



***Staphylococcus aureus* Programme 2012 (SAP 2012)
Community Survey
MRSA Epidemiology and Typing Report**

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Epidemiology and Typing Report of Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolates from the Australian Group on Antimicrobial Resistance (AGAR) 2012
***Staphylococcus aureus* Surveillance Programme (SAP 2012)**

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***Staphylococcus aureus* Programme 2012 (SAP 2012)**

Community Survey

MRSA Epidemiology and Typing Report

1. Overview

Of the 510 S aureus classified as MRSA in the SAP 2012 Community Survey, molecular typing was performed on 499 (97.8%) isolates. The mean age of patients with infections due to community-associated MRSA (CA-MRSA) strains (41 years; median 38 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 (70 years; median 75 years). Although the percentage of S aureus characterized as HA-MRSA in this survey (5.1%) was lower when compared to the 2010 survey (5.9%), ST22-IV [2B] (EMRSA-15) remains a major HA-MRSA clone in most Australian communities surveyed, accounting for 21.0% of all community-onset MRSA infections. Of continuing concern has been the rapid emergence of this clone in Victorian (0% in 2002 to 21.2% in 2012), and New South Wales communities (18.0% in 2000 to 34.3% in 2012). CA-MRSA accounted for 71.1% of MRSA and 12.5% of all S aureus. Since 2000 the percentage of S aureus characterized as CA-MRSA has more than doubled (5.3% in 2000 to 12.5% in 2012). As in previous surveys, although CA-MRSA was multiclonal (32 clones) 82.5% 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 36.3% of all CA-MRSA and 25.9% of all MRSA infections. Overall 62.8% 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 (32 years; median 29 years) was significantly lower ($P < 0.0001$) than the mean age of patients with PVL negative CA-MRSA infections (56 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] (SWP MRSA), ST8-IV [2B] (USA300) ST59-V [5C2&5] (Taiwan CA-MRSA), and the hypervirulent multiresistant ST772-V [5C2] (Bengal Bay). Four 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

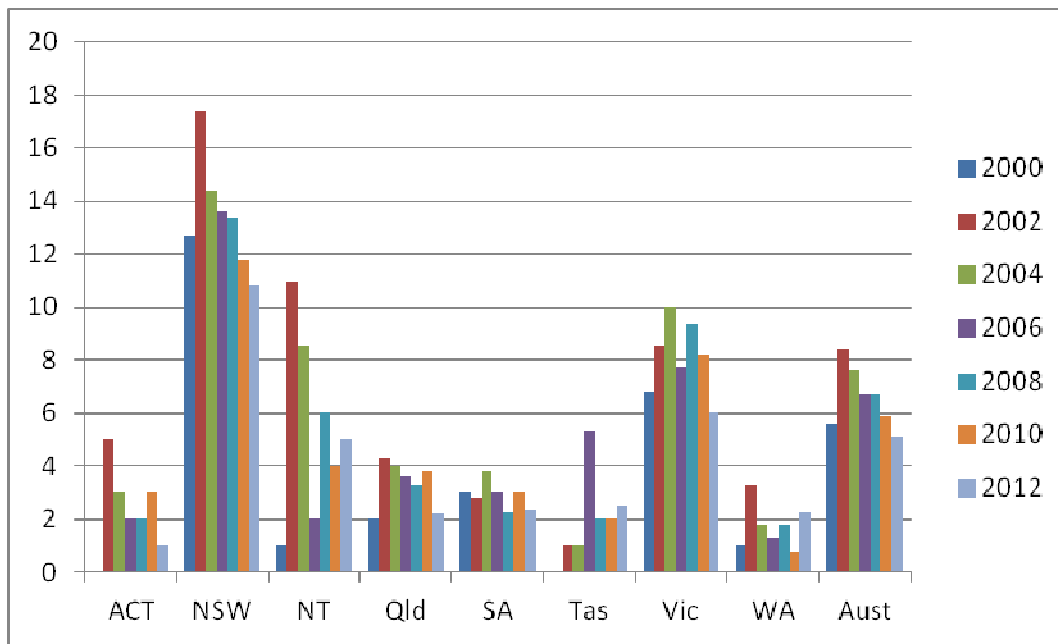
The Australian Group for Antimicrobial Resistance (AGAR) biennial community *Staphylococcus aureus* surveillance programme commenced in 2000. In the 2012 programme (SAP 2012) up to 100 clinically significant, community onset, consecutive isolates of *S aureus* from different outpatients were collected by each of 29 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 510 (17.9%) *S aureus* classified as MRSA in SAP 2012, 499 (97.8%) were referred to **ACCESS** Typing and Research. Overall 71.1% and 28.9% 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 (41 years; median 38 years) was significantly lower ($P < 0.0001$) than the mean age of patients with HA-MRSA infections (70 years; median 75 years).

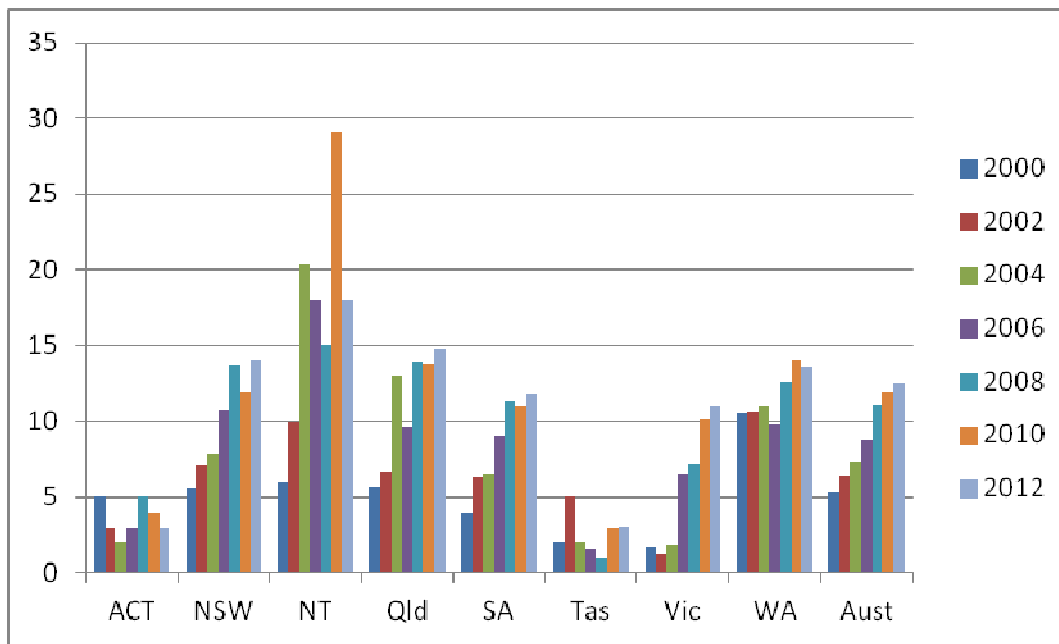
Since the initial community *S aureus* surveillance study performed in 2000 there has been a significant increase ($P < 0.0001$) in the percentage of patients with MRSA infections in most regions of Australia such that in 2012 one in six patients with a staphylococcal infection have MRSA and one in eight are infected with a CA-MRSA clone.

Throughout Australia the percentage of *S aureus* characterized as HA-MRSA was 5.1% ranging from 1.0% in the Australian Capital Territory to 10.8% in New South Wales.



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

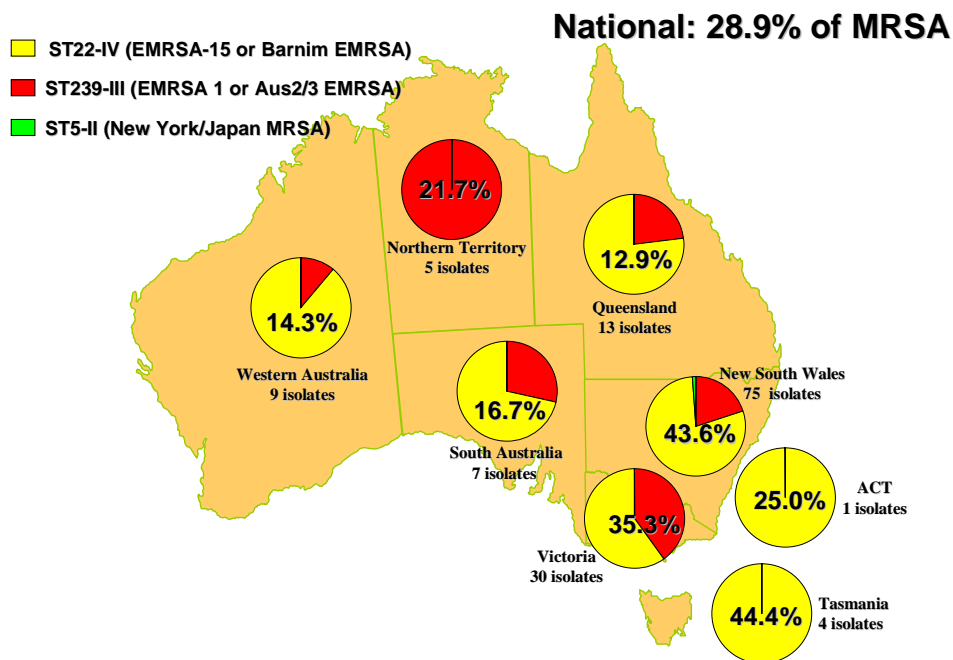
The percentage of *S aureus* characterized as CA-MRSA was 12.5% ranging from 3.0% in the Australian Capital Territory to 18% in the Northern Territory.



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: 72.9% were ST22-IV [2B] (EMRSA-15), 26.4% ST239-III [3A] (Aus-2/3 EMRSA), and 0.7% ST5-II [2A] (New York/Japan MRSA/USA100).



Percentage of MRSA characterized as HA-MRSA

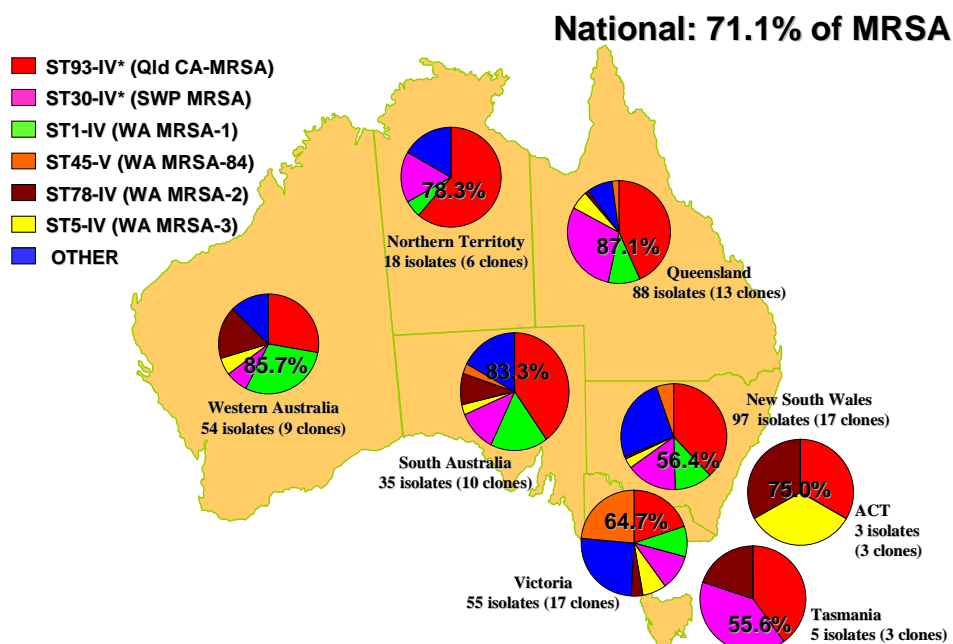
EMRSA-15, which was initially reported in Australia in 1997, accounted for 21.0% of all MRSA isolated in this study, ranging from 0% in the Northern Territory to 44.4% in Tasmania. The percentage of MRSA characterized as EMRSA-15 has increased in most Australian regions over the six surveys noticeably in Victorian (0% in 2002 to 21.2% in 2012), and New South Wales communities (18.0% in 2000 to 34.3% in 2012). Aus-2/3 EMRSA was isolated in most Australian regions, accounting for 21.7% of MRSA in the Northern Territory. Over the six community surveys the percentage of isolates characterized as Aus-2/3 has decreased throughout Australia.

2.2. Community Onset CA-MRSA clones

Thirty two CA-MRSA clones were identified by pulsed-field gel electrophoresis (corresponding to 25 MLST/SCC*mec* clones) of which 82.5% were made up of six clones:

- ST93-IV [2B] {Qld CA-MRSA} (36.3%)
- ST30-IV [2B] {SWP CA-MRSA} (16.9%)
- ST1-IV [2B] {WA MRSA-1} (13.5%)
- ST45-V [5C2&5] {WA MRSA-84} (5.9%)
- ST78-IV [2B] {WA MRSA-2} (5.1%)
- ST5-IV [2B] {WA MRSA-3} (4.8%)
-

ST93-MRSA-IV [2B] (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 62.8% (n=223) of CA-MRSA (15 clones) were PVL positive:

- ST93-IV [2B](Qld CA-MRSA) – 127 of 129 isolates
- The following recognised international clones:
 - o ST30-IV [2B] (SWP) – 56 of 60 isolates
 - o ST8-IV [2B] (USA300) – 9 of 10 isolates
 - o ST772-V [5C2] (Bengal Bay) – 2 of 2 isolates
 - o ST59-V_T [5C2&5] (Taiwan CA-MRSA) – 5 of 5 isolates
 - o ST952-V_T [5C2&5] (Taiwan A CA-MRSA) – 5 of 5 isolates
- Three of the 48 ST1-MRSA-IV [2B] (WA MRSA-1) isolates. It is possible that these are USA400 strains however further molecular studies are required to confirm.
- In addition, the following seven “Australian CA-MRSA” clones also contained PVL positive isolates
 - o ST5-IV [2B] (WA MRSA-3) – 5 of 17 isolates
 - o ST5-IV [2B] (WA MRSA-121) – 4 of 4 isolates
 - o ST6-IV [2B] (WA MRSA-51) – 3 of 3 isolates
 - o ST78-IV [2B] (WA MRSA-2) – 1 of 18 isolates
 - o ST30-V [5C2] (WA MRSA-124) -1 of 1 isolate
 - o ST59-IV [2B] (WA MRSA-55) – 1 of 1 isolate
 - o ST5-IV [2B] (WA MRSA-71) - 1 of 1 isolate

Although PVL positive CA-MRSA were isolated throughout Australia, the percentage of CA-MRSA that were positive varied from 39% in Western Australia to 78% and 80% in the Northern Territory and Tasmania respectively. In the previous community survey (SAP 2010), 62.5% of CA-MRSA were PVL positive ranging from 36% in South Australia to 83% in Queensland.

The mean age of patients with PVL positive CA-MRSA infections (32 years; median 29 years) was significantly lower ($P < 0.0001$) than the mean age of patients with PVL negative CA-MRSA infections (56 years; median 57 years).

HA-MRSA

Four PVL-positive ST22-MRSA-IV [2B] (EMRSA-15) isolates were identified by PCR (two in New South Wales, one in Queensland and one in South Australia). 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 2012 Protocol

3.1. Commencement Date

1st July 2012

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 29 laboratories located across Australia (total number of isolates = 2,844). Fifteen isolates were from Nursing Homes, Long-Term Care Facilities and Hospice patients. 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 (5)
Alfred Hospital
Austin Health
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[®] 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:

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). 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. Pantone-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 [5C2&5] (Taiwan CA-MRSA)
4. ST1-IV [2B] (USA400)
5. ST772-V [5C2] (Bengal Bay CA-MRSA)

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 β -lactamase production using nitrocefin. High-level mupirocin resistance was determined by disc diffusion (200 ug disc, Oxoid).

Resistogram

Disk Diffusion (14,15)

mercuric chloride (HgCl₂) (0.4 μ 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_{mec} 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
- DNA Micro-Array 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
- CHEF
- DNA Micro-Array on selected isolates

4.3. Identification of CA-MRSA Clones

ST30-IV [2B] (South West Pacific MRSA - SWP MRSA)

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

ST93-IV [2B] (Queensland MRSA)

- Antibiogram
- Urea broth
- CHEF

ST8-IV [2B] (USA300 MRSA)

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

ST59-V [5C2&5] (Taiwan MRSA)

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP

ST952-V [5C2&5] (Taiwan A MRSA)

Antibiogram
Urea broth
CHEF

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

Antibiogram
Urea broth
CHEF

ST72-IV [2B] (Korean CA-MRSA)

Antibiogram
Urea broth
CHEF

“WA MRSA”

ST1-IV [2B] (WA1)
ST78-IV [2B] (WA2)
ST5-IV [2B] (WA3)
ST8-IV [2B] (WA5)
ST59-IV [2B] (WA15)
ST577-V [5C2] (WA22)
ST188-IV [2B] (WA38)
ST883-IV [2B] (WA47)
ST835-IV [2B] (WA48)
ST6-IV [2B] (WA51)
ST953-IV [2B] (WA54)
ST59-IV [2B] (WA55)
ST12-novel (WA59)
ST73-IV [2B] (WA65)
ST5-IV [2B] (WA71)
ST45-IV [2B] (WA75)
ST1303-IV [2B] (WA76)
ST45-V [5C2&5] (WA-84)
ST5-IV [2B] (WA96)
ST5-V [5C2] (WA109)
ST247-IV [2B] (WA120)
ST5-IV [2B] (WA121)
ST30-V [5C2] (WA124)
ST5-V [5C2]

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP on selected isolates
DNA Micro-Array on selected isolates

CC1-V [5C2]

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

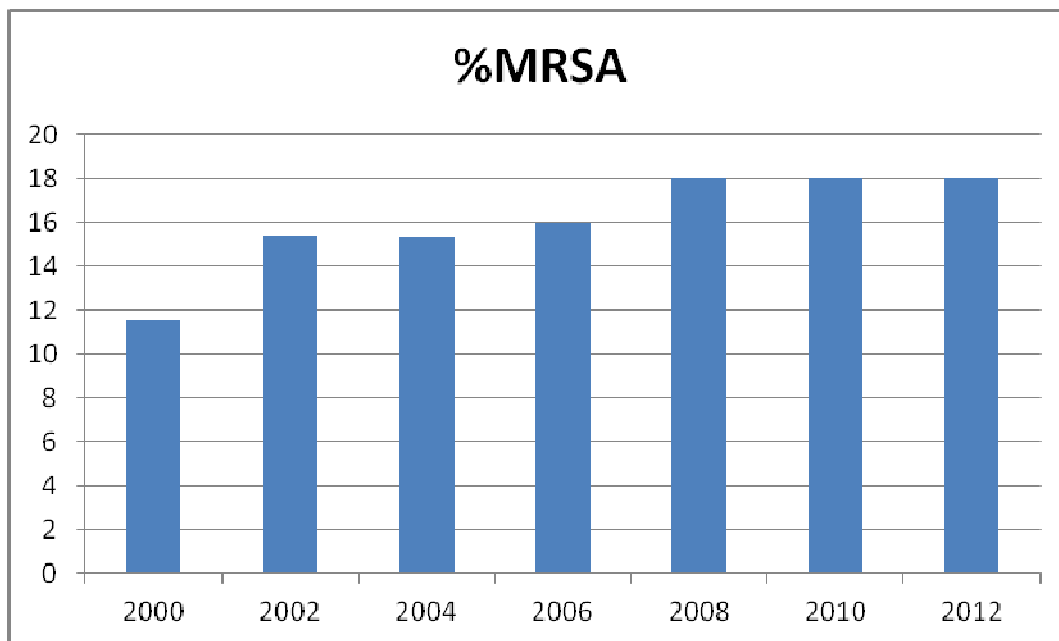
In SAP 2012, 510 (17.9%) *Staphylococcus aureus* were classified as MRSA.

5.1. AGAR Community Onset SAP 2000 – 2012

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
2012	29	2,844	510	17.9

Percentage of *Staphylococcus aureus* Identified as MRSA

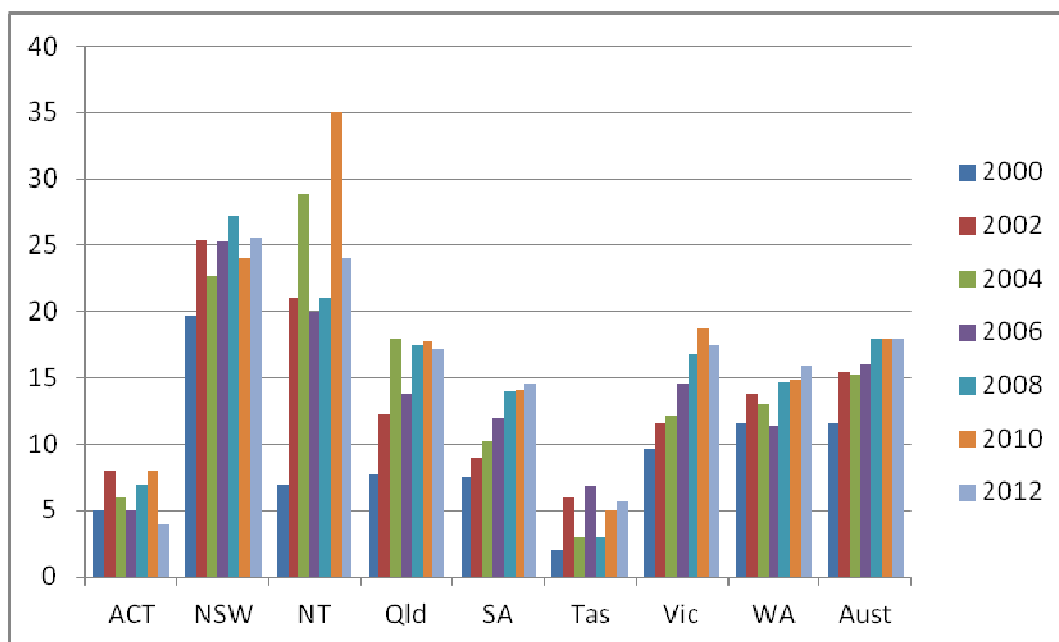


Regional Distribution of MRSA

Region	2000	2002	2004	2006	2008	2010	2012
ACT	5 (5.0)	8 (8.0)	6 (6.0)	5 (5.0)	7 (7.0)	8 (8.0)	4 (4.0)
NSW	138 (19.7)	175 (25.4)	159 (22.6)	201 (25.3)	214 (27.2)	167 (24.0)	177 (25.5)
NT	7 (7.0)	21 (21.0)	17 (28.8)	20 (20.0)	21 (21.0)	35 (35.0)	24 (24.0)
Qld	23 (7.7)	37 (12.3)	54 (18.0)	69 (13.8)	104 (17.4)	106 (17.7)	103 (17.2)
SA	30 (7.5)	36 (9.0)	41 (10.3)	36 (12.0)	42 (14.0)	42 (14.1)	43 (14.5)
Tas	2 (2.0)	6 (6.0)	3 (3.0)	13 (6.8)	6 (3.0)	10 (5.0)	9 (5.7)
Vic	45 (9.6)	46 (11.5)	61 (12.12)	87 (14.5)	100 (16.8)	112 (18.7)	87 (17.4)
WA	46 (11.5)	55 (13.8)	52 (13.0)	45 (11.3)	58 (14.6)	59 (14.8)	63 (15.9)
Total	296 (11.5)	384 (15.4)	393 (15.3)	476 (16.0)	553 (18.0)	539 (18.0)	510 (17.9)

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

Regional Distribution of MRSA



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

5.2. SAP 2012 Epidemiological Typing of MRSA

Of the 510 MRSA identified in SAP 2012, 499 (97.8%) 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	499
Coagulase Gene PCR-RFLP Assay	32
Resistogram	41
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	499
Urease Reaction	499
Multi Locus Sequencing Typing (MLST)	1
SCCmec PCR	1
Panton-Valentine Leucocidin PCR	499

Regional Distribution of HA-MRSA and CA-MRSA

Region	HA-MRSA (%)	CA-MRSA (%)	Total MRSA
ACT	1 (25.0)	3 (75.0)	4
NSW	75 (43.6)	97 (56.4)	172
NT	5 (21.7)	18 (78.3)	23
Qld	13 (12.9)	88 (87.1)	101
SA	7 (16.7)	35 (83.3)	42
Tas	4 (44.4)	5 (55.6)	9
Vic	30 (35.3)	55 (64.7)	85
WA	9 (14.3)	54 (85.7)	63
TOTAL	144 (28.9)	355 (71.1)	499

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

SAP 2000 – 2012: Regional Distribution of HA-MRSA and CA-MRSA

Region	2000 (n = 279) ^a		2002 (n = 367) ^b		2004 (n = 383) ^c		2006 (n = 462) ^d		2008 (n=547) ^e	
	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)
TOTAL	144 (51.6)	135 (48.4)	208 (56.7)	159 (43.3)	194 (50.7)	189 (49.3)	200 (43.3)	262 (56.7)	207 (37.8)	340 (62.2)

Percentage figures relate to the total number of MRSA isolates

^aIn SAP 2000, 279 of the 296 MRSA were fully characterized

^bIn SAP 2002, 367 of the 384 MRSA were fully characterized

^cIn SAP 2004, 383 of the 393 MRSA were fully characterized

^dIn SAP 2006, 462 of the 476 MRSA were fully characterized

^eIn SAP 2008, 547 of the 552 MRSA were fully characterized

SAP 2000 – 2012: Regional Distribution of HA-MRSA and CA-MRSA cont

Region	2010 (n = 532) ^f		2012 (n=499) ^g	
	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)
ACT	3 (42.9)	4 (57.1)	1 (25.0)	3 (75.0)
NSW	82 (49.7)	83 (50.3)	75 (43.6)	97 (56.4)
NT	4 (12.1)	29 (87.9)	5 (21.7)	18 (78.3)
Qld	23 (21.7)	83 (78.3)	13 (12.9)	88 (87.1)
SA	9 (21.4)	33 (78.6)	7 (16.7)	35 (83.3)
Tas	4 (40.0)	6 (60.0)	4 (44.4)	5 (55.6)
Vic	49 (44.5)	61 (55.5)	30 (35.3)	55 (64.7)
WA	3 (5.1)	56 (94.9)	9 (14.3)	54 (85.7)
TOTAL	177 (33.3)	355 (66.7)	144 (28.9)	355 (71.1)

^fIn SAP 2010, 532 of the 539 MRSA were fully characterized

^gIn SAP 2012, 499 of the 510 MRSA were fully characterized

SAP 2000 – 2012: Regional Distribution of HA-MRSA and CA-MRSA as a Proportion of *Staphylococcus aureus*

Region	2000			2002			2004			2006		
	Total	HA-MRSA (%)	CA-MRSA (%)	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)	100	2 (2.0)	3 (3.0)
NSW	700	89 (12.7)	39 (5.6)	689	120 (17.4)	49 (7.1)	703	101 (14.4)	55 (7.8)	795	108 (13.6)	85 (10.7)
NT	100	1 (1.0)	6 (6.0)	100	11 (11.0)	10 (10.0)	59	5 (8.5)	12 (20.3)	100	2 (2.0)	18 (18.0)
Qld	300	6 (2.0)	17 (5.7)	300	13 (4.3)	20 (6.7)	300	12 (4.0)	39 (13.0)	500	18 (3.6)	48 (9.6)
SA	400	12 (3.0)	16 (4.0)	400	11 (2.8)	25 (6.3)	399	15 (3.8)	26 (6.5)	299	9 (3.0)	27 (9.0)
Tas	100	0	2 (2.0)	100	1 (1.0)	5 (5.0)	99	1 (1.0)	2 (2.0)	190	10 (5.3)	3 (1.6)
Vic	469	32 (6.8)	8 (1.7)	399	34 (8.5)	5 (1.3)	500	50 (10.0)	9 (1.8)	598	46 (7.7)	39 (6.5)
WA	400	4 (1.0)	42 (10.5)	398	13 (3.3)	42 (10.6)	400	7 (1.8)	44 (11.0)	397	5 (1.3)	39 (9.8)
TOTAL	2,569	144 (5.6)	135 (5.3)	2,486	208 (8.4)	159 (6.4)	2,560	194 (7.6)	189 (7.4)	2,979	200 (6.7)	262 (8.8)

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

Region	2008			2010			2012		
	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)
ACT	100	2 (2.0)	5 (5.0)	100	3 (3.0)	4 (4.0)	100	1 (1.0)	3 (3.0)
NSW	786	105 (13.4)	108 (13.7)	696	82 (11.8)	83 (11.9)	693	75 (10.8)	97 (14.0)
NT	100	6 (6.0)	15 (15.0)	100	4 (4.0)	29 (29.0)	100	5 (5.0)	18 (18.0)
Qld	598	20 (3.3)	83 (13.9)	600	23 (3.8)	83 (13.8)	599	13 (2.2)	88 (14.7)
SA	300	7 (2.3)	34 (11.3)	299	9 (3.0)	33 (11.0)	296	7 (2.4)	35 (11.8)
Tas	198	4 (2.0)	2 (1.0)	200	4 (2.0)	6 (3.0)	159	4 (2.5)	5 (3.1)
Vic	597	56 (9.4)	43 (7.2)	599	49 (8.2)	61 (10.2)	500	30 (6.0)	55 (11.0)
WA	396	7 (1.8)	50 (12.6)	400	3 (0.8)	56 (14.0)	397	9 (2.3)	54 (13.6)
TOTAL	3,075	207 (6.7)	340 (11.1)	2,994	177 (5.9)	355 (11.6)	2,844	144 (5.1)	355 (12.5)

SAP 2012: HA-MRSA by AGAR Laboratory

LAB	ST22-IV [2B] (EMRSA-15)	ST239-III [3A] (Aus2/3 EMRSA)	ST5-II [2A] (NY/Japan MRSA)	TOTAL
ACT (1)				
TCH	1			1
NSW(75)				
CRGH	15			15
DHM	4	1	1	6
LH	13	5		18
NH	7			7
RNSH	5	1		6
RPAH	10	2		12
WH	5	6		11
NT (5)				
RDH		5		5
Qld (13)				
CBH				0
GCH	5	1		6
PAH	2			2
PCH	3	1		4
RBWH		1		1
SNP				0
SA (7)				
FMC		1		1
IMVS	5	1		6
WCH				0
Tas (4)				
LGH	4			4
RHH				0
Vic (30)				
AH	5	3		8
AUH	6	4		10
MMC	3	4		7
RCH	2			2
SVH	2	1		3
WA (9)				
FH	1			1
QEII	1			1
RPH	2	1		3
SJOG	4			4
TOTAL	105	38	1	144

SAP 2012: CA-MRSA by AGAR Laboratory

ST SCCmec	CC1				CC5								CC8			CC12	C30		
	1 IV WA1	1 V	772 V Bengal Bay	188 IV WA38	5 IV WA3	5 IV WA71	5 IV WA96	5 IV WA121	5 V WA109	5 V	6 IV WA51	73 IV WA65	835 IV WA48	8 IV USA300	8 IV WA5	2471 V WA120	12 Novel WA59	30 IV WSPP	30 V WA124
ACT (3)																			
TCH					1														
NSW (97)																			
CRGH	1						1					1		1				1	
DHM	2				2									1	1			1	
LH	1				1									1	1			2	
NH	1						1											5	
RNSH												1						1	
RPAH	2						1							2	1			3	
WH	4		2							3	2							2	
NT (18)																			
RDH	1																1	3	
QLD (88)																			
PCH	1	1																5	
RBWH	2				3													7	
SNP	2																	3	
CBH	2				2	1								1				7	
GCH	1																	1	
PAH	1										1							3	
SA (35)																			
FMC	2				1													1	
IMVS	3											1						1	
WCH	1													1				2	
Tas (5)																			
LGH																		2	

SAP 2012: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

	CC1				CC5								CC8			CC12	C30			
ST SCCmec	1 IV WA1	1 V	772 V Bengal Bay	188 IV WA38	5 IV WA3	5 IV WA71	5 IV WA96	5 IV WA121	5 V WA109	5 V	6 IV WA51	73 IV WA65	835 IV WA48	8 IV USA300	8 IV WA5	2471 V WA120	12 Novel WA59	30 IV WSPP	30 V WA124	
RHH																				
Vic (55)																				
AH	1													1						
AuH	1			1	1					1								1		
MMC	2				2				1			1						2		
RCH					1										2			3	1	
SVH	1																			
WA (54)																				
FH	3											1	1					3		
QEII	4				2			2				1								
RPH	4											1				1				
SJOG	5				1													1		
Total	48	1	1	1	17	1	1	4	1	1	3	10	1	10	3	1	1	60	1	

SAP 2012: CA-MRSA by AGAR Laboratory cont

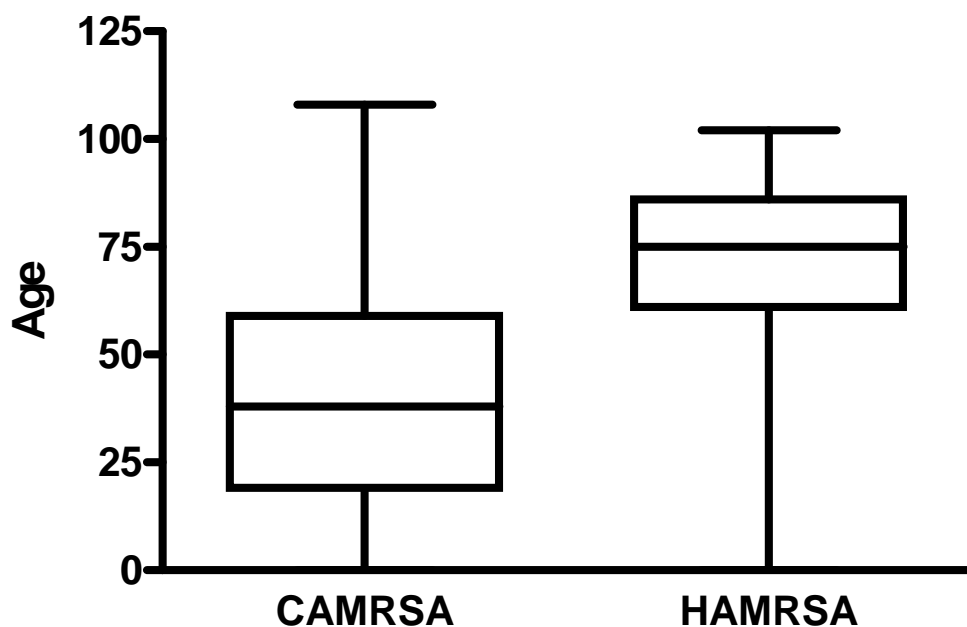
	CC45		CC59				CC72	CC88	CC97	CC121	Singleton	Singleton	Undetermined	TOTAL
ST SCCmec	45 IV WA75	45 V WA84	59 IV WA15	59 IV WA55	59 V Taiwan	952 V Taiwan A	72 IV Korean	78 IV WA2	953 IV WA54	577 V WA22	93 IV Qld	883 IV WA47	1303 IV WA76	
ACT (3)														
TCH								1			1			3
NSW (97)														
CRGH														5
DHM											4			11
LH		2				1					7			16
NH											12			19
RNSH		1			1	1	1							6
RPAH	1	2									3			15
WH								1			11			25
NT (18)														
RDH											11	1	1	18
Qld (88)														
PCH					1						9			17
RBWH											10			22
SNP		1	1								3			10
CBH											3			16
GCH		1				1					10			14
PAH								1			3			9
SA (35)														
FMC		1							2		5			12
IMVS								2			4			12
WCH						2		1			5			11
Tas (5)														
LGH								1			2			5

SAP 2012: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

	CC45		CC59				CC72	CC88	CC97	CC121	Singleton	Singleton	Undetermined	TOTAL
ST SCCmec	45 IV WA75	45 V WA84	59 IV WA15	59 IV WA55	59 V Taiwan	952 V Taiwan A	72 IV Korean	78 IV WA2	953 IV WA54	577 V WA22	93 IV Qld	883 IV WA47	1303 IV WA76	
RHH														0
Vic (55)														
AH		2		1					1		2			8
AuH		2			1			1			1			10
MMC		7									4			19
RCH		2			1			1		1				12
SVH					1						4			6
WA (54)														
FH								4			1			13
QEII								1			9			19
RPH											5			11
SJOG								4						11
Total	1	21	1	1	5	5	1	18	3	1	129	1	1	355

Age statistics for Clone Type

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

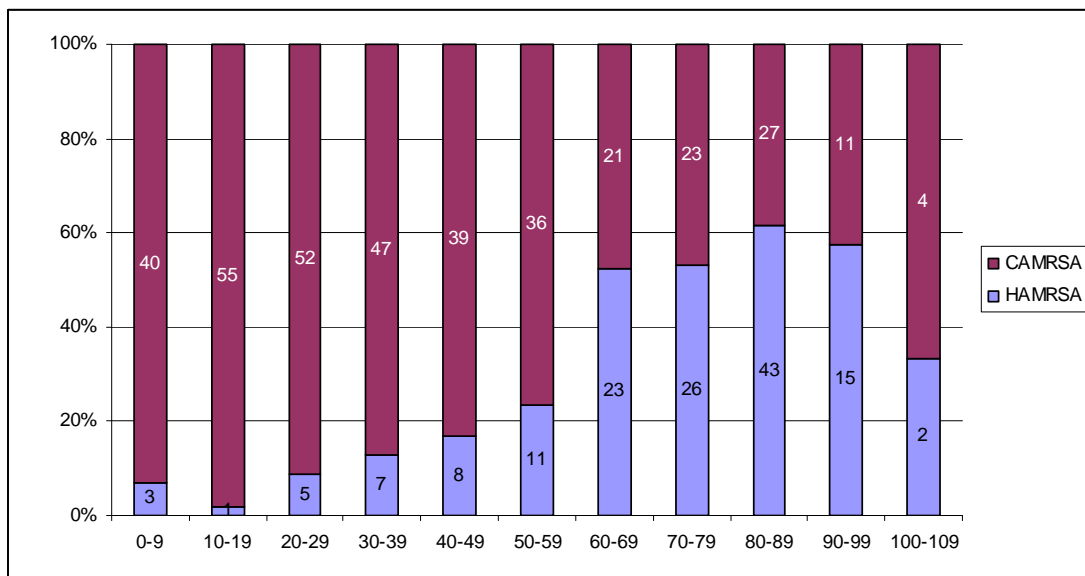


Mean, median and percentile data

Age (years)	CA-MRSA	HA-MRSA
Mean (95% Confidence Interval [CI])	40.6 (37.8 – 43.4)	69.8 (66.2 – 73.4)
Median	38	75
25 th percentile	19	61
75 th percentile	59	85

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



Figures in the columns indicate the number of patients with CA-MRSA and HA-MRSA per 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)].

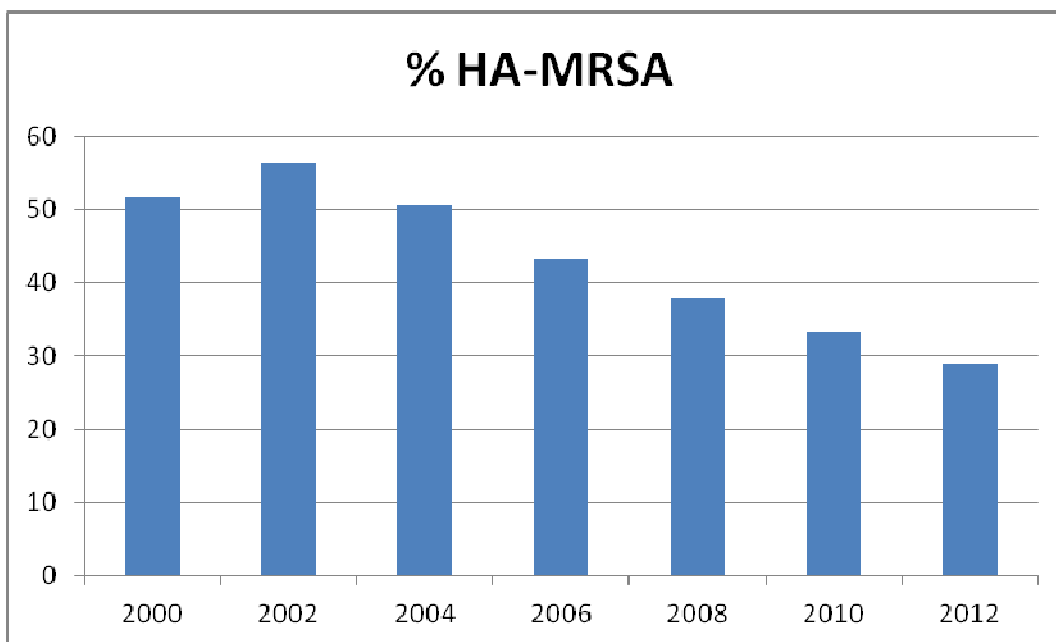
SAP 2012 HA-MRSA

In SAP 2012 three international HA-MRSA clones (144 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST22-IV [4B]	EMRSA-15	105 (72.9)
ST239-III [3A]	Aus -2/3 EMRSA/ EA-EMRSA	38 (26.4)
ST5-II [2A]	New York /Japan MRSA/USA100	1 (0.7)
TOTAL		144

Percentage figures relate to HA- MRSA isolates

SAP 2000 – 2012: Percentage of MRSA Identified as HA-MRSA



ST22-IV [2B]

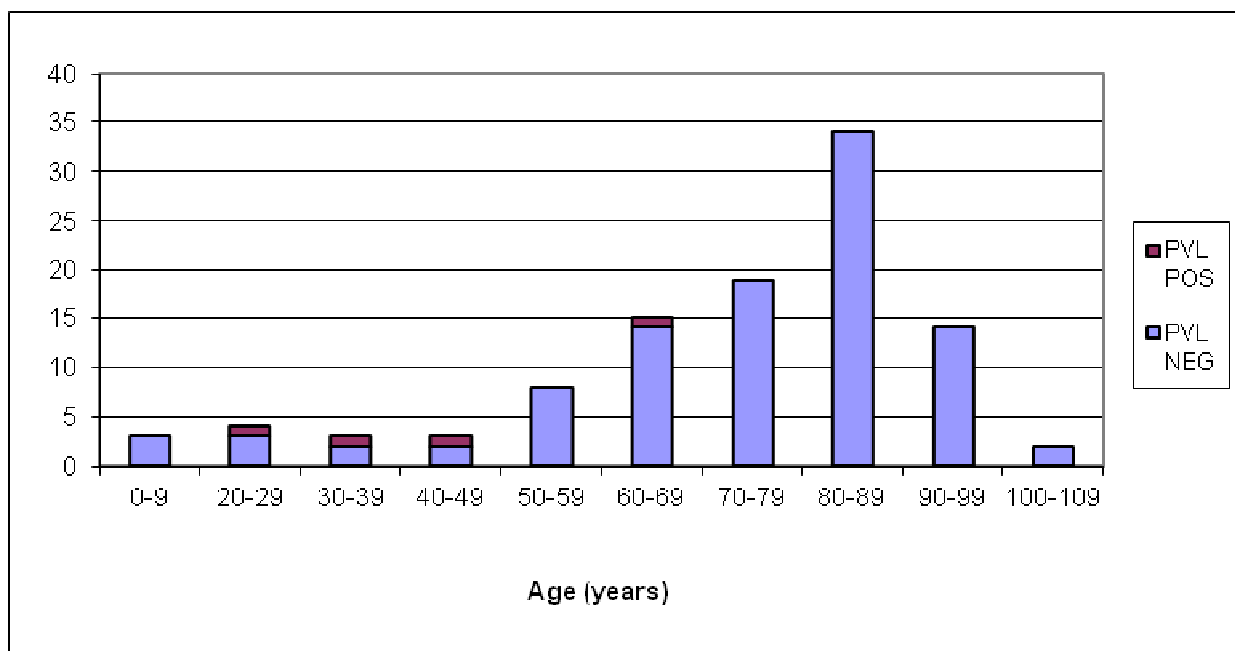
Also known as “EMRSA-15” or the “German Barnim” strain, ST22-IV [2B] has become a major EMRSA clone in many parts of the world including Australia, United Kingdom, New Zealand, several European countries and recently Singapore. First identified in the Midlands and South-East England in the early 1990s EMRSA-15 is non-multiresistant (typically resistant to ciprofloxacin and erythromycin only) and is staphylococcal enterotoxin C, G and I positive. In 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 ^R	99%
	Erythromycin ^R	61%
	Fusidic Acid ^R	3%
	Rifampicin ^R	3%
	Tetracycline ^R	3%
	Gentamicin ^R	0%
	Cotrimoxazole ^R	0%
	High Level Mupirocin ^R	0%

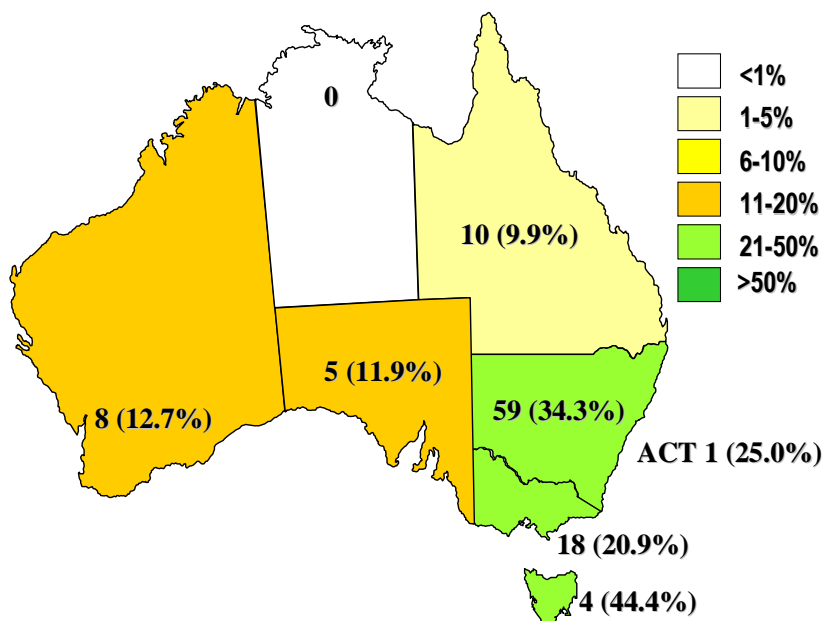
Urease: Negative

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



Regional distribution of ST22-IV [2B]

ST22-IV [2B] (EMRSA-15): n =105 (21.0%)



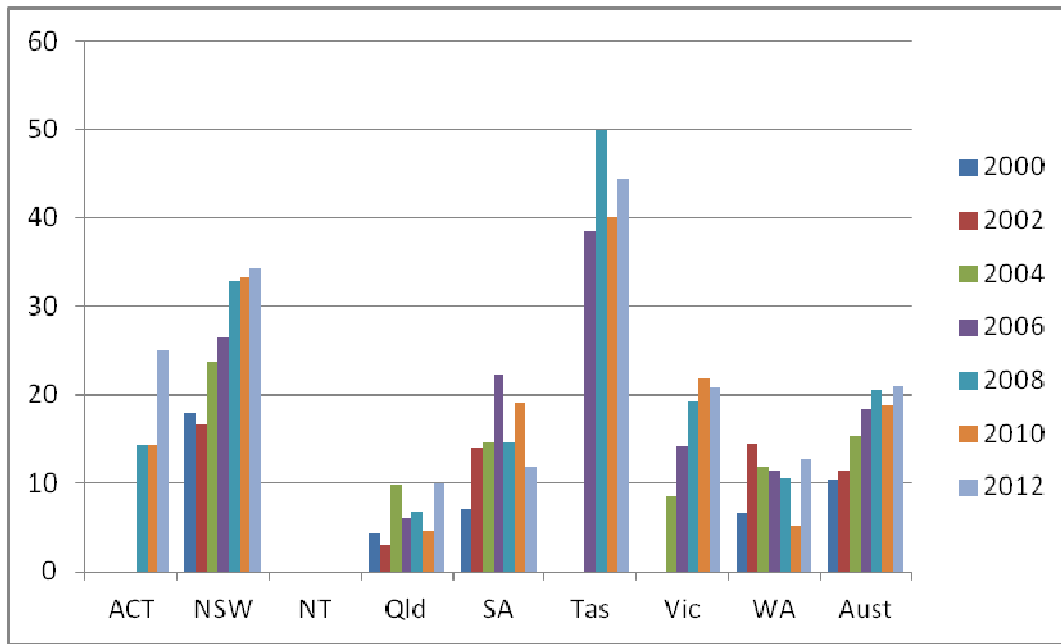
Percentage figures relate to total MRSA isolates characterized

SAP 2000 – 2012: Regional Distribution of ST22-IV [2B]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	0	0	0	0	1 (14.3)	1 (14.3)	1 (25.0)
NSW	23 (18.0)	28 (16.6)	37 (23.7)	51 (26.4)	70 (32.9)	55 (33.3)	59 (34.3)
NT	0	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)	10 (9.9)
SA	2 (7.1)	5 (13.9)	6 (14.6)	8 (22.2)	6 (14.6)	8 (19.0)	5 (11.9)
Tas	0	0	0	5 (38.5)	3 (50)	4 (40.0)	4 (44.4)
Vic	0	0	5 (8.5)	12 (14.1)	19 (19.2)	24 (21.8)	18 (21.2)
WA	3 (6.5)	8 (14.5)	6 (11.8)	5 (11.4)	6 (10.5)	3 (5.1)	8 (12.7)
Total	29 (10.4)	42 (11.4)	59 (15.4)	85 (18.4)	112 (20.5)	100 (18.8)	105 (21.0)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 – 2012: Regional Distribution of ST22-IV [2B]



Percentage figures relate to total MRSA isolates characterized

ST239-III [3A]

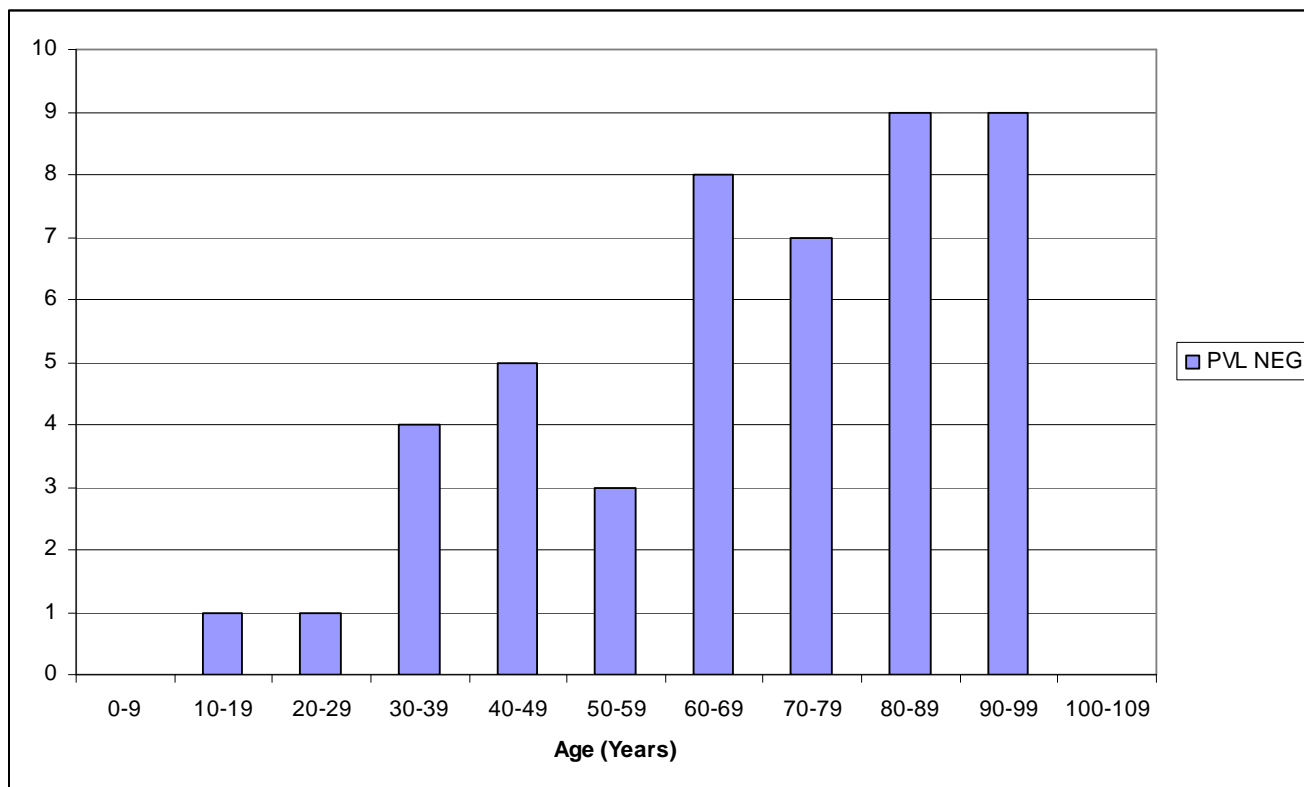
In Australia ST239-III [3A] evolved from the “Eastern Australian EMRSA” clone described in the 1980s. ST239-III [3A] is one of the most commonly encountered and internationally disseminated multidrug-resistant HA-MRSA clones. It is also known as “Aus2/3 EMRSA”, “EMRSA-1”, “Portuguese/Brazilian” clone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

Phenotypic Characteristics

Antibiogram:

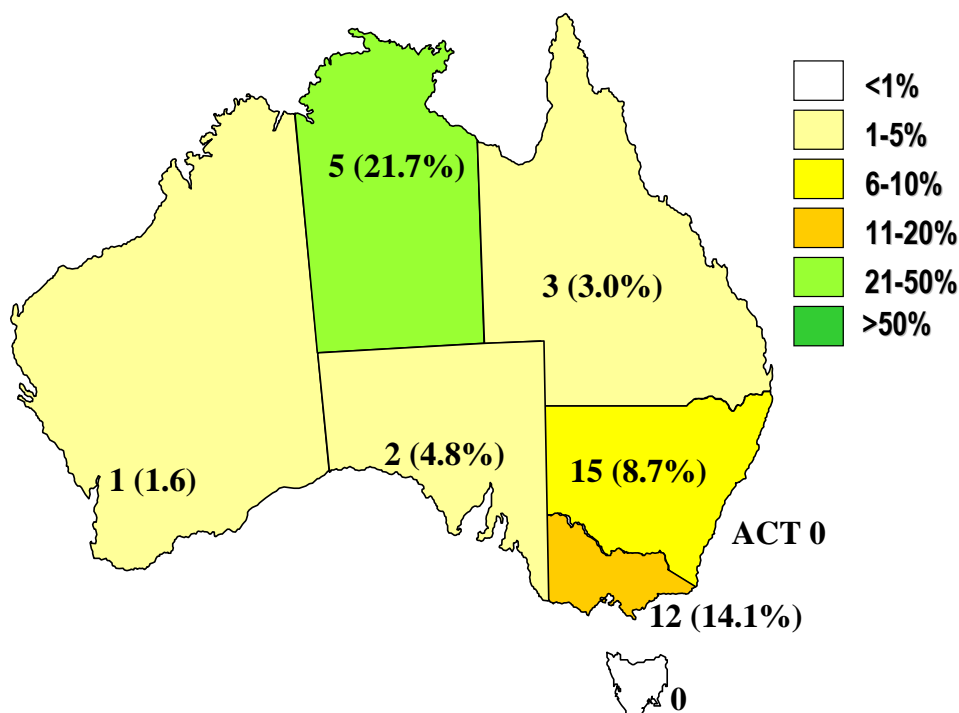
Erythromycin ^R	100%
Tetracycline ^R	100%
Gentamicin ^R	97%
Ciprofloxacin ^R	92%
Cotrimoxazole ^R	92%
Fusidic Acid ^R	3%
Rifampicin ^R	0%
High Level Mupirocin ^R	0%

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



Regional Distribution of ST239-III [3A]

ST239-III [3A]: n = 38 (7.6%)



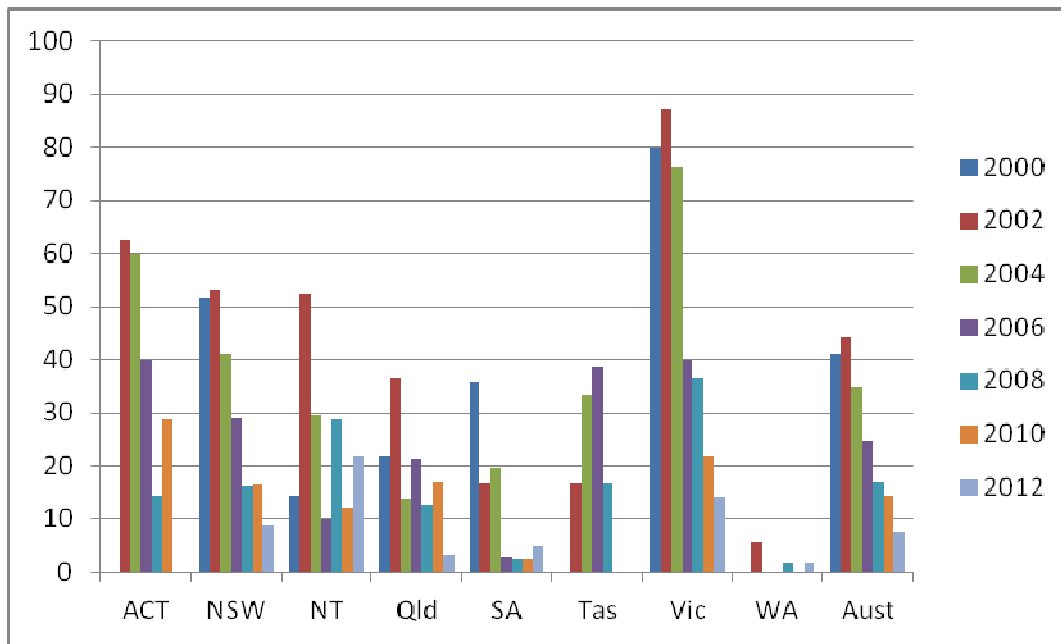
Percentage figures relate to total MRSA isolates characterized

SAP 2000 – 2012: Regional Distribution of ST239-III [3A]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	0	5 (62.5)	3 (60)	2 (40.0)	1 (14.3)	2 (28.6)	0
NSW	66 (51.6)	90 (53.3)	64 (41.0)	56 (29.0)	34 (16.0)	27 (16.4)	15 (8.7)
NT	1 (14.3)	11 (52.4)	5 (29.4)	2 (10.0)	6 (28.6)	4 (12.1)	5 (21.7)
Qld	5 (21.7)	12 (36.4)	7 (13.7)	14 (21.2)	13 (12.6)	18 (17.0)	3 (3.0)
SA	10 (35.7)	6 (16.7)	8 (19.5)	1 (2.8)	1 (2.4)	1 (2.4)	2 (4.8)
Tas	0	1 (16.7)	1 (33.3)	5 (38.5)	1 (16.7)	0	0
Vic	32 (80.0)	34 (87.2)	45 (76.3)	34 (40.0)	36 (36.4)	24 (21.8)	12 (14.1)
WA	0	3 (5.5)	0	0	1 (1.8)	0	1 (1.6)
Total	114 (40.9)	162 (44.1)	133 (34.7)	114 (24.7)	93 (17.0)	76 (14.3)	38 (7.6)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 – 2012: 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. New York/Japan MRSA is the major HA-MRSA strain in the USA, Japan and several South American and Asian countries

Phenotypic Characteristics

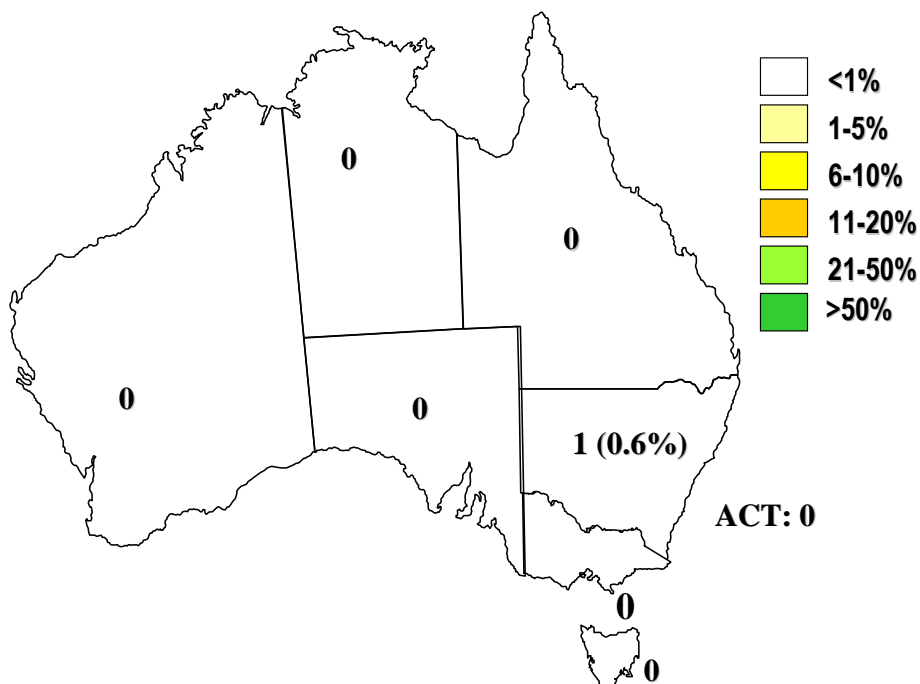
Antibiogram:

Erythromycin ^R	100%
Tetracycline ^R	100%
Ciprofloxacin ^R	100%
Fusidic Acid ^R	100%
Cotrimoxazole ^R	0%
Gentamicin ^R	0%
Rifampicin ^R	0%
High Level Mupirocin ^R	0%

Urease: Positive

Regional Distribution of ST5-II [2A]

ST5-II [2A] (New York/Japan MRSA/USA100): n = 1 (0.7%)



Percentage figures relate to total MRSA isolates characterized

Summary of Community onset HA-MRSA clones Isolated in AGAR SAPs 2000 – 2012

Clone	Alternative Name	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ST22-IV	EMRSA-15	290 (20.1)	42 (20.2)	59 (30.4)	85 (42.5)	112 (54.1)	100 (56.5)	105 (72.9)
ST239-III	Aus-2, -3 EMRSA	114 (79.2)	162 (77.9)	133 (68.6)	114 (57.0)	93 (44.9)	76 (42.9)	38 (26.4)
ST5-II	New York/Japan /USA100	0	0	0	1 ^e (0.5)	1 ^f (0.5)	1 ^h (0.6)	1 ⁱ (0.7)
ST36-II	EMRSA-16/USA200	0	1 ^b (0.5)	2 ^d (1.0)	0	1 ^g (0.5)	0	0
ST8-II	Irish-1 EMRSA	0	3 ^c (1.4)	0	0	0	0	0
ST8-VI	Irish-2 EMRSA	1 ^a (0.7)	0	0	0	0	0	0
Total		144	208	194	200	207	177	144

Percentage figures in parenthesis relate to the healthcare associated MRSA isolates

^aIsolated in WA

^bIsolated in WA

^cIsolated in NSW (n=2) and WA (n=1)

^dIsolated in SA (n=1) and WA (n=1)

^eIsolated in NSW

^fIsolated in Vic

^gIsolated in NSW

^hIsolated in Vic

ⁱIsolated in NSW

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- β -lactams antibiotics. “WA MRSA” has acquired the community associated *SCCmec* types IV and V, which generally 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 “South West Pacific MRSA” (SWP MRSA). SWP 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 2012 CA-MRSA

In SAP 2012, 32 CA-MRSA pulsotypes (25 MLST/*SCCmec* clone types) were identified:

Clone	CC	Alternative Name	n (% of CA-MRSA)
ST93-IV	Singleton	Queensland CA-MRSA	129 (36.3%)
ST30-IV	30	WSPP MRSA	60 (16.9%)
ST1-IV	1	WA MRSA -1	48 (13.5%)
ST45-V	45	WA MRSA-84	21 (5.9%)
ST78-IV	88	WA MRSA-2	18 (5.1%)
ST5-IV	5	WA MRSA-3	17(4.8%)
ST73-IV	5	WA MRSA-65	10 (2.8%)
ST8-IV	8	USA 300	10 (2.8%)
ST59-V _T	59	Taiwan MRSA	5 (1.4%)
ST952-V _T	59	Taiwan A MRSA	5 (1.4%)
ST5-IV	5	WA MRSA-121	4 (1.1%)
ST6-IV	5	WA MRSA-51	3 (0.8%)
ST8-IV	8	WA MRSA-5	3 (0.8%)
953-IV	97	WA MRSA-54	3 (0.8%)
ST772-V	1	Bengal Bay CA-MRSA	2 (0.6%)
ST1-V	1		1 (0.3%)
ST188-IV	1	WA MRSA-38	1 (0.3%)
ST5-IV	5	WA MRSA-71	1 (0.3%)

SAP 2012: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

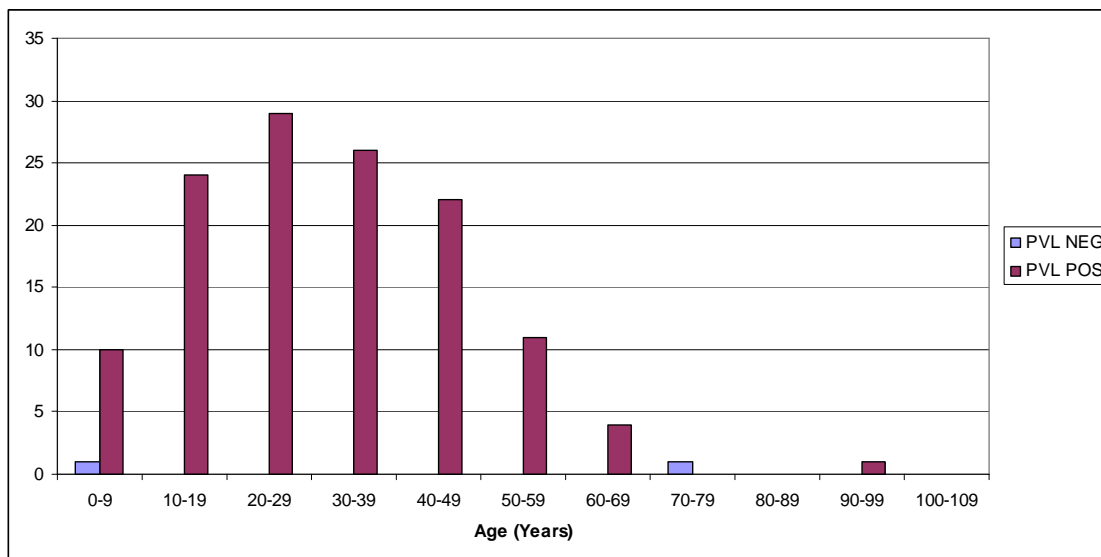
Clone	CC	Alternative Name	n (% of CA-MRSA)
ST5-IV	5	WA MRSA-96	1 (0.3%)
ST5-V	5	WA MRSA-109	1 (0.3%)
ST5-V	5		1 (0.3%)
ST835-IV	5	WA MRSA-48	1 (0.3%)
ST2471-V	8	WA MRSA-120	1 (0.3%)
ST12-novel	12	WA MRSA-59	1 (0.3%)
ST30-V	30	WA MRSA-124	1 (0.3%)
ST45-IV	45	WA MRSA-75	1 (0.3%)
ST59-IV	59	WA MRSA-15	1 (0.3%)
ST59-IV	59	WA MRSA-55	1 (0.3%)
ST72-IV	72	Korean Clone	1 (0.3%)
ST577-IV	121	WA MRSA-22	1 (0.3%)
ST883-IV	Singleton	WA MRSA-47	1 (0.3%)
ST1303-IV	Undetermined	WA MRSA-76	1 (0.3%)
Total			355

Major CA-MRSA Clones

ST93-IV [2B]

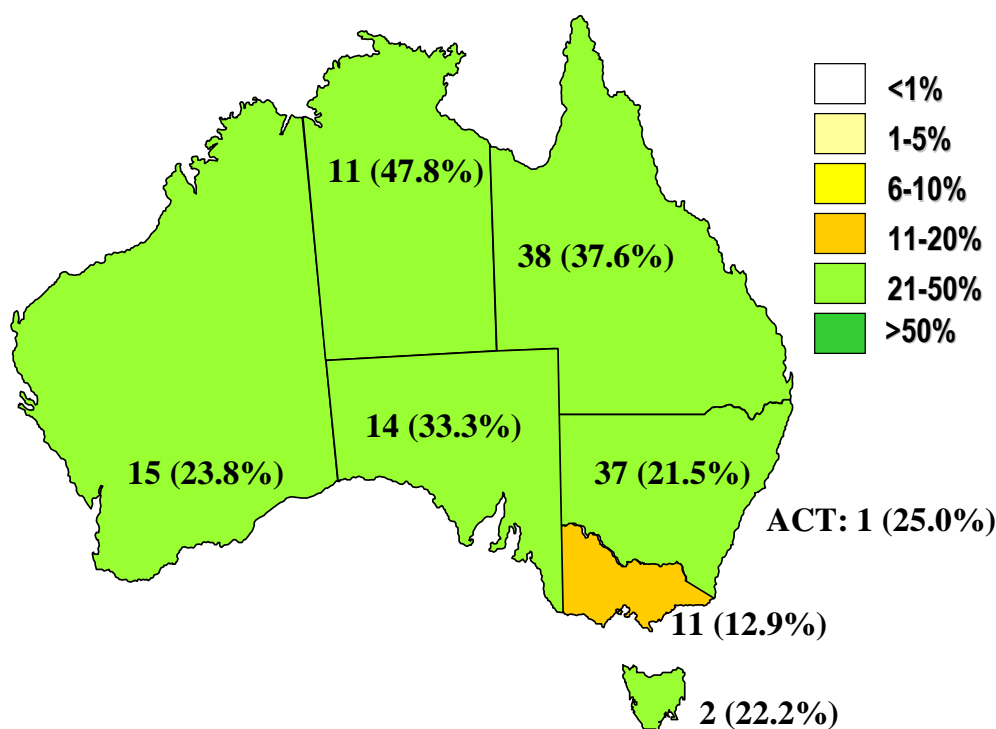
Also known as the “Queensland MRSA” clone, ST93-IV [2B] is a singleton (ie does not form part of a clonal complex) and is PVL positive.

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



Regional Distribution of ST93-IV [2B]

ST93-IV [2B] (Queensland MRSA): n = 129 (25.9%)



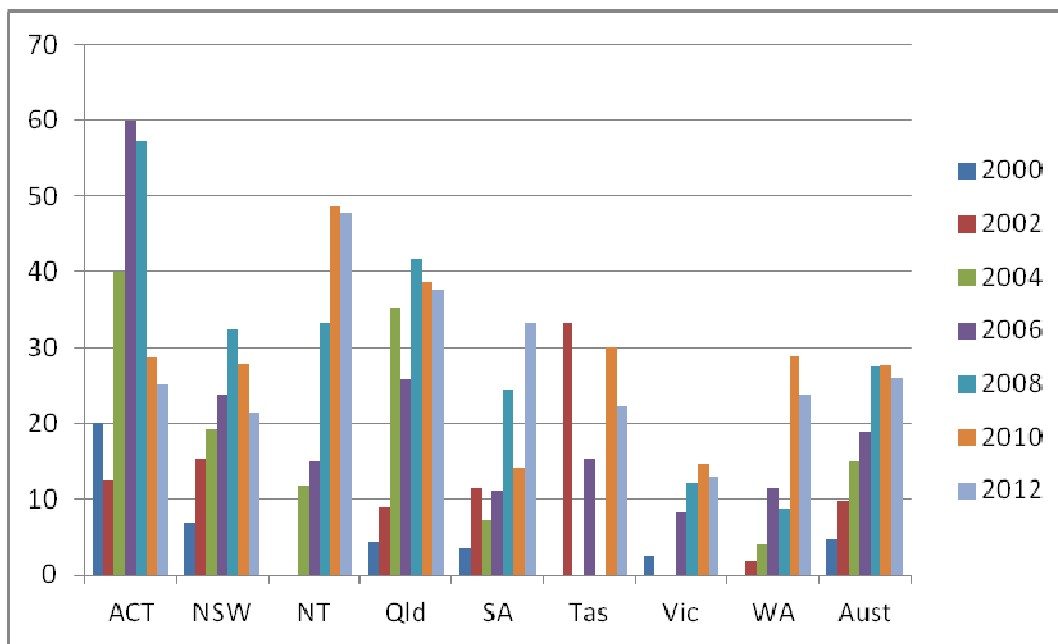
Percentage figures relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST93-IV [2B]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	1 (20.0)	1 (12.5)	2 (40.0)	3 (60.0)	4 (57.1)	2 (28.6)	1 (25.0)
NSW	9 (7.0)	26 (15.4)	30 (19.2)	46 (23.8)	69 (32.4)	46 (27.9)	37 (21.5)
NT	0	0	2 (11.8)	3 (15.0)	7 (33.3)	16 (48.5)	11 (47.8)
Qld	1 (4.3)	3 (9.0)	18 (35.3)	17 (25.8)	43 (41.7)	41 (38.7)	38 (37.6)
SA	1 (3.6)	3 (11.5)	3 (7.3)	4 (11.1)	10 (24.4)	6 (14.3)	14 (33.3)
Tas	0	2 (33.3)	0	2 (15.4)	0	3 (30.0)	2 (22.2)
Vic	1 (2.5)	0	0	7 (8.2)	12 (12.1)	16 (14.5)	11 (12.9)
WA	0	1 (1.8)	2 (3.9)	5 (11.4)	5 (8.8)	17 (28.8)	15 (23.8)
Total	13 (4.7)	36 (9.8)	57 (14.9)	87 (18.8)	150 (27.4)	147 (27.6)	129 (25.9)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST93-IV [2B]

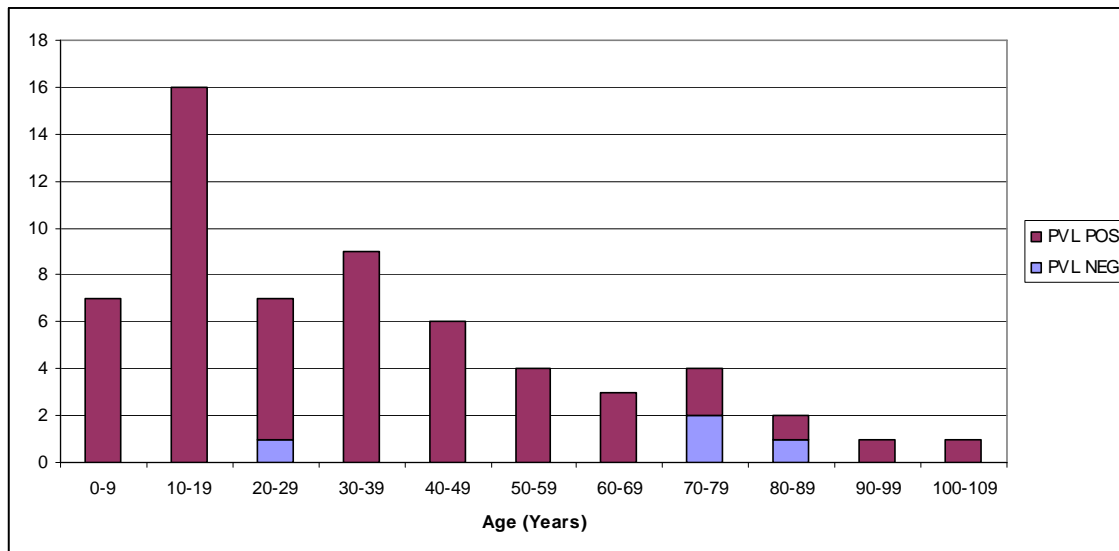


Percentage figures relate to total MRSA isolates characterized

ST30-IV [2B]

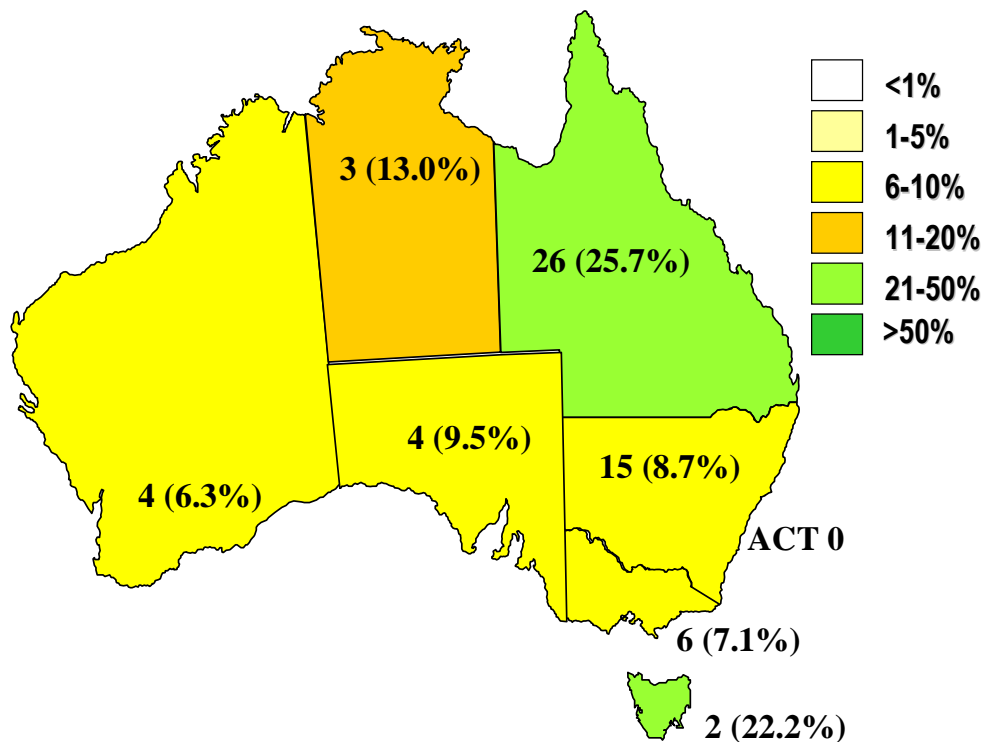
Also known as “SWP MRSA”, ST30-IV [2B] was originally described in Polynesians living in New Zealand and the Pacific islands and is PVL positive.

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



Regional Distribution of ST30-IV [2B]

ST30-IV [2B] (SWP MRSA): n = 60 (12.0%)



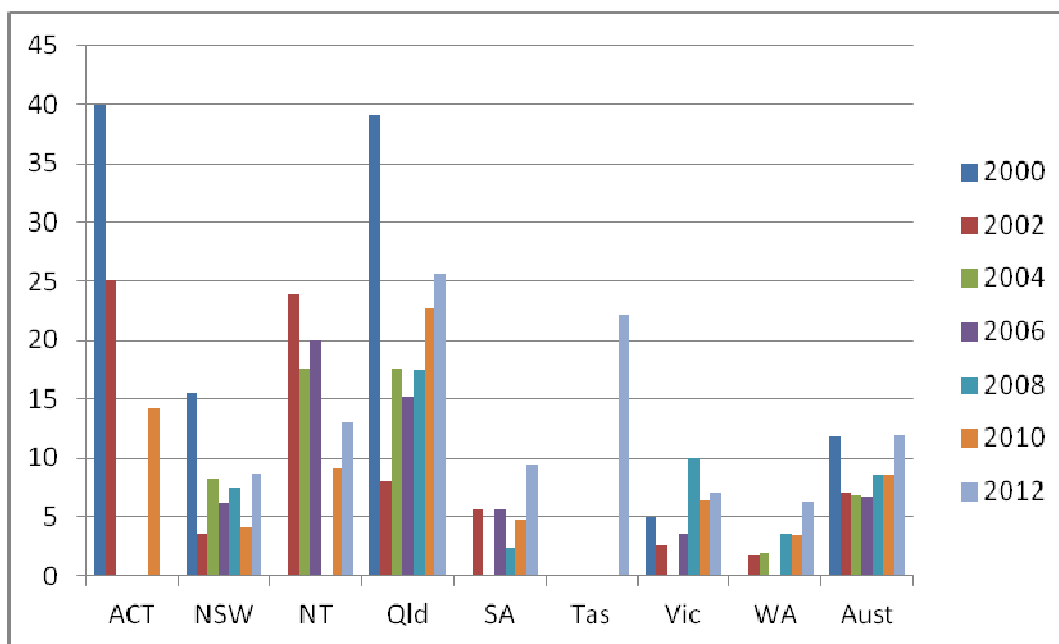
Percentage figures relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST30-IV [2B]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	2 (40.0)	2 (25.0)	0	0	0	1 (14.3)	0
NSW	20 (15.6)	6 (3.6)	13 (8.3)	12 (6.2)	16 (7.5)	7 (4.2)	15 (8.7)
NT	0	5 (23.8)	3 (17.6)	4 (20.0)	0	3 (9.1)	3 (13.0)
Qld	9 (39.1)	9 (8.0)	9 (17.6)	10 (15.2)	18 (17.5)	24 (22.6)	26 (25.7)
SA	0	2 (5.6)	0	2 (5.6)	1 (2.4)	2 (4.8)	4 (9.5)
Tas	0	0	0	0	0	0	2 (22.2)
Vic	2 (5.0)	1 (2.6)	0	3 (3.5)	10 (10.1)	7 (6.4)	6 (7.1)
WA	0	1 (1.8)	1 (2.0)	0	2 (3.5)	2 (3.4)	4 (6.3)
Total	33 (11.8)	26 (7.1)	26 (6.8)	31 (6.7)	47 (8.6)	46 (8.6)	60 (12.0)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST30-IV [2B]

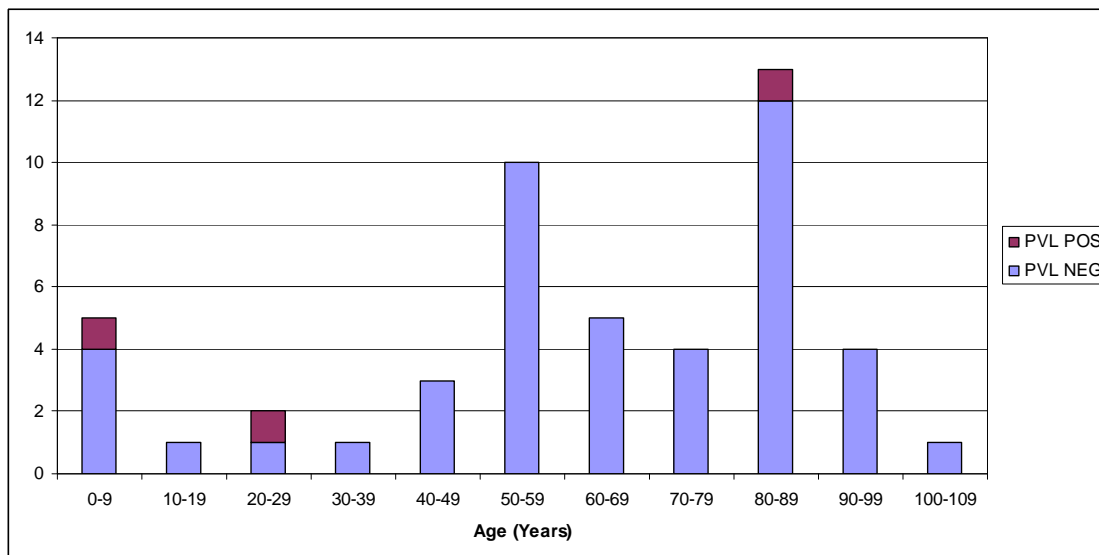


Percentage figures relate to total MRSA isolates characterized

ST1-IV [2B]

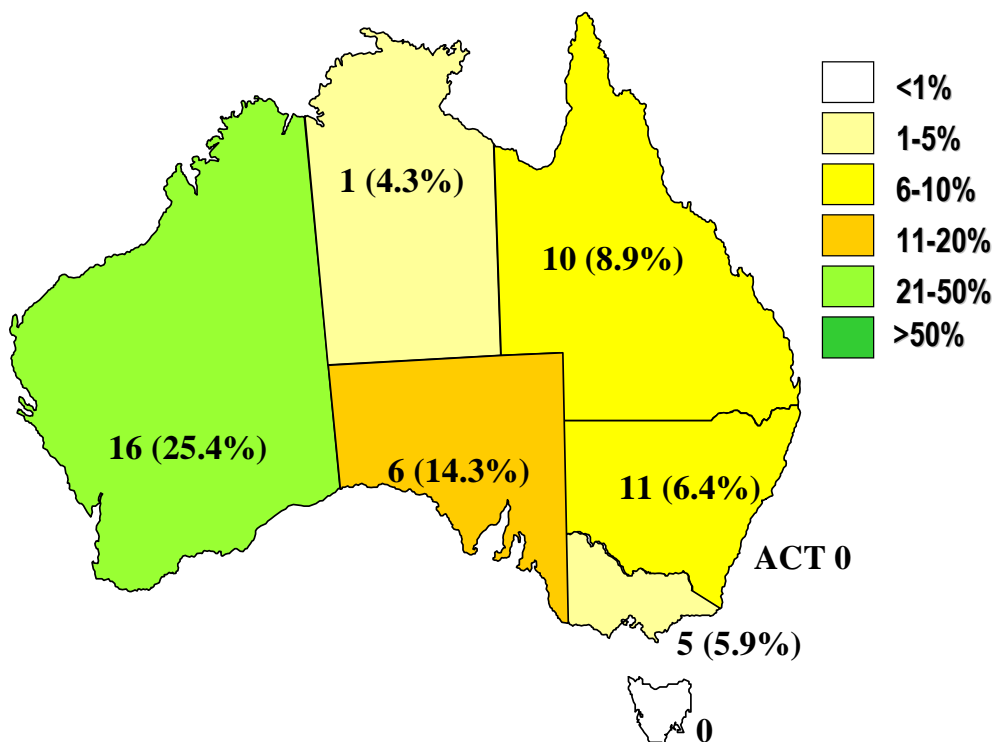
Also known as “WA MRSA-1”, ST1-IV forms part of clonal complex 1. Although normally PVL-negative, PVL-positive “USA400” MRSA-like strains have been identified in Australia.

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



Regional Distribution of ST1-IV [2B]

ST1-IV [2B] (WA MRSA-1): n = 48 (9.6%)



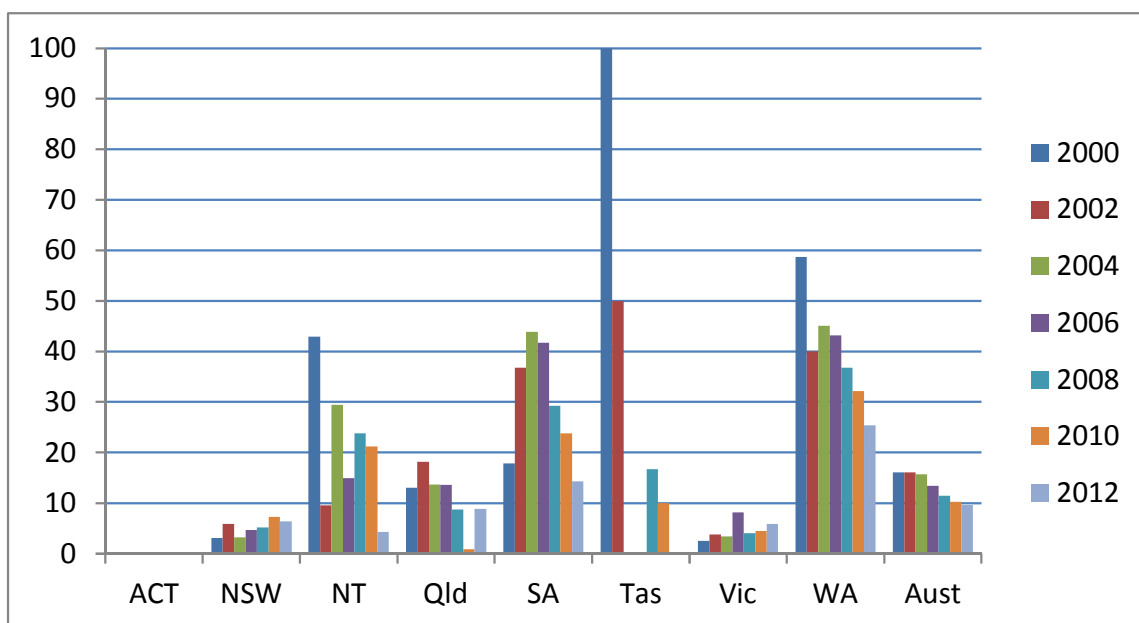
Percentage figures relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST1-IV [2B]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	0	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)	11 (6.4)
NT	3 (42.9)	2 (9.5)	5 (29.4)	3 (15.0)	5 (23.8)	7 (21.2)	1 (4.3)
Qld	3 (13.0)	6 (18.2)	7 (13.7)	9 (13.6)	9 (8.7)	1 (0.9)	9 (8.9)
SA	5 (17.90)	14 (36.8)	18 (43.9)	15 (41.7)	12 (29.3)	10 (23.8)	6 (14.3)
Tas	2 (100)	3 (50.0)	0	0	1 (16.7)	1 (10)	0
Vic	1 (2.5)	2 (3.8)	2 (3.4)	7 (8.2)	4 (4.0)	5 (4.5)	5 (5.9)
WA	27 (58.7)	22 (40)	23 (45.1)	19 (43.2)	21 (36.8)	19 (32.2)	16 (25.4)
Total	45 (16.1)	59 (16.1)	60 (15.7)	62 (13.4)	63 (11.5)	55 (10.3)	48 (9.6)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST1-IV [2B]

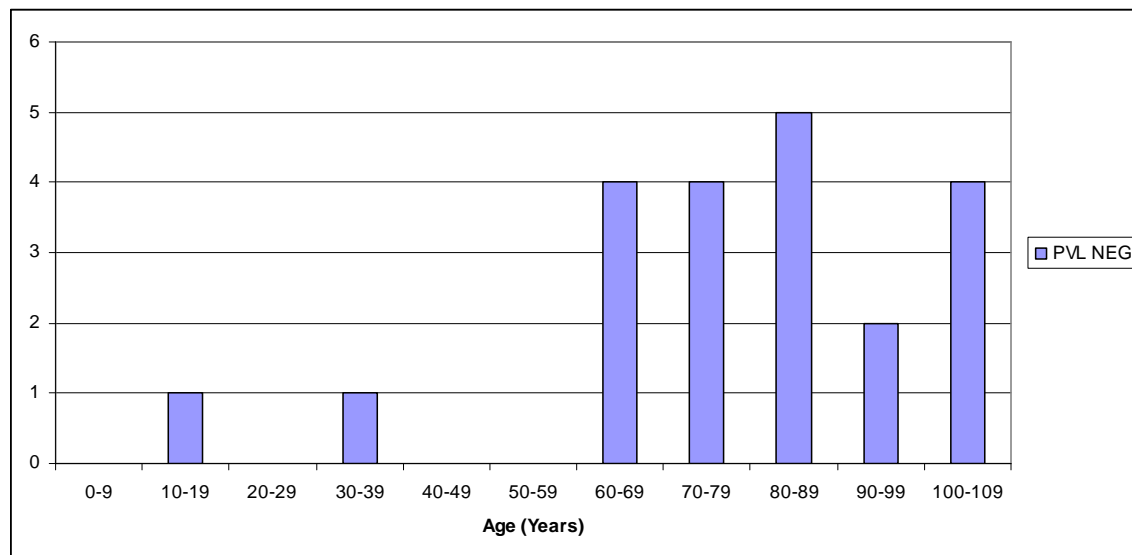


Percentage figures relate to total MRSA isolates characterized

ST45-V [5C2&5]

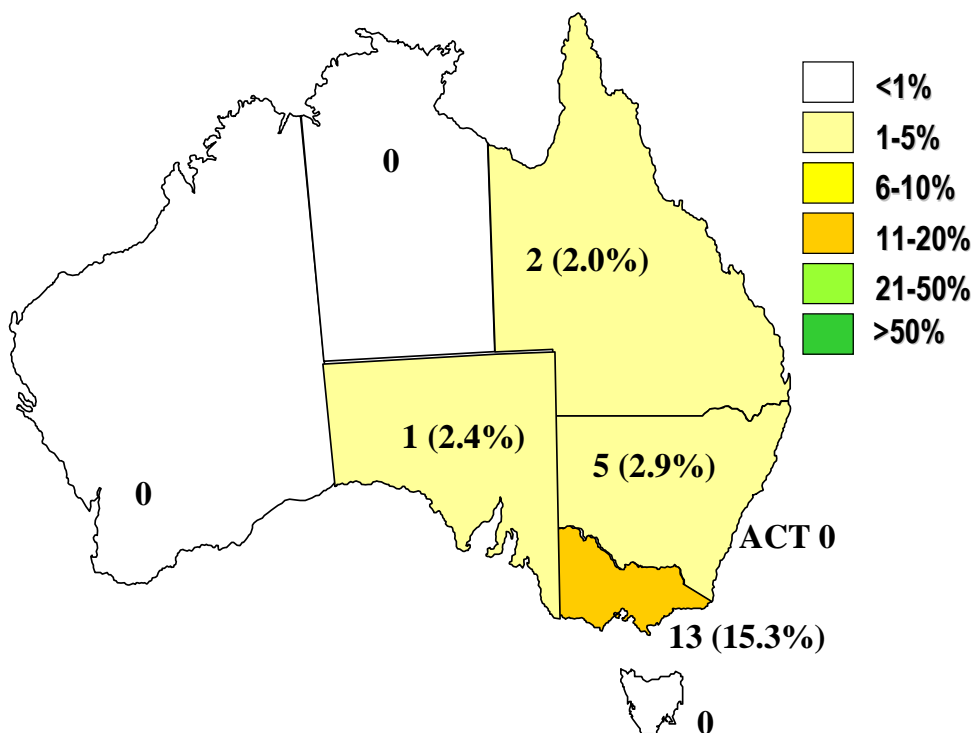
Also known as “WA MRSA-84” and typically PVL negative

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 = 21 (4.2%)



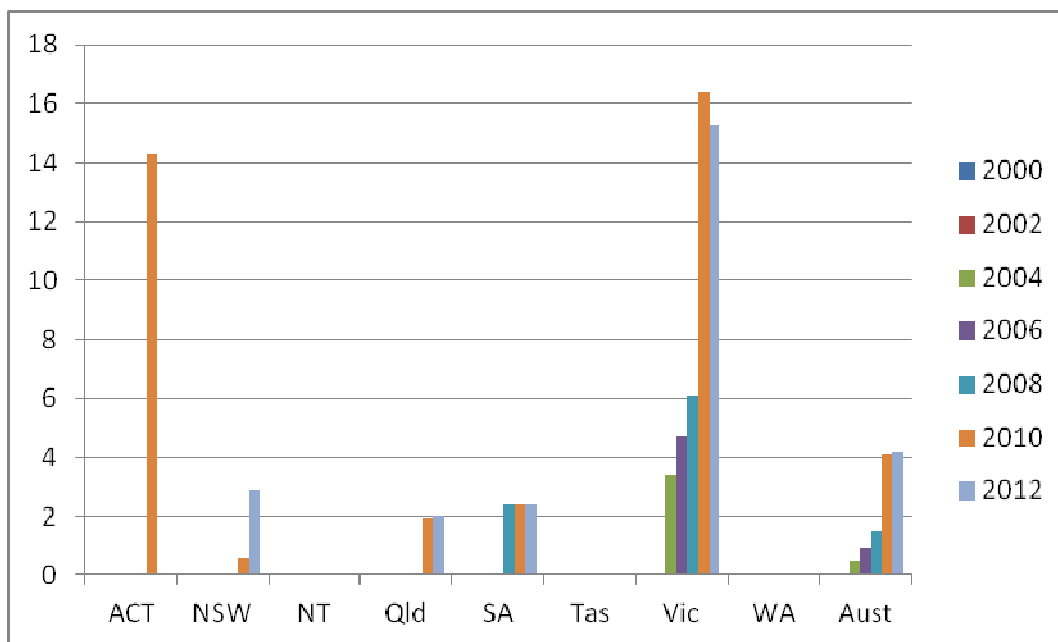
Percentage figures relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST45-V [5C2&5]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	0	0	0	0	1 (14.3)	0	0
NSW	0	0	0	0	0	1 (0.6)	5 (2.9)
NT	0	0	0	0	0	0	0
Qld	0	0	0	0	0	2 (1.9)	2 (2.0)
SA	0	0	0	0	1 (2.4)	1 (2.4)	1 (2.4)
Tas	0	0	0	0	0	0	0
Vic	0	0	2 (3.4)	4 (4.7)	6 (6.1)	18 (16.4)	13 (15.3)
WA	0	0	0	0	0	0	0
Total	0	0	2 (0.5)	4 (0.9)	8 (1.5)	22 (4.1)	21 (4.2)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST45-V [5C2&5]

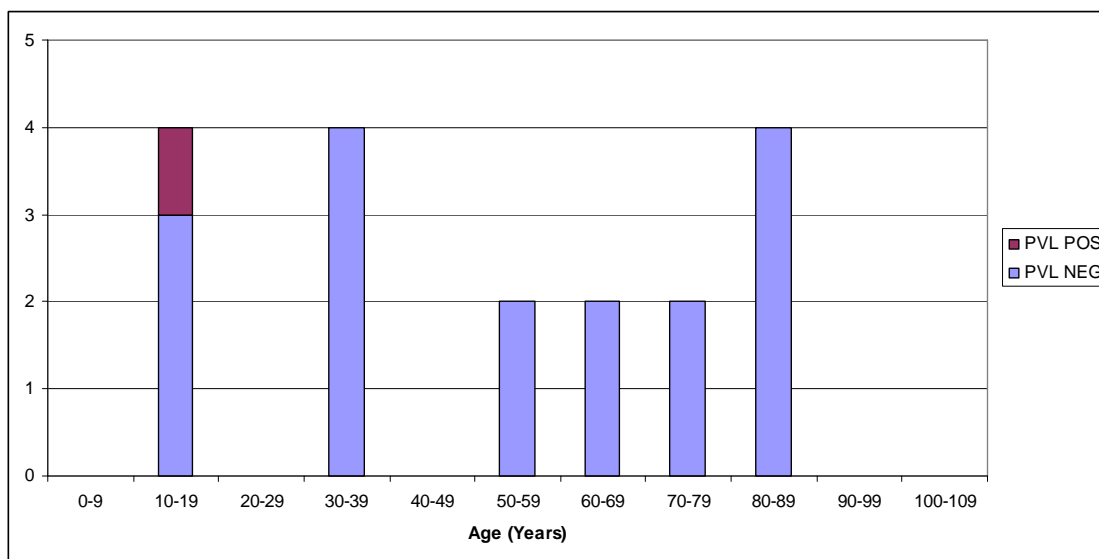


Percentage figures relate to total MRSA isolates characterized

ST78- IV [2B]

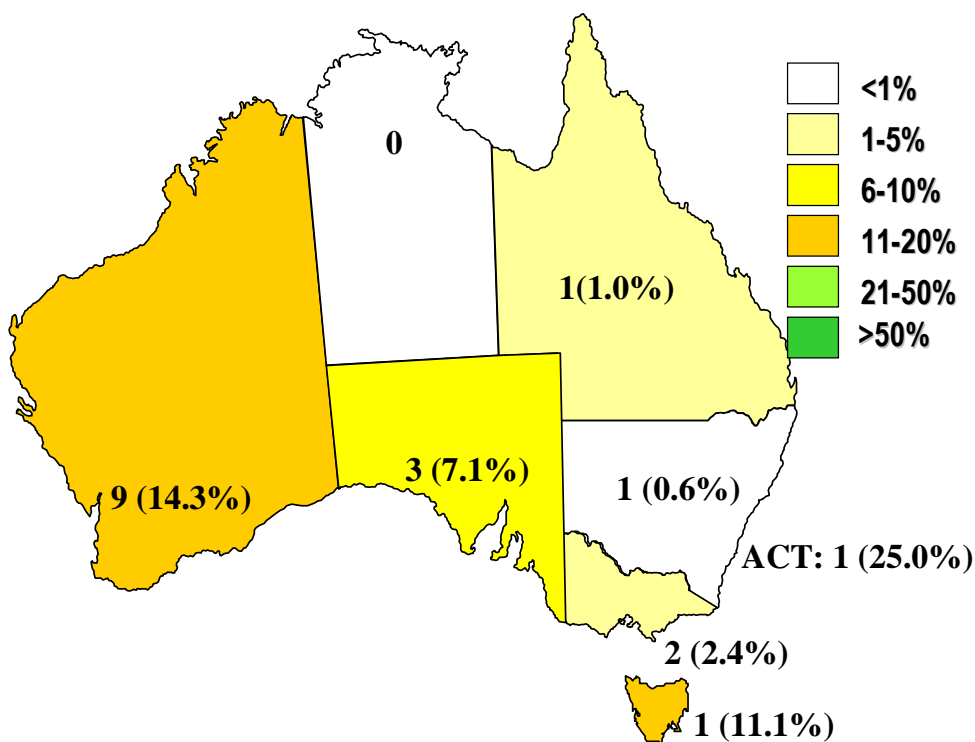
Also known as “WA MRSA-2” and typically PVL negative

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



Regional Distribution of ST78-IV [2B]

ST78-IV [2B] (WA MRSA-2): n = 18 (3.6%)



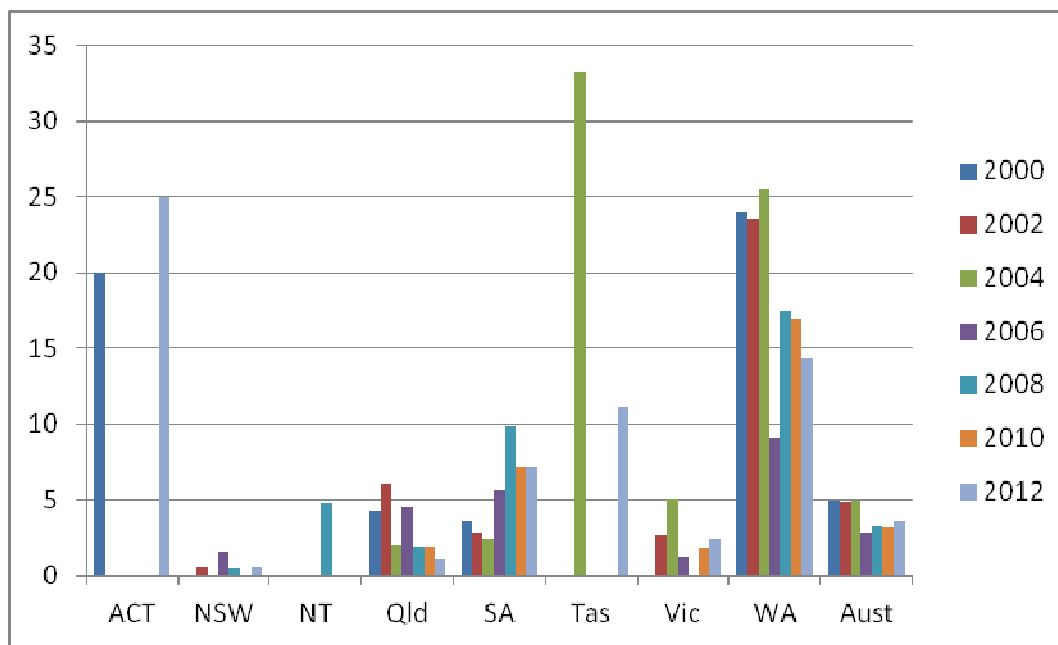
Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST78-IV [2B]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	1 (20.0)	0	0	0	0	0	1 (25.0)
NSW	0	1 (0.6)	0	3 (1.6)	1 (0.5)	0	1 (0.6)
NT	0	0	0	0	1 (4.8)	0	0
Qld	1 (4.3)	2 (6.1)	1 (2.0)	3 (4.5)	2 (1.9)	2 (1.9)	1 (1.0)
SA	1 (3.6)	1 (2.8)	1 (2.4)	2 (5.6)	4 (9.8)	3 (7.1)	3 (7.1)
Tas	0	0	1 (33.3)	0	0	0	1 (11.1)
Vic	0	1 (2.6)	3 (5.1)	1 (1.2)	0	2 (1.8)	2 (2.4)
WA	11 (23.9)	13 (23.6)	13 (25.5)	4 (9.1)	10 (17.5)	10 (16.9)	9 (14.3)
Total	14 (5.0)	18 (4.9)	19 (4.8)	13 (2.8)	18 (3.3)	17 (3.2)	18 (3.6)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST78-IV [2B]

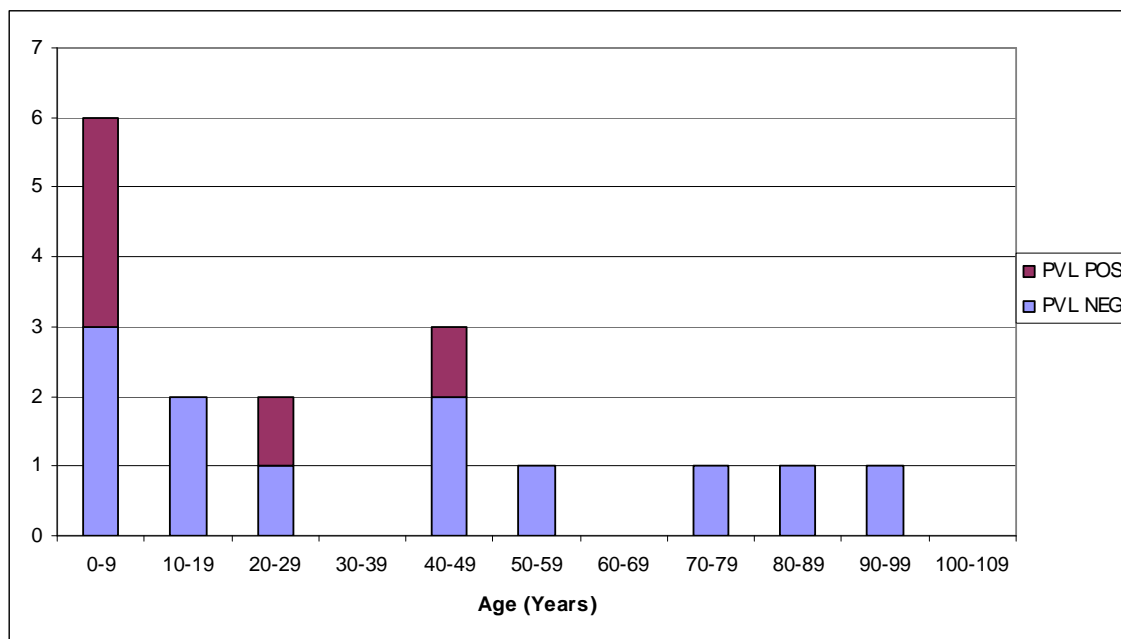


Percentage figures relate to total MRSA isolates characterized

ST5-IV [2B]

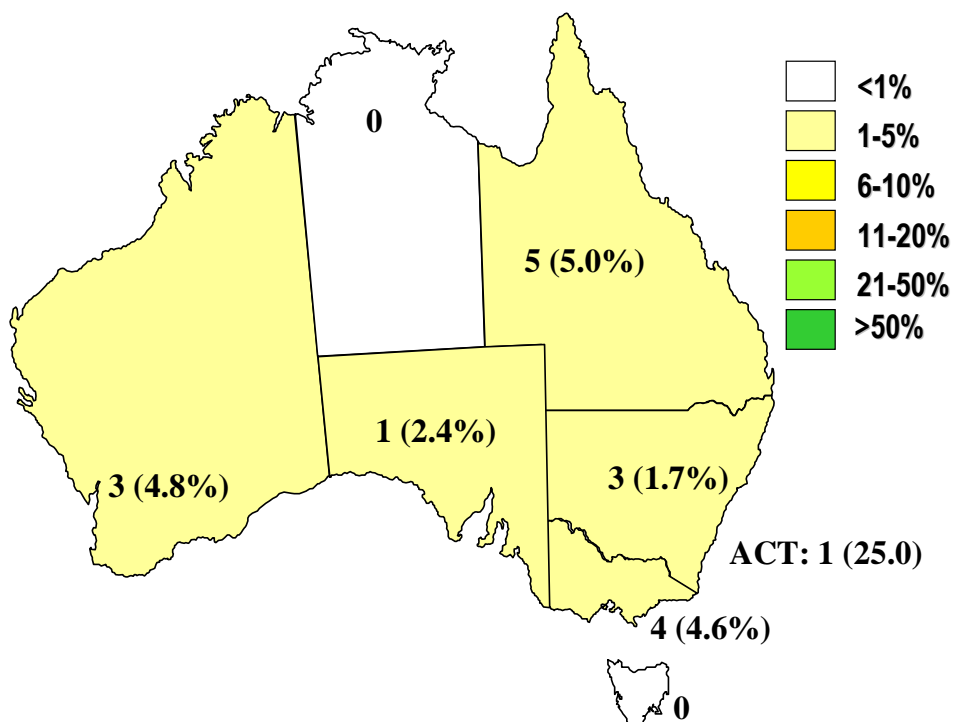
Also known as “WA MRSA-3” and typically PVL negative

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



Regional Distribution of ST5-IV [2B]

ST5-IV [2B] (WA MRSA-3): n = 17 (3.4%)



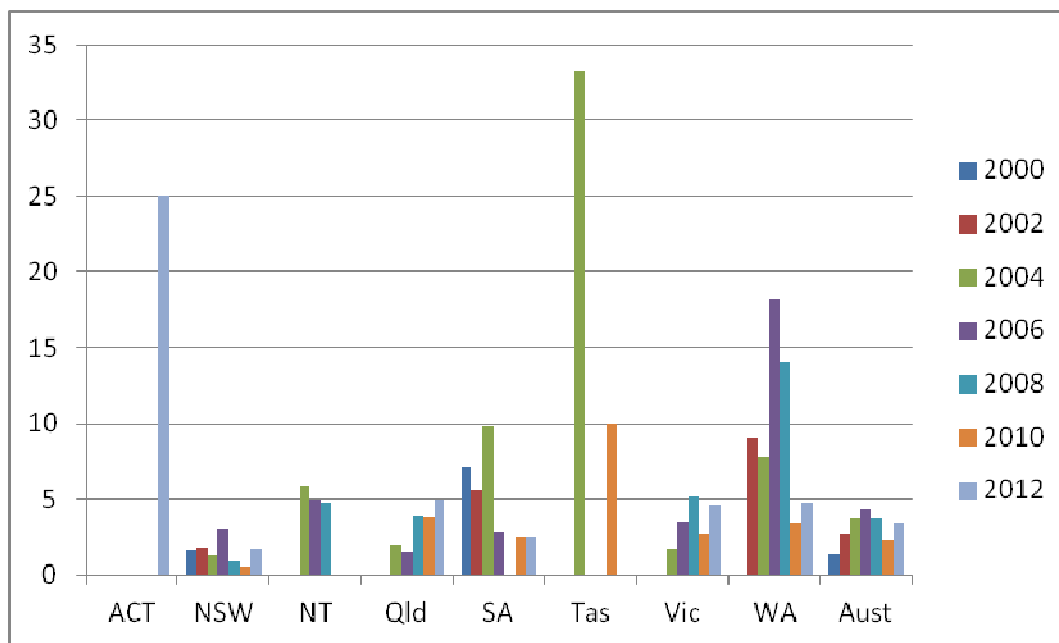
Percentage figures relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST5-IV [2B]

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008	SAP 2010	SAP 2012
ACT	0	0	0	0	0	0	1 (25.0)
NSW	2 (1.6)	3 (1.8)	2 (1.3)	6 (3.1)	2 (0.9)	1 (0.6)	3 (1.7)
NT	0	0	1 (5.9)	1 (5.0)	1 (4.8)	0	0
Qld	0	0	1 (2.0)	1 (1.5)	4 (3.9)	4 (3.8)	5 (5.0)
SA	2 (7.1)	2 (5.6)	4 (9.8)	1 (2.8)	0	1 (2.4)	1 (2.4)
Tas	0	0	1 (33.3)	0	0	1 (10.0)	0
Vic	0	0	1 (1.7)	3 (3.5)	3 (5.1)	3 (2.7)	4 (4.6)
WA	0	5 (9.1)	4 (7.8)	8 (18.2)	8 (14.0)	2 (3.4)	3 (4.8)
Total	4 (1.4)	10 (2.7)	14 (3.7)	20 (4.3)	20 (3.7)	12 (2.3)	17 (3.4)

Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2000 to SAP 2012 Regional Distribution of ST5-IV [2B]



Percentage figures relate to total MRSA isolates characterized

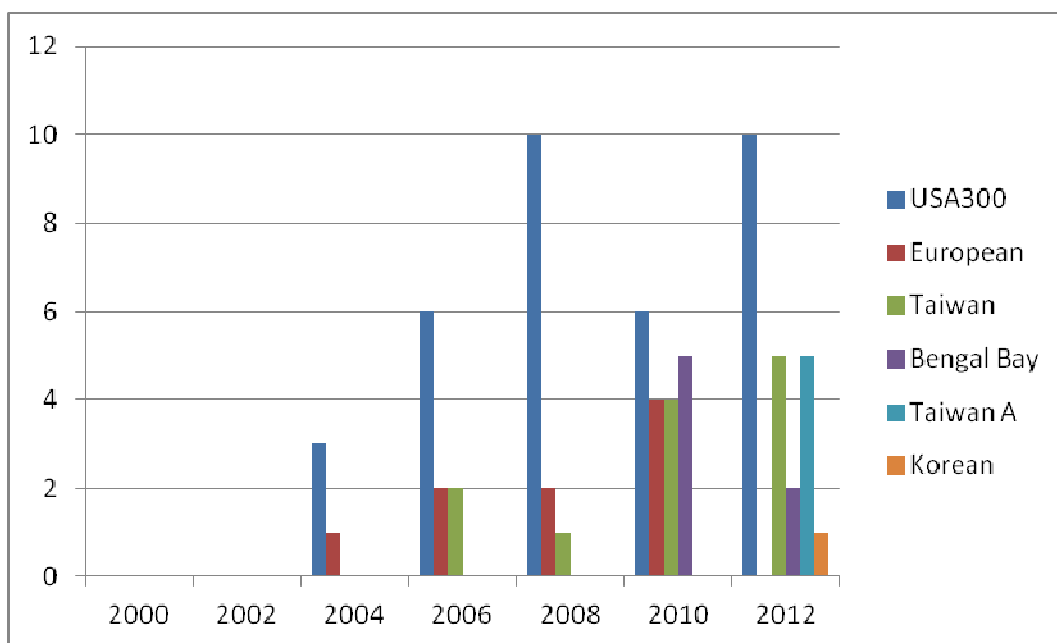
International CA-MRSA Clones

In SAP 2012, five international CA-MRSA clones were characterized. Four of the five clones are Panton Valentine leucocidin (PVL) positive.

CLONE	ALTERNATIVE NAME	n (%)
ST8-IV	USA300	10 (2.8)
ST59-V _T	Taiwan CA-MRSA	5 (1.4)
ST952-V _T	Taiwan A CA-MRSA	5 (1.4)
ST772-IV	Bengal Bay	2 (0.6)
ST72-V	Korean CA-MRSA	1 (0.3)
TOTAL		23 (6.5)

Percentage figures relate to CA-MRSA isolates characterized

2012: Number of MRSA Identified as International CA-MRSA



SAP 2000 – 2012: Number of MRSA Identified as International CA-MRSA

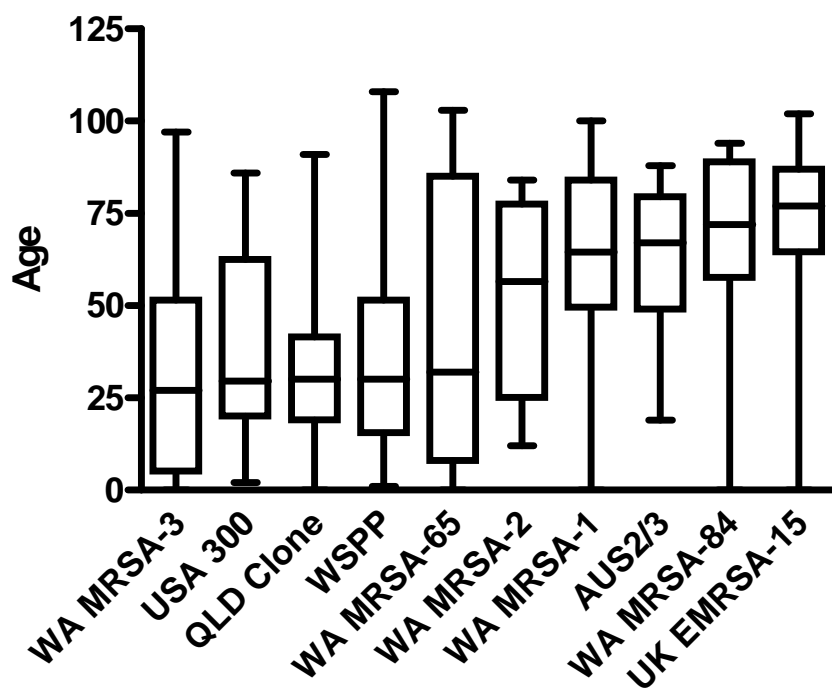
CLONE	SAP 2004				SAP 2006				SAP 2008				SAP 2010			
	USA 300	Europe	Taiwan	Bengal Bay	USA 300	Europe	Taiwan	Bengal Bay	USA 300	Europe	Taiwan	Bengal Bay	USA 300	Europe	Taiwan	Bengal Bay
ACT	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
NSW	3	1	0	0	4	0	0	0	4	1	0	0	3	2	1	0
NT	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Qld	0	0	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
Total	3	1	0	0	6	2	2	0	10	2	1	0	6	4	4	5

SAP 2000 – 2012: Number of MRSA Identified as International CA-MRSA cont

CLONE	SAP 2012				
	USA 300	Taiwan	Taiwan A	Bengal Bay	Korean
ACT	0	0	0	0	0
NSW	5	1	2	2	1
NT	0	0	0	0	0
Qld	1	1	1	0	0
SA	1	0	2	0	0
Tas	0	0	0	0	0
Vic	3	3	0	0	0
WA	0	0	0	0	0
Total	10	5	5	2	1

Age Statistics for Major clones (≥ 10 isolates)

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



Mean, median and percentile data

Age (years)	ST5 IV WA MRSA 3	ST8 IV USA300	ST93-IV Qld	ST30 IV WSPP	ST73 IV WA MRSA 65	ST78 IV WA MRSA 2	ST1 IV WA MRSA 1	ST239 III EMRSA	ST45 V WA MRSA 84	ST22 IV EMRSA 15
Mean (95% CI)	33	38	31	35	43	51	60	63	68	73
95% CI of mean	17 - 49	18 - 57	28 - 34	28 - 42	19 - 68	38 - 64	52 - 68	56 - 69	57 - 79	68 - 77
Median	27	30	30	30	32	56	64	67	72	77
25 th percentile	5	20	19	16	8	25	50	49	58	65
75 th percentile	52	62	42	52	85	78	84	80	89	87

FOOTNOTE:

ST5-IV (WA MRSA-3) PVL Positive (5 isolates): Mean Age 18 years (95% CI -7 to 43) median age 6 years

ST5-IV (WA MRSA-3) PVL Negative (12 isolates): Mean Age 39 years (95% CI 18 to 60) median age 36 years

5.5. Panton-Valentine Leucocidin (PVL) Toxin

CA-MRSA

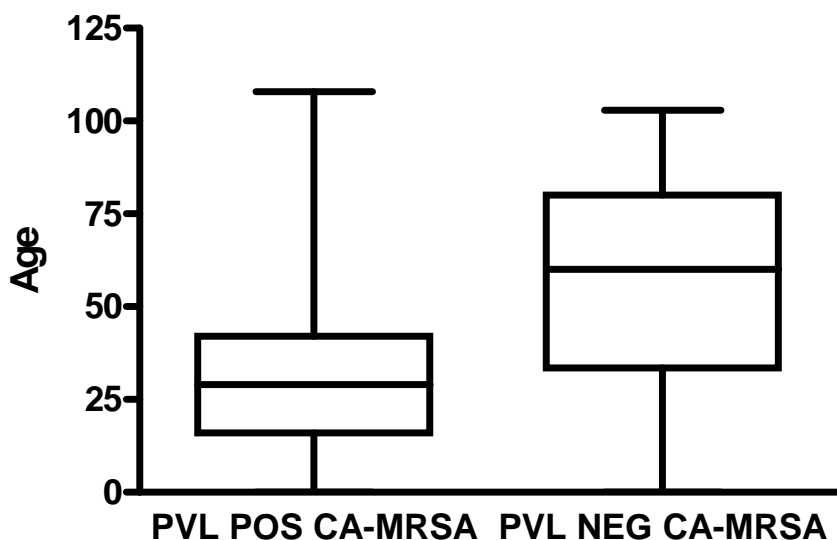
Clone	Alternative Name	Positive	Negative	Total
ST93-IV	Queensland CA-MRSA	127	2	129
ST30-IV	WSPP MRSA	56	4	60
ST1-IV	WA MRSA-1	3	45	48
ST45-V	WA MRSA-84	0	21	21
ST78-IV	WA MRSA-2	1	17	18
ST5-IV	WA MRSA-3	5	12	17
ST73-IV	WA MRSA-65	0	10	10
ST8-IV	USA-300	9	1	10
ST952-V	Taiwan A MRSA	5	0	5
ST59-V	Taiwan MRSA	5	0	5
ST5-IV	WA MRSA-121	4	0	4
ST8-IV	WA MRSA-5	0	3	3
ST6-IV	WA MRSA-51	3	0	3
ST953-IV	WA MRSA-54	0	3	3
ST772-V	Bengal Bay MRSA	2	0	2
ST1-V		0	1	1
ST5-IV	WA MRSA-71	1	0	1
ST5-IV	WA MRSA-96	0	1	1
ST5-V	WA MRSA-109	0	1	1
ST5-V		0	1	1
ST12-novel	WA MRSA-59	0	1	1
ST30-V	WA MRSA-124	1	0	1
ST45-IV	WA MRSA-75	0	1	1
ST59-IV	WA MRSA-15	0	1	1
ST59-IV	WA MRSA-55	1	0	1
ST72-IV	Korean Clone	0	1	1
ST188-IV	WA MRSA-38	0	1	1
ST577-IV	WA MRSA-22	0	1	1

SAP 2012: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

Clone	Alternative Name	Positive	Negative	Total
ST835-IV	WA MRSA-48	0	1	1
ST883-IV	WA MRSA-47	0	1	1
ST1303-IV	WA MRSA-76	0	1	1
ST2471-V	WA MRSA-120	0	1	1
Total		223 (62.8)	132 (37.2)	355

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)	31.7 (28.9 – 34.5)	55.7 (50.7 – 60.6)
Median	29	57
25 th percentile	16	28
75 th percentile	42	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

Clone	Alternative Name	Positive	Negative	Total
ST22-IV	EMRSA-15	4	101	105
ST239-III	Aus2/3 EMRSA	0	38	38
ST5-II	New York/Japan EMRSA	0	1	1
Total		4 (2.8%)	140 (97.2%)	144

5.6. CA-MRSA Antibigram

	CC1				CC5									CC8			CC12
	1 IV WA1	1 V	188 IV WA38	772 V Bengal Bay	5 IV WA3	5 IV WA71	5 IV WA96	5 IV WA121	5 V WA109	5 V	6 IV WA51	73 IV WA65	835 IV WA48	8 IV USA300	8 IV WA5	2471 V WA120	12 novel WA59
Oxacillin only:																	
Ox ^R	24				8	1	1				3	5		1			1
Oxacillin plus one non beta lactam antibiotic:																	
Em ^R	5				3							1		3			
Cp ^R	1								1		1			1			
FA ^R	8										3						
Tc ^R					1												
Rf ^R																	
Mp ^R	1				3												
Cot ^R								4									
Oxacillin plus two non beta lactam antibiotics:																	
Em ^R Tc ^R	3																
Er ^R FA ^R	2																
Em ^R Mp ^R					1												
Em ^R Cp ^R	1											1	3				
Tc ^R FA ^R	1	1															

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	CC1				CC5									CC8			CC12
	1 IV WA1	1 V	188 IV WA38	772 V Bengal Bay	5 IV WA3	5 IV WA71	5 IV WA96	5 IV WA121	5 V WA109	5 V	6 IV WA51	73 IV WA65	835 IV WA48	8 IV USA300	8 IV WA5	2471 V WA120	12 novel WA59
Tc ^R Mp ^R														1			
Gm ^R Er ^R															1		
Rf ^R Cp ^R																	
Rf ^R Er ^R					1												
Er ^R Cot ^R																	
Oxacillin plus three non beta lactam antibiotics:																	
Em ^R Tc ^R Cp ^R																	
Gm ^R Er ^R Cp ^R																1	
Gm ^R Cot ^R Cp ^R				1													
Gm ^R Cot ^R Em ^R																	
Em ^R Tc ^R FA ^R	1																
Em ^R Mp ^R Cp ^R															1		
Em ^R Cot ^R Cp ^R															1		
Em ^R Cp ^R FA ^R	1																
Tc ^R Cp ^R FA ^R																	
Oxacillin plus four non beta lactam antibiotics:																	
Em ^R Tc ^R Cp ^R Gm ^R																	

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	CC1				CC5									CC8			CC12
	1 IV WA1	1 V	188 IV WA38	772 V Bengal Bay	5 IV WA3	5 IV WA71	5 IV WA96	5 IV WA121	5 V WA109	5 V	6 IV WA51	73 IV WA65	835 IV WA48	8 IV USA300	8 IV WA5	2471 V WA120	12 novel WA59
Em ^R Cot ^R Cp ^R Gm ^R				1													
Em ^R Cot ^R Cp ^R FA ^R									1								
Oxacillin plus five non beta lactam antibiotics:																	
Em ^R Tc ^R Cp ^R Cot ^R Gm ^R			1														
Em ^R Tc ^R Cp ^R Mp ^R Gm ^R														1			
TOTAL	48	1	1	2	17	1	1	4	1	1	3	10	1	10	3	1	1

SAP 2010: CA-MRSA Antibiogram cont

	CC30		CC45		CC59				CC72	CC88	CC97	CC121	S	S	Undetermined	TOTAL
	30 IV WSP	30 V WA124	45 IV WA75	45 V WA84	59 IV WA15	59 IV WA55	59 V Taiwan	952 V Taiwan A	72 IV Korean	78 IV WA2	953 IV WA54	577 V WA22	93 IV Qld	883 IV WA47	1303 IV WA76	
Oxacillin only:																
Ox ^R	54		1						1	4	2		110	1	1	218
Oxacillin plus one non beta lactam antibiotic:																
Em ^R							1	1		13	1		17			45
Cp ^R	1			10	1											16
FA ^R																11
Tc ^R		1				1							1			4
Rf ^R	1															1
Mp ^R																4
Cot ^R																4
Oxacillin plus two non beta lactam antibiotics:																
Em ^R Tc ^R							4	4					1			12
Et ^R FA ^R																2
Em ^R Mp ^R																1
Em ^R Cp ^R	2			3												10

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	CC30		CC45		CC59				CC72	CC88	CC97	CC121	S	S	Undetermined	TOTAL
	30 IV WSPP	30 V WA124	45 IV WA75	45 V WA84	59 IV WA15	59 IV WA55	59 V Taiwan	952 V Taiwan A	72 IV Korean	78 IV WA2	953 IV WA54	577 V WA22	93 IV Qld	883 IV WA47	1303 IV WA76	
Tc ^R FA ^R																2
Tc ^R Mp ^R																1
Gm ^R Er ^R																1
Rf ^R Cp ^R	1															1
Rf ^R Er ^R																1
Er ^R Cot ^R									1							1
Oxacillin plus three non beta lactam antibiotics:																
Em ^R Tc ^R Cp ^R				4												4
Gm ^R Er ^R Cp ^R																1
Gm ^R Cot ^R Cp ^R																1
Gm ^R Cot ^R Em ^R											1					1
Em ^R Tc ^R FA ^R																1
Em ^R Mp ^R Cp ^R																1
Em ^R Cot ^R Cp ^R	1			1												3
Em ^R Cp ^R FA ^R																1
Tc ^R Cp ^R FA ^R				1												1
Oxacillin plus four non beta lactam antibiotics:																
Em ^R Tc ^R Cp ^R Gm ^R				2												2

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	CC30		CC45		CC59				CC72	CC88	CC97	CC121	S	S	Undetermined	TOTAL
	30 IV WSPP	30 V WA124	45 IV WA75	45 V WA84	59 IV WA15	59 IV WA55	59 V Taiwan	952 V Taiwan A	72 IV Korean	78 IV WA2	953 IV WA54	577 V WA22	93 IV Qld	883 IV WA47	1303 IV WA76	
Em ^R Cot ^R Cp ^R Gm ^R																1
Em ^R Cot ^R Cp ^R FA ^R																1
Oxacillin plus five non beta lactam antibiotics:																
Em ^R Tc ^R Cp ^R Cot ^R Gm ^R																1
Em ^R Tc ^R Cp ^R Mp ^R Gm ^R																1
TOTAL	60	1	1	21	1	1	5	5	1	18	3	1	129	1	1	355

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

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