	NSW	0.06	-	I	8	t1510	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-455	ST45	NSW	0.06	-	I	8	t1510	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-456	ST45	NSW	≤0.03	-	I	8	t026	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-468	ST45	QLD	≤0.03	-	I	8	t589	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-470	ST45	QLD	0.06	-	I	8	t1078	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-473	ST45	QLD	≤0.03	-	I	8	t026	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-26	ST508	NSW	≤0.03	-	I	8	UD	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-35	ST508	NSW	0.12	-	I	8	t015	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-154	ST508	TAS	≤0.03	-	I	8	t073	*egc-cluster*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
								(seg+sei+sem+sen+seo+selw), selx		
ISTOP-163	ST508	NSW	0.06	-	I	8	t015	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-169	ST508	WA	0.06	-	I	8	t015	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-253	ST508	WA	0.12	-	I	8	t015	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-269	ST508	NSW	0.125	-	I	8	t026	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-336	ST508	SA	0.125	-	I	8	t050	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-408	ST508	VIC	0.06	-	I	8	t015	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-75	ST7254	NSW	≤0.03	-	I	8	t132	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-84	ST7255	TAS	0.12	**DETECTED**	I	8	t230	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-147	ST7258	ACT	0.06	-	I	8	UD	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-203	ST7261	SA	≤0.03	-	I	8	t2726	*sec3+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
ISTOP-268	ST7268	NSW	0.06	-	I	8	t015	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-346	ST7279	VIC	0.06	-	I	8	t050	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-419	ST7284	NSW	0.12	-	I	8	t715	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-463	ST7289	QLD	0.12	-	I	8	t026	*sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	*tst*	*sak, chp, scn* (B)
Clonal Complex 59 (n=9)										
ISTOP-67	ST59	WA	0.12	-	I	8	t437	*sea, seb, sek+seq, selx, sely*	-	*sea*, *sak*, *scn* (D)
ISTOP-77	ST59	ACT	0.06	-	I	8	t216	*seb, sek+seq, selx, sely*	-	*sak, chp, scn* (B)
ISTOP-343	ST59	TAS	0.06	-	I	8	t471	*selx, sely*	-	*chp, scn* (C)
ISTOP-368	ST59	NSW	0.12	-	I	8	t316	*selx, sely*	-	*sak, chp, scn* (B)
ISTOP-403	ST59	VIC	0.12	-	I	8	t437	*selx, sely*	-	*chp, scn* (C)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-437	ST59	NSW	0.06	-	I	8	t1293	*seb, sek+seq, selx, sely*	-	*chp, scn* (C)
ISTOP-256	ST87	WA	0.12	-	I	8	t316	*seb, sek+seq, selx, sely*	-	*sak, chp, scn* (B)
ISTOP-186	ST1224	NSW	≤0.03	-	I	8	t471	*selx, sely*		*chp, scn* (C)
ISTOP-354	ST7280	WA	0.06	-	I	8	t216	*sea, seb, sek+seq, selx, sely*	-	*sea, sak, chp, scn* (A)
Clonal Complex 80 (n=1)										
ISTOP-199	ST80	VIC	0.12	-	III	8	t042	*seb, seh, sel+ seq, selx, sely*	*edinB*	*sak, chp, scn* (B)
Clonal Complex 88 (n=17)										
ISTOP-47	ST78	NSW	0.12	-	III	8	t1814	*selx*	-	*sak, scn* (E)
ISTOP-76	ST78	ACT	0.12	-	III	8	UD	*selx*	-	*sak, scn* (E)
ISTOP-182	ST78	VIC	0.12	-	III	8	t786	*Selx*	-	*sak, scn* (E)
ISTOP-217	ST78	TAS	0.06	-	III	8	t2311	*Selx*	-	*sak, scn* (E)
ISTOP-261	ST78	ACT	0.06	-	III	8	t2177	*sec2+sel, selx*	-	*sak, scn* (E)
ISTOP-312	ST78	NSW	0.06	-	III	8	t2191	*sec2+sel, selx*	-	-
ISTOP-471	ST78	QLD	0.06	-	III	8	t186	*selx*	-	*sak, scn* (E)
ISTOP-8	ST88	WA	0.12	-	III	8	UD	*selx*	-	*sak, scn* (E)
ISTOP-71	ST88	NSW	0.06	-	III	8	t4013	*selx*	-	*sak, scn* (E)
ISTOP-120	ST88	WA	0.12	-	III	8	UD	*selx*	-	*sak, scn* (E)
ISTOP-135	ST88	NSW	0.12	-	III	8	t2649	*selx*	-	*sak, scn* (E)
ISTOP-175	ST88	VIC	0.06	-	III	8	UD	*selx*	-	*sak, scn* (E)
ISTOP-308	ST88	VIC	0.12	-	III	8	t3341	*selx*	*lukF/S-PVL*	*sak, scn* (E)
ISTOP-333	ST88	NSW	0.12	-	III	8	t6928	*selx*	-	*sak, scn* (E)
ISTOP-441	ST88	NT	0.12	-	III	8	t4013	*selx*	-	*sak, scn* (E)
ISTOP-444	ST88	NT	≤0.03	-	III	8	UD	*selx*	-	*sak, scn* (E)
ISTOP-355	ST7281	WA	≤0.03	-	III	8	t730	*sec2+sel, selx*	-	*sak, scn* (E)
Clonal Complex 97 (n=48)										
ISTOP-37	ST97	NSW	0.06	-	I	5	t9432	*selx*	-	*sak, scn* (E)
ISTOP-54	ST97	NSW	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-57	ST97	NSW	0.06	-	I	5	t359	*selx*	-	*sak, scn* (E)
ISTOP-65	ST97	NSW	0.12	-	I	5	t14122	*selx*	-	*sak, scn* (E)
ISTOP-73	ST97	NSW	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-80	ST97	NSW	0.12	-	I	5	t359	*selx*	-	*sak, scn* (E)
ISTOP-96	ST97	VIC	≤0.03	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-138	ST97	VIC	0.06	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-172	ST97	VIC	0.06	-	I	5	t1028	*selx*	-	*sak, scn* (E)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-198	ST97	SA	0.12	-	I	5	t1236	*selx*	-	*sak, scn* (E)
ISTOP-211	ST97	QLD	0.06	-	I	5	t231	*selx*	-	*sak, scn* (E)
ISTOP-242	ST97	SA	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-245	ST97	WA	0.12	-	I	5	t359	*selx*	-	*sak, scn* (E)
ISTOP-250	ST97	WA	0.12	-	I	5	t3380	*selx*	-	*sak, scn* (E)
ISTOP-280	ST97	NSW	0.12	-	I	5	t7753	*selx*	-	*sak, scn* (E)
ISTOP-291	ST97	QLD	0.06	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-298	ST97	VIC	0.12	-	I	5	t224	*sec3+sel, selx*	*tst*	*sak, scn* (E)
ISTOP-307	ST97	VIC	≤0.03	-	I	5	t224	*sec3+sel, selx*	*tst*	*sak, scn* (E)
ISTOP-320	ST97	VIC	0.12	-	I	5	t2734	*selx*	-	*sak, scn* (E)
ISTOP-335	ST97	SA	≤0.03	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-352	ST97	WA	0.12	-	I	5	t693	*selx*	-	*sak, scn* (E)
ISTOP-358	ST97	WA	0.06	-	I	5	t10212	*selx*	-	*sak, scn* (E)
ISTOP-359	ST97	WA	≤0.03	-	I	5	UD	*selx*	-	*sak, scn* (E)
ISTOP-367	ST97	NSW	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-385	ST97	QLD	0.06	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-414	ST97	NSW	0.06	-	I	5	t359	*selx*	-	*sak, scn* (E)
ISTOP-416	ST97	NSW	0.12	-	I	5	t1028	*selx*	-	*sak, scn* (E)
ISTOP-420	ST97	NSW	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-422	ST97	NSW	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-434	ST97	TAS	0.12	-	I	5	t231	*selx*	-	*sak, scn* (E)
ISTOP-449	ST97	NSW	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-469	ST97	QLD	0.06	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-474	ST97	QLD	0.06	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-477	ST97	QLD	0.06	-	I	5	UD	*selx*	-	*sak, scn* (E)
ISTOP-10	ST953	WA	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-45	ST953	NSW	0.06	-	1	5	t359	*selx*	-	*sak, scn* (E)
ISTOP-58	ST953	NSW	0.12	-	I	5	t1109	*selx*	-	*sak, scn* (E)
ISTOP-126	ST953	SA	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-234	ST953	WA	≤0.03	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-237	ST953	WA	0.12	-	I	5	t2802	*selx*	-	*sak, scn* (E)
ISTOP-255	ST953	NSW	0.06	-	I	5	t359	*selx*	-	*sak, scn* (E)
ISTOP-273	ST953	TAS	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-392	ST953	NSW	≤0.03	-	I	5	t267	*selx*	-	*sak, scn* (E)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-443	ST953	NT	≤0.03	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-5	ST1179	WA	0.12	-	I	5	t237	*selx*	-	*sak, scn* (E)
ISTOP-404	ST1179	VIC	0.12	-	I	5	t267	*selx*	-	*sak, scn* (E)
ISTOP-99	ST7256	VIC	0.06	-	I	5	t359	*selx*	-	*sak, scn* (E)
ISTOP-344	ST7278	TAS	0.12	-	I	5	t359	*selx*	-	*sak, scn* (E)
Clonal Complex 101 (n=16)										
ISTOP-136	ST101	TAS	0.06	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-174	ST101	VIC	0.12	**DETECTED**	I	8	t2078	*selx*	-	*sak, scn* (E)
ISTOP-192	ST101	VIC	0.12	-	I	8	t643	*selx*	-	*sak, scn* (E)
ISTOP-284	ST101	NSW	0.12	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-289	ST101	NSW	0.06	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-294	ST101	VIC	0.06	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-332	ST101	NSW	0.06	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-340	ST101	NSW	0.12	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-361	ST101	NSW	0.12	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-393	ST101	NSW	≤0.03	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-411	ST101	NSW	0.06	-	I	8	t2078	*selx*	-	*sak, scn* (E)
ISTOP-484	ST101	QLD	0.12	-	I	8	t528	*selx*	-	*sak, scn* (E)
ISTOP-72	ST1155	QLD	0.12	-	I	8	t4171	*sec2+sel, selx*	-	*sak, scn* (E)
ISTOP-168	ST1155	WA	0.06	-	I	8	UD	*sec2+sel, selx*	-	*sak, scn* (E)
ISTOP-133	ST7257	NSW	0.06	-	I	8	UD	*selx*	-	*sak, scn* (E)
ISTOP-305	ST7274	QLD	0.06	-	I	8	t528	*selx*	-	*sak, scn* (E)
Clonal Complex 188 (n=23)										
ISTOP-2	ST188	NSW	0.06	-	I	8	t189	*selx*	-	*sak, scn* (E)
ISTOP-24	ST188	VIC	0.12	-	I	8	t189	*sep, selx*	-	*sep, sak, scn* (G)
ISTOP-25	ST188	NSW	≤0.03	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-44	ST188	NSW	0.12	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-52	ST188	NSW	0.12	-	I	8	t2883	*selx*	-	*sak, chp, scn* (B)
ISTOP-56	ST188	NSW	0.06	-	I	8	t189	*selx*	-	*sak, scn* (E)
ISTOP-92	ST188	SA	0.06	-	I	8	t189	*selx*	-	*sak, scn* (E)
ISTOP-112	ST188	NSW	0.06	-	I	8	t189	*selx*	-	*sak, scn* (E)
ISTOP-155	ST188	TAS	0.12	-	I	8	t189	*selx*	-	*sak, scn* (E)
ISTOP-156	ST188	NSW	0.06	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-165	ST188	NSW	0.12	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-205	ST188	NSW	0.12	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-317	ST188	VIC	0.12	-	I	8	t189	*selx*	-	*sak, scn* (E)
ISTOP-417	ST188	NSW	≤0.03	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-440	ST188	NT	0.12	-	I	8	t189	*seb, selx*	-	*sak, scn* (E)
ISTOP-446	ST188	NSW	0.06	-	I	8	UD	*sep, selx*	-	*sep, sak, scn* (G)
ISTOP-458	ST188	QLD	0.12	**DETECTED**	I	8	t189	*selx*	-	*sak, scn* (E)
ISTOP-460	ST188	QLD	0.06	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-464	ST188	QLD	0.06	-	I	8	T416	*selx*	-	*sak, chp, scn* (B)
ISTOP-467	ST188	QLD	0.06	-	I	8	UD	*sep, selx*	-	*sep, sak, scn* (G)
ISTOP-472	ST188	QLD	0.06	-	I	8	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-185	ST7259	NSW	0.06	-	I	ND	t189	*selx*	-	*sak, chp, scn* (B)
ISTOP-287	ST7271	NSW	0.125	-	I	8	t189	*sep, selx*	-	*sep, sak, scn* (G)
Clonal Complex 291 (n=4)										
ISTOP-55	ST291	NSW	0.12	-	I	5	t3096	*sea*	*edinB*	*sea, sak, chp, scn* (A)
ISTOP-326	ST291	VIC	≤0.03	-	I	5	t937		*edinB*	*sak, chp, scn* (B)
ISTOP-418	ST291	NSW	0.06	-	I	5	t16392		*edinB*	*sak, chp, scn* (B)
ISTOP-453	ST7287	NSW	0.12	-	I	5	t937		*edinB*	*sak, chp, scn* (B)
Clonal Complex 361 (n=5)										
ISTOP-108	ST672	NSW	≤0.03	-	I	8	t3841	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-131	ST672	ACT	0.06	-	I	8	t2379	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-151	ST672	WA	0.12	-	I	8	t14090	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, chp, scn* (B)
ISTOP-222	ST672	QLD	0.06	-	I	8	t1309	*egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
ISTOP-302	ST672	NSW	0.06	-	I	8	t1309	*see, egc-cluster (seg+sei+sem+sen+seo+selw), selx*	-	*sak, scn* (E)
Clonal Complex 398 (n=16)										
ISTOP-11	ST398	WA	0.06	-	I	5	t2928		-	*sak, scn* (E)
ISTOP-16	ST398	VIC	0.06	-	I	5	t1451		-	*chp, scn* (C)
ISTOP-97	ST398	VIC	≤0.03	-	UD	5	t1451		-	*chp, scn* (C)
ISTOP-132	ST398	NSW	0.12	-	I	5	t1130		-	*chp, scn* (C)
ISTOP-213	ST398	VIC	0.12	-	I	5	t1451		-	*chp, scn* (C)

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	*agr* type	Capsule type	*spa* type [c]	Enterotoxins	Other Virulence Genes	IEC (Type)
ISTOP-214	ST398	VIC	0.06	-	I	5	UD		-	*chp, scn* (C)
ISTOP-226	ST398	WA	0.06	-	I	5	t1451		-	*chp, scn* (C)
ISTOP-240	ST398	SA	0.06	-	I	5	t6605		-	*chp, scn* (C)
ISTOP-304	ST398	QLD	0.12	-	I	5	t1451		-	*chp, scn* (C)
ISTOP-362	ST398	NSW	≤0.03	-	I	5	t1451		-	*chp, scn* (C)
ISTOP-363	ST398	NSW	0.06	-	I	5	t1451		-	*chp, scn* (C)
ISTOP-448	ST398	NSW	≤0.03	-	I	5	t1451		-	*chp, scn* (C)
ISTOP-98	ST3332	VIC	≤0.03	-	I	5	t011		-	*sak, chp, scn* (B)
ISTOP-100	ST3332	VIC	≤0.03	-	I	5	t011		-	*sak, chp, scn* (B)
ISTOP-323	ST7275	NSW	0.12	-	I	5	UD		-	*chp, scn* (C)
ISTOP-328	ST7277	NSW	0.06	-	I	5	t1451		-	*chp, scn* (C)
Singletons (n=7)										
ISTOP-146	ST425	ACT	0.06	-	II	5	UD	*selx*	-	*sak, chp, scn* (B)
ISTOP-162	ST2867	NSW	0.12	-	II	5	t2016	*selx*	*edinB*	*sak, scn* (E)
ISTOP-208	ST2867	QLD	0.12	-	II	5	UD	*selx*	*edinB*	-
ISTOP-288	ST2867	NSW	0.06	-	II	5	t148	*selx*	*edinB*	*sak, scn* (E)
ISTOP-190	ST5491	VIC	≤0.03	-	III	8	t5925	*selx*	-	*sak, scn* (E)
ISTOP-277	ST7270	NSW	0.06	-	I	5	UD	*seb, sep, selx, selz*	-	*sep, sak, scn* (G)
ISTOP-483	ST573	QLD	0.12	-	II	5	t1839	*Sec2+sel, egc-cluster (seg+sei+sem+sen+seo+selw), selx, swl27, sel28*	-	*scn*

ST, sequence type; Pen, penicillin; MIC, minimum inhibitory concentration; *agr*, accessory gene regulator; *spa*, staphylococcal protein A; IEC, immune evasion cluster

[a] ACT, Australian Capital Territory; NSW, New South Wales; QLD, Queensland; SA, South Australia; TAS, Tasmania; VIC, Victoria; WA, Western Australia

[b] Penicillin-resistant, >0.125 mg/L; penicillin-susceptible, <0.125 mg/L

[c] UD, undetermined *spa* type

Supplementary Table 3. Antibiogram and antimicrobial resistance genes identified in 470 penicillin-susceptible *Staphylococcus aureus* isolates

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
Clonal Complex 1 (n=17)						
ISTOP-48	ST1	NSW	0.12	-	FA^R	*fusC*
ISTOP-127	ST1	SA	0.12	-	FA^R	*fusC*
ISTOP-141	ST1	VIC	≤0.03	-	FA^R	*fusC*
ISTOP-152	ST1	TAS	≤0.03	-		
ISTOP-212	ST1	QLD	0.06	-		*fusC*
ISTOP-219	ST1	TAS	0.06	-		*fusC*
ISTOP-281	ST1	NSW	0.06	-	FA^R	*fusC*
ISTOP-330	ST1	NSW	≤0.03	-		
ISTOP-364	ST1	NSW	0.12	-	Cip^R, FA^R	*fusC,* GrlA S80F and GyrA S84 mutations
ISTOP-396	ST1	WA	0.12	-	Cip^R, FA^R	*fusc,* GrlA S80F and GyrA S84 mutations
ISTOP-407	ST1	VIC	0.12	-		
ISTOP-409	ST1	NSW	0.06	-	FA^R	*fusC*
ISTOP-433	ST1	TAS	0.06	-	FA^R	*fusC*
ISTOP-442	ST1	NT	≤0.03	-	FA^R	*fusC*
ISTOP-130	ST3949	NSW	0.12	-	FA^R	*fusC*
ISTOP-21	ST4100	VIC	≤0.03	-		
ISTOP-69	ST4100	NSW	0.06	-		
Clonal Complex 5 (n=150)						
ISTOP-3	ST5	WA	0.06	-		
ISTOP-9	ST5	WA	≤0.03	-		
ISTOP-15	ST5	VIC	0.06	-		
ISTOP-18	ST5	VIC	0.06	-		
ISTOP-19	ST5	VIC	0.12	-		
ISTOP-22	ST5	VIC	≤0.03	-		
ISTOP-28	ST5	VIC	0.06	-		
ISTOP-32	ST5	QLD	0.12	-		
ISTOP-33	ST5	NSW	0.06	-		
ISTOP-36	ST5	NSW	0.06	-		
ISTOP-38	ST5	TAS	0.12	-		
ISTOP-49	ST5	NSW	≤0.03	-		
ISTOP-60	ST5	VIC	0.06	-		
ISTOP-63	ST5	VIC	0.06	-		
ISTOP-64	ST5	NSW	0.12	-		
ISTOP-66	ST5	NSW	0.06	-		
ISTOP-81	ST5	NSW	0.12	-		
ISTOP-82	ST5	TAS	≤0.03	-		
ISTOP-83	ST5	TAS	0.06	-		
ISTOP-89	ST5	TAS	0.06	-		
ISTOP-90	ST5	SA	0.12	-		
ISTOP-93	ST5	SA	0.12	-		
ISTOP-95	ST5	SA	0.06	-		
ISTOP-102	ST5	VIC	≤0.03	-		
ISTOP-103	ST5	SA	0.06	-		
ISTOP-106	ST5	NSW	0.06	-	SXT^R	*dfrG*
ISTOP-107	ST5	NSW	0.12	-		
ISTOP-110	ST5	QLD	≤0.03	-		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-111	ST5	QLD	0.06	-	Cli^R, Ery^R	*ermC*
ISTOP-113	ST5	NSW	≤0.03	-		
ISTOP-116	ST5	SA	0.12	-		
ISTOP-118	ST5	WA	0.12	-		
ISTOP-124	ST5	SA	0.12	-		
ISTOP-128	ST5	SA	0.12	-		
ISTOP-142	ST5	SA	0.06	-		*fexA*
ISTOP-145	ST5	ACT	0.06	-		
ISTOP-148	ST5	ACT	0.06	-		
ISTOP-158	ST5	NSW	≤0.03	**DETECTED**		
ISTOP-159	ST5	NSW	0.06	-		
ISTOP-161	ST5	NSW	0.12	-		
ISTOP-166	ST5	NSW	0.12	-		
ISTOP-167	ST5	NSW	0.12	-		
ISTOP-173	ST5	VIC	0.12	**DETECTED**		
ISTOP-176	ST5	VIC	0.12	-		
ISTOP-178	ST5	VIC	0.06	-	Cip^R, SXT^R	*dfrG,* GrlA S80F and GyrA S84 mutations
ISTOP-179	ST5	VIC	0.12	-		
ISTOP-180	ST5	VIC	0.12	-		
ISTOP-184	ST5	NSW	≤0.03	-		
ISTOP-187	ST5	NSW	0.12	**DETECTED**		
ISTOP-188	ST5	NSW	0.06	**DETECTED**		
ISTOP-191	ST5	VIC	0.12	-		
ISTOP-193	ST5	SA	0.06	-		
ISTOP-200	ST5	VIC	0.12	-		
ISTOP-201	ST5	VIC	0.06	-	Cip^R, SXT^R	*dfrG,* GrlA S80F and GyrA S84 mutations
ISTOP-206	ST5	NSW	0.06	-		
ISTOP-207	ST5	QLD	0.12	**DETECTED**	Cli^R, Ery^R	*ermC*
ISTOP-209	ST5	QLD	0.06	-	Ery^R	
ISTOP-218	ST5	TAS	0.12	-		
ISTOP-224	ST5	WA	0.12	-		
ISTOP-227	ST5	WA	0.06	-		
ISTOP-231	ST5	WA	0.12	-		
ISTOP-232	ST5	WA	0.12	-		
ISTOP-233	ST5	WA	0.12	**DETECTED**		*ant(9)-Ia_1, ermA, ermC, tetK, penA*
ISTOP-241	ST5	SA	≤0.03	-		
ISTOP-249	ST5	WA	0.06	-		
ISTOP-252	ST5	WA	0.12	-		
ISTOP-262	ST5	ACT	≤0.03	-		
ISTOP-265	ST5	ACT	0.12	-		
ISTOP-267	ST5	ACT	0.06	-		
ISTOP-270	ST5	NSW	0.06	-		
ISTOP-272	ST5	TAS	≤0.03	-		
ISTOP-275	ST5	TAS	≤0.03	-		
ISTOP-282	ST5	NSW	0.12	-		
ISTOP-290	ST5	NSW	0.06	-		
ISTOP-301	ST5	QLD	0.06	-		*ermB, tetM*
ISTOP-303	ST5	QLD	0.06	-		
ISTOP-310	ST5	VIC	0.06	-		
ISTOP-313	ST5	NSW	0.06	-		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-315	ST5	VIC	0.06	-		
ISTOP-316	ST5	VIC	0.12	-		
ISTOP-321	ST5	NSW	0.06	-		
ISTOP-322	ST5	NSW	0.06	-		
ISTOP-327	ST5	VIC	≤0.03	-		
ISTOP-329	ST5	NSW	0.06	-		
ISTOP-334	ST5	SA	0.06	-		
ISTOP-339	ST5	NSW	0.06	-		
ISTOP-350	ST5	WA	0.12	-		
ISTOP-351	ST5	WA	0.12	-		
ISTOP-353	ST5	WA	≤0.03	-		
ISTOP-357	ST5	WA	0.06	-		
ISTOP-365	ST5	NSW	0.12	-		
ISTOP-369	ST5	NSW	0.12	-		
ISTOP-372	ST5	QLD	0.06	-		
ISTOP-374	ST5	VIC	0.06	-		
ISTOP-378	ST5	ACT	0.12	-		
ISTOP-380	ST5	ACT	0.06	-		
ISTOP-381	ST5	ACT	0.06	-		*mdf(A)_1*
ISTOP-382	ST5	VIC	≤0.03	-		
ISTOP-388	ST5	VIC	0.06	-		
ISTOP-389	ST5	VIC	0.06	-		
ISTOP-390	ST5	VIC	0.06	-		
ISTOP-391	ST5	VIC	0.06	-		
ISTOP-394	ST5	WA	≤0.03	-		
ISTOP-395	ST5	WA	0.06	-		
ISTOP-398	ST5	WA	0.06	-		
ISTOP-399	ST5	WA	0.12	-		
ISTOP-400	ST5	WA	0.12	-	Tet^R	*fexA, tetM*
ISTOP-410	ST5	NSW	0.06	-		
ISTOP-412	ST5	NSW	0.06	-	Cli^R, Ery^R, Tet^R	*ermC, tetM*
ISTOP-413	ST5	NSW	0.06	-		*tetM*
ISTOP-415	ST5	NSW	0.06	-		
ISTOP-421	ST5	NSW	0.06	-		
ISTOP-423	ST5	NSW	0.12	-		
ISTOP-424	ST5	NSW	0.06	-		
ISTOP-425	ST5	NSW	0.12	-		
ISTOP-430	ST5	TAS	0.06	-		
ISTOP-431	ST5	TAS	≤0.03	-		
ISTOP-432	ST5	TAS	0.06	-		
ISTOP-436	ST5	NSW	0.12	-		
ISTOP-450	ST5	NSW	≤0.03	-		
ISTOP-451	ST5	NSW	0.12	-		
ISTOP-452	ST5	NSW	0.06	**DETECTED**		
ISTOP-459	ST5	QLD	0.12	**DETECTED**		
ISTOP-461	ST5	QLD	0.06	-	Cip^R, Cli^R, Ery^R, SXT^R	*dfrG, ermC,* GrlA S80F and GyrA S84 mutations
ISTOP-476	ST5	QLD	≤0.03	-	Cli^R, Ery^R, Tet^R	*ermC, tetM*
ISTOP-478	ST5	QLD	0.06	-		
ISTOP-480	ST5	QLD	0.06	-		
ISTOP-481	ST5	QLD	0.12	-		*ermC*
ISTOP-4	ST2967	WA	≤0.03	-		
ISTOP-13	ST3628	WA	0.06	-	Ery^R	*ermC*
ISTOP-34	ST3628	NSW	≤0.03	-		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-39	ST3628	TAS	0.12	-		
ISTOP-121	ST3628	WA	0.12	**DETECTED**		
ISTOP-338	ST3628	WA	0.06	-		
ISTOP-349	ST3628	WA	0.12	-		
ISTOP-104	ST3724	SA	0.06	-	Tet^R	*tetM*
ISTOP-62	ST5189	VIC	0.06	-		
ISTOP-228	ST5189	WA	0.06	-		
ISTOP-41	ST7252	VIC	0.12	-		
ISTOP-61	ST7252	VIC	0.06	-		
ISTOP-195	ST7260	SA	≤0.03	-		
ISTOP-229	ST7262	WA	0.12	**DETECTED**		
ISTOP-238	ST7263	WA	0.12	-		
ISTOP-246	ST7265	WA	≤0.03	-	Rif^R	
ISTOP-251	ST7267	WA	0.12	-		
ISTOP-482	ST7267	QLD	0.06	-		
ISTOP-271	ST7269	NSW	0.06	-		
ISTOP-370	ST7282	NSW	0.06	-		
ISTOP-457	ST7288	NSW	0.06	-		
ISTOP-466	ST7290	QLD	0.12	-		
Clonal Complex 6 (n=16)						
ISTOP-1	ST6	NSW	0.06	-		
ISTOP-53	ST6	NSW	0.12	**DETECTED**		
ISTOP-87	ST6	TAS	≤0.03	-		
ISTOP-91	ST6	SA	0.12	-		
ISTOP-105	ST6	NSW	0.12	-	Rif^R	
ISTOP-114	ST6	NSW	0.12	-		
ISTOP-204	ST6	SA	0.12	-		
ISTOP-244	ST6	SA	0.06	-		
ISTOP-248	ST6	WA	0.12	-		
ISTOP-257	ST6	WA	0.06	-		
ISTOP-285	ST6	NSW	0.12	-		
ISTOP-375	ST6	VIC	0.06	-		
ISTOP-402	ST6	VIC	0.06	-		
ISTOP-428	ST6	VIC	≤0.03	-		
ISTOP-429	ST6	VIC	0.06	-		
ISTOP-479	ST6	QLD	0.06	-		
Clonal Complex 7 (n=3)						
ISTOP-125	ST7	SA	0.12	-		
ISTOP-220	ST7	TAS	0.06	-	FA^R	
ISTOP-345	ST7	VIC	0.06	-		
Clonal Complex 8 (n=14)						
ISTOP-17	ST8	VIC	0.12	-		
ISTOP-78	ST8	ACT	0.06	-		
ISTOP-143	ST8	SA	≤0.03	-		
ISTOP-144	ST8	ACT	0.06	-		
ISTOP-164	ST8	NSW	0.06	**DETECTED**		
ISTOP-181	ST8	VIC	0.06	-		
ISTOP-215	ST8	VIC	0.12	-		
ISTOP-239	ST8	SA	0.06	-		
ISTOP-259	ST8	ACT	≤0.03	-		
ISTOP-286	ST8	NSW	0.06	-	Ery^R	*ermC*
ISTOP-331	ST8	NSW	0.06	-		
ISTOP-397	ST8	WA	0.06	-		
ISTOP-405	ST8	VIC	0.12	-		
ISTOP-6	ST5234	WA	0.06	-		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
Clonal Complex 9 (n=1)						
ISTOP-293	ST9	VIC	0.12	**DETECTED**		
Clonal Complex 12 (n=16)						
ISTOP-12	ST12	WA	≤0.03	-		
ISTOP-14	ST12	WA	0.06	-		
ISTOP-29	ST12	QLD	≤0.03	-		
ISTOP-30	ST12	QLD	0.06	-		
ISTOP-40	ST12	TAS	0.12	-		
ISTOP-51	ST12	NSW	0.06	-		
ISTOP-74	ST12	NSW	0.06	-		
ISTOP-86	ST12	TAS	0.06	-		
ISTOP-117	ST12	WA	0.06	-		
ISTOP-140	ST12	VIC	0.12	-		
ISTOP-150	ST12	ACT	0.06	-		
ISTOP-254	ST12	WA	0.06	-		
ISTOP-274	ST12	TAS	0.06	-		
ISTOP-377	ST12	NSW	0.06	-		
ISTOP-406	ST12	VIC	0.06	-		
ISTOP-23	ST7251	VIC	0.06	**DETECTED**		
Clonal Complex 15 (n=41)						
ISTOP-7	ST15	WA	0.06	-		
ISTOP-46	ST15	NSW	0.12	-		
ISTOP-59	ST15	NSW	0.06	-		
ISTOP-79	ST15	ACT	0.06	-	SXT^R	*dfrG*
ISTOP-109	ST15	QLD	0.12	-		
ISTOP-119	ST15	WA	0.12	-		
ISTOP-129	ST15	NSW	0.06	-		
ISTOP-134	ST15	NSW	0.12	-	Cli^R, Ery^R	*ermC*
ISTOP-137	ST15	VIC	0.06	-		
ISTOP-221	ST15	TAS	≤0.03	-		
ISTOP-225	ST15	WA	0.12	-		
ISTOP-235	ST15	WA	0.06	-		
ISTOP-236	ST15	WA	0.12	-		
ISTOP-299	ST15	VIC	0.12	-		
ISTOP-309	ST15	VIC	0.12	-		
ISTOP-348	ST15	WA	0.06	-		
ISTOP-356	ST15	WA	0.06	-		
ISTOP-379	ST15	ACT	0.06	-		
ISTOP-438	ST15	NSW	0.12	**DETECTED**		
ISTOP-20	ST333	VIC	0.06	-		
ISTOP-50	ST582	NSW	0.12	**DETECTED**	Cip^R,FA^R	*fusC,* GrlA S80F and GyrA S84 mutations
ISTOP-153	ST582	TAS	0.12	**DETECTED**		
ISTOP-157	ST582	NSW	0.12	**DETECTED**		
ISTOP-223	ST582	WA	0.06	**DETECTED**		
ISTOP-306	ST582	Qld	0.12	**DETECTED**		
ISTOP-318	ST582	VIC	0.12	**DETECTED**		
ISTOP-324	ST582	VIC	0.06	**DETECTED**		
ISTOP-447	ST582	NSW	0.06	**DETECTED**		
ISTOP-462	ST582	QLD	0.12	**DETECTED**		
ISTOP-465	ST582	QLD	0.12	**DETECTED**		
ISTOP-475	ST582	QLD	0.12	**DETECTED**		
ISTOP-27	ST3911	VIC	0.06	**DETECTED**		
ISTOP-171	ST3911	WA	0.12	**DETECTED**		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-210	ST3911	QLD	0.06	**DETECTED**		
ISTOP-276	ST3911	NSW	0.12	**DETECTED**		
ISTOP-295	ST3911	VIC	0.12	**DETECTED**		
ISTOP-115	ST5059	NSW	0.12	**DETECTED**		
ISTOP-243	ST7264	SA	0.06	-		
ISTOP-300	ST7273	QLD	0.12	**DETECTED**		
ISTOP-401	ST7283	VIC	0.12	**DETECTED**		
ISTOP-445	ST7286	NSW	≤0.03	-		
Clonal Complex 20 (n=3)						
ISTOP-85	ST20	TAS	0.12	-		
ISTOP-342	ST20	TAS	0.12	-		
ISTOP-427	ST20	SA	0.12	**DETECTED**		
Clonal Complex 22 (n=8)						
ISTOP-266	ST22	ACT	0.06	-		
ISTOP-278	ST22	NSW	0.12	-		
ISTOP-347	ST22	WA	0.12	-		
ISTOP-360	ST22	WA	0.06	**DETECTED**		
ISTOP-383	ST22	VIC	0.12	-		
ISTOP-384	ST22	VIC	≤0.03	-		
ISTOP-292	ST7272	QLD	≤0.03	-		
ISTOP-435	ST7285	TAS	0.06	-		
Clonal Complex 25 (n=1)						
ISTOP-325	ST7276	VIC	≤0.03	**DETECTED**		
Clonal Complex 30 (n=7)						
ISTOP-311	ST30	VIC	0.06	-	Cip^R,	*dfrG,* GrlA S80F and GyrA S84 mutations
ISTOP-319	ST30	VIC	0.12	**DETECTED**		
ISTOP-42	ST34	VIC	0.06	**DETECTED**		
ISTOP-101	ST34	VIC	≤0.03	-	Cli^R, Ery^R	
ISTOP-263	ST34	ACT	0.06	**DETECTED**		
ISTOP-264	ST34	ACT	0.06	**DETECTED**		
ISTOP-296	ST39	VIC	≤0.03	-	Ery^R	*ant(9)-Ia_1, ermA*
Clonal Complex 45 (n=47)						
ISTOP-31	ST45	QLD	0.06	-		
ISTOP-68	ST45	WA	0.06	-		
ISTOP-70	ST45	NSW	0.06	-		
ISTOP-88	ST45	TAS	0.12	**DETECTED**		
ISTOP-94	ST45	SA	0.12	-		
ISTOP-122	ST45	WA	0.06	-		
ISTOP-123	ST45	SA	0.12	-		
ISTOP-139	ST45	VIC	≤0.03	-		
ISTOP-149	ST45	ACT	0.06	-		
ISTOP-160	ST45	NSW	0.06	-		
ISTOP-170	ST45	WA	≤0.03	-		
ISTOP-189	ST45	NSW	0.06	-		
ISTOP-216	ST45	TAS	0.06	-		
ISTOP-230	ST45	WA	0.06	-		
ISTOP-260	ST45	ACT	0.06	-		
ISTOP-279	ST45	NSW	0.12	-		
ISTOP-283	ST45	NSW	0.06	-		
ISTOP-337	ST45	WA	0.06	-		
ISTOP-366	ST45	NSW	0.06	-		
ISTOP-373	ST45	VIC	0.06	-		
ISTOP-376	ST45	WA	0.06	-		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-386	ST45	QLD	0.06	-	Cli^R, Ery^R	*ant(4')-Ia, aadD, ermC, mphC*
ISTOP-426	ST45	SA	0.06	-		
ISTOP-439	ST45	NT	0.12	-		
ISTOP-454	ST45	NSW	0.06	-		
ISTOP-455	ST45	NSW	0.06	-		
ISTOP-456	ST45	NSW	≤0.03	-		
ISTOP-468	ST45	QLD	≤0.03	-		
ISTOP-470	ST45	QLD	0.06	-		
ISTOP-473	ST45	QLD	≤0.03	-		
ISTOP-26	ST508	NSW	≤0.03	-		
ISTOP-35	ST508	NSW	0.12	-		
ISTOP-154	ST508	TAS	≤0.03	-		
ISTOP-163	ST508	NSW	0.06	-		
ISTOP-169	ST508	WA	0.06	-		
ISTOP-253	ST508	WA	0.12	-		
ISTOP-269	ST508	NSW	0.125	-		
ISTOP-336	ST508	SA	0.125	-		
ISTOP-408	ST508	VIC	0.06	-		
ISTOP-75	ST7254	NSW	≤0.03	-		
ISTOP-84	ST7255	TAS	0.12	**DETECTED**		
ISTOP-147	ST7258	ACT	0.06	-		
ISTOP-203	ST7261	SA	≤0.03	-		
ISTOP-268	ST7268	NSW	0.06	-		
ISTOP-346	ST7279	VIC	0.06	-		
ISTOP-419	ST7284	NSW	0.12	-		
ISTOP-463	ST7289	QLD	0.12	-		
Clonal Complex 59 (n=9)						
ISTOP-67	ST59	WA	0.12	-		
ISTOP-77	ST59	ACT	0.06	-		
ISTOP-343	ST59	TAS	0.06	-		
ISTOP-368	ST59	NSW	0.12	-	Ery^R	*ant(9)-Ia_1, ermA*
ISTOP-403	ST59	VIC	0.12	-		
ISTOP-437	ST59	NSW	0.06	-		
ISTOP-256	ST87	WA	0.12	-		
ISTOP-186	ST1224	NSW	≤0.03	-		
ISTOP-354	ST7280	WA	0.06	-		
Clonal Complex 80 (n=1)						
ISTOP-199	ST80	VIC	0.12	-		
Clonal Complex 88 (n=17)						
ISTOP-47	ST78	NSW	0.12	-	Ery^R	*ant(9)-Ia_1, ermA*
ISTOP-76	ST78	ACT	0.12	-	Ery^R	*ant(9)-Ia_1, ermA*
ISTOP-182	ST78	VIC	0.12	-		
ISTOP-217	ST78	TAS	0.06	-		*ant(9)-Ia_1, ermA*
ISTOP-261	ST78	ACT	0.06	-	Ery^R	*ant(9)-Ia_1, ermA*
ISTOP-312	ST78	NSW	0.06	-		
ISTOP-471	ST78	QLD	0.06	-		
ISTOP-8	ST88	WA	0.12	-	FA^R	
ISTOP-71	ST88	NSW	0.06	-		
ISTOP-120	ST88	WA	0.12	-	FA^R	
ISTOP-135	ST88	NSW	0.12	-		
ISTOP-175	ST88	VIC	0.06	-		
ISTOP-308	ST88	VIC	0.12	-		
ISTOP-333	ST88	NSW	0.12	-		
ISTOP-441	ST88	NT	0.12	-		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-444	ST88	NT	≤0.03	-		
ISTOP-355	ST7281	WA	≤0.03	-	Ery^R	*ant(9)-Ia_1, ermA*
Clonal Complex 97 (n=48)						
ISTOP-37	ST97	NSW	0.06	-		
ISTOP-54	ST97	NSW	0.12	-		
ISTOP-57	ST97	NSW	0.06	-		
ISTOP-65	ST97	NSW	0.12	-		
ISTOP-73	ST97	NSW	0.12	-		
ISTOP-80	ST97	NSW	0.12	-		
ISTOP-96	ST97	VIC	≤0.03	-		
ISTOP-138	ST97	VIC	0.06	-		
ISTOP-172	ST97	VIC	0.06	-		
ISTOP-198	ST97	SA	0.12	-		
ISTOP-211	ST97	QLD	0.06	-	FA^R	
ISTOP-242	ST97	SA	0.12	-		
ISTOP-245	ST97	WA	0.12	-	Ery^R	*ant(9)-Ia_1, ermA*
ISTOP-250	ST97	WA	0.12	-		
ISTOP-280	ST97	NSW	0.12	-		
ISTOP-291	ST97	QLD	0.06	-		
ISTOP-298	ST97	VIC	0.12	-		
ISTOP-307	ST97	VIC	≤0.03	-		
ISTOP-320	ST97	VIC	0.12	-		
ISTOP-335	ST97	SA	≤0.03	-		
ISTOP-352	ST97	WA	0.12	-		
ISTOP-358	ST97	WA	0.06	-		
ISTOP-359	ST97	WA	≤0.03	-		
ISTOP-367	ST97	NSW	0.12	-		
ISTOP-385	ST97	QLD	0.06	-		
ISTOP-414	ST97	NSW	0.06	-		
ISTOP-416	ST97	NSW	0.12	-		
ISTOP-420	ST97	NSW	0.12	-		
ISTOP-422	ST97	NSW	0.12	-		
ISTOP-434	ST97	TAS	0.12	-		
ISTOP-449	ST97	NSW	0.12	-		
ISTOP-469	ST97	QLD	0.06	-		
ISTOP-474	ST97	QLD	0.06	-		
ISTOP-477	ST97	QLD	0.06	-		
ISTOP-10	ST953	WA	0.12	-		
ISTOP-45	ST953	NSW	0.06	-		
ISTOP-58	ST953	NSW	0.12	-		
ISTOP-126	ST953	SA	0.12	-		
ISTOP-234	ST953	WA	≤0.03	-		
ISTOP-237	ST953	WA	0.12	-		
ISTOP-255	ST953	NSW	0.06	-		
ISTOP-273	ST953	TAS	0.12	-		*lnuA*
ISTOP-392	ST953	NSW	≤0.03	-		
ISTOP-443	ST953	NT	≤0.03	-		
ISTOP-5	ST1179	WA	0.12	-	Tet^R	*tetK*
ISTOP-404	ST1179	VIC	0.12	-		
ISTOP-99	ST7256	VIC	0.06	-		
ISTOP-344	ST7278	TAS	0.12	-		
Clonal Complex 101 (n=16)						
ISTOP-136	ST101	TAS	0.06	-		
ISTOP-174	ST101	VIC	0.12	**DETECTED**		
ISTOP-192	ST101	VIC	0.12	-		

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-284	ST101	NSW	0.12	-		
ISTOP-289	ST101	NSW	0.06	-		
ISTOP-294	ST101	VIC	0.06	-		
ISTOP-332	ST101	NSW	0.06	-		
ISTOP-340	ST101	NSW	0.12	-		
ISTOP-361	ST101	NSW	0.12	-		
ISTOP-393	ST101	NSW	≤0.03	-		
ISTOP-411	ST101	NSW	0.06	-		
ISTOP-484	ST101	QLD	0.12	-		
ISTOP-72	ST1155	QLD	0.12	-		
ISTOP-168	ST1155	WA	0.06	-		
ISTOP-133	ST7257	NSW	0.06	-		
ISTOP-305	ST7274	QLD	0.06	-		
Clonal Complex 188 (n=23)						
ISTOP-2	ST188	NSW	0.06	-		
ISTOP-24	ST188	VIC	0.12	-		
ISTOP-25	ST188	NSW	≤0.03	-		
ISTOP-44	ST188	NSW	0.12	-		
ISTOP-52	ST188	NSW	0.12	-		
ISTOP-56	ST188	NSW	0.06	-		
ISTOP-92	ST188	SA	0.06	-		
ISTOP-112	ST188	NSW	0.06	-		
ISTOP-155	ST188	TAS	0.12	-		*aph(3')-IIIa*
ISTOP-156	ST188	NSW	0.06	-		
ISTOP-165	ST188	NSW	0.12	-		
ISTOP-205	ST188	NSW	0.12	-		
ISTOP-317	ST188	VIC	0.12	-		
ISTOP-417	ST188	NSW	≤0.03	-		
ISTOP-440	ST188	NT	0.12	-		
ISTOP-446	ST188	NSW	0.06	-		
ISTOP-458	ST188	QLD	0.12	**DETECTED**		
ISTOP-460	ST188	QLD	0.06	-		
ISTOP-464	ST188	QLD	0.06	-		
ISTOP-467	ST188	QLD	0.06	-		
ISTOP-472	ST188	QLD	0.06	-		
ISTOP-185	ST7259	NSW	0.06	-		
ISTOP-287	ST7271	NSW	0.125	-		
Clonal Complex 291 (n=4)						
ISTOP-55	ST291	NSW	0.12	-		
ISTOP-326	ST291	VIC	≤0.03	-	Cip^R	GrlA S80F and GyrA 84 mutations
ISTOP-418	ST291	NSW	0.06	-		
ISTOP-453	ST7287	NSW	0.12	-		
Clonal Complex 361 (n=5)						
ISTOP-108	ST672	NSW	≤0.03	-	Cip^R	GrlA S80F and GyrA 84 mutations
ISTOP-131	ST672	ACT	0.06	-		
ISTOP-151	ST672	WA	0.12	-		
ISTOP-222	ST672	QLD	0.06	-		
ISTOP-302	ST672	NSW	0.06	-		
Clonal Complex 398 (n=16)						
ISTOP-11	ST398	WA	0.06	-		
ISTOP-16	ST398	VIC	0.06	-	Ery^R	*ermT*
ISTOP-97	ST398	VIC	≤0.03	-		*ermT*
ISTOP-132	ST398	NSW	0.12	-	Ery^R	*ermT*

Isolate	ST	State [a]	Vitek® 2 Pen MIC (mg/L) [b]	*blaZ*	Antibiogram [c]	Resistance Genes
ISTOP-213	ST398	VIC	0.12	-	Ery^R	*ermT*
ISTOP-214	ST398	VIC	0.06	-		*ermT*
ISTOP-226	ST398	WA	0.06	-	Ery^R	*ermT*
ISTOP-240	ST398	SA	0.06	-	Ery^R	*ermT*
ISTOP-304	ST398	QLD	0.12	-	Ery^R	*ermT*
ISTOP-362	ST398	NSW	≤0.03	-	Cli^R, Ery^R	*ermC*
ISTOP-363	ST398	NSW	0.06	-	Ery^R	*ermT*
ISTOP-448	ST398	NSW	≤0.03	-	Ery^R	*ermT*
ISTOP-98	ST3332	VIC	≤0.03	-		
ISTOP-100	ST3332	VIC	≤0.03	-		
ISTOP-323	ST7275	NSW	0.12	-	Ery^R	*ermT*
ISTOP-328	ST7277	NSW	0.06	-	Ery^R	*ermT*
Singletons (n=7)						
ISTOP-146	ST425	ACT	0.06	-		
ISTOP-162	ST2867	NSW	0.12	-		
ISTOP-208	ST2867	QLD	0.12	-		
ISTOP-288	ST2867	NSW	0.06	-		*ant(4')-Ia, aadD*
ISTOP-190	ST5491	VIC	≤0.03	-		
ISTOP-277	ST7270	NSW	0.06	-		
ISTOP-483	ST573	QLD	0.12	-		

ST, sequence type; Pen, penicillin; MIC, minimum inhibitory concentration

[a] ACT, Australian Capital Territory; NSW, New South Wales; QLD, Queensland; SA, South Australia; TAS, Tasmania; VIC, Victoria; WA, Western Australia

[b] Penicillin-resistant, >0.125 mg/L; penicillin-susceptible, <0.125 mg/L

[c] Antimicrobial resistance labelled ^{R}. Cli, Clindamycin; Cip, Ciprofloxacin; Ery, Erythromycin; FA, fusidic acid; Rif, Rifampicin; SXT, Trimethoprim/Sulfamethoxazole; Tet, Tetracycline.