

**The Australian Group on Antimicrobial Resistance**

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***Staphylococcus aureus* Programme 2010 (SAP 2010)  
Community Survey  
MRSA Epidemiology and Typing Report**

**PREPARED BY:**

**Mr Geoffrey Coombs**

**Department of Microbiology and Infectious Diseases, Royal Perth Hospital.  
PathWest Laboratory Medicine-WA, Western Australia.**

**Ms Julie Pearson**

**Department of Microbiology and Infectious Diseases, Royal Perth Hospital.  
PathWest Laboratory Medicine-WA, Western Australia.**

**Clinical Professor Keryn Christiansen**

**Department of Microbiology and Infectious Diseases, Royal Perth Hospital.  
PathWest Laboratory Medicine-WA, Western Australia.**

**Professor Graeme Nimmo**

**Division of Microbiology, Pathology Queensland Central Laboratory, Queensland.**

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**Epidemiology and Typing Report of Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolates from the Australian Group on Antimicrobial Resistance (AGAR) 2010**  
***Staphylococcus aureus* Surveillance Programme (SAP 2010)**

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# ***Staphylococcus aureus* Programme 2010 (SAP 2010)**

## **Community Survey**

### **MRSA Epidemiology and Typing Report**

#### **1. Overview**

*Of the 539 S aureus classified as MRSA in the SAP 2010 Community Survey, molecular typing was performed on 532 (98.7%) isolates. The mean age of patients with infections due to community-associated MRSA (CA-MRSA) strains (39 years; median 33 years) was found to be significantly lower ( $P < 0.0001$ ) than the mean age of patients with infections due to healthcare-associated MRSA (HA-MRSA) strains (69 years; median 73 years). Although the percentage of S aureus characterized as HA-MRSA in this survey (5.9%) was lower when compared to the 2008 survey (6.7%), ST22-IV [2B] (EMRSA-15) remains a major HA-MRSA clone in most Australian communities surveyed, accounting for 18.8% of all community-onset MRSA infections. Of continuing concern has been the rapid emergence of this clone in the Victorian (0% in 2002 to 21.8% in 2010), South Australian (7.1% in 2000 to 19.0% in 2010), and New South Wales communities (18.0% in 2000 to 33.3% in 2010). CA-MRSA accounted for 66.7% of MRSA and 11.6% of all S aureus. Since 2000 the percentage of S aureus characterized as CA-MRSA has almost doubled (6.6% in 2000 to 11.6% in 2010). As in previous surveys, although CA-MRSA was multiclonal (32 clones) 84.3% of strains could be characterized into six clones. ST93-IV [2B] (Queensland CA-MRSA), a Panton Valentine leucocidin (PVL)-positive clone, remains the most frequently isolated CA-MRSA clone in the Australian community accounting for 41.4% of all CA-MRSA and 27.6% of all MRSA infections. Overall 62.5% of CA-MRSA were PVL positive, a 21% increase when compared to the 2006 survey. The mean age of patients with PVL positive CA-MRSA infections (31 years; median 25 years) was significantly lower ( $P < 0.0001$ ) than the mean age of patients with PVL negative CA-MRSA infections (53 years; median 57 years). The increase in PVL-positive MRSA is not only due to the expansion of the ST93-IV [2B] clone but also due to the introduction of several international CA-MRSA clones including ST30-IV [2B] (WSPP MRSA), ST8-IV [2B] (USA300) ST59-V<sub>T</sub> [5C2&5] (Taiwan CA-MRSA), ST80-IV [2B] (European CA-MRSA) and more recently the hypervirulent multiresistant ST772-V [5C2] (Bengal Bay). Three ST22-IV [2B] (EMRSA-15) isolates carrying the PVL determinant were also identified. For this clone, which has been demonstrated to have enhanced transmission in the Australian community, to acquire the PVL determinant continues to be a major public health concern.*

#### **2. Summary**

The Australian Group for Antimicrobial Resistance (AGAR) biennial community *Staphylococcus aureus* surveillance programme commenced in 2000. In the 2010 programme (SAP 2010) up to 100 clinically significant, community onset, consecutive isolates of *S aureus* from different outpatients were collected by each of 30 institutions located across Australia Day surgery and dialysis patients were excluded. Methicillin-resistant *S aureus* (MRSA) isolates were referred to the Australian Collaborating Centre for *Enterococcus* and *Staphylococcus* Species (**ACCESS**) Typing and Research for clone characterization and Panton-Valentine leucocidin (PVL) toxin determination.

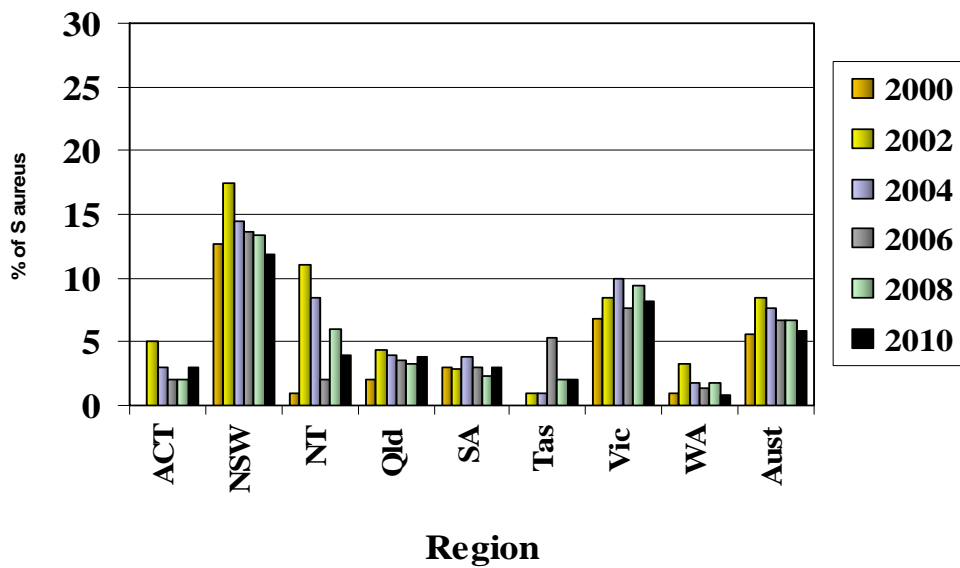
The molecular characterization of the MRSA isolates is designed to provide a “snapshot” of MRSA clones circulating in the Australian community.

Of the 539 (18.0%) *S aureus* classified as MRSA in SAP 2010, 532 (98.7%) were referred to **ACCESS** Typing and Research. Overall 66.7% and 33.3% of MRSA were characterized as Community-associated (CA-MRSA) and Healthcare-associated (HA-MRSA) clones respectively. The mean age of

patients with CA-MRSA infections (39 years; median 33 years) was significantly lower ( $P < 0.0001$ ) than the mean age of patients with HA-MRSA infections (69 years; median 73 years).

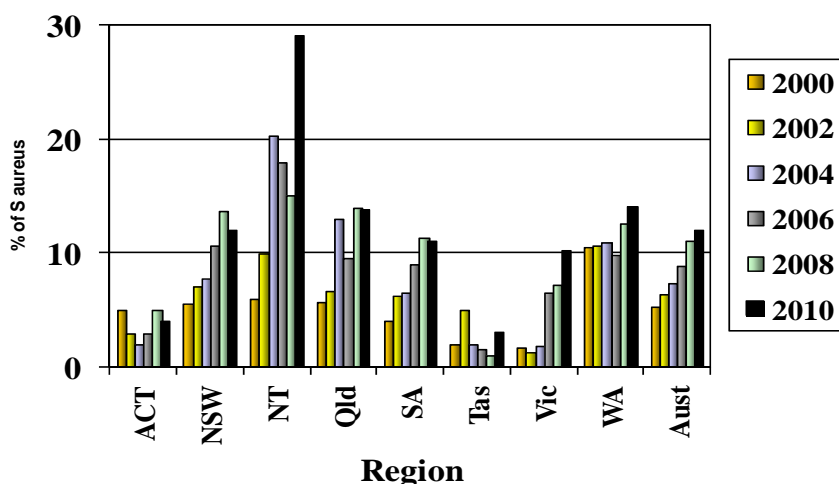
Since the initial community *S aureus* surveillance study performed in 2000 there has been a significant increase ( $p < 0.0001$ ) in the percentage of patients with MRSA infections in most regions of Australia such that in 2010 one in six patients with a staphylococcal infection have MRSA and one in ten are infected with a CA-MRSA clone.

Throughout Australia the percentage of *S aureus* characterized as HA-MRSA was 5.9% ranging from 0.8% in Western Australia to 11.8% in New South Wales.



Percentage of *S aureus* characterized as HA-MRSA clones

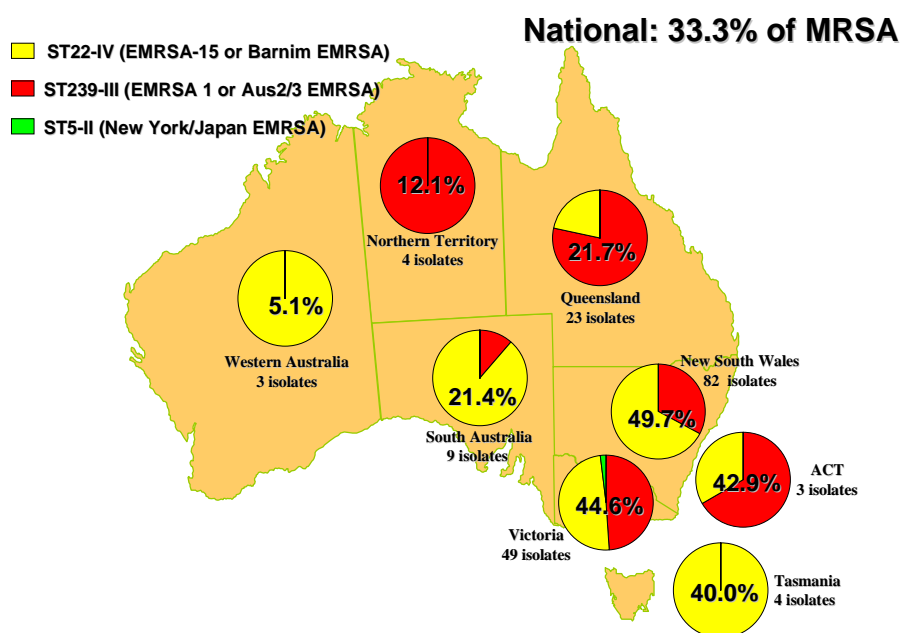
The percentage of *S aureus* characterized as CA-MRSA was 11.9% ranging from 3.0% in Tasmania to 29.0% in the Northern Territory.



Percentage of *S aureus* characterized as CA-MRSA

### 2.1. Community Onset HA-MRSA clones

Three HA-MRSA clones were identified in the Australian community; 56.5% were ST22-IV [2B] (EMRSA-15), 42.9% ST239-III [3A] (Aus-2/3 EMRSA), and 0.6% ST5-II [2A] (New York Japan MRSA/USA100).



Percentage of MRSA characterized as HA-MRSA

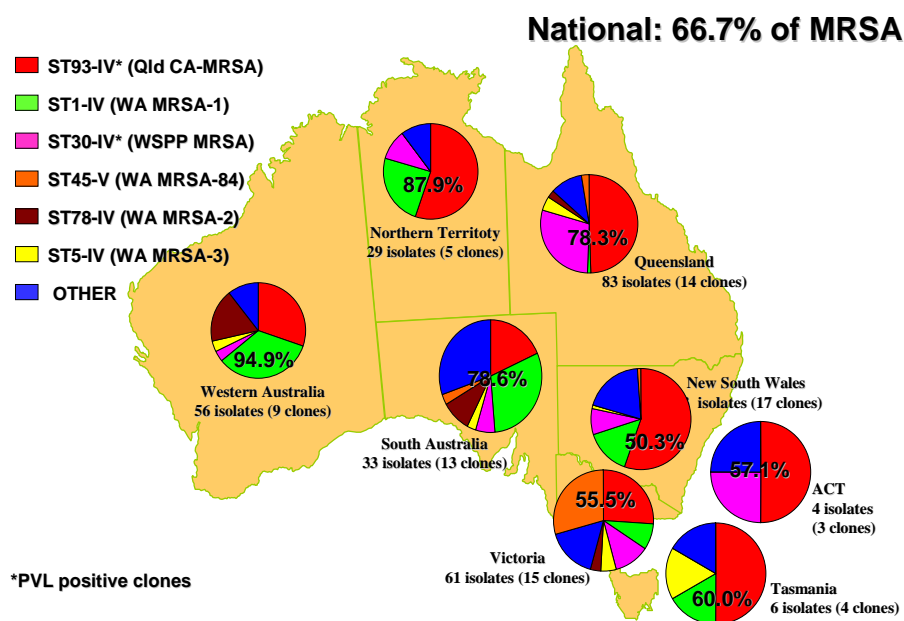
Aus2/3 EMRSA was isolated in most Australian regions, accounting for 28.6% of MRSA in the Australian Capital Territory. Over the six community surveys the percentage of isolates characterized as Aus-2/3 has decreased throughout Australia. EMRSA-15, which was initially reported in Australia in 1997, accounted for 18.8% of all MRSA isolated in this study, ranging from 0% in the Northern Territory to 40.0% in Tasmania. The percentage of MRSA characterized as EMRSA-15 has increased in most Australian regions over the six surveys noticeably in Victoria (0% in 2002 to 21.8% in 2010), South Australia (7.1% in 2000 to 19.0% in 2010) and New South Wales (18.0% in 2000 to 33.3% in 2010).

## 2.2. Community Onset CA-MRSA clones

Thirty two CA-MRSA clones were identified by pulsed-field gel electrophoresis (corresponding to 26 MLST/SCC*mec* clones) of which 84.3% were made up of six clones:

- ST93-IV [2B] {Qld CA-MRSA} (41.4%)
- ST1-IV [2B] {WA MRSA-1} (15.5%)
- ST30-IV [2B] {WSPP CA-MRSA} (13.0%)
- ST45-V [5C2&5] {WA MRSA-84} (6.2%)
- ST78-MRSA-IV [2B] {WA MRSA-2} (4.8%)
- ST5-MRSA-IV [2B] {WA MRSA-3} (3.4%)

ST93-MRSA-IV (PVL-positive Queensland clone), which was isolated in all regions, remained the predominant CA-MRSA clone isolated in Australia



Percentage of MRSA characterized as CA-MRSA

### **2.3. Panton-Valentine Leucocidin (PVL) Toxin**

#### **CA-MRSA**

Overall 62.5% (n=222) of CA-MRSA (11 clones) were PVL positive:

- ST93-IV [2B](Qld CA-MRSA) – 146 isolates
- The following recognised international clones:
  - o ST30-IV [2B] (WSPP) – 46 isolates
  - o ST8-IV [2B] (USA300) – 6 isolates
  - o ST772-V [5C2] (Bengal Bay) – 5 isolates
  - o ST80-IV [2B] (European CA-MRSA) – 4 isolates
  - o ST59-V<sub>T</sub> [5C2&5] (Taiwan CA-MRSA) – 4 isolates
- Five isolates of ST1-MRSA-IV [2B] (WA MRSA-1). It is possible that these are USA400 strains however further molecular studies are required to confirm.
- In addition, the following four “Australian CA-MRSA” clones also contained PVL positive isolates
  - o ST5-IV [2B] (WA MRSA-3) – 3 isolates
  - o ST78-IV [2B] (WA MRSA-2) – 1 isolate
  - o ST72-IV [2B] (WA MRSA-44) – 1 isolate
  - o ST1-V [5C2] – 1 isolate

Although PVL positive CA-MRSA were isolated throughout Australia, the percentage of CA-MRSA that were positive varied from 36% in South Australia to 73% and 83% in New South Wales and Queensland respectively. In the previous community survey (SAP 2008), 64.7% of CA-MRSA were PVL positive ranging from 16% in Western Australia to 88% in New South Wales.

The mean age of patients with PVL positive CA-MRSA infections (31 years; median 25 years) was significantly lower ( $P < 0.0001$ ) than the mean age of patients with PVL negative CA-MRSA infections (53 years; median 57 years).

#### **HA-MRSA**

Three PVL-positive ST22-MRSA-IV [2B] (EMRSA-15) isolates were identified by PCR (two in Queensland and one in New South Wales). The detection of PVL in a prevalent HA-MRSA strain is a cause of serious concern because of the potential increased virulence associated with PVL-positive strains and the rapid expansion of EMRSA-15 in both the hospital and community setting.

### 3. SAP 2010 Protocol

#### 3.1. Commencement Date

1<sup>st</sup> July 2010

#### 3.2. Isolates

Approximately 100 consecutive isolates of *Staphylococcus aureus* from 100 different outpatients, excluding dialysis and day surgery patients, at each site were tested by 30 laboratories located across Australia (total number of isolates = 2,994). Isolates from Nursing Homes, Long-Term Care Facilities and Hospice patients were included. Each *S aureus* isolate was judged to have come from a potentially infected site.

#### 3.3. Participating Laboratories

Australian Capital Territory (1)  
The Canberra Hospital

New South Wales (7)  
Concord Hospital  
Douglass Hanly Moir Pathology  
Nepean Hospital  
Royal Prince Alfred Hospital  
Royal North Shore Hospital  
Sydney South West Pathology Service  
Westmead Hospital

Northern Territory (1)  
Royal Darwin Hospital

Queensland (6)  
Pathology Queensland Cairns Base  
Hospital  
Pathology Queensland Gold Coast  
Hospital  
Pathology Queensland Prince Charles  
Hospital  
Pathology Queensland Princess  
Alexandra Hospital  
Pathology Queensland Central Laboratory  
Sullivan Nicolaides Pathology

South Australia (3)  
SA Pathology, Flinders Medical Centre  
SA Pathology, Institute of Medical Veterinary Science  
SA Pathology, Women's and Children's Hospital

Tasmania (2)  
Launceston General Hospital  
Royal Hobart Hospital

Victoria (6)  
Alfred Hospital  
Austin Health  
Healthscope Pathology  
Monash Medical Centre  
Royal Children's Hospital  
St Vincent's Hospital

Western Australia (4)  
PathWest WA - Fremantle Hospital  
PathWest WA - Queen Elizabeth Medical Centre  
PathWest WA - Royal Perth Hospital  
Saint John of God Pathology

#### 3.4. Methicillin Susceptibility Testing

Vitek2<sup>®</sup> AST-P612 susceptibility card according to the manufacturer's guidelines.

#### 3.5. Epidemiological Typing

Performed by the Australian Collaborating Centre for *Enterococcus* and *Staphylococcus* Species (**ACCESS**) Typing and Research:

Department of Microbiology and Infectious Diseases, PathWest Laboratory Medicine-WA,  
Royal Perth Hospital, Perth Western Australia.

Molecular Genetics Research Unit, School of Biomedical Sciences, Curtin University of  
Technology, Bentley, Western Australia.

### 3.6. MRSA Nomenclature

**ACCESS** Typing and Research employs the international MRSA nomenclature system described by *Enright et al.* (1). This system provides a universally standardised MRSA nomenclature allowing MRSA clones to be readily compared between laboratories and countries. It is based upon the combination of the sequences of seven housekeeping genes combined to define a sequence type (ST) using multilocus sequence typing (MLST), and the *SCCmec* type. The MRSA genotype is therefore the sum of the *SCCmec* type and the type of its recipient chromosome. For example, an MRSA clone of ST22 and *SCCmec* type IV is referred to as ST22-IV [2B] (previously known as EMRSA-15).

#### Multi Locus Sequence Typing (MLST)

MLST is a highly discriminatory method of characterizing MRSA. For each of the seven housekeeping gene fragments, different sequences are assigned as distinct alleles, and an isolate is defined by the alleles of each of the seven housekeeping loci (the allelic profile or ST). The ST can be compared with the STs of other strains using the program BURST which is located on the MLST website ([www.saureus.mlst.net](http://www.saureus.mlst.net)). As there are many alleles for each loci, isolates are highly unlikely to have identical ST by chance, and therefore isolates with the same ST or STs that differ at no more than two alleles are considered to belong to the same clonal complex (CC) and be members of the same clone. Isolates that are found to have a one or two housekeeping gene(s) that have not previously been reported may be referred to as single (slv) or double locus variants (dlv) of a previously described sequence type (eg ST30slv).

#### Staphylococcal Cassette Chromosome *mec* (*SCCmec*)

The gene for methicillin resistance, *mecA*, is contained within a mobile element known as the *mec* region or staphylococcal cassette chromosome *mec* (*SCCmec*). The *SCCmecs* differ depending on variations in the *mecA* regulatory region (*mec* complex), the type of cassette chromosome recombinases (*ccr* genes), and the resistance determinants they have acquired due to the integration of plasmids and transposons.

Eleven *SCCmec* types have been identified globally. Types I [1B], II [2A], III [3A] and VI [4B] are associated with “health-care-associated MRSA” (HA-MRSA) while Types IV [2B], V [5C2], VII [5C1], VIII [4A], IX [1C2], X [7C1] and XI [8E] are normally associated with “community associated MRSA” (CA-MRSA).

In this report MRSA are classified as either “healthcare-associated MRSA (HA-MRSA) clones” or “community-associated MRSA (CA-MRSA) clones” and are assigned an MLST/*SCCmec* type. The previous nomenclature that was applied to HA-MRSA and CA-MRSA clones is also reported. HA-MRSA clones are also known as Epidemic MRSA (EMRSA) clones, however with the epidemic properties of several CA-MRSA clones, the term HA-MRSA is used in this report.

### **3.7. Panton-Valentine Leucocidin (PVL) Toxin**

CA-MRSA clones have been shown to acquire several virulence genes including the determinants for PVL (2). PVL is a necrotizing toxin that causes leucocyte destruction and tissue necrosis and is associated with abscesses and severe pneumonia. It is present in the majority of CA-MRSA studied in Europe and USA (3). In Australia, it was initially reported that CA-MRSA infrequently carried the genes encoding PVL (4). However, two CA-MRSA clones now frequently isolated in Australia are PVL positive; ST30-IV [2B] and ST93-IV [2B]. These clones were originally reported in Auckland, New Zealand and Queensland, Australia respectively. ST30-IV [2B] was first noted in Australia in 1997 in the Polynesian population living in the eastern Australian states and the Australian Capital Territory (5). ST93-IV [2B] was first identified as a cause of community-acquired infection in the Caucasian population in Ipswich, Queensland in 2000 (6). Both clones are now frequently isolated in most regions of Australia (7).

Several imported PVL-positive CA-MRSA clones have recently been identified in Australia including (8):

1. ST8-IV [2B] (USA300)
2. ST80-IV [2B] (European CA-MRSA)
3. ST59-V<sub>T</sub> [5C2&5] (Taiwan CA-MRSA)
4. ST1-IV [2B] (USA400)

PVL genes have been shown to be transmitted by a temperate phage indicating that the PVL determinants are transferable (9). PVL-positive ST1-IV [2B] strains have been isolated in Queensland (10) and New South Wales (11), Australian states that have reported an increasing incidence of ST30-IV [2B] and ST93-IV [2B] (6,12,13). This may suggest that the PVL determinants are being transferred and raises the prospect that more CA-MRSA in Australia may become PVL positive in the future.

## 4. Methods

### 4.1. Epidemiological Typing Methods

#### Antibiogram

Participating laboratories performed antimicrobial susceptibility tests using the Vitek2® AST-P612 card (BioMerieux, Durham, NC). Antimicrobials tested were benzylpenicillin, oxacillin, cefoxitin, vancomycin, rifampicin, fusidic acid, gentamicin, erythromycin, clindamycin, tetracycline, trimethoprim/sulphamethoxazole (cotrimoxazole), ciprofloxacin, daptomycin, teicoplanin, linezolid, nitrofurantoin and mupirocin. Penicillin susceptible strains were tested for  $\beta$ -lactamase production using nitrocefin. High-level mupirocin resistance was determined by disc diffusion (200 ug disc, Oxoid).

#### Resistogram

Disk Diffusion (14,15)

mercuric chloride (HgCl<sub>2</sub>) (0.4  $\mu$ M)  
phenylmercuric acetate (PMA) (5 mM)

#### Urease

Christensen's Urea broth incubated for 24hrs at 37°C (16).

#### Coagulase Gene PCR-Restriction Fragment Length Polymorphisms (RFLP) Assay

Coagulase gene restriction fragment length polymorphism typing was performed as previously described (17).

#### Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)

Electrophoresis of chromosomal DNA was performed as previously described (18) using the CHEF DR III System (Bio-Rad Laboratories Pty Ltd). Chromosomal patterns were examined visually, scanned with a Quantity One® and digitally analysed using FPQuest™ software (Bio-Rad Laboratories). CHEF patterns were grouped according to the criteria of *Tenover et al.* (19) and using a dendrogram similarity of 80% or greater to assign strain relatedness. *S aureus* NCTC 8325 was used as the size marker.

#### Chromosomal DNA Preparation

Chromosomal DNA for MLST and SCC<sub>mec</sub> typing was prepared using the DNeasy Tissue kit (Qiagen Pty Ltd, Clifton Hill, Victoria, Australia 3068).

#### Multi Locus Sequence Typing (MLST)

MLST was performed on selected isolates as specified by *Enright et al.* (1). The sequences obtained were compared with the sequences at the MLST web site at <http://www.mlst.net/>, to assign a sequence type (ST). Using the MLST database, clones were subsequently grouped into clonal complexes.

### **Staphylococcal Chromosomal Cassette *mec* (SCC*mec*)**

The SCC*mec* was typed by PCR using previously published primers that identified the class of *mec* complex and type of cassette chromosome recombinase (*ccr*) encoded on the element (20,21,22)

SCC*mec* nomenclature is used as proposed by the International Working Group on the Classification of Staphylococcal Cassette Chromosome Elements (IWG-SCC) (23). Briefly, the structural type is indicated by a Roman numeral, with a lowercase letter indicating the subtype, and the *ccr* complex and the *mec* complex are indicated by an Arabic numeral and an uppercase letter respectively in parenthesis. Where there is an extra *ccr* element, this is indicated by “&” and an Arabic numeral designating the *ccr* type.

## **4.2. Identification of HA-MRSA Clones**

### **ST239-III [3A] (Aus-2/3 EMRSA)**

- Antibiogram
- Resistogram
- Urea broth
- CHEF
- Coagulase PCR-RFLP on selected isolates

### **ST22-IV [2B] (EMRSA-15)**

- Antibiogram
- Urea broth
- CHEF
- Coagulase PCR-RFLP on selected isolates

### **ST5-II [2A] (New York Japan MRSA/USA100)**

- Antibiogram
- Urea broth
- Coagulase PCR/RFLP
- CHEF
- Multilocus Sequence Typing
- SCC*mec* PCR

## **4.3. Identification of CA-MRSA Clones**

### **ST30-IV [2B] (Western Samoan Phage Pattern MRSA - WSPP MRSA)**

- Antibiogram
- Urea broth
- CHEF
- Coagulase PCR-RFLP on selected isolates

### **ST93-IV [2B] (Queensland MRSA)**

- Antibiogram
- Urea broth
- CHEF
- Coagulase PCR-RFLP on selected isolates

### **ST8-IV [2B] (USA300 MRSA)**

- Antibiogram
- Urea broth

CHEF

Coagulase PCR-RFLP on selected isolates

**ST59-V<sub>T</sub> [5C2&5] (Taiwan MRSA)**

Antibiogram

Urea broth

CHEF

Coagulase PCR-RFLP

**ST80-IV [2B] (European MRSA)**

Antibiogram

Urea broth

CHEF

Coagulase PCR-RFLP on selected isolates

**ST772-V [2B] (Bengal Bay MRSA)**

Antibiogram

Urea broth

CHEF

Coagulase PCR-RFLP on selected isolates

**“WA MRSA”**

ST1-IV [2B] (WA1)

ST78-IV [2B] (WA2)

ST5-IV [2B] (WA3)

ST8-IV [2B] (WA5)

ST75-IV [2B] (WA8)

ST59-IV [2B] (WA15)

ST45-IV [2B] (WA23)

ST188-IV [2B] (WA38)

ST72-IV [2B] (WA44)

ST6-IV [2B] (WA51)

ST73-IV [2B] (WA65)

ST6-IV [2B] (WA66)

ST5-IV [2B] (WA71)

ST1304-IV [2B] (WA72)

ST45-IV [2B] (WA75)

ST1303-IV [2B] (WA76)

ST188-IV [2B] (WA78)

ST207-V [5C2]

ST779-IV [2B]

Antibiogram

Urea broth

CHEF

Coagulase PCR-RFLP on selected isolates

**ST45-V [5C2&5] (WA-84)**

Antibiogram

Urea broth

CHEF

Coagulase PCR-RFLP on selected isolates

*SCCmec* PCR

ST5-V [5C2] (WA35)  
ST73-IV [2B] (WA95)  
ST72-V [5C2] (WA91)  
ST1-V [5C2]  
ST672-novel  
ST2149-IV [2B]

Antibiogram  
Coagulase PCR/RFLP  
CHEF  
Multilocus Sequence Typing  
*SCCmec* PCR

#### **4.4. Detection of Panton-Valentine Leucocidin (PVL) Toxin Genes**

The presence of the PVL determinants was detected by PCR using previously published primers (24).

## 5. Results

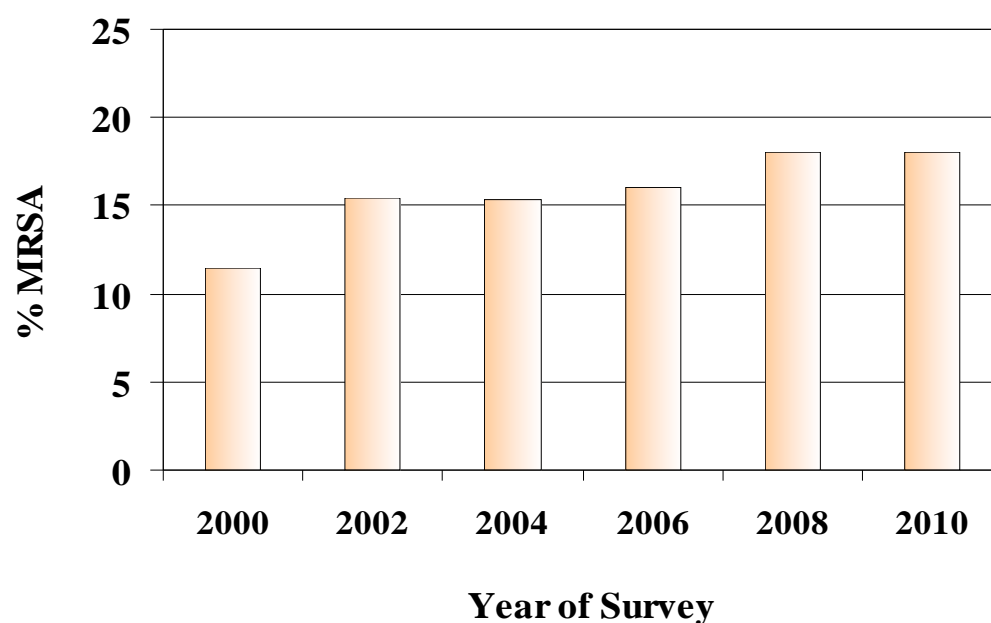
In SAP 2010, 539 (18.0%) *Staphylococcus aureus* were classified as MRSA.

### 5.1. AGAR Community Onset SAP 2000 – 2010

#### Percentage of *Staphylococcus aureus* Identified as MRSA

SAP	Laboratories (n)	<i>S aureus</i> (n)	MRSA (n)	MRSA (%)
2000	25	2,569	296	11.5
2002	24	2,486	384	15.4
2004	27	2,560	393	15.3
2006	30	2,979	476	16.0
2008	31	3,075	552	18.0
2010	30	2,994	539	18.0

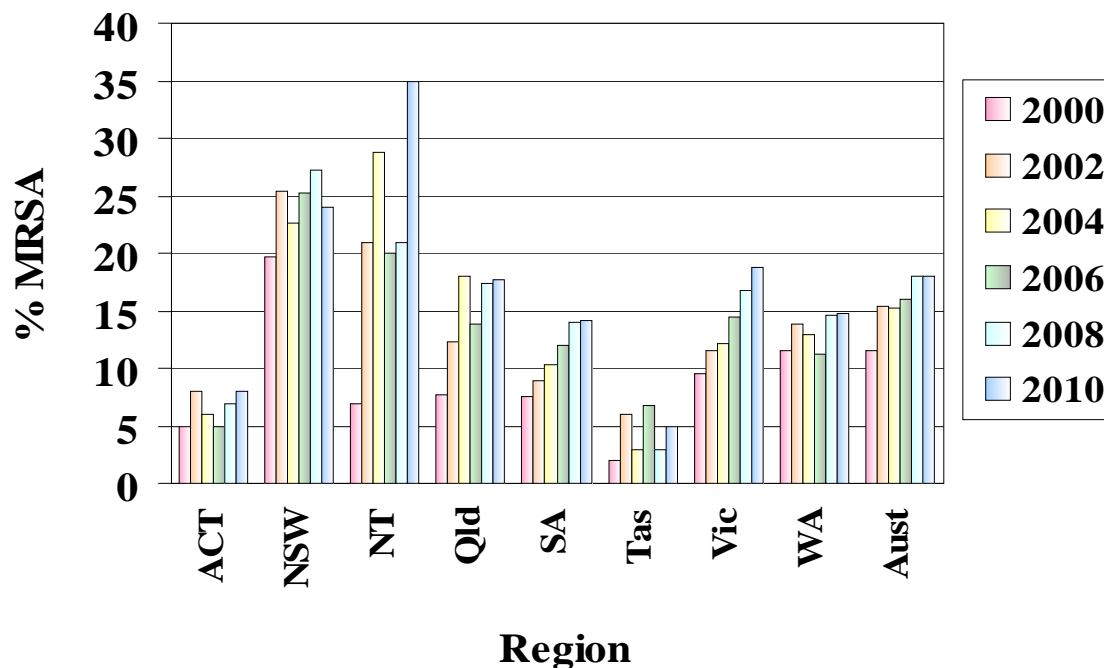
#### Percentage of *Staphylococcus aureus* Identified as MRSA



**Regional Distribution of MRSA**

Region	2000	2002	2004	2006	2008	2010
ACT	5 (5.0)	8 (8.0)	6 (6.0)	5 (5.0)	7 (7.0)	8 (8.0)
NSW	138 (19.7)	175 (25.4)	159 (22.6)	201 (25.3)	214 (27.2)	167 (24.0)
NT	7 (7.0)	21 (21.0)	17 (28.8)	20 (20.0)	21 (21.0)	35 (35.0)
Qld	23 (7.7)	37 (12.3)	54 (18.0)	69 (13.8)	104 (17.4)	106 (17.7)
SA	30 (7.5)	36 (9.0)	41 (10.3)	36 (12.0)	42 (14.0)	42 (14.1)
Tas	2 (2.0)	6 (6.0)	3 (3.0)	13 (6.8)	6 (3.0)	10 (5.0)
Vic	45 (9.6)	46 (11.5)	61 (12.12)	87 (14.5)	100 (16.8)	112 (18.7)
WA	46 (11.5)	55 (13.8)	52 (13.0)	45 (11.3)	58 (14.6)	59 (14.8)
<b>Total</b>	<b>296 (11.5)</b>	<b>384 (15.4)</b>	<b>393 (15.3)</b>	<b>476 (16.0)</b>	<b>553 (18.0)</b>	<b>539 (18.0)</b>

Figures in parenthesis are percentages of the total number of *Staphylococcus aureus* isolates



Percentage figures relate to the total number of *Staphylococcus aureus* isolates

## 5.2. SAP 2010 Epidemiological Typing of MRSA

Of the 539 MRSA identified in SAP 2010, 532 (98.7%) were referred to the Australian Collaborating Centre for *Enterococcus* and *Staphylococcus* Species ([ACCESS](#)) Typing and Research for epidemiological typing

### Typing Tests Performed

Test	Number
Cefoxitin Susceptibility Testing	532
Coagulase Gene PCR-RFLP Assay	72
Resistogram	77
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	532
Urease Reaction	532
Multi Locus Sequencing Typing (MLST)	8
SCC <i>mec</i> PCR	9
Panton-Valentine Leucocidin PCR	532

### Regional Distribution of HA-MRSA and CA-MRSA

Region	HA-MRSA (%)	CA-MRSA (%)	Total MRSA
ACT	3 (42.9)	4 (57.1)	7
NSW	82 (49.7)	83 (50.3)	165
NT	4 (12.1)	29 (87.9)	33
Qld	23 (21.7)	83 (78.3)	106
SA	9 (21.4)	33 (78.6)	42
Tas	4 (40.0)	6 (60.0)	10
Vic	49 (44.5)	61 (55.5)	110
WA	3 (5.1)	56 (94.9)	59
<b>TOTAL</b>	<b>177 (33.3)</b>	<b>355 (66.7)</b>	<b>532</b>

Figures in parenthesis are percentages of the total number of MRSA isolates

**SAP 2000 – 2010: Regional Distribution of HA-MRSA and CA-MRSA**

2000 (n = 279) <sup>a</sup>		2002 (n = 367) <sup>b</sup>		2004 (n = 383) <sup>c</sup>		2006 (n = 462) <sup>d</sup>		2008 (n=547) <sup>e</sup>		
Region	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)
ACT	0	5 (100)	5 (62.5)	3 (37.5)	3 (60.0)	2 (40.0)	2 (40.0)	3 (60.0)	2 (28.6)	5 (71.4)
NSW	89 (69.5)	39 (30.5)	120 (71.0)	49 (29.0)	101 (64.7)	55 (35.3)	108 (56.0)	85 (44.0)	105 (49.3)	108 (50.7)
NT	1 (14.3)	6 (85.7)	11 (52.4)	10 (47.6)	5 (29.4)	12 (70.6)	2 (10.0)	18 (90.0)	6 (28.6)	15 (71.4)
Qld	6 (26.1)	17 (73.9)	13 (39.4)	20 (60.6)	12 (23.5)	39 (76.5)	18 (27.3)	48 (72.7)	20 (19.4)	83 (80.6)
SA	12 (42.9)	16 (57.1)	11 (30.6)	25 (69.4)	15 (36.6)	26 (63.4)	9 (25.0)	27 (75.0)	7 (17.1)	34 (82.9)
Tas	0	2 (100)	1 (16.7)	5 (83.3)	1 (33.3)	2 (66.7)	10 (76.9)	3 (23.1)	4 (66.7)	2 (33.3)
Vic	32 (80.0)	8 (20.0)	34 (87.2)	5 (12.8)	50 (84.7)	9 (15.3)	46 (54.1)	39 (45.9)	56 (56.6)	43 (43.4)
WA	4 (8.7)	42 (91.3)	13 (23.6)	42 (76.4)	7 (13.4)	44 (86.3)	5 (11.4)	39 (88.6)	7 (12.3)	50 (87.8)
<b>TOTAL</b>	<b>144 (51.6)</b>	<b>135 (48.4)</b>	<b>208 (56.7)</b>	<b>159 (43.3)</b>	<b>194 (50.7)</b>	<b>189 (49.3)</b>	<b>200 (43.3)</b>	<b>262 (56.7)</b>	<b>207 (37.8)</b>	<b>340 (62.2)</b>

Percentage figures relate to the total number of MRSA isolates

<sup>a</sup>In SAP 2000, 279 of the 296 MRSA were fully characterized

<sup>b</sup>In SAP 2002, 367 of the 384 MRSA were fully characterized

<sup>c</sup>In SAP 2004, 383 of the 393 MRSA were fully characterized

<sup>d</sup>In SAP 2006, 462 of the 476 MRSA were fully characterized

<sup>e</sup>In SAP 2008, 547 of the 552 MRSA were fully characterized

**SAP 2000 – 2008: Regional Distribution of HA-MRSA and CA-MRSA cont**

<b>2010 (n = 532)<sup>f</sup></b>		
<b>Region</b>	<b>HA-MRSA (%)</b>	<b>CA-MRSA (%)</b>
<b>ACT</b>	<b>3 (42.9)</b>	<b>4 (57.1)</b>
<b>NSW</b>	<b>82 (49.7)</b>	<b>83 (50.3)</b>
<b>NT</b>	<b>4 (12.1)</b>	<b>29 (87.9)</b>
<b>Qld</b>	<b>23 (21.7)</b>	<b>83 (78.3)</b>
<b>SA</b>	<b>9 (21.4)</b>	<b>33 (78.6)</b>
<b>Tas</b>	<b>4 (40.0)</b>	<b>6 (60.0)</b>
<b>Vic</b>	<b>49 (44.5)</b>	<b>61 (55.5)</b>
<b>WA</b>	<b>3 (5.1)</b>	<b>56 (94.9)</b>
<b>TOTAL</b>	<b>177 (33.3)</b>	<b>355 (66.7)</b>

<sup>f</sup>In SAP 2010, 532 of the 539 MRSA were fully characterized

**SAP 2000 – 20010: Regional Distribution of HA-MRSA and CA-MRSA as a Proportion of *Staphylococcus aureus***

Region	2000			2002			2004		
	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)
ACT	100	0	5 (5.0)	100	5 (5.0)	3 (3.0)	100	3 (3.0)	2 (2.0)
NSW	700	89 (12.7)	39 (5.6)	689	120 (17.4)	49 (7.1)	703	101 (14.4)	55 (7.8)
NT	100	1 (1.0)	6 (6.0)	100	11 (11.0)	10 (10.0)	59	5 (8.5)	12 (20.3)
Qld	300	6 (2.0)	17 (5.7)	300	13 (4.3)	20 (6.7)	300	12 (4.0)	39 (13.0)
SA	400	12 (3.0)	16 (4.0)	400	11 (2.8)	25 (6.3)	399	15 (3.8)	26 (6.5)
Tas	100	0	2 (2.0)	100	1 (1.0)	5 (5.0)	99	1 (1.0)	2 (2.0)
Vic	469	32 (6.8)	8 (1.7)	399	34 (8.5)	5 (1.3)	500	50 (10.0)	9 (1.8)
WA	400	4 (1.0)	42 (10.5)	398	13 (3.3)	42 (10.6)	400	7 (1.8)	44 (11.0)
<b>TOTAL</b>	<b>2,569</b>	<b>144 (5.6)</b>	<b>135 (5.3)</b>	<b>2,486</b>	<b>208 (8.4)</b>	<b>159 (6.4)</b>	<b>2,560</b>	<b>194 (7.6)</b>	<b>189 (7.4)</b>

**SAP 2000 – 2010: Regional Distribution of HA-MRSA and CA-MRSA as a Proportion of *Staphylococcus aureus* cont**

Region	2006			2008			2010		
	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)
ACT	100	2 (2.0)	3 (3.0)	100	2 (2.0)	5 (5.0)	100	3 (3.0)	4 (4.0)
NSW	795	108 (13.6)	85 (10.7)	786	105 (13.4)	108 (13.7)	696	82 (11.8)	83 (11.9)
NT	100	2 (2.0)	18 (18.0)	100	6 (6.0)	15 (15.0)	100	4 (4.0)	29 (29.0)
Qld	500	18 (3.6)	48 (9.6)	598	20 (3.3)	83 (13.9)	600	23 (3.8)	83 (13.8)
SA	299	9 (3.0)	27 (9.0)	300	7 (2.3)	34 (11.3)	299	9 (3.0)	33 (11.0)
Tas	190	10 (5.3)	3 (1.6)	198	4 (2.0)	2 (1.0)	200	4 (2.0)	6 (3.0)
Vic	598	46 (7.7)	39 (6.5)	597	56 (9.4)	43 (7.2)	599	49 (8.2)	61 (10.2)
WA	397	5 (1.3)	39 (9.8)	396	7 (1.8)	50 (12.6)	400	3 (0.8)	56 (14.0)
<b>TOTAL</b>	<b>2,979</b>	<b>200 (6.7)</b>	<b>262 (8.8)</b>	<b>3,075</b>	<b>207 (6.7)</b>	<b>340 (11.1)</b>	<b>2,994</b>	<b>177 (5.9)</b>	<b>355 (11.6)</b>

**SAP 2010: HA-MRSA by AGAR Laboratory**

LAB	ST22-IV [2B] (EMRSA-15)	ST239-III [3A] (Aus2/3 EMRSA)	ST5-II [2A] (NY/Japan MRSA)	TOTAL
<b>ACT (3)</b>				
TCH	1	2		3
<b>NSW(82)</b>				
CRGH	5	4		9
DHM	7			7
LH	11	7		18
NH	9			9
RNSH	14	4		18
RPAH	5	3		8
WH	4	9		13
<b>NT (4)</b>				
RDH		4		4
<b>Qld (23)</b>				
CBH				0
GCH	2	7		9
PAH	1	3		4
PCH		6		6
RBH	1	1		2
SNP	1	1		2
<b>SA (9)</b>				
FMC	3			3
IMVS	4	1		5
WCH	1			1
<b>Tas (4)</b>				
LGH	4			4
RHH				0
<b>Vic (49)</b>				
AH	6	14		20
AUH	10	3		13
GP Vic		1		1
MMC	3	3		6
RCH		1	1	2
SVH	5	2		7
<b>WA (3)</b>				
FH				0
QEII	1			1
RPH	1			1
SJOG	1			1
<b>TOTAL</b>	<b>100</b>	<b>76</b>	<b>1</b>	<b>177</b>

**SAP 2010: CA-MRSA by AGAR Laboratory**

ST SCCmec	CC1					CC5							CC8			CC30	CC45		
	1 IV WA1	1 V	772 V Bengal Bay	188 IV WA38	188 IV WA78	5 IV WA3	5 IV WA71	5 V WA35	6 IV WA51	6 IV WA66	73 IV WA65	73 IV WA95	8 IV WA5	8 IV USA300	2149 IV	30 IV WSPP	45 IV WA23	45 IV WA75	45 V WA84
<b>ACT (4)</b>																			
TCH														1		1			
<b>NSW (83)</b>																			
CRGH																			
DHM	1									1				2					
LH	1			2	1								1	1		3			
NH	2	1													3		1	1	
RNSH	4																		
RPAH	2			1															
WH	2						1									1			
<b>NT (29)</b>																			
RDH	7										2					3			
<b>Qld (83)</b>																			
PCH										1						2			
RBH						1										5			
SNP											1					1			

SAP 2010: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

ST SCCmec	CC1					CC5							CC8			CC30	CC45		
	1 IV WA1	1 V	772 V Bengal Bay	188 IV WA38	188 IV WA78	5 IV WA3	5 IV WA71	5 V WA35	6 IV WA51	6 IV WA66	73 IV WA65	73 IV WA95	8 IV WA5	8 IV USA300	2149 IV	30 IV WSPP	45 IV WA23	45 IV WA75	45 V WA84
CBH						2					1					6			
GCH			1			1								1		4			2
PAH	1															6			
<b>SA (33)</b>																			
FMC	6															2		3	1
IMVS	1		1									1							
WCH	3					1					1	1							
<b>Tas (6)</b>																			
LGH						1													
RHH	1								1										
<b>Vic (61)</b>																			
AH	1		1	1												1			5
AUH						1													4
GP Vic																1	1		
MMC	2		1			2		1								4			9
RCH	1															1			
SVH	1													1	1				

SAP 2010: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

	CC1					CC5							CC8			CC30	CC45		
<b>ST SCCmec</b>	1 IV WA1	1 V	772 V Bengal Bay	188 IV WA38	188 IV WA78	5 IV WA3	5 IV WA71	5 V WA35	6 IV WA51	6 IV WA66	73 IV WA65	73 IV WA95	8 IV WA5	8 IV USA300	2149 IV	30 IV WSPP	45 IV WA23	45 IV WA75	45 V WA84
<b>WA (56)</b>																			
<b>FH</b>	9		1													1			
<b>QEII</b>	3					2					1					1			
<b>RPH</b>	3																	1	
<b>SJOG</b>	4																		
<b>Total</b>	<b>55</b>	<b>1</b>	<b>5</b>	<b>2</b>	<b>2</b>	<b>12</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>7</b>	<b>2</b>	<b>1</b>	<b>6</b>	<b>1</b>	<b>46</b>	<b>1</b>	<b>5</b>	<b>22</b>

## SAP 2010: CA-MRSA by AGAR Laboratory cont

ST SCCmec	CC59		CC72		CC75		CC80	CC88	CC509	CC672	Singleton	Undetermined		TOTAL
	59 IV WA15	59 V Taiwan	72 IV WA44	72 V WA91	75 IV WA8	1304 IV WA72	80 IV European	78 IV WA2	207 V	672 novel	93 IV Qld	1303 IV WA76	779 IV WA100	
<b>ACT (4)</b>														
TCH											2			4
<b>NSW (83)</b>														
CRGH											3			3
DHM							1		1		3			9
LH							1				10			20
NH	1										14			23
RNSH											2			6
RPAH											5			8
WH		1									9			14
<b>NT (29)</b>														
RDH						1					16			29
<b>Qld (83)</b>														
PCH											5			8
RBH								2			12		1	21
SNP											10			12

SAP 2010: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

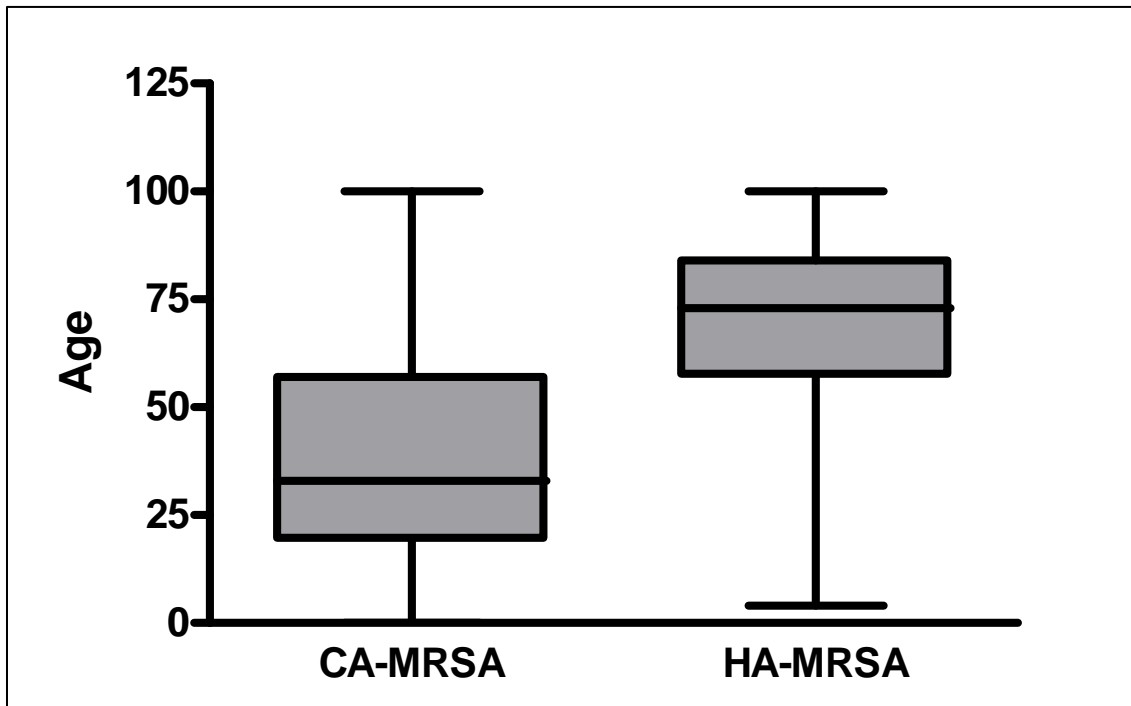
ST SCCmec	CC59		CC72		CC75		CC80	CC88	CC509	CC672	Singleton	Undetermined		TOTAL
	59 IV WA15	59 V Taiwan	72 IV WA44	72 V WA91	75 IV WA8	1304 IV WA72	80 IV European	78 IV WA2	207 V	672 novel	93 IV Qld	1303 IV WA76	779 IV WA100	
<b>CBH</b>	1				1	1						5		17
<b>GCH</b>												3		12
<b>PAH</b>												6		13
<b>SA (33)</b>														
<b>FMC</b>							1	1				1		15
<b>IMVS</b>								2		1		4		10
<b>WCH</b>												1	1	8
<b>Tas (6)</b>														
<b>LGH</b>												2		3
<b>RHH</b>												1		3
<b>Vic (61)</b>														
<b>AH</b>												5		14
<b>AUH</b>			1	1								2		9
<b>GP Vic</b>		1										5		8
<b>MMC</b>								1				1		21
<b>RCH</b>								1						3
<b>SVH</b>												3		6

SAP 2010: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

	CC59		CC72		CC75		CC80	CC88	CC509	CC672	Singleton	Undetermined		TOTAL
ST SCCmec	59 IV WA15	59 V Taiwan	72 IV WA44	72 V WA91	75 IV WA8	1304 IV WA72	80 IV European	78 IV WA2	207 V	672 novel	93 IV Qld	1303 IV WA76	779 IV WA100	
<b>WA (56)</b>														
FH		1										3		15
QEII							1	2				3		13
RPH								5				10		19
SJOG		1						3				1		9
<b>Total</b>	<b>2</b>	<b>4</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>2</b>	<b>4</b>	<b>17</b>	<b>1</b>	<b>1</b>	<b>147</b>	<b>1</b>	<b>1</b>	<b>355</b>

Age statistics for Clone Type

Boxplot of age of patients infected with CA-MRSA and HA-MRSA clones

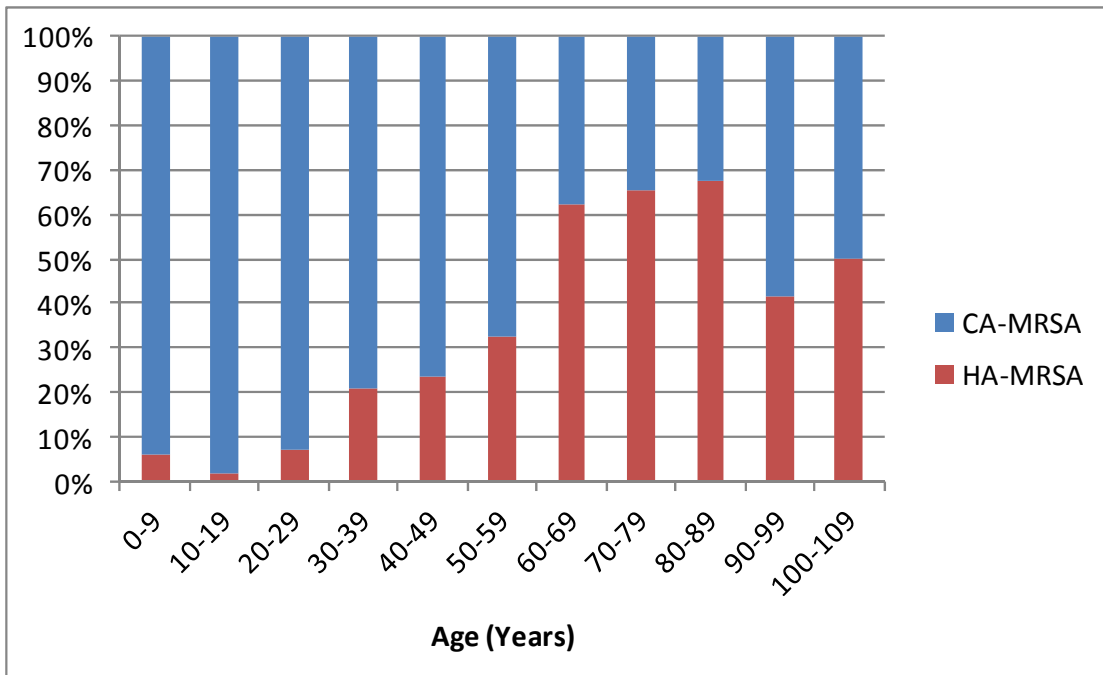


Mean, median and percentile data

Age (years)	CA-MRSA	HA-MRSA
Mean (95% Confidence Interval [CI])	39.0 (36.4 – 41.7)	68.5 (65.6 – 71.3)
Median	33	73
25 <sup>th</sup> percentile	19	57
75 <sup>th</sup> percentile	57	84

The mean age of patients with CA-MRSA is significantly lower ( $P < 0.0001$ ) than the mean age of patients with HA-MRSA.

**MRSA Acquisition (CA- or HA-MRSA) by decade of life**



### 5.3. HA-MRSA

Certain strains of MRSA are known to spread easily between and within hospitals and are designated healthcare-associated MRSA (HA-MRSA) [previously known as epidemic MRSA (EMRSA)].

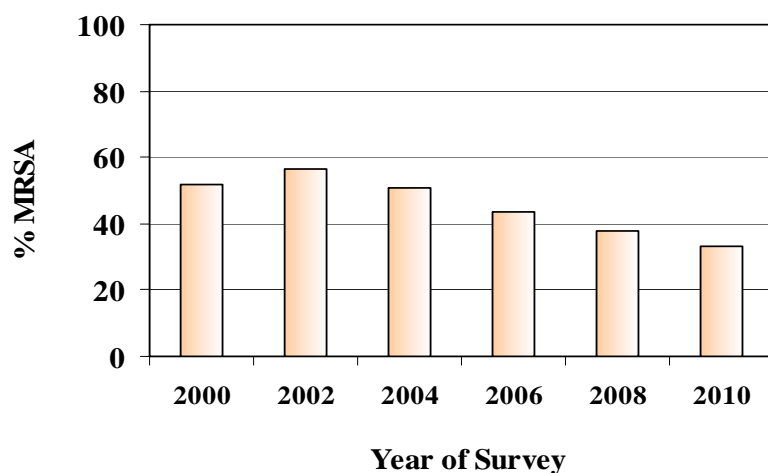
#### SAP 2010 HA-MRSA

In SAP 2010 three international HA-MRSA clones (177 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST22-IV [4B]	EMRSA-15	100 (56.5)
ST239-III [3A]	Aus -2/3 EMRSA/ EA-EMRSA	76 (42.9)
ST5-II [2A]	New York Japan MRSA/USA100	1 (0.6)
<b>TOTAL</b>		<b>177</b>

Percentage figures relate to HA- MRSA isolates

#### SAP 2000 – 2010: Percentage of MRSA Identified as HA-MRSA



### ST22-IV [2B]

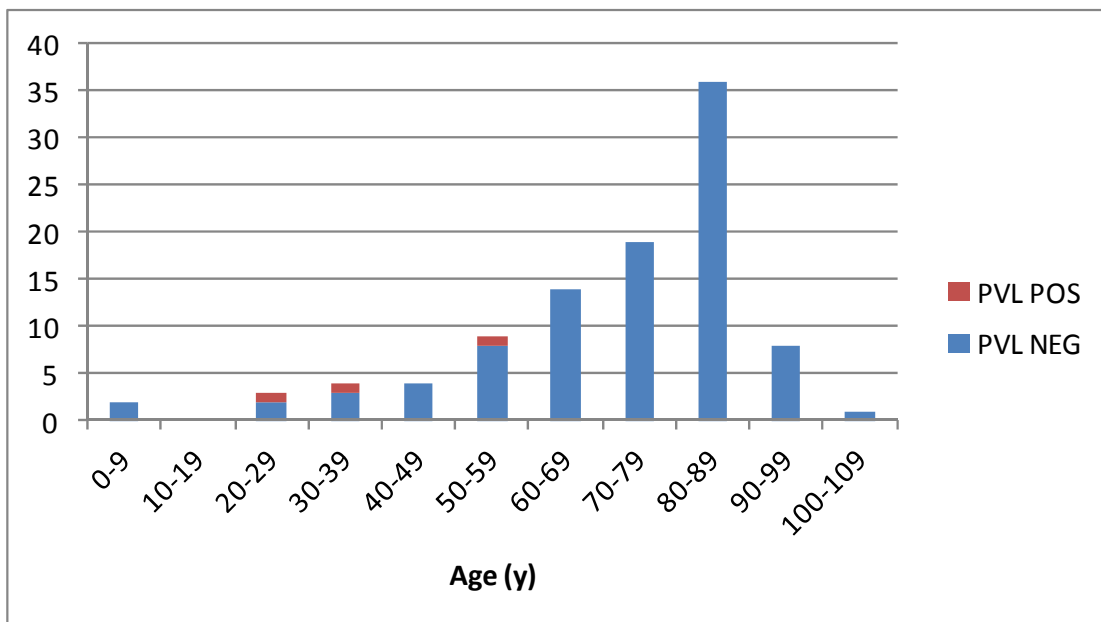
Also known as “EMRSA-15” or the “German Barnim” strain, ST22-IV [2B] has become a major EMRSA clone in many parts of the world including Australia, United Kingdom, New Zealand, several European countries and recently Singapore. First identified in the Midlands and South-East England in the early 1990s EMRSA-15 is non-multiresistant (typically resistant to ciprofloxacin and erythromycin only) and is staphylococcal enterotoxin C, G and I positive. In New Zealand and Australia, ST22-IV [2B] is frequently isolated from patients in long term care facilities and is associated with pre-employment screening of health staff from the United Kingdom.

### Phenotypic Characteristics

Antibiogram:	Ciprofloxacin <sup>R</sup>	99%
	Erythromycin <sup>R</sup>	54%
	Fusidic Acid <sup>R</sup>	2%
	Rifampicin <sup>R</sup>	2%
	Gentamicin <sup>R</sup>	1%
	Cotrimoxazole <sup>R</sup>	1%
	Tetracycline <sup>R</sup>	0%
	High Level Mupirocin <sup>R</sup>	0%

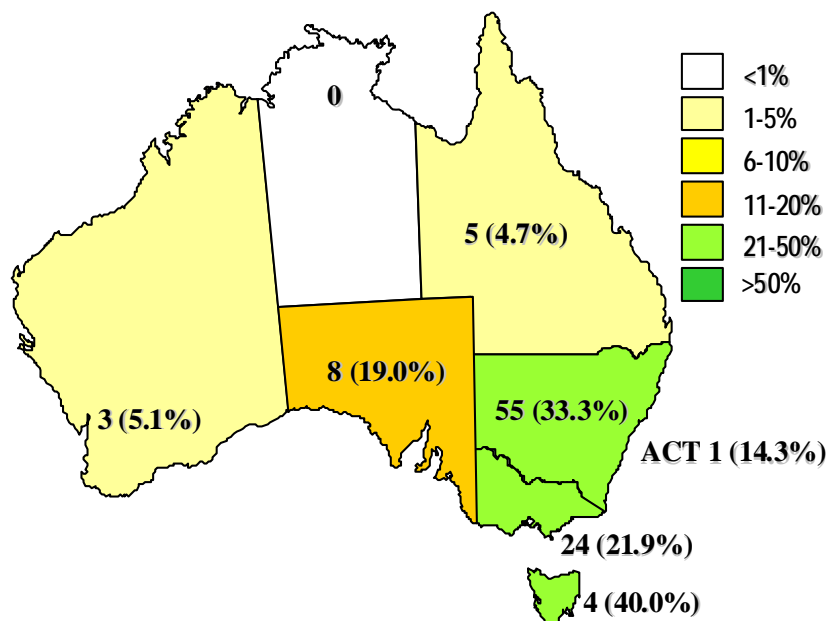
Urease: Negative

### Patients Infected with ST22-IV [2B] by Decade of Life



**Regional distribution of ST22-IV [2B]**

**ST22-IV [2B] (EMRSA-15): n =100 (18.8%)**



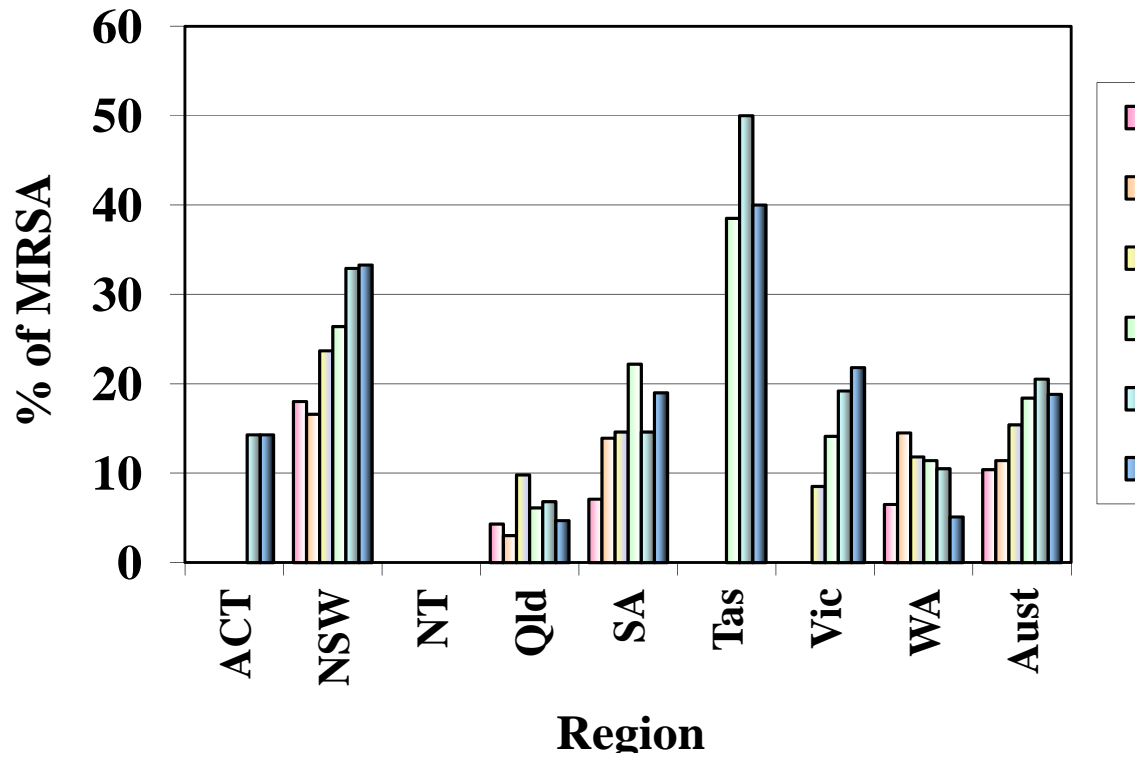
Percentage figures relate to total MRSA isolates characterized

**SAP 2000 – 2010: Regional Distribution of ST22-IV [2B]**

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010
ACT	0	0	0	0	1 (14.3)	1 (14.3)
NSW	23 (18.0)	28 (16.6)	37 (23.7)	51 (26.4)	70 (32.9)	55 (33.3)
NT	0	0	0	0	0	0
Qld	1 (4.3)	1 (3.0)	5 (9.8)	4 (6.1)	7 (6.8)	5 (4.7)
SA	2 (7.1)	5 (13.9)	6 (14.6)	8 (22.2)	6 (14.6)	8 (19.0)
Tas	0	0	0	5 (38.5)	3 (50)	4 (40.0)
Vic	0	0	5 (8.5)	12 (14.1)	19 (19.2)	24 (21.8)
WA	3 (6.5)	8 (14.5)	6 (11.8)	5 (11.4)	6 (10.5)	3 (5.1)
<b>Total</b>	<b>29 (10.4)</b>	<b>42 (11.4)</b>	<b>59 (15.4)</b>	<b>85 (18.4)</b>	<b>112 (20.5)</b>	<b>100 (18.8)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

**SAP 2000 – 2010: Regional Distribution of ST22-IV [2B]**



Percentage figures relate to total MRSA isolates characterized

### ST239-III [3A]

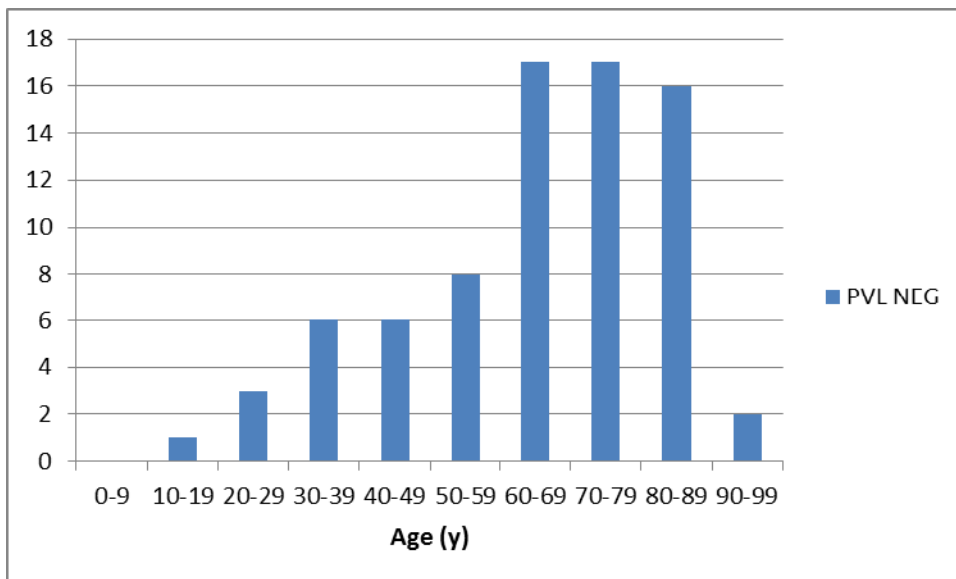
In Australia ST239-III [3A] evolved from the “Eastern Australian EMRSA” clone described in the 1980s. ST239-III [3A] is one of the most commonly encountered and internationally disseminated multidrug-resistant HA-MRSA clones. It is also known as “Aus2/3 EMRSA”, “EMRSA-1”, “Portuguese/Brazilian” clone or the “Vienna” clone.

### Phenotypic Characteristics

Antibiogram:

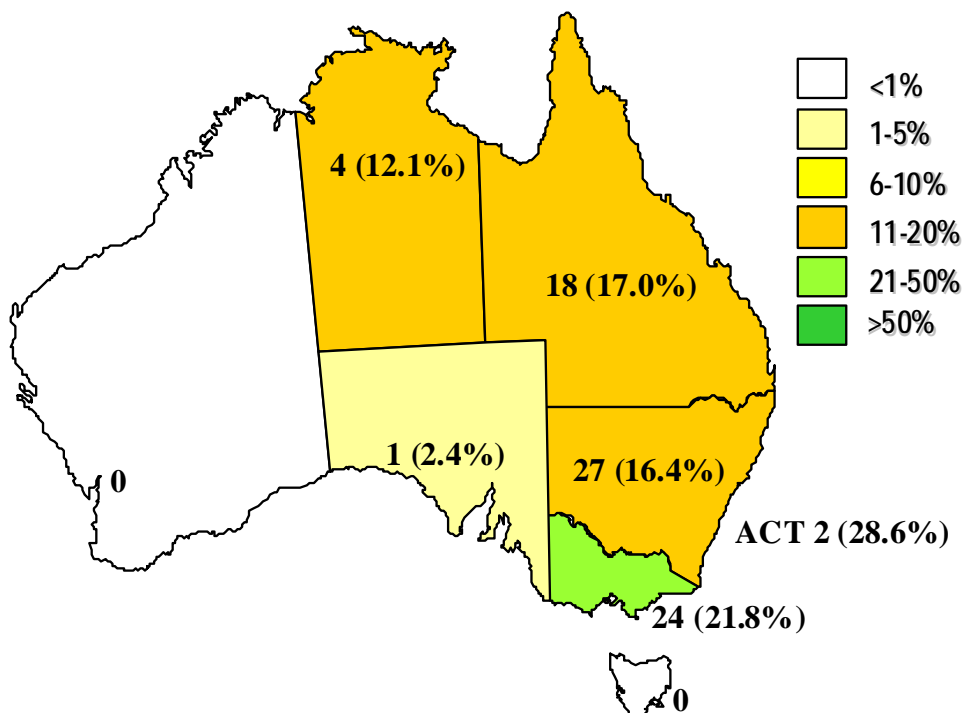
Erythromycin <sup>R</sup>	100%
Tetracycline <sup>R</sup>	100%
Cotrimoxazole <sup>R</sup>	99%
Ciprofloxacin <sup>R</sup>	97%
Gentamicin <sup>R</sup>	97%
Rifampicin <sup>R</sup>	5%
Fusidic Acid <sup>R</sup>	4%
High Level Mupirocin <sup>R</sup>	0%

### Patients Infected with ST239-III [3A] by Decade of Life



**Regional Distribution of ST239-III [3A]**

**ST239-III [3A]: n = 76 (14.3%)**



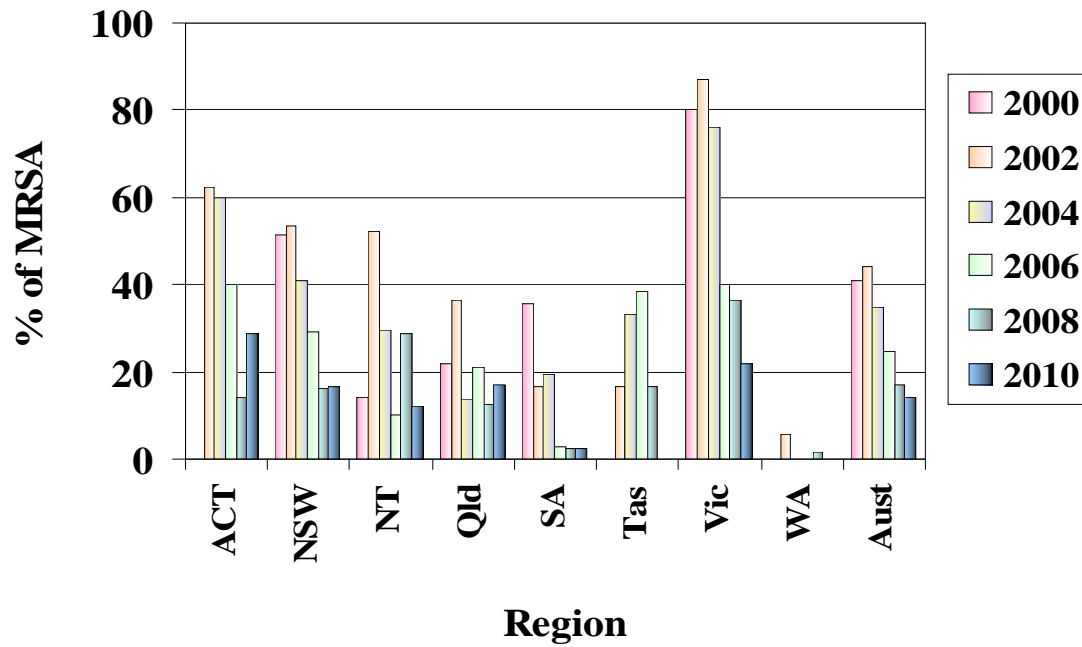
Percentage figures relate to total MRSA isolates characterized

**SAP 2000 – 2010: Regional Distribution of ST239-III [3A]**

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP2010
ACT	0	5 (62.5)	3 (60)	2 (40.0)	1 (14.3)	2 (28.6)
NSW	66 (51.6)	90 (53.3)	64 (41.0)	56 (29.0)	34 (16.0)	27 (16.4)
NT	1 (14.3)	11 (52.4)	5 (29.4)	2 (10.0)	6 (28.6)	4 (12.1)
Qld	5 (21.7)	12 (36.4)	7 (13.7)	14 (21.2)	13 (12.6)	18 (17.0)
SA	10 (35.7)	6 (16.7)	8 (19.5)	1 (2.8)	1 (2.4)	1 (2.4)
Tas	0	1 (16.7)	1 (33.3)	5 (38.5)	1 (16.7)	0
Vic	32 (80.0)	34 (87.2)	45 (76.3)	34 (40.0)	36 (36.4)	24 (21.8)
WA	0	3 (5.5)	0	0	1 (1.8)	0
<b>Total</b>	<b>114 (40.9)</b>	<b>162 (44.1)</b>	<b>133 (34.7)</b>	<b>114 (24.7)</b>	<b>93 (17.0)</b>	<b>76 (14.3)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

**SAP 2000 – 2010: Regional Distribution of ST239-III [3A]**



Percentage figures relate to total MRSA isolates characterized

**ST5-II [2A]**

The original hVISA, ST5-GISA-II, is thought to have evolved from the New York Japan MRSA/USA100 clone.

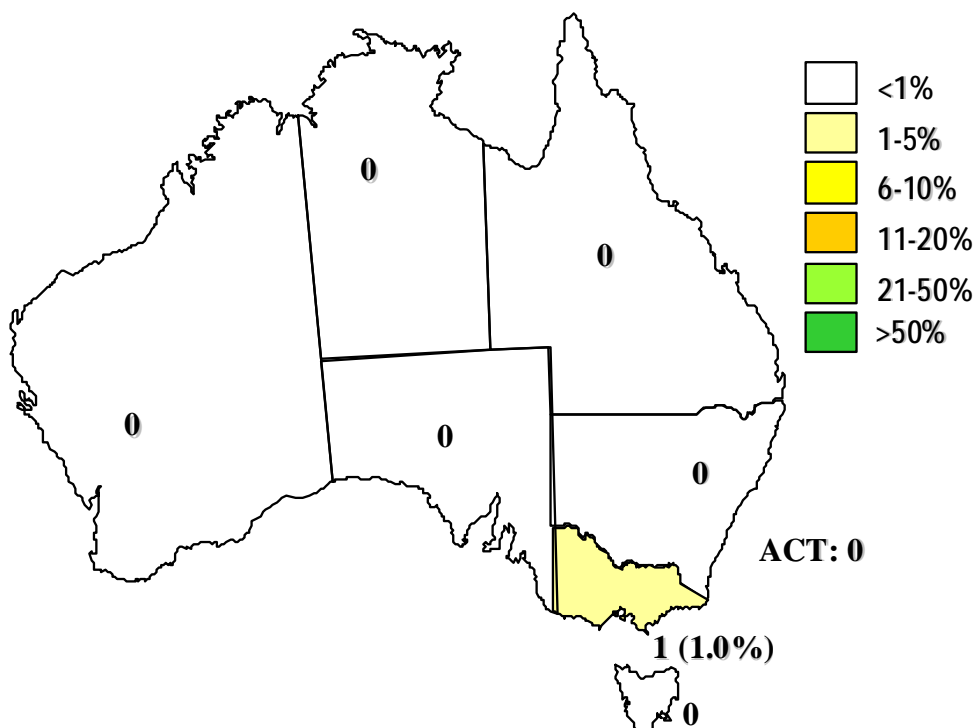
**Phenotypic Characteristics**

Antibiogram:	Erythromycin <sup>R</sup>	100%
	Ciprofloxacin <sup>R</sup>	100%
	Tetracycline <sup>R</sup>	100%
	Cotrimoxazole <sup>R</sup>	0%
	Gentamicin <sup>R</sup>	0%
	Rifampicin <sup>R</sup>	0%
	Fusidic Acid <sup>R</sup>	0%
	High Level Mupirocin <sup>R</sup>	0%

Urease: Positive

**Epidemiology**

**ST5-II [2A] (New York Japan MRSA/USA100): n = 1 (0.2%)**



Percentage figures relate to total MRSA isolates characterized

### Summary of Community onset HA-MRSA clones Isolated in AGAR SAPs 2000 – 2010

Clone	Alternative Name	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP2010
ST22-IV	EMRSA-15	290 (20.1)	42 (20.2)	59 (30.4)	85 (42.5)	112 (54.1)	100 (56.5)
ST239-III	Aus-2, -3 EMRSA	114 (79.2)	162 (77.9)	133 (68.6)	114 (57.0)	93 (44.9)	76 (42.9)
ST5-II	New York/Japan/USA100	0	0	0	1 <sup>e</sup> (0.5)	1 <sup>f</sup> (0.5)	1 <sup>h</sup> (0.6)
ST36-II	EMRSA-16/USA200	0	1 <sup>b</sup> (0.5)	2 <sup>d</sup> (1.0)	0	1 <sup>g</sup> (0.5)	0
ST8-II	Irish-1 EMRSA	0	3 <sup>c</sup> (1.4)	0	0	0	0
ST8-VI	Irish-2 EMRSA	1 <sup>a</sup> (0.7)	0	0	0	0	0
<b>Total</b>		<b>144</b>	<b>208</b>	<b>194</b>	<b>200</b>	<b>207</b>	<b>177</b>

Percentage figures in parenthesis relate to the healthcare associated MRSA isolates

<sup>a</sup>Isolated in WA

<sup>b</sup>Isolated in WA

<sup>c</sup>Isolated in NSW (n=2) and WA (n=1)

<sup>d</sup>Isolated in SA (n=1) and WA (n=1)

<sup>e</sup>Isolated in NSW

<sup>f</sup>Isolated in Vic

<sup>g</sup>Isolated in NSW

<sup>h</sup>Isolated in Vic

## 5.4. CA-MRSA

CA-MRSA was first reported in Australia in the early 1980s in aboriginal communities living in the Kimberley region of Western Australia (WA). Known collectively as “WA MRSA” they were subsequently isolated in other remote communities in WA, South Australia and Northern Territory. These strains are usually susceptible to most non- $\beta$ -lactams antibiotics. “WA MRSA” has acquired the community associated *SCCmec* types IV and V, which lack transposons, integrated plasmids and other antibiotic resistance genes. Although they have been introduced into teaching hospitals they rarely cause outbreaks. In the 1990s, non-multiresistant MRSA were isolated on the eastern seaboard in suburban/regional areas of south-east Queensland, Sydney and Canberra (5). They were frequently isolated in people of Pacific Island descent and were subsequently identified as “Western Samoan Phage Pattern MRSA” (WSPP MRSA). WSPP MRSA has previously been reported in New Zealand and several Pacific islands. In 2000, a non-multiresistant MRSA was identified as a cause of community acquired infection in the Caucasian population living in Ipswich Queensland and was subsequently identified as “Queensland MRSA” (6). Although both strains initially caused skin infections they have now been associated with serious invasive disease and have been shown to be PVL positive.

### SAP 2010 CA-MRSA

In SAP 2010, 32 CA-MRSA pulsotypes (27 MLST/*SCCmec* clone types) were identified:

Clone	CC	Alternative Name	n (% of CA-MRSA)
ST93-IV	Singleton	Queensland CA-MRSA	147 (41.4%)
ST1-IV	1	WA MRSA -1	55 (15.5%)
ST30-IV	30	WSPP MRSA	46 (13.0%)
ST45-V	45	WA MRSA-84	22 (6.2%)
ST78-IV	88	WA MRSA-2	17 (4.8%)
ST5-IV	5	WA MRSA-3	12 (3.4%)
ST73-IV	5	WA MRSA-65	7 (2.0%)
ST8-IV	8	USA 300	6 (1.7%)
ST45-IV	45	WA MRSA-75	5 (1.4%)
ST772-V	1	Bengal Bay MRSA	5 (1.4%)
ST80-IV	80	European MRSA	4 (1.1%)
ST59-V <sub>T</sub>	59	Taiwan MRSA	4 (1.1%)
ST1304-IV	75	WA MRSA-72	2 (0.6%)
ST188-IV	1	WA MRSA-78	2 (0.6%)
ST59-IV	59	WA MRSA-15	2 (0.6%)
ST188-IV	1	WA MRSA-38	2 (0.6%)
ST73-IV	5	WA MRSA- 95	2 (0.6%)
ST72-V	72	WA MRSA-91	1 (0.3%)

## SAP 2010: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

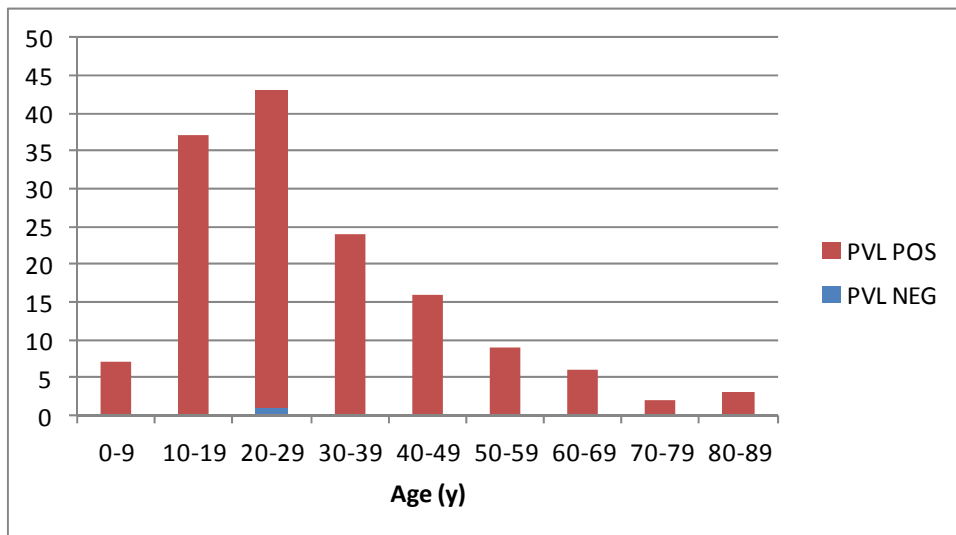
Clone	CC	Alternative Name	n (% of CA-MRSA)
ST1303-IV	Undetermined	WA MRSA-76	1 (0.3%)
ST672-novel	672		1 (0.3%)
ST5-V	5	WA MRSA-35	1 (0.3%)
ST75-IV	75	WA MRSA-8	1 (0.3%)
ST2149-IV	8		1 (0.3%)
ST72-IV	72	WA MRSA-44	1 (0.3%)
ST8-IV	8	WA MRSA-5	1 (0.3%)
ST1-V	1		1 (0.3%)
ST6-IV	5	WA MRSA-51	1 (0.3%)
ST207-V	509		1 (0.3%)
ST779-IV	Undetermined	WA MRSA-100	1 (0.3%)
ST6-IV	5	WA MRSA-66	1 (0.3%)
ST5-IV	5	WA MRSA-71	1 (0.3%)
ST45-IV	45	WA MRSA-23	1 (0.3%)
<b>Total</b>			<b>355</b>

### Major CA-MRSA Clones

#### ST93-IV [2B]

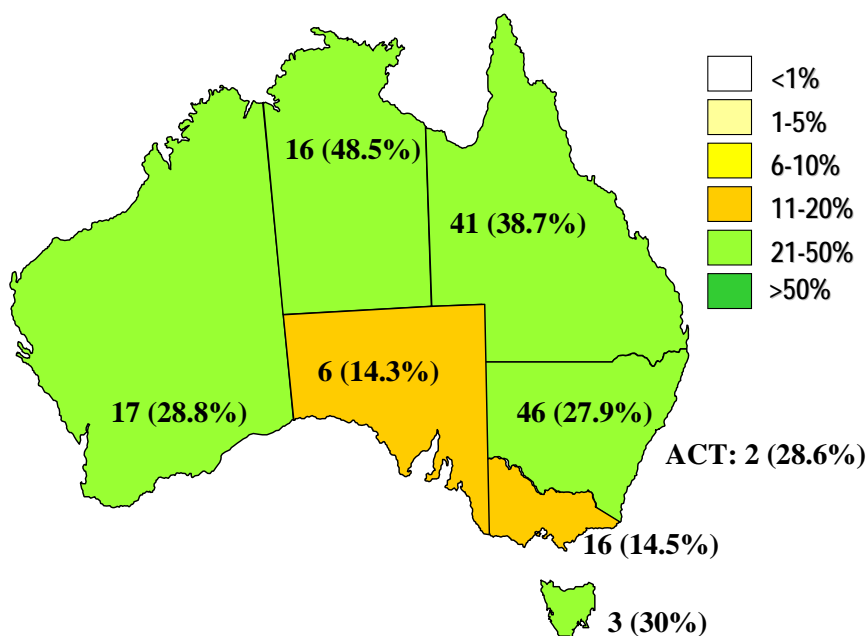
Also known as the “Queensland MRSA” clone, ST93-IV [2B] is a singleton (ie does not form part of a clonal complex) and is PVL positive.

#### Patients Infected with ST93-IV [2B] (Queensland MRSA) by Decade of Life



#### Regional Distribution of ST93-IV [2B]

ST93-IV [2B] (Queensland MRSA): n = 147 (27.6%)



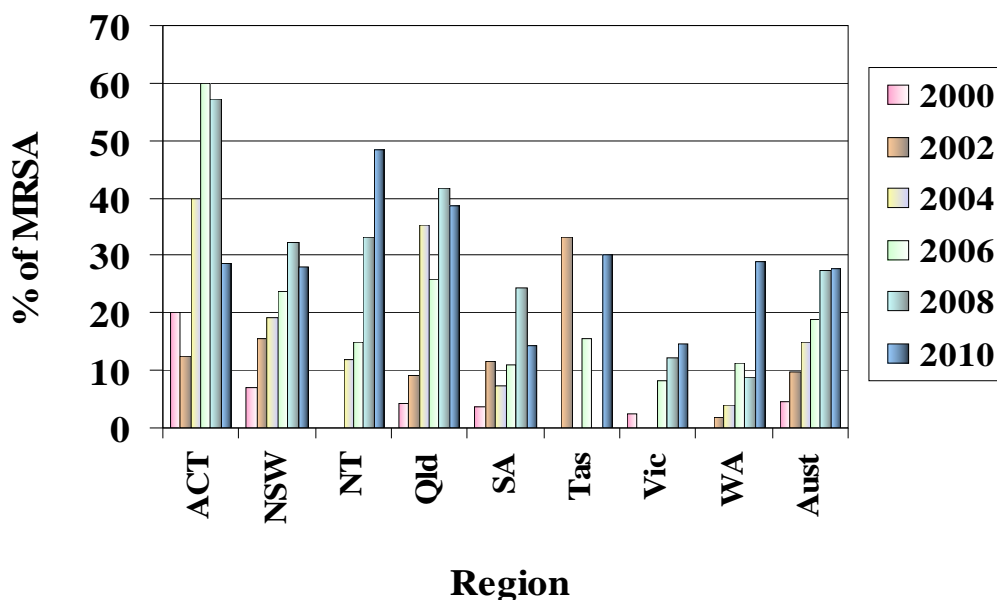
Percentage figures relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST93-IV [2B]**

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP2010
ACT	1 (20.0)	1 (12.5)	2 (40.0)	3 (60.0)	4 (57.1)	2 (28.6)
NSW	9 (7.0)	26 (15.4)	30 (19.2)	46 (23.8)	69 (32.4)	46 (27.9)
NT	0	0	2 (11.8)	3 (15.0)	7 (33.3)	16 (48.5)
Qld	1 (4.3)	3 (9.0)	18 (35.3)	17 (25.8)	43 (41.7)	41 (38.7)
SA	1 (3.6)	3 (11.5)	3 (7.3)	4 (11.1)	10 (24.4)	6 (14.3)
Tas	0	2 (33.3)	0	2 (15.4)	0	3 (30.0)
Vic	1 (2.5)	0	0	7 (8.2)	12 (12.1)	16 (14.5)
WA	0	1 (1.8)	2 (3.9)	5 (11.4)	5 (8.8)	17 (28.8)
<b>Total</b>	<b>13 (4.7)</b>	<b>36 (9.8)</b>	<b>57 (14.9)</b>	<b>87 (18.8)</b>	<b>150 (27.4)</b>	<b>147 (27.6)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST93-IV [2B]**

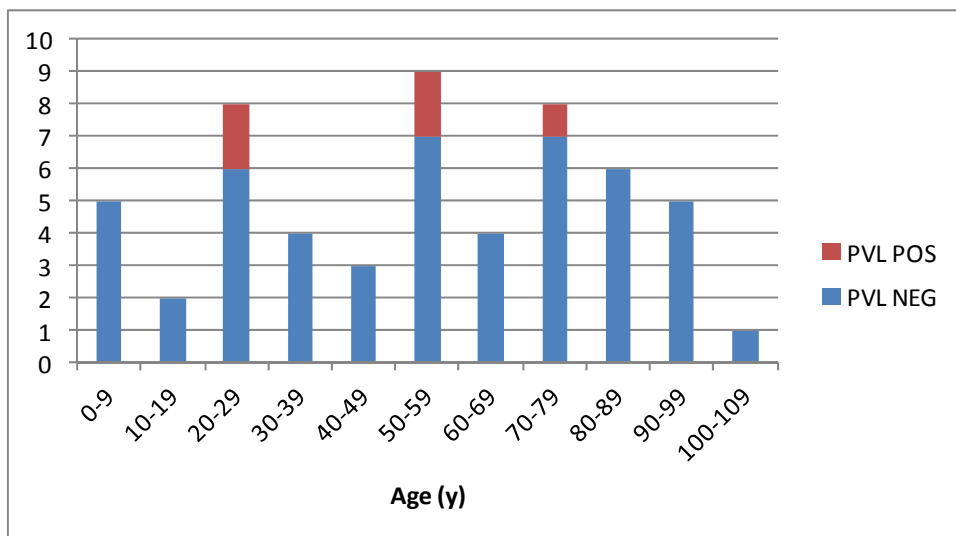


Percentage figures relate to total MRSA isolates characterized

### ST1-IV [2B]

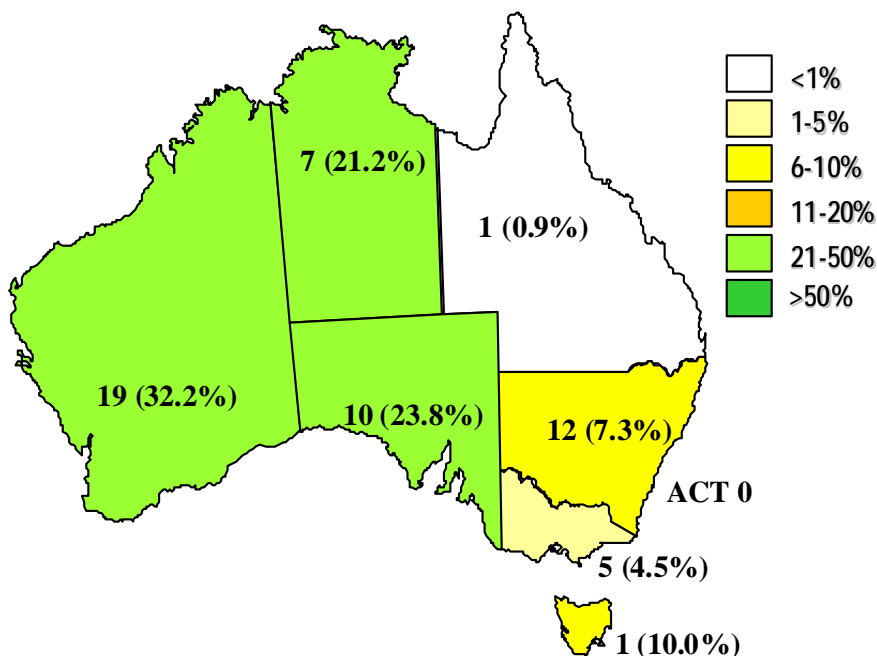
Also known as “WA MRSA-1”, ST1-IV forms part of clonal complex 1. Although normally PVL-negative, PVL-positive “USA400” MRSA-like strains have been identified in Australia.

### Patients Infected with ST1-IV [2B] by Decade of Life



### Regional Distribution of ST1-IV [2B]

**ST1-IV [2B] (WA MRSA-1): n = 55 (10.3%)**



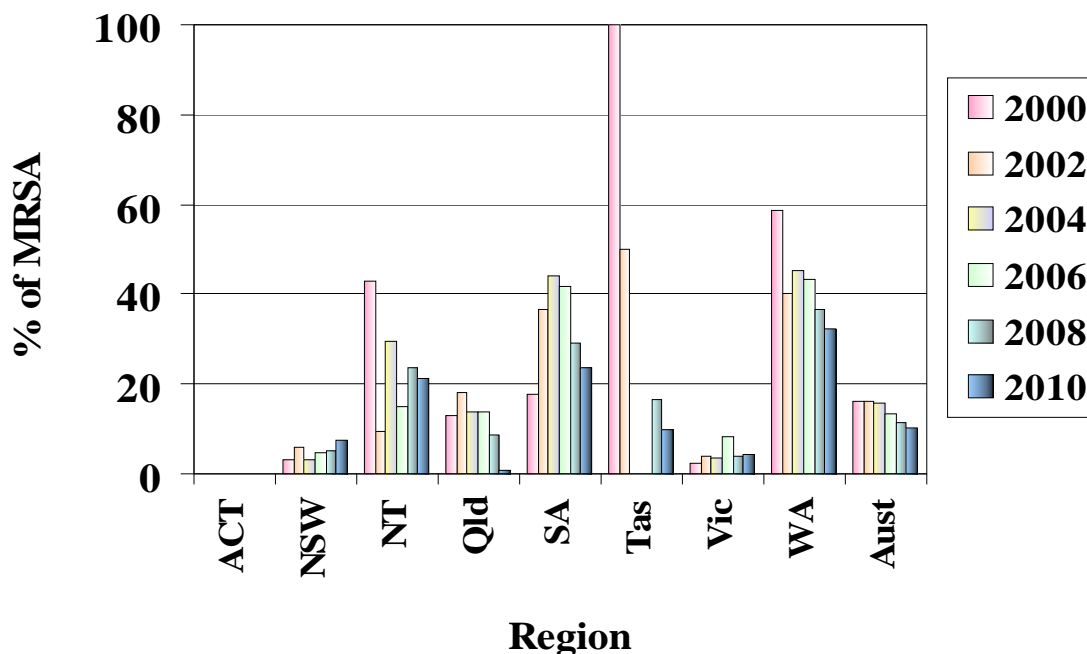
Percentage figures relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST1-IV [2B]**

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010
ACT	0	0	0	0	0	0
NSW	4 (3.1)	10 (5.9)	5 (3.2)	9 (4.7)	11 (5.2)	12 (7.3)
NT	3 (42.9)	2 (9.5)	5 (29.4)	3 (15.0)	5 (23.8)	7 (21.2)
Qld	3 (13.0)	6 (18.2)	7 (13.7)	9 (13.6)	9 (8.7)	1 (0.9)
SA	5 (17.90)	14 (36.8)	18 (43.9)	15 (41.7)	12 (29.3)	10 (23.8)
Tas	2 (100)	3 (50.0)	0	0	1 (16.7)	1 (10)
Vic	1 (2.5)	2 (3.8)	2 (3.4)	7 (8.2)	4 (4.0)	5 (4.5)
WA	27 (58.7)	22 (40)	23 (45.1)	19 (43.2)	21 (36.8)	19 (32.2)
<b>Total</b>	<b>45 (16.1)</b>	<b>59 (16.1)</b>	<b>60 (15.7)</b>	<b>62 (13.4)</b>	<b>63 (11.5)</b>	<b>55 (10.3)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST1-IV [2B]**

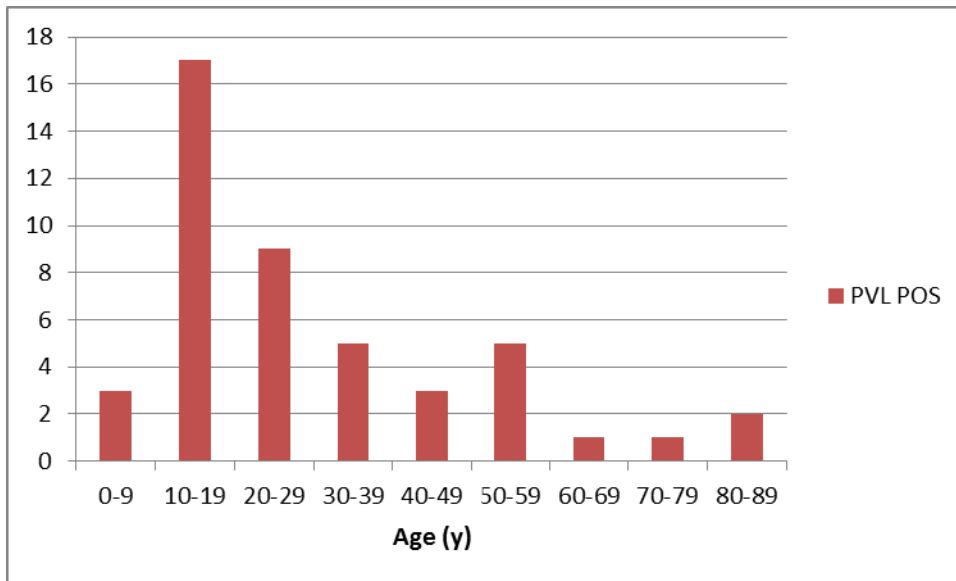


Percentage figures relate to total MRSA isolates characterized

**ST30-IV [2B]**

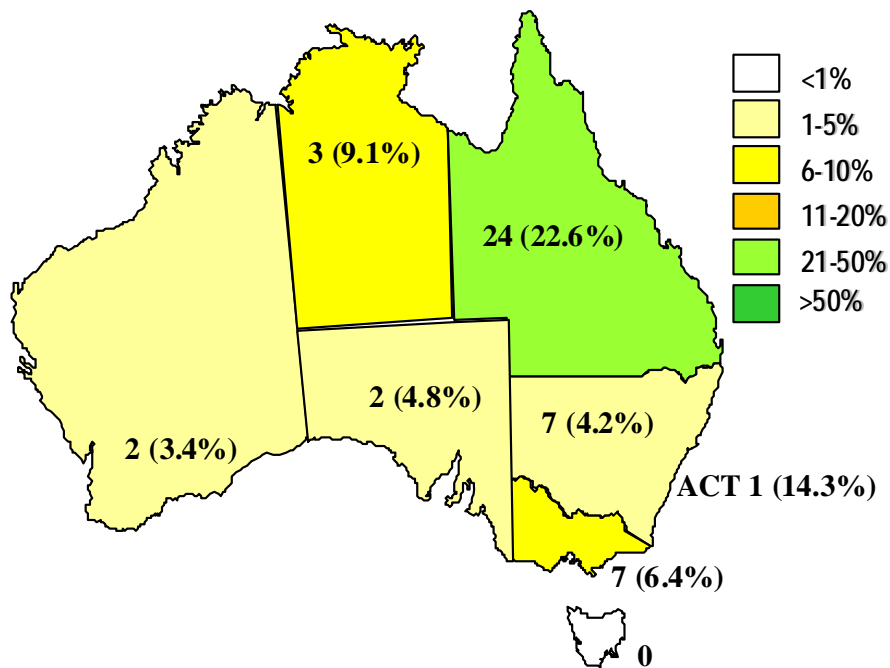
Also known as “WSPP MRSA”, ST30-IV [2B] was originally described in Polynesians living in New Zealand and the Pacific islands and is PVL positive.

**Patients Infected with ST30-IV [2B] by Decade of Life**



**Regional Distribution of ST30-IV [2B]**

**ST30-IV [2B] (WSPP MRSA): n = 46 (8.6%)**



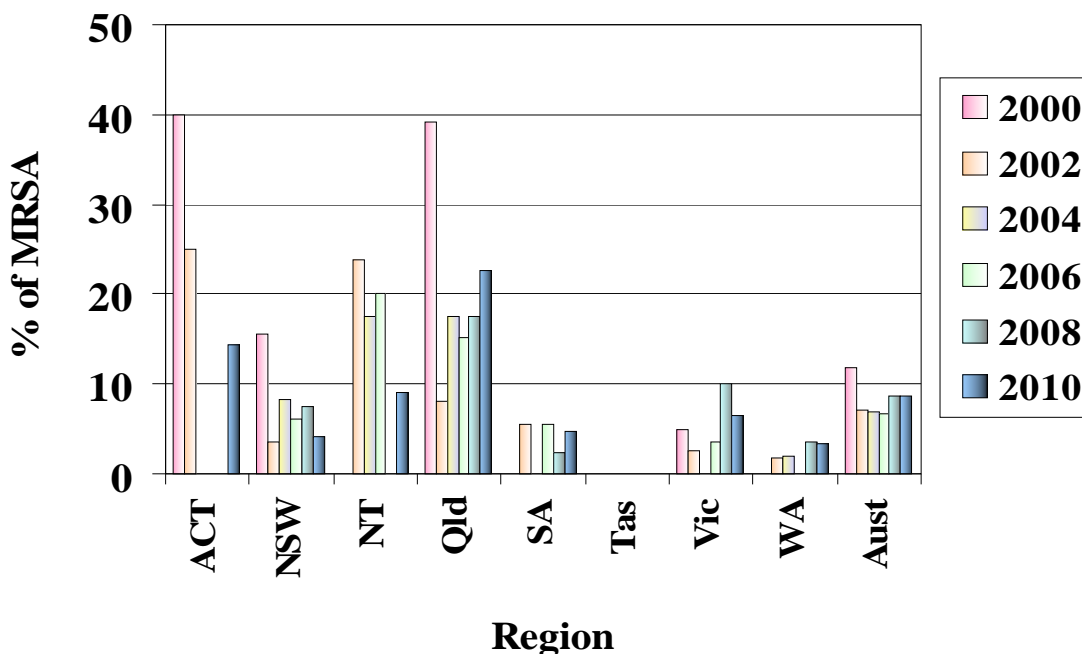
Percentage figures relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST30-IV [2B]**

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010
ACT	2 (40.0)	2 (25.0)	0	0	0	1 (14.3)
NSW	20 (15.6)	6 (3.6)	13 (8.3)	12 (6.2)	16 (7.5)	7 (4.2)
NT	0	5 (23.8)	3 (17.6)	4 (20.0)	0	3 (9.1)
Qld	9 (39.1)	9 (8.0)	9 (17.6)	10 (15.2)	18 (17.5)	24 (22.6)
SA	0	2 (5.6)	0	2 (5.6)	1 (2.4)	2 (4.8)
Tas	0	0	0	0	0	0
Vic	2 (5.0)	1 (2.6)	0	3 (3.5)	10 (10.1)	7 (6.4)
WA	0	1 (1.8)	1 (2.0)	0	2 (3.5)	2 (3.4)
<b>Total</b>	<b>33 (11.8)</b>	<b>26 (7.1)</b>	<b>26 (6.8)</b>	<b>31 (6.7)</b>	<b>47 (8.6)</b>	<b>46 (8.6)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST30-IV [2B]**

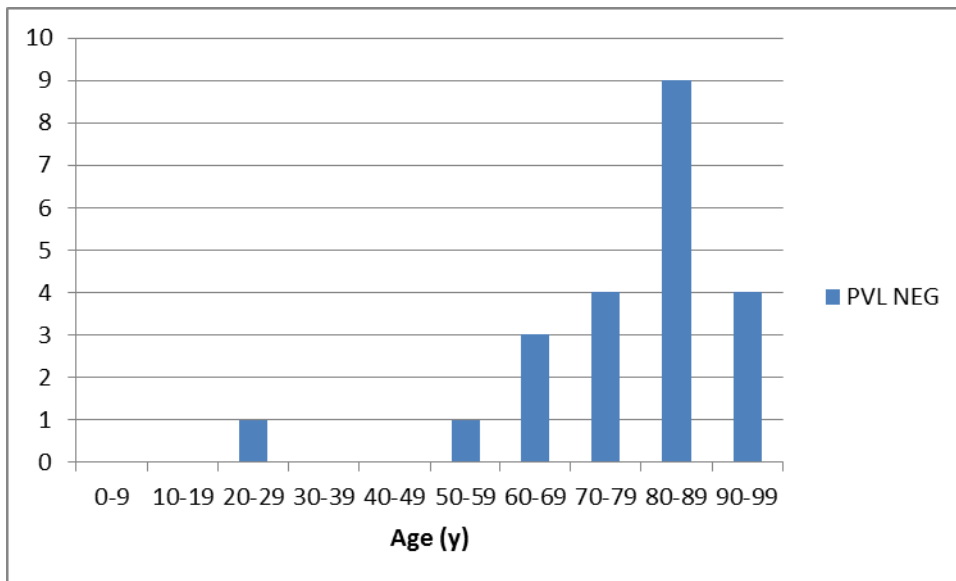


Percentage figures relate to total MRSA isolates characterized

**ST45-V [5C2&5]**

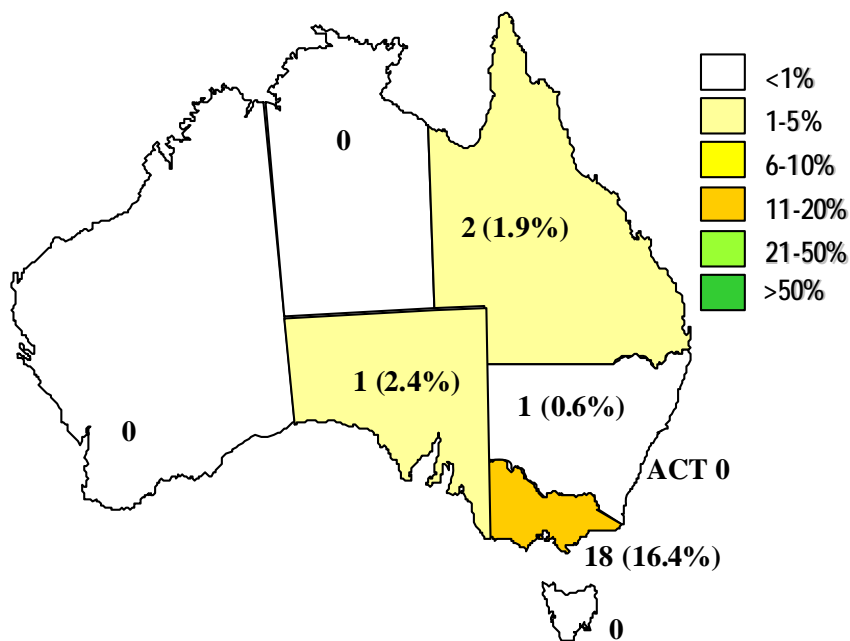
Also known as “WA MRSA-84” and is typically PVL negative

**Patients Infected with ST45-V [5C2&5] by Decade of Life**



**Regional Distribution of ST45-V [5C2&5]**

**ST45-V [5C2&5] (WA MRSA-84): n = 22 (4.1%)**



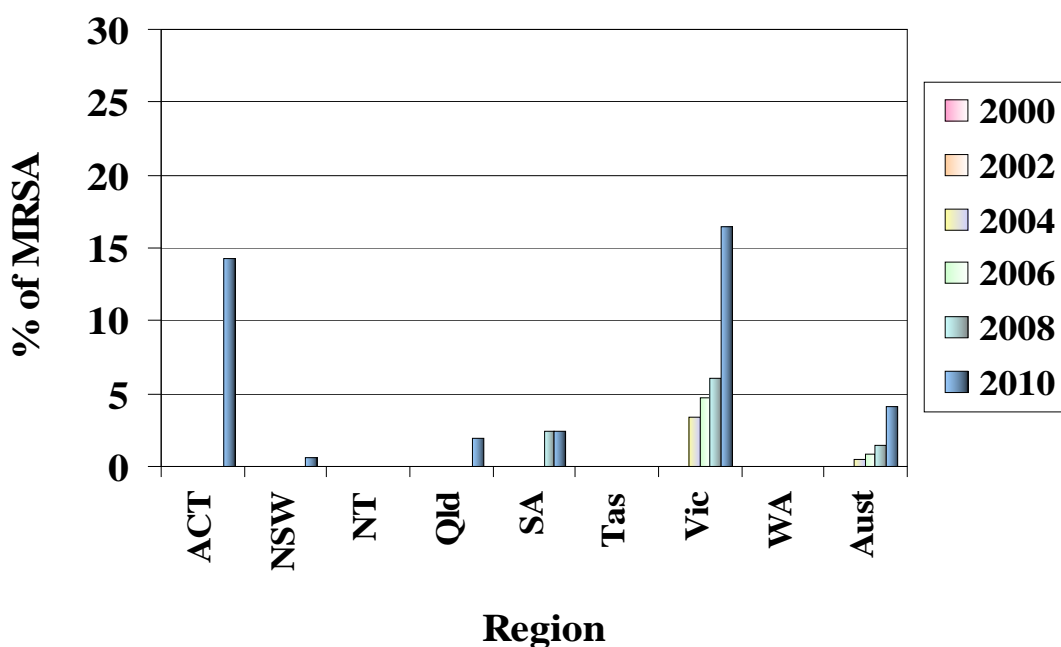
Percentage figures relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST45-V [5C2&5]**

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP2010
ACT	0	0	0	0	1 (14.3)	0
NSW	0	0	0	0	0	1 (0.6)
NT	0	0	0	0	0	0
Qld	0	0	0	0	0	2 (1.9)
SA	0	0	0	0	1 (2.4)	1 (2.4)
Tas	0	0	0	0	0	0
Vic	0	0	2 (3.4)	4 (4.7)	6 (6.1)	18 (16.4)
WA	0	0	0	0	0	0
<b>Total</b>	<b>0</b>	<b>0</b>	<b>2 (0.5)</b>	<b>4 (0.9)</b>	<b>8 (1.5)</b>	<b>22 (4.1)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST45-V [5C2&5]**

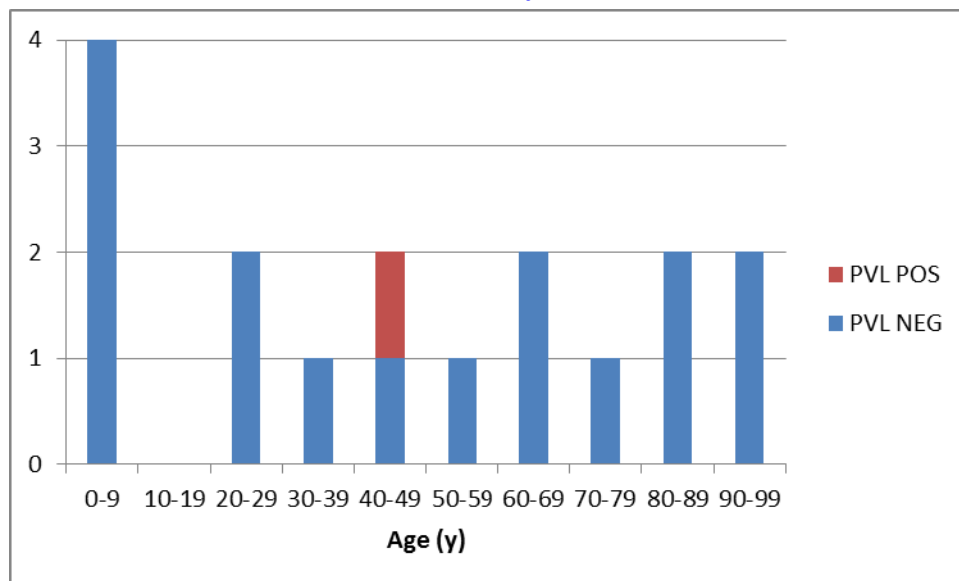


Percentage figures relate to total MRSA isolates characterized

**ST78- IV [2B]**

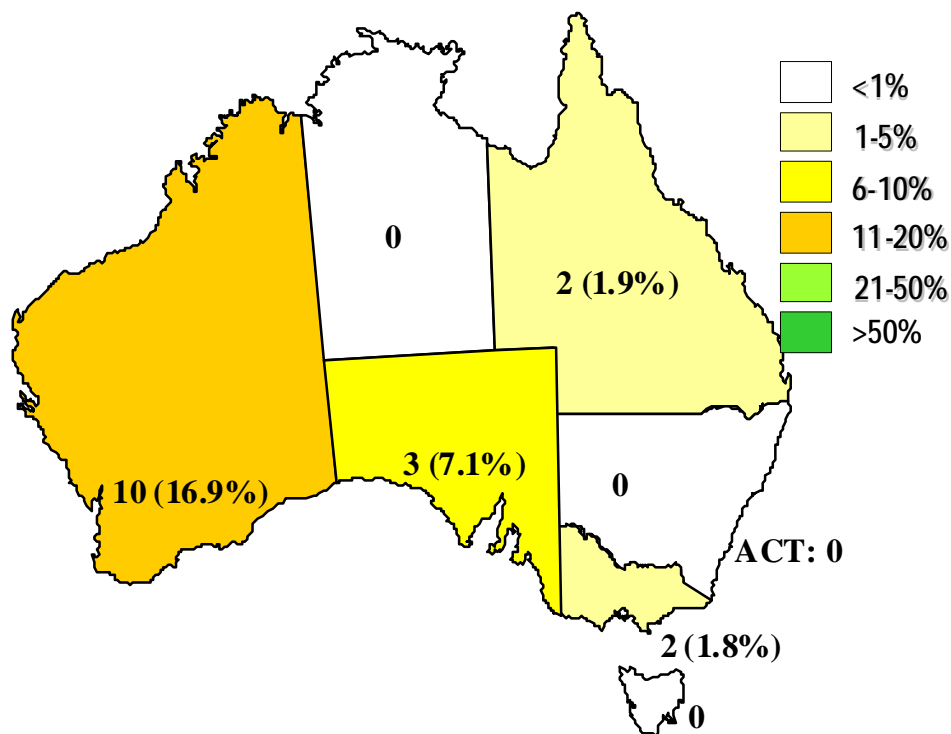
Also known as “WA MRSA-2” and is typically PVL negative

**Patients Infected with ST78-IV [2B] by Decade of Life**



**Regional Distribution of ST78-IV [2B]**

**ST78-IV [2B] (WA MRSA-2): n = 17 (3.2%)**



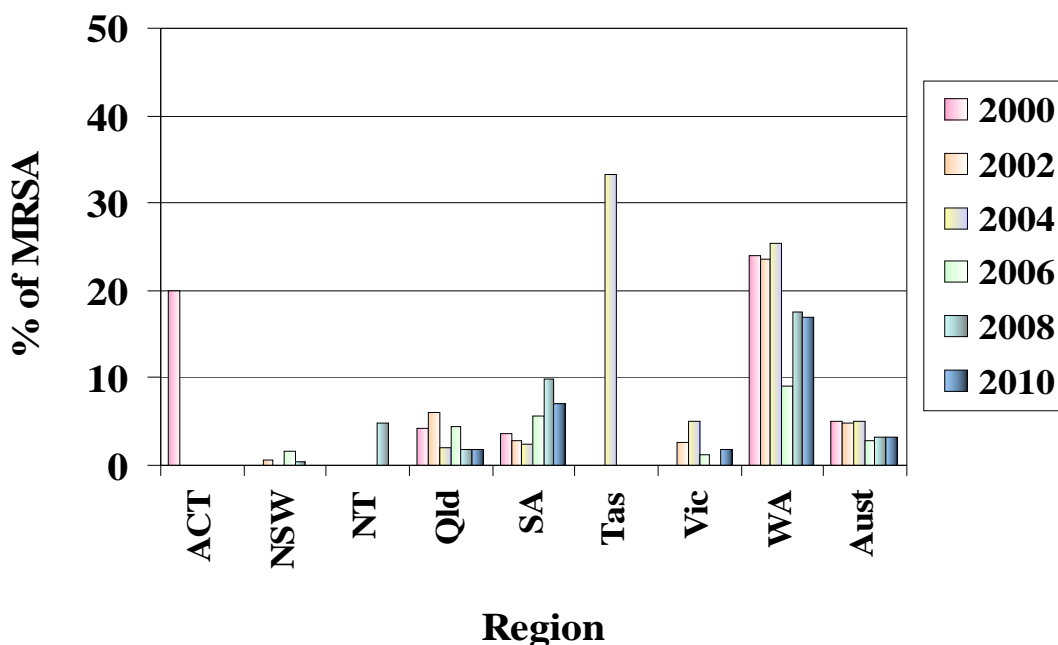
Percentage figures relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST78-IV [2B]**

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP2010
ACT	1 (20.0)	0	0	0	0	0
NSW	0	1 (0.6)	0	3 (1.6)	1 (0.5)	0
NT	0	0	0	0	1 (4.8)	0
Qld	1 (4.3)	2 (6.1)	1 (2.0)	3 (4.5)	2 (1.9)	2 (1.9)
SA	1 (3.6)	1 (2.8)	1 (2.4)	2 (5.6)	4 (9.8)	3 (7.1)
Tas	0	0	1 (33.3)	0	0	0
Vic	0	1 (2.6)	3 (5.1)	1 (1.2)	0	2 (1.8)
WA	11 (23.9)	13 (23.6)	13 (25.5)	4 (9.1)	10 (17.5)	10 (16.9)
<b>Total</b>	<b>14 (5.0)</b>	<b>18 (4.9)</b>	<b>19 (4.8)</b>	<b>13 (2.8)</b>	<b>18 (3.3)</b>	<b>17 (3.2)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

**SAP 2000 to SAP 2010 Regional Distribution of ST78-IV [2B]**

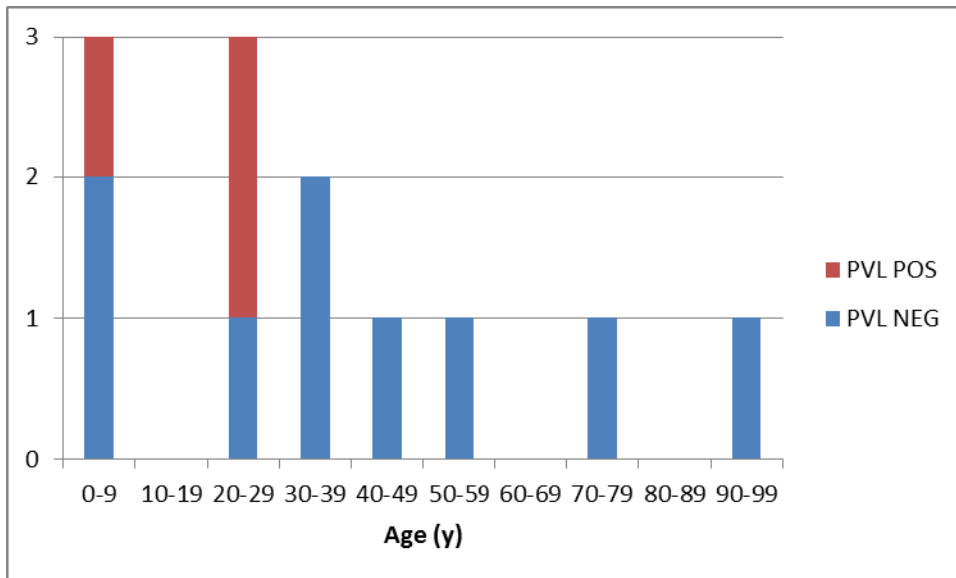


Percentage figures relate to total MRSA isolates characterized

**ST5-IV [2B]**

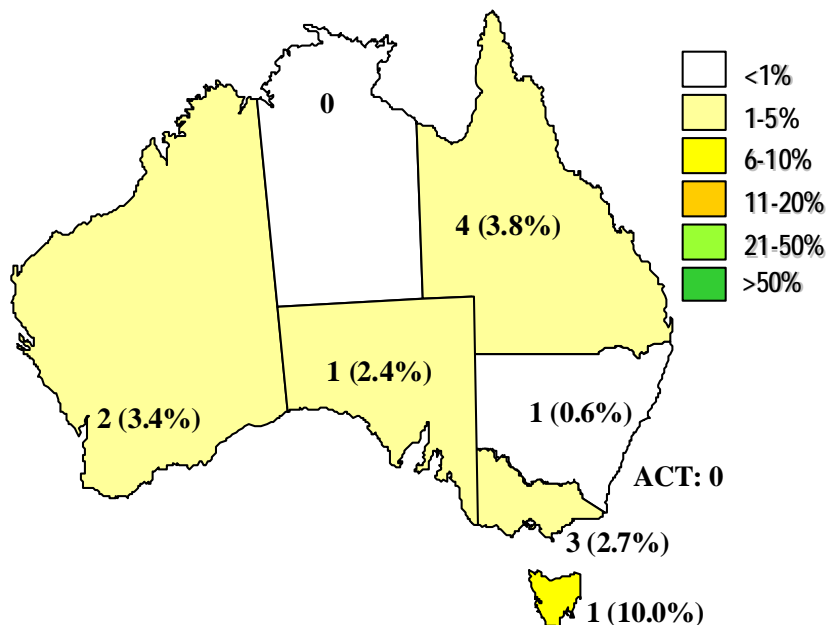
Also known as “WA MRSA-3” and is typically PVL negative

**Patients Infected with ST5-IV [2B] by Decade of Life**



**Regional Distribution of ST5-IV [2B]**

**ST5-IV [2B] (WA MRSA-3): n = 12 (2.3%)**



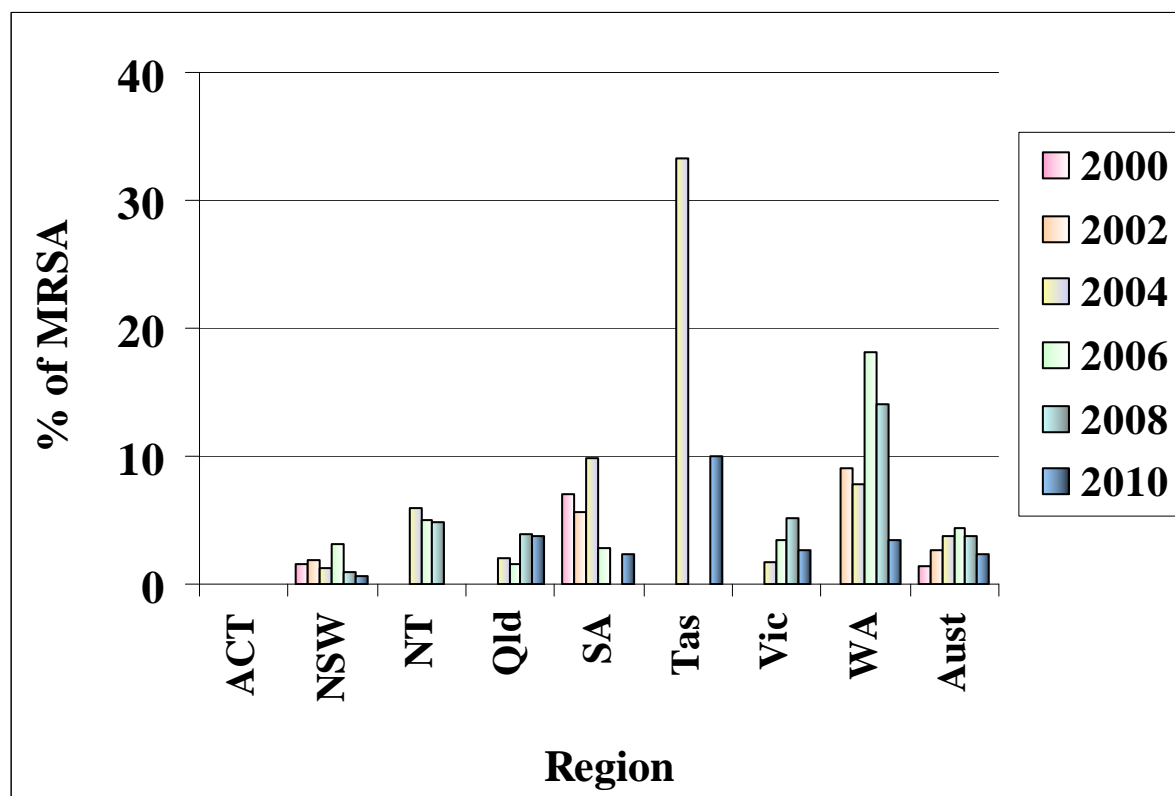
Percentage figures relate to total MRSA isolates characterized

## SAP 2000 to SAP 2010 Regional Distribution of ST5-IV [2B]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010
ACT	0	0	0	0	0	0
NSW	2 (1.6)	3 (1.8)	2 (1.3)	6 (3.1)	2 (0.9)	1 (0.6)
NT	0	0	1 (5.9)	1 (5.0)	1 (4.8)	0
Qld	0	0	1 (2.0)	1 (1.5)	4 (3.9)	4 (3.8)
SA	2 (7.1)	2 (5.6)	4 (9.8)	1 (2.8)	0	1 (2.4)
Tas	0	0	1 (33.3)	0	0	1 (10.0)
Vic	0	0	1 (1.7)	3 (3.5)	3 (5.1)	3 (2.7)
WA	0	5 (9.1)	4 (7.8)	8 (18.2)	8 (14.0)	2 (3.4)
<b>Total</b>	<b>4 (1.4)</b>	<b>10 (2.7)</b>	<b>14 (3.7)</b>	<b>20 (4.3)</b>	<b>20 (3.7)</b>	<b>12 (2.3)</b>

Percentage figures in parenthesis relate to total MRSA isolates characterized

## SAP 2000 to SAP 2010 Regional Distribution of ST5-IV [2B]



Percentage figures relate to total MRSA isolates characterized

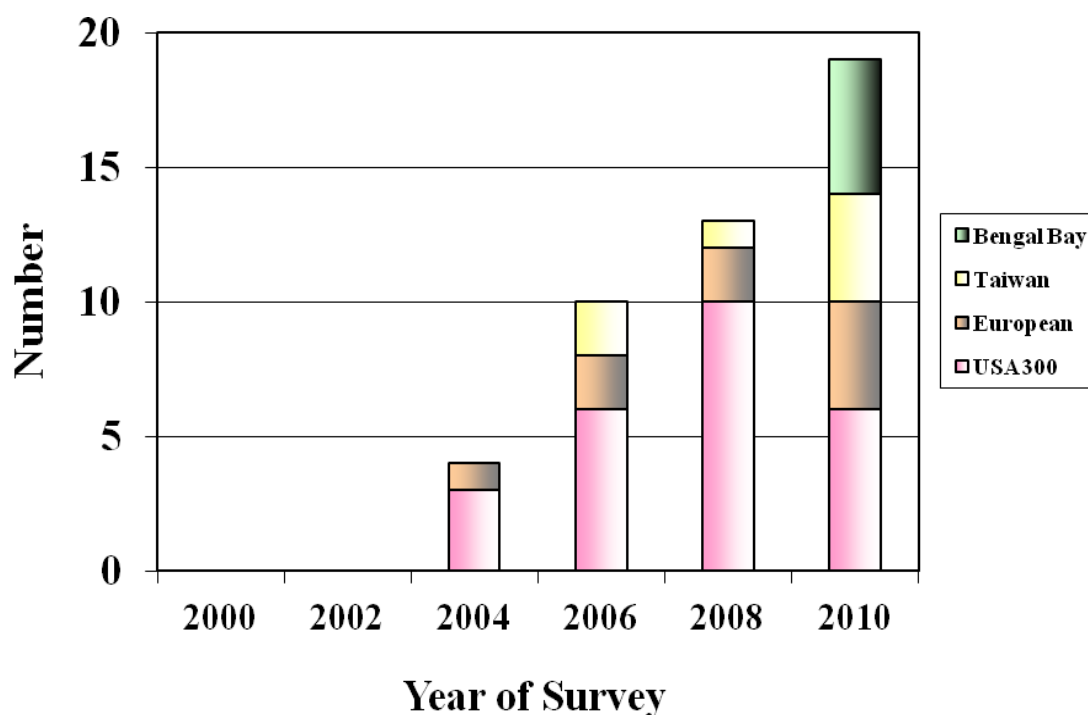
**International CA-MRSA Clones**

In SAP 2010, four international CA-MRSA clones were characterized. All were Panton Valentine leucocidin (PVL) positive.

CLONE	ALTERNATIVE NAME	n (%)
ST8-IV	USA300	6 (1.7%)
ST772-IV	Bengal Bay	5 (1.4%)
ST80-IV	European CA-MRSA	4 (1.1%)
ST59-V <sub>T</sub>	Taiwan CA-MRSA	4 (1.1%)
<b>TOTAL</b>		<b>19 (5.4%)</b>

Percentage figures relate to CA-MRSA isolates characterized

**2010: Number of MRSA Identified as International CA-MRSA**

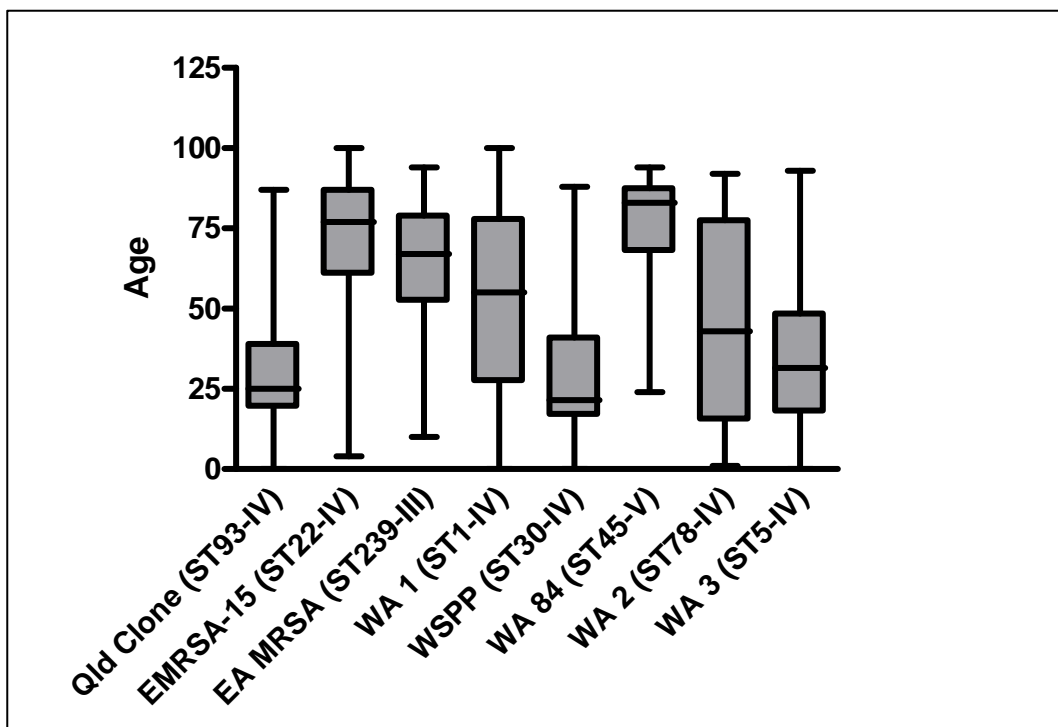


**SAP 2000 – 2010: Number of MRSA Identified as International CA-MRSA**

CLONE	SAP 2004				SAP 2006				SAP 2008				SAP 2010			
	USA 300	Europe	Taiwan	Bengal Bay	USA 300	Europe	Taiwan	Bengal Bay	USA 300	Europe	Taiwan	Bengal Bay	USA 300	Europe	Taiwan	Bengal Bay
ACT	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
NSW	3	1	0	0	4	0	0	0	4	1	0	0	3	2	1	0
NT	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Qld	0	0	0	0	1	0	0	0	2	0	0	0	1	0	0	1
SA	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1
Tas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vic	0	0	0	0	0	2	2	0	3	1	0	0	1	0	1	2
WA	0	0	0	0	0	0	0	0	1	0	0	0	0	1	2	1
<b>Total</b>	<b>3</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>6</b>	<b>2</b>	<b>2</b>	<b>0</b>	<b>10</b>	<b>2</b>	<b>1</b>	<b>0</b>	<b>6</b>	<b>4</b>	<b>4</b>	<b>5</b>

Age Statistics for Major clones ( $\geq 10$  isolates)

Box Plot of Age of Patients Infected with a Major MRSA Clone



Mean, median and percentile data

Age (years)	ST93-IV Queensland	ST22-IV EMRSA-15	ST239-III EMRSA	ST1-IV WA MRSA-1	ST30-IV WSPP	ST45-V WA MRSA-84	ST78-IV WA MRSA-2	ST5-IV WA MRSA-3
Mean (95% CI)	31	72	65	53	30	77	47	36
95% CI of mean	27.8 - 33.5	67.9 - 75.6	60.4 - 68.9	44.9 - 60.6	24.1 - 35.9	69.6 - 84.1	30.3 - 63.4	18.6 - 53.4
Median	25	77	67	55	22	83	43	32
25 <sup>th</sup> percentile	19	61	52	27	17	68	15	18
75 <sup>th</sup> percentile	39	87	79	78	41	88	78	49

## 5.5. Panton-Valentine Leucocidin (PVL) Toxin

### CA-MRSA

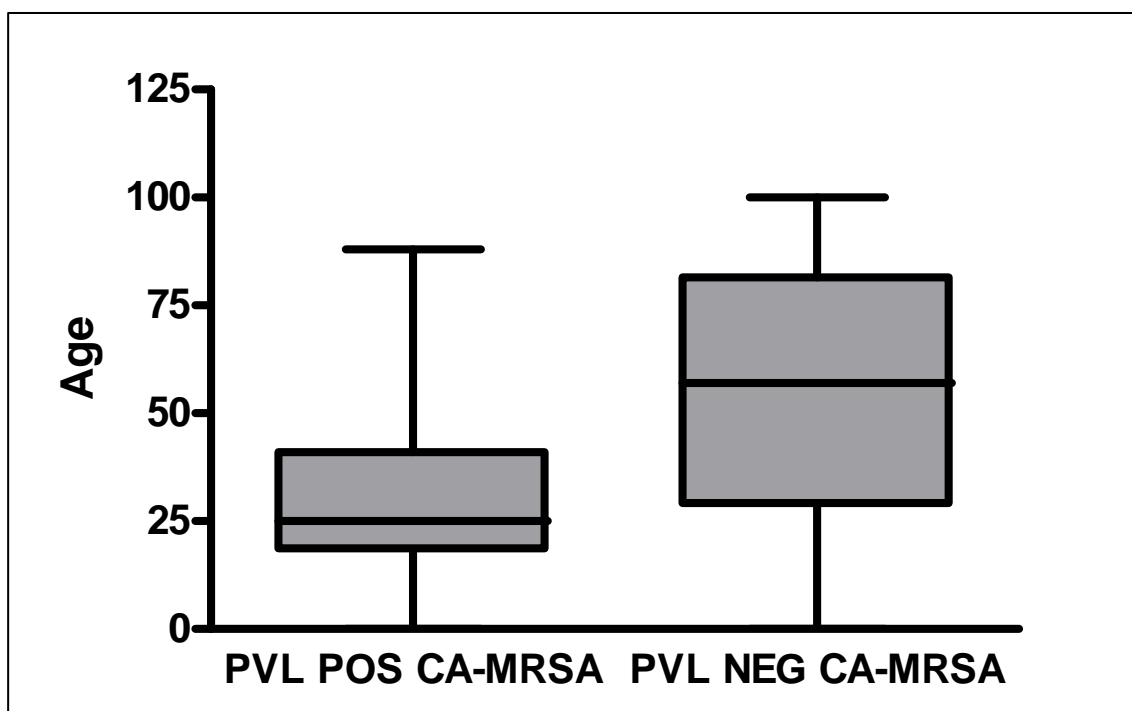
Clone	Alternative Name	Positive	Negative	Total
ST93-IV	Queensland CA-MRSA	146	1	147
ST1-IV	WA MRSA -1	5	50	55
ST30-IV	WSPM MRSA	46		46
ST45-V	WA MRSA-84		22	22
ST78-IV	WA MRSA-2	1	16	17
ST5-IV	WA MRSA-3	3	9	12
ST73-IV	WA MRSA-65		7	7
ST8-IV	USA 300	6		6
ST45-IV	WA MRSA-75		5	5
ST772-V	Bengal Bay MRSA	5		5
ST80-IV	European MRSA	4		4
ST59-V <sub>T</sub>	Taiwan MRSA	4		4
ST1304-IV	WA MRSA-72		2	2
ST188-IV	WA MRSA-78		2	2
ST59-IV	WA MRSA-15		2	2
ST188-IV	WA MRSA-38		2	2
ST73-IV	WA MRSA-95		2	2
ST72-V	WA MRSA-91		1	1
ST1303-IV	WA MRSA-76		1	1
ST672-novel			1	1
ST5-V	WA MRSA-35		1	1
ST75-IV	WA MRSA-8		1	1
ST2149-IV			1	1
ST72-IV	WA MRSA-44	1		1
ST8-IV	WA MRSA-5		1	1
ST1-V		1		1
ST6-IV	WA MRSA-51		1	1
ST207-V			1	1

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<b>Clone</b>	<b>Alternative Name</b>	<b>Positive</b>	<b>Negative</b>	<b>Total</b>
ST779-IV	WA MRSA-100		1	1
ST6-IV	WA MRSA-66		1	1
ST5-IV	WA MRSA-71		1	1
ST45-IV	WA MRSA-23		1	1
<b>Total</b>		<b>222 (62.5%)</b>	<b>133(37.5%)</b>	<b>355</b>

Age statistics for CA-MRSA clones by PVL status

Box Plot of Age of Patients Infected with PVL Positive and PVL Negative CA-MRSA



Mean, median and percentile data

Age (years)	PVL positive	PVL negative
Mean (95% CI)	30.6 (28.2 – 32.9)	53.2 (48.1 – 58.2)
Median	25	57
25 <sup>th</sup> percentile	18	28
75 <sup>th</sup> percentile	41	82

The mean age of patients with PVL-positive CA-MRSA is significantly lower ( $P < 0.0001$ ) than the mean age of patients with PVL-negative CA-MRSA

**HA- MRSA**

<b>Clone</b>	<b>Alternative Name</b>	<b>Positive</b>	<b>Negative</b>	<b>Total</b>
<b>ST22-IV</b>	<b>EMRSA-15</b>	<b>3</b>	<b>97</b>	<b>100</b>
<b>ST239-III</b>	<b>Aus2/3 EMRSA</b>	<b>0</b>	<b>76</b>	<b>76</b>
<b>ST5-II</b>	<b>New York/Japan EMRSA</b>	<b>0</b>	<b>1</b>	<b>1</b>
<b>Total</b>		<b>3 (1.7%)</b>	<b>174 (98.3%)</b>	<b>177</b>

## 5.6. CA-MRSA Antibiogram

	CC1					CC5							CC8			CC30
	1 IV WA1	1 V	772 V Bengal Bay	188 IV WA38	188 IV WA78	5 IV WA3	5 IV WA71	5 V WA35	6 IV WA51	6 IV WA66	73 IV WA65	73 IV WA95	8 IV WA5	8 IV USA300	2149 IV	30 IV WSPP
<b>Oxacillin only:</b>																
Ox <sup>R</sup>	28					7	1		1		6					42
<b>Oxacillin plus one non beta lactam antibiotic:</b>																
Em <sup>R</sup>	7					1					1	2		2	1	2
Cp <sup>R</sup>	1					1		1					1			
FA <sup>R</sup>	8															
Tc <sup>R</sup>																
Rf <sup>R</sup>																1
Mp <sup>R</sup>	1															
<b>Oxacillin plus two non beta lactam antibiotics:</b>																
Em <sup>R</sup> Tc <sup>R</sup>	1					2										
Er <sup>R</sup> FA <sup>R</sup>	9															
Em <sup>R</sup> Mp <sup>R</sup>						1								1		
Em <sup>R</sup> Cp <sup>R</sup>														3		
Tc <sup>R</sup> FA <sup>R</sup>										1						
Gn <sup>R</sup> Cot <sup>R</sup>																

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	CC1					CC5							CC8			CC30
	1 IV WA1	1 V	772 V Bengal Bay	188 IV WA38	188 IV WA78	5 IV WA3	5 IV WA71	5 V WA35	6 IV WA51	6 IV WA66	73 IV WA65	73 IV WA95	8 IV WA5	8 IV USA300	2149 IV	30 IV WSPP
Gn <sup>R</sup> Cp <sup>R</sup>																
<b>Oxacillin plus three non beta lactam antibiotics:</b>																
Em <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup>																
Gn <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup>																
Gn <sup>R</sup> Cot <sup>R</sup> Cp <sup>R</sup>			1													1
Gn <sup>R</sup> Cot <sup>R</sup> Em <sup>R</sup>			1													
Em <sup>R</sup> Tc <sup>R</sup> FA <sup>R</sup>																
<b>Oxacillin plus four non beta lactam antibiotics:</b>																
Em <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup>				1												
Em <sup>R</sup> Cot <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup>			2		2											
Cot <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup> Tc <sup>R</sup>		1														
Mp <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup> Tc <sup>R</sup>																
<b>Oxacillin plus five non beta lactam antibiotics:</b>																
Em <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup> Cot <sup>R</sup> Gn <sup>R</sup>				1												
Em <sup>R</sup> FA <sup>R</sup> Cp <sup>R</sup> Cot <sup>R</sup> Gn <sup>R</sup>			1													
TOTAL	55	1	5	2	2	12	1	1	1	1	7	2	1	6	1	46

## SAP 2010: CA-MRSA Antibigram cont

	CC45			CC59		CC72		CC75		CC80	CC88	CC509	CC672	Singleton	Undetermined		TOTAL	
	45 IV WA23	45 IV WA75	45 V WA84	59 IV WA15	59 V Taiwan	72 IV WA44	72 V WA91	75 IV WA8	1304 IV WA72	80 IV European	78 IV WA2	207 V	672 novel	93 IV Qld	1303 IV WA76	779 IV WA100		
<b>Oxacillin only:</b>																		
Ox <sup>R</sup>		2			2	1					3			129	1	1	224	
<b>Oxacillin plus one non beta lactam antibiotic:</b>																		
Em <sup>R</sup>		2		2	1			1	1		13	1		18			55	
Cp <sup>R</sup>	1	1	14														20	
FA <sup>R</sup>																	8	
Tc <sup>R</sup>											1						1	
Rf <sup>R</sup>																	1	
Mp <sup>R</sup>																	1	
<b>Oxacillin plus two non beta lactam antibiotics:</b>																		
Em <sup>R</sup> Tc <sup>R</sup>					1												4	
Er <sup>R</sup> FA <sup>R</sup>																	9	
Em <sup>R</sup> Mp <sup>R</sup>																	2	
Em <sup>R</sup> Cp <sup>R</sup>			4														7	
Tc <sup>R</sup> FA <sup>R</sup>										3							4	
Gn <sup>R</sup> Cot <sup>R</sup>							1										1	

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	CC45			CC59		CC72		CC75		CC80	CC88	CC509	CC672	Singleton	Undetermined		TOTAL
	45 IV WA23	45 IV WA75	45 V WA84	59 IV WA15	59 V Taiwan	72 IV WA44	72 V WA91	75 IV WA8	1304 IV WA72	80 IV European	78 IV WA2	207 V	672 novel	93 IV Qld	1303 IV WA76	779 IV WA100	
Gn <sup>R</sup> Cp <sup>R</sup>													1				1
<b>Oxacillin plus three non beta lactam antibiotics:</b>																	
Em <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup>			2														2
Gn <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup>			2														2
Gn <sup>R</sup> Cot <sup>R</sup> Cp <sup>R</sup>																	2
Gn <sup>R</sup> Cot <sup>R</sup> Em <sup>R</sup>																	1
Em <sup>R</sup> Tc <sup>R</sup> FA <sup>R</sup>										1							1
<b>Oxacillin plus four non beta lactam antibiotics:</b>																	
Em <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup>																	1
Em <sup>R</sup> Cot <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup>																	4
Cot <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup> Tc <sup>R</sup>																	1
Mp <sup>R</sup> Cp <sup>R</sup> Gn <sup>R</sup> Tc <sup>R</sup>									1								1
<b>Oxacillin plus five non beta lactam antibiotics:</b>																	
Em <sup>R</sup> Tc <sup>R</sup> Cp <sup>R</sup> Cot <sup>R</sup> Gn <sup>R</sup>																	1
Em <sup>R</sup> FA <sup>R</sup> Cp <sup>R</sup> Cot <sup>R</sup> Gn <sup>R</sup>																	1
<b>TOTAL</b>	<b>1</b>	<b>5</b>	<b>22</b>	<b>2</b>	<b>4</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>2</b>	<b>4</b>	<b>17</b>	<b>1</b>	<b>1</b>	<b>147</b>	<b>1</b>	<b>1</b>	<b>355</b>

Ox = oxacillin, Em = erythromycin, Cp = ciprofloxacin, FA = fusidic acid, Gm = gentamicin, Tc = tetracycline, Rf = rifampicin, Mp = mupirocin, Cot = Cotrimoxazole

## 6. References

1. **Enright M. C., D. A. Robinson, R. Randle, E. J. Feil, G. Grundmann and B. G. Spratt.** 2002. The evolutionary history of methicillin-resistant *Staphylococcus aureus* (MRSA). *Proc Natl. Acad Sci. USA.* **99**:7687-7692.
2. **Baba T., F. Takeuchi, M. Kuroda, H. Yuzawa, K. Aoki, A. Oguchi, Y. Nagai, N. Iwama, K. Asano, T. Naimi, H. Kuroda, L. Cui, K. Yamamoto, and K. Hiramatsu.** 2002. Genome and virulence determinants of high virulence community-acquired MRSA. *Lancet.* **359**:1819-27.
3. **Vandenesch F., T. Naimi, M. Enright, G. Lina, G. R. Nimmo, H. Heffernan, N. Liassine, M. Bes, T. Greenland, M-E Reverdy and J. Etienne.** 2003. Community-acquired methicillin-resistant *Staphylococcus aureus* carrying Panton-Valentine leukocidin genes: worldwide emergence. *Emerg Infect Dis.* **9**:978-984
4. **O'Brien F. G., T. T. Lim, F. N. Chong, G. W. Coombs, M. C. Enright, D. A. Robinson, A. Monk, B. Said-Salim, B. N. Kreisworth, and W. B. Grubb.** 2004. Diversity among isolates of methicillin resistant *Staphylococcus aureus* in Australia. *J Clin Microb.* **42**:3185-3190.
5. **Collignon P., I. Gosbell, A. Vickery, G. Nimmo, T. Stylianopoulos, and T. Gottlieb.** 1998. Community-acquired methicillin-resistant *Staphylococcus aureus* in Australia. *Lancet.* **352**:146-147
6. **Munckhof W. J., J Schooneveldt, G. W. Coombs, J. Hoare and G. R. Nimmo.** 2003. Emergence of community-acquired methicillin-resistant *Staphylococcus aureus* (MRSA) infection in Queensland, Australia *Inter J Infect Dis.* **7**:259-267.
7. **Coombs G.W., G.R. Nimmo, J.C. Pearson, K.J. Christiansen, J.M. Bell, P.J. Collignon, M-L McLaws, on behalf of the Australian Group on Antimicrobial Resistance.** 2009. Prevalence of MRSA strains among *Staphylococcus aureus* isolated from outpatients. 2006. *Commun Dis Intell.* **33**:10-20.
8. **Nimmo G.R., and G.W. Coombs.** 2008. Community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) in Australia. *Int J Antimicrob Agents* **31**:401-410.
9. **Kaneko J., T. Kimura, S. Narita, T. Tomita, and Y. Kamio.** 1998. Complete nucleotide sequence and molecular characterisation of the temperate staphylococcal phage  $\phi$ PVL carrying Panton-Valentine leukocidin genes. *Gene* **28**:393-397.
10. **Stephens A.J., F. Huygens, G.R. Nimmo, J.M. Schooneveldt, G.W. Coombs, E.P. Price, and P.M. Giffard.** 2004 Variable binary gene typing increases resolution of methicillin-resistant *Staphylococcus aureus* MLST clonal groups defined by SNP typing. In: Abstracts of the 11th International Symposium on Staphylococci and Staphylococcal Infections; Charleston, South Carolina. Abstract ME-30.
11. **Gosbell I.B., T. Barbagiannakos, H. Burke, C. Kenned, A. Vickery, P. Lambie, A. Morton and J. Mercer.** 2004. Community MRSA in far western New South Wales: Emergence of two epidemic clones and emergence of Panton-Valentine leukocidin in a previous naïve clone. In: Abstracts of the 11th International Symposium on Staphylococci and Staphylococcal Infections; Charleston, South Carolina. Abstract CA-10.

12. **Nimmo G.R., J. Schooneveldt, G. O’Kane, B. McCall, and A. Vickery.** 2000. Community acquisition of gentamicin-sensitive MRSA in southeast Queensland. *J Clin Microbiol.* **38**:3926-3931
13. **Gosbell I.B., J.L. Mercer, S.A. Neville, K.G. Chant, and R. Munro.** 2001. Non-Multiresistant and multiresistant methicillin-resistant *Staphylococcus aureus* in community-acquired infections. *Med J Aust.* 174:627-630.
14. **Townsend D. E., N. Ashdown, S. Bolton, J. Bradley, G. Duckworth, E.C. Moorhouse and W.B. Grubb.** 1987. The international spread of methicillin- resistant *Staphylococcus aureus*. *J Hosp Infect* **9**:60-71.
15. **Townsend D. E., N. Ashdown, J. W. Pearman, D. I. Annear and W. B. Grubb.** 1985. Genetics and epidemiology of methicillin- resistant *Staphylococcus aureus* in a Western Australian Hospital. *Med J Aust* **142**:108-111.
16. **Ayliffe G. A. J., A. Buckles, M. S. Casewell, B. D. Cookson, R. A. Cox, G. J. Duckworth, G. L. French, A. Griffiths-Jones, R. Heathcock, H. Humphreys, C.T. Keane, R. R. Marples, D. C. Shanson, R. Slack and E. Tebbs.** 1998. Revised guidelines for the control of methicillin-resistant *Staphylococcus aureus* infections in hospitals. Report of a combined working party at the British Society of Antimicrobial Chemotherapy, the Hospital Infection Society, and the Infection Control Nurses’s Association. *J Hosp Infect* **39**:253-290.
17. **Goh, S-H. S. B. Byrne, J. L. Zhang, and A. W. Chow.** 1992. Molecular typing of *Staphylococcus aureus* on the basis of coagulase gene polymorphisms. *J Clin Microbiol* **30**:
18. **O’Brien F. G., J. W. Pearman, M. Gracey, T. V. Riley, and W. B. Grubb.** 1999. Community strain of methicillin-resistant *Staphylococcus aureus* involved in a hospital outbreak. *J Clin Microbiol* **37**:2858-2862
19. **Tenover F. C., R. D. Arbeit, R. V. Goering, P. A. Mickelsen, B. E. Murray, D. H. Persing, and B. Swaminathan.** 1995. Interpreting chromosomal DNA restriction patterns produced by pulsed-field gel electrophoresis; criteria for bacterial strain typing. *J Clin Microbiol.* **33**:2233-2239
20. **Okuma K., K. Iwakawa, J.D. Turnidge, W.B. Grubb, J.M. Bell, F.G. O’Brien, G.W. Coombs, J.W. Pearman, F.C. Tenover, M. Kapi, C. Tiensasitorn, T. Ito, and K. Hiramatsu.** 2002. Dissemination of new methicillin-resistant *Staphylococcus aureus* clones in the community. *J Clin Microbiol.* **40**:4289-94.
21. **Lim T. T., F. N. Chong, F. G. O’Brien, and W. B. Grubb.** 2003. Are all community methicillin-resistant *Staphylococcus aureus* related? A comparison of their *mec* regions. *Pathol.* **35**:336-343.
22. **Ito T, X.X. Ma, F. Takeuchi, K Okuma, H. Yuzawa, and K. Hiramatsi.** 2004. Novel type V staphylococcal cassette chromosome *mec* driven by a novel cassette chromosome recombinase, *ccrC*. *Antimicrob Agents Chemother.* 48:2637-51.
23. **IWG-SCC.** 2009. Classification of Staphylococcal Cassette Chromosome *mec* (SCC*mec*): Guidelines for reporting novel SCC*mec* elements. *Antimicrob Agents Chemother.* 53:4961-4967
24. **Fey P.D., B. Said-Salim, M.E. Rupp, S.H. Henrichs, D.J. Boxrud, C.C. Davis, B.N. Kreiswirth, and P.M. Schlievert.** 2003. Comparative molecular analysis of community- or

hospital-acquired methicillin-resistant *Staphylococcus aureus*. *Antimicrob Agents Chemother.* **47**:196-203.

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SA Pathology, Women's and Children's Hospital, SA	John Turnidge and Jan Bell

### ACCESS Typing and Research Unit

Curtin University, WA	Frances O'Brien
PathWest, Royal Perth Hospital, WA	Yung Lee

### Lottery West State Biomedical Facility: Genomics

Dept of Clinical Immunology and  
Immunogenetics, Royal Perth Hospital. PathWest Laboratory Medicine – WA