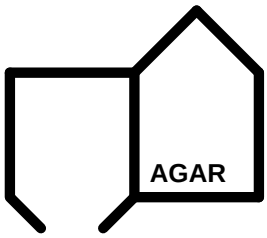

The Australian Group on Antimicrobial Resistance
http://antimicrobial-resistance.com

Staphylococcus aureus Programme 2011 (SAP 2011)
Hospital-onset Survey
MRSA Epidemiology and Typing Report

PREPARED BY:

Mr Geoffrey Coombs
Department of Microbiology and Infectious Diseases, PathWest Laboratory Medicine, Royal Perth Hospital. Western Australia.
Molecular Genetics Research Unit, Curtin University. Western Australia.

Ms Julie Pearson
Department of Microbiology and Infectious Diseases, PathWest Laboratory Medicine, Royal Perth Hospital. Western Australia.

Professor Graeme Nimmo
Division of Microbiology, Queensland Pathology – Central Laboratory Brisbane, Queensland.

Clinical Professor Keryn Christiansen
Department of Microbiology and Infectious Diseases, PathWest Laboratory Medicine, Royal Perth Hospital. Western Australia.

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

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Epidemiology and Typing Report of Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolates from the Australian Group on Antimicrobial Resistance (AGAR) 2011 *Staphylococcus aureus* Surveillance Programme (SAP 2011)

Contents

Staphylococcus aureus Programme 2011 (SAP 2011)
Hospital-onset Survey
MRSA Epidemiology and Typing Report

1.0. Overview

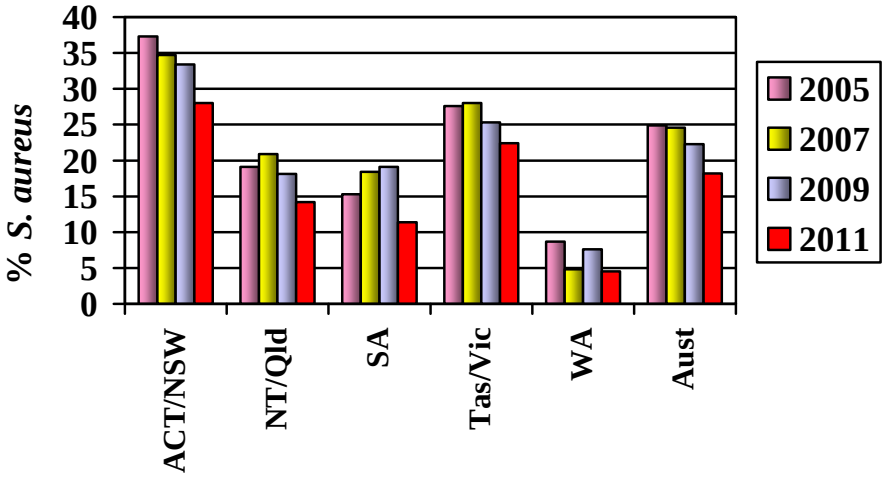
Of the 713 S. aureus *classified as MRSA in the SAP 2011 Hospital-onset Survey, molecular typing was performed on 703 (98.6%) isolates. The percentage of* S. aureus *characterized as "Healthcare-Associated MRSA (HA-MRSA)" was significantly lower in this survey (18.2%) when compared to the 2005 survey (24.2%) (P<0.001). Although four HA-MRSA clones were characterized, 98.8% of HA-MRSA were classified as either ST22-IV [2B] (EMRSA-15) or ST239-III [3A] (Aus-2/3 EMRSA). EMRSA-15 has become the predominant HA-MRSA in Australia. Aus-2/3 EMRSA, however, remains the predominant HA-MRSA clone in the Northern Territory/Queensland and Tasmania/Victoria regions. Australia-wide Aus2/3 EMRSA has decreased significantly from 19.8% to 8.9% of all* S. aureus *(2005 to 2011, P<0.0001). Over the same period EMRSA-15 increased significantly in several regions particularly in the Tasmania/Victoria region (5.8% of MRSA in 2005 to 33.3% in 2011). In SAP 2011 EMRSA-15 accounted for 9% of all* S. aureus *infections. Community-Associated MRSA clones (CA-MRSA) increased markedly from 6.5% in 2005 to 11.7% of all S. aureus in 2011 (P<0.0001). As in the previous surveys CA-MRSA were multiclonal (32 clones) however 79.6% of isolates could be characterized into six clones. Although ST1-IV [2B] was the most frequently isolated CA-MRSA clone in most regions of Australia (22.9% of CA-MRSA), approximately 26% of CA-MRSA were characterized as either ST93-IV [2B] (Queensland CA-MRSA) or ST30-IV [2B] (SWP CA-MRSA). These two clones are Panton Valentine leucocidin (PVL) positive. Two international PVL positive clones were also characterized: ST8-IV [2B] (USA300) and ST772-V [5C2] (Bengal Bay CA-MRSA). Overall 31.6% of CA-MRSA were PVL positive, a much lower proportion than seen in outpatient/community surveys.*

2.0. Summary

The Australian Group for Antimicrobial Resistance (AGAR) biennial hospital-onset *Staphylococcus aureus* surveillance programme commenced in 2005. In the 2011 programme (SAP 2011) up to 100 clinically significant consecutive isolates of *S. aureus* from different patients were collected by each of 29 institutions located across Australia. Isolates were collected from hospitalised patients (>48 hours at the time of specimen collection). 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 Australian hospitals.

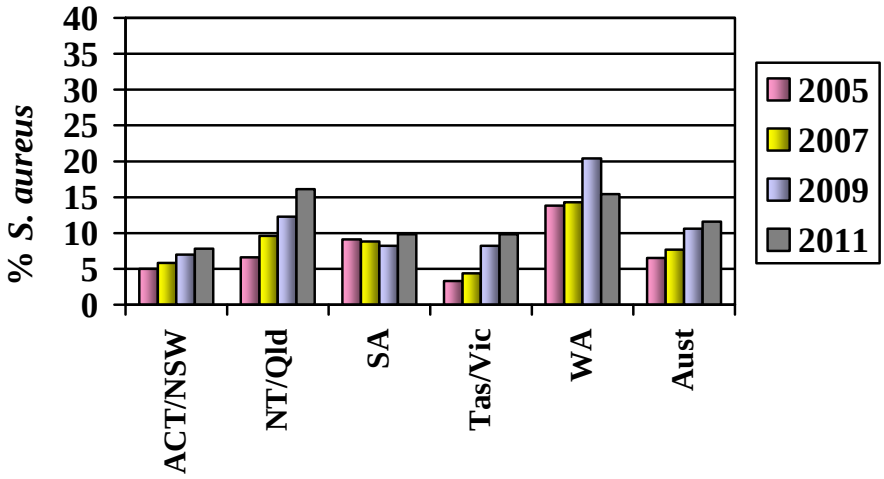
Of the 713 (30.3%) *S. aureus* classified as MRSA in SAP 2011, 703 (98.6%) were referred to the ***ACCESS*** Typing and Research. Overall 61% and 39% of MRSA were characterized as "healthcare-associated MRSA" (HA-MRSA) strains and "community-associated MRSA" (CA-MRSA) strains respectively.

Throughout Australia the percentage of *S. aureus* characterized as HA-MRSA was 18.2% ranging from 4.5% in WA to 28.0% in the ACT/NSW region. Since 2005 significant falls in the proportion of *S. aureus* charactised as HA-MRSA occurred in ACT/NSW (P=0.0002), NT/Qld (P<0.0001), Tas/Vic (P=0.0023), and nationally (P<0.0001) Within HA-MRSA the proportion of ST239-III [3A] decreased even more markedly while it was only partially replaced by ST22-IV (see below).



Percentage of *S. aureus* characterised as HA-MRSA

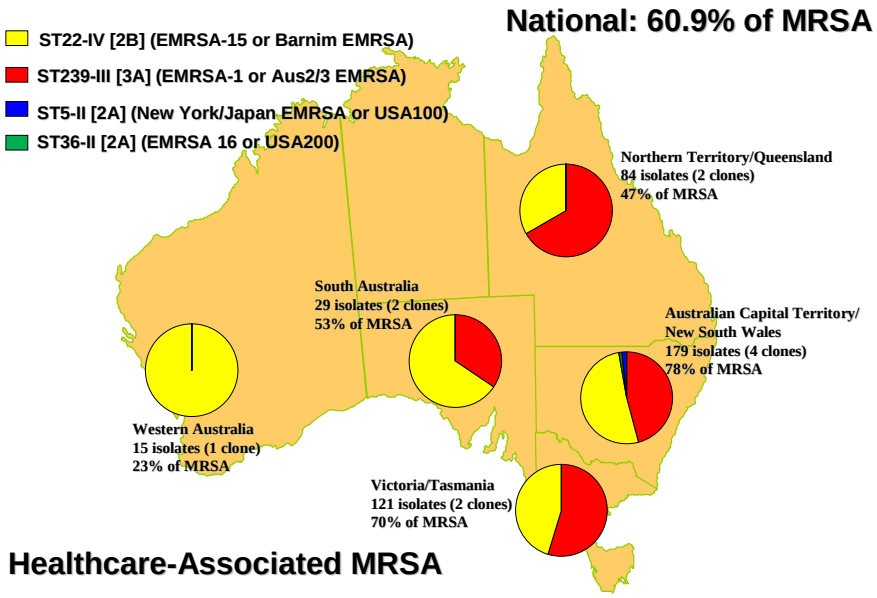
Overall 11.7% of *S aureus* were characterized as CA-MRSA ranging from 7.8% in the ACT/NSW region to 16.1% in NT/Qld. Since 2005, CA-MRSA as a proportion of S. aureus has significantly increased in ACT/NSW (P=0.0012), NT/Qld (P<0.001), Tas/Vic (P<0.0001) and nationally (P<0.0001). There continues to be a marked heterogeneity of strains constituting CA-MRSA seen in the hospital setting, although the proportion that are PVL-positive is much lower than is seen in community onset infections (see below and SAP 2010 Community Survey).



Percentage of *S. aureus* characterised as CA-MRSA

2.1. Healthcare-Associated MRSA (HA-MRSA) Clones

Four HA-MRSA clones were identified: 49.5% were ST22-IV (EMRSA-15), 49.3% ST239-III (Aus-2/3 EMRSA), and three isolates of ST5-II (New York Japan EMRSA or USA100), and two isolates of ST36-II (EMRSA-16 or USA200).

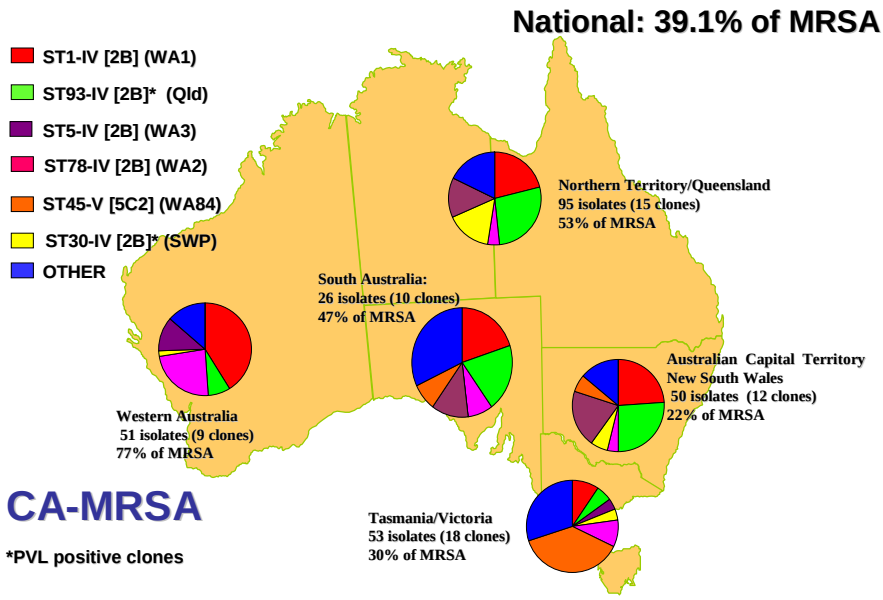


ST239-III [3A] (Aus-2/3 EMRSA) was isolated in most regions, accounting for 36.2% and 35.8% of MRSA in the Tas/Vic and ACT/NSW regions respectively. As a consequence of the state's MRSA prevention policy ST239-III [3A] was not isolated in WA. Overall 30.0% of MRSA were identified as Aus-2/3 EMRSA compared to 42.7%, 63.1% and 62.8% in SAP 2009, 2007 and 2005 respectively. ST22-IV [2B] (EMRSA-15), which was initially reported in Australia in 1997, accounted for 30.2% of all MRSA isolated in Australia (24.5% in SAP 2009), ranging from 15.6% in the NT/Qld region to 40.2% in the ACT/NSW region. The percentage of MRSA characterized as EMRSA-15 has increased in four Australian regions over the four surveys noticeably in the ACT/NSW and Tas/Vic regions, and has become the predominant HA-MRSA clone in Australia.

2.2. Community-Associated MRSA (CA-MRSA) Clones

Thirty two community MRSA clones were identified by pulsed-field gel electrophoresis (corresponding to 25 MLST/SCC*mec* clones) of which 79.6% were:

- ST1-IV [2B] [WA MRSA-1] (22.9% of CA-MRSA)
- ST93-IV [2B] [Queensland CA-MRSA] (18.6%)
- ST5-IV [2B] [WA MRSA-3] (12.4%)
- ST78-IV [2B] [WA MRSA-2] (9.1%)
- ST45-V [5C2] [WA MRSA-84 or Victorian CA-MRSA] (9.1%)
- ST30-IV [2B] [SWP MRSA] (7.6%)



2.3. Panton Valentine Leucocidin (PVL) Toxin

HA-MRSA Clones

Eight PVL positive ST22-IV [2B] were isolated (One isolate in SAP 2009).

CA-MRSA Clones

87 CA-MRSA (8 clones) were PVL positive:

- ST93-IV [2B] (Queensland CA-MRSA) – 51 isolates (100% PVL positive)
- ST30-IV [2B] (SWP MRSA) – 18 isolates (85.7%)
- ST8-IV [2B] (USA300] – 8 isolates (100%)
- ST772-V [5C2] (Bengal Bay CA-MRSA) – 3 isolates (100%)
- ST1-IV [2B] (WA MRSA-1) – 3 isolates (4.8%)
- ST5-IV [2B] (WA MRSA-3) – 2 isolates (5.9%)
- ST573-V [5C2] (WA MRSA-10) - 1 isolate (100%)
- ST59-IV [2B] (WA MRSA-55) – 1 isolate (100%)

It is possible that the threer WA MRSA-1 isolates are USA400 strains however further molecular studies are required to confirm.

Overall 31.6% of CA-MRSA were identified as PVL positive (28.3% in SAP 2009).

3.0. SAP 2011 Protocol

3.1. Commencement Date

1st July 2011

3.2. Isolates

Approximately 100 consecutive clinical isolates of *Staphylococcus aureus* from 100 different inpatients (hospital stay >48 hours at the time of specimen collection) at each site were tested by 29 laboratories located across Australia (total number of isolates = 2,357).

3.3. Participating Laboratories

Australian Capital Territory (1)

The Canberra Hospital

New South Wales (7)

Concord Hospital
Nepean Hospital
Royal North Shore Hospital
Sydney South West Pathology Services
Westmead Hospital
Douglass Hanly Moir Pathology
Royal Prince Alfred Hospital

Queensland (6)

Pathology Queensland
- Princess Alexandra Hospital
- Central Laboratory
- Cairns Base Hospital
- Gold Coast Hospital
- Prince Charles Hospital

Sullivan Nicolaides Pathology

Northern Territory (1)

Royal Darwin Hospital

South Australia (3)

Flinders Medical Centre
Institute of Medical & Veterinary Science
Women's and Children's Hospital

Tasmania (2)

Royal Hobart Hospital
Launceston General Hospital

Victoria (5)

Alfred Hospital
Royal Children's Hospital
St Vincent's Hospital
Austin Health
Monash Medical Centre

Western Australia (4)

PathWest-WA Fremantle Hospital
PathWest-WA Queen Elizabeth II
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

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 standardized 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 SCC*mec* type. The MRSA genotype is therefore the sum of the SCC*mec* type and the type of its recipient chromosome. For example, an MRSA clone of ST22 and SCC*mec* type IV is referred to as ST22-IV [2B] (previously known as EMRSA-15).

Multilocus Sequence Typing (MLST)

MLST is a highly discriminatory method of characterising 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). A clonal complex (CC) comprises genetically related isolates that differ at only one or two loci (termed single [slv] or double locus variant [dlv] respectively). The primary founder of a complex is defined as the ST that differs from the largest number of other STs at only a single locus (ie the ST that has the greatest number of SLVs). DLVs of the founder are only linked if the intermediate SLV on the path from the founder to the DLV is present. Some STs may not share alleles at five out of the seven loci with any STs and are termed 'singleton' STs.

Staphylococcal Cassette Chromosome *mec* (SCC*mec*)

The gene for methicillin resistance, *mecA*, is contained within a mobile element known as the *mec* region or staphylococcal cassette chromosome *mec* (SCC*mec*). The SCC*mec*s

differ depending on variations in the *mec*A 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 SCC*mec* 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 HA-MRSA or CA-MRSA clones and are assigned an MLST/SCC*mec* 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_T [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.

4.0. 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 (screen), vancomycin, rifampicin, fusidic acid, gentamicin, erythromycin, clindamycin, inducible clindamycin resistance, tetracycline, trimethoprim/sulphamethoxazole (cotrimoxazole), ciprofloxacin, teicoplanin, linezolid, nitrofurantoin, mupirocin and daptomycin. Penicillin susceptible strains were tested for β-lactamase production using nitrocefin. A cefoxitin disc diffusion test was used to confirm methicillin-resistance. High-level mupirocin resistance was determined by disc diffusion (200 ug disc, Oxoid).

Resistogram

Disk Diffusion (14, 15)

mercuric chloride ($HgCl_2$) (0.4μM)
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 Quantity One and digitally analysed using FPQuest (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).

Multilocus 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

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

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP on selected isolates

ST239-III [3A] (Aus-2 and Aus-3 EMRSA)

Antibiogram
Resistogram
Urea broth
CHEF
Coagulase PCR-RFLP on selected isolates
Multilocus Sequence Typing on selected isolates
SCC*mec* PCR on selected isolates

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

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF
SCC*mec* PCR

ST36-II [2A] (EMRSA-16 or USA200)

Antibiogram
Urea broth
CHEF

4.3. Identification of CA-MRSA Clones

ST93-IV [2B] (Queensland CA-MRSA)

Antibiogram
Urea Broth
Coagulase PCR-RFLP on selected isolates
CHEF

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

Antibiogram
Urea Broth
CHEF

ST8-IV [2B] (USA300)

Antibiogram
Urea Broth
Coagulase PCR-RFLP on selected isolates
CHEF

ST772-V [5C2] (Bengal Bay CA-MRSA)

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

"WA MRSA"

ST1-IV [2B] (WA-MRSA-1)
ST78-IV [2B] (WA-MRSA-2)

Antibiogram
Urea Broth
CHEF
Coagulase PCR-RFLP on selected isolates
Multilocus Sequence Typing on selected isolates

ST5-IV [2B] (WA-MRSA-3)
ST5-V [5C2] (WA-MRSA-14)
ST5-V [5C2] (WA-MRSA-90)
ST5-V [5C2] (WA-MRSA-109)
ST5-V [5C2] (WA-MRSA-35)
ST5-V [5C2] (WA-MRSA-108)
ST575-IV [2B] (WA-MRSA-25)
ST45-IV [2B] (WA-MRSA-75)
ST45-V [5C2] (WA-MRSA-4)
ST45-V [5C2] (WA-MRSA-84)
ST59-IV [2B] (WA-MRSA-15)
ST59-IV [2B] (WA-MRSA-55)
ST72-IV [2B] (WA-44)
ST73-IV [2B] (WA-MRSA-65)
ST75-IV [2B] (WA-MRSA-8)
ST188-IV [2B] (WA-MRSA-38)
ST573-V [5C2] (WA-MRSA-10)
ST575-IV [2B] (WA-MRSA-25)
ST835-IV [2B] (WA-MRSA-48)
ST953-IV [2B] (WA-MRSA-54)
ST1304-IV [2B] (WA-MRSA-72)
ST1970-V [5C2] (WA-MRSA-106)

Antibiogram
Urea Broth
Coagulase PCR-RFLP on selected isolates
CHEF
SCC*mec* PCR on selected isolates

ST1-V [5C2] (unique)
ST7-V [5C2] (unique)
ST45-V [5C2]&4 (unique)
ST1756-V [5C2] (unique)

Antibiogram
Urea Broth
Coagulase PCR-RFLP on selected isolates
CHEF
Multilocus Sequence Typing on selected isolates
SCC*mec* PCR on selected isolates

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).

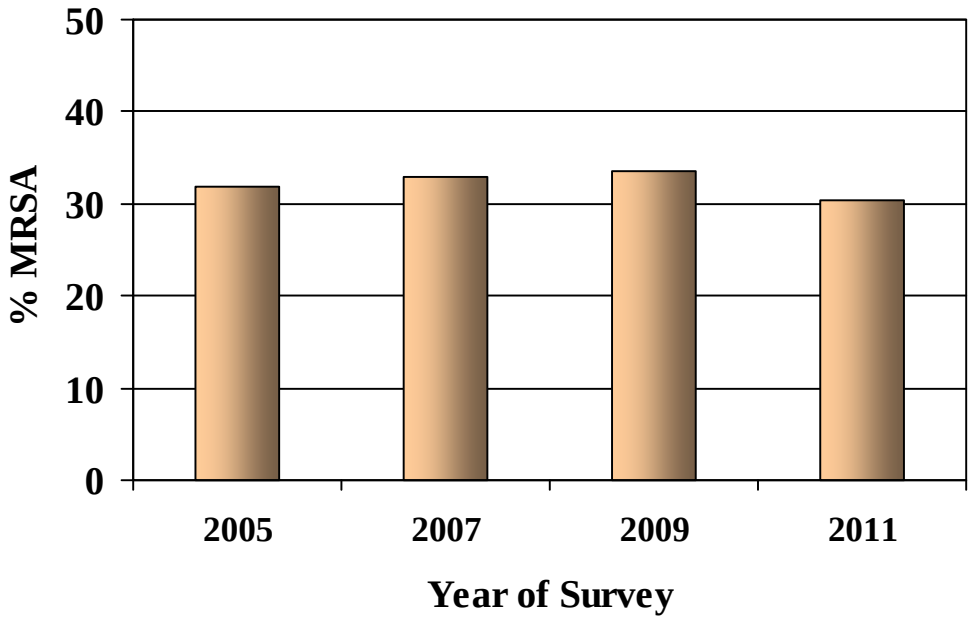
5.0. Results

In SAP 2011, 713 (30.3%) *Staphylococcus aureus* were classified as MRSA. To ensure institutional anonymity, data from New South Wales (NSW) and the Australian Capital Territory (ACT), from Tasmania (Tas) and Victoria (Vic), and from Queensland (Qld) and Northern Territory (NT) have been combined.

5.1. AGAR Hospital SAP 2005 – 2011

Percentage of *Staphylococcus aureus* Identified as MRSA

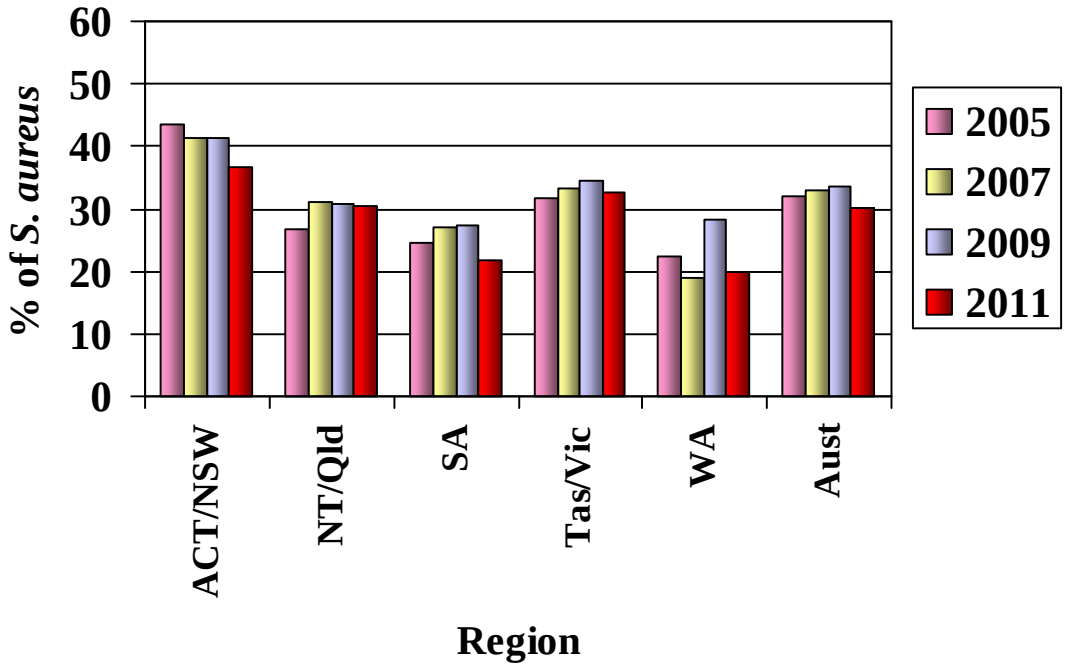
SAP	Laboratories (n)	*S aureus* (n)	MRSA (n)	MRSA (%)
2005	32	2,908	928	31.9%
2007	31	2,705	889	32.9%
2009	30	2,728	916	33.6%
2011	29	2,357	713	30.3%



Regional Distribution of MRSA

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	358 (43.4%)	333 (41.3%)	271 (41.4%)	235 (36.9%)
Qld/NT	177 (26.7%)	212 (31.0%)	210 (30.7%)	180 (30.5%)
SA	84 (24.7%)	71 (27.2%)	77 (27.3%)	55 (21.7%)
Tas/Vic	229 (31.6%)	213 (33.3%)	250 (34.6%)	177 (32.7%)
WA	80 (22.5%)	60 (19.0%)	108 (28.2%)	66 (19.9%)
TOTAL	928 (31.9%)	889 (32.9%)	916 (33.6%)	713 (30.3%)

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



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

5.2. SAP 2011 Epidemiological Typing of MRSA

Of the 713 MRSA identified in SAP 2011, 703 (98.6%) were referred to the ***ACCESS*** Typing and Research for epidemiological typing.

Typing Tests Performed

Test	N
Cefoxitin Susceptibility Testing	**738**
Coagulase Gene PCR-RFLP Assay	**107**
Resistogram	**218**
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	**708**
Urease Reaction	**717**
Multilocus Sequencing Typing (MLST)	**2**
SCC*mec* PCR	**2**
Panton-Valentine leucocidin PCR	**725**

Regional Distribution of HA-MRSA and CA-MRSA Clones

Region	HA-MRSA (%)	CA-MRSA (%)	Total MRSA
ACT/NSW	**179 (78.2)**	**50 (21.8)**	**229**
Qld/NT	**84 (46.9)**	**95 (53.1)**	**179**
SA	**29 (52.7)**	**26 (47.3)**	**55**
Tas/Vic	**121 (69.5)**	**53 (30.5)**	**174**
WA	**15 (22.7)**	**51 (77.3)**	**66**
TOTAL	**428 (60.9)**	**275 (39.1)**	**703**

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - SAP 2011 Regional Distribution of HA-MRSA and CA-MRSA Clones

	SAP 2005 (n = 881)		SAP 2007 (n = 874)		SAP 2009 (n = 899)	
Region	**HA-MRSA (%)**	**CA-MRSA (%)**	**HA-MRSA (%)**	**CA-MRSA (%)**	**HA-MRSA (%)**	**CA-MRSA (%)**
ACT/NSW	**309 (88.5)**	**40 (11.5)**	**280 (85.6)**	**47 (14.4)**	**219 (82.6)**	**46 (17.4)**
NT/Qld	**114 (72.2)**	**44 (27.8)**	**143 (68.4)**	**66 (31.6)**	**124 (59.6)**	**84 (40.4)**
SA	**51 (61.4)**	**32 (38.6)**	**48 (67.6)**	**23 (32.4)**	**54 (70.1)**	**23 (29.9)**
Tas/Vic	**200 (89.3)**	**24 (10.7)**	**179 (86.5)**	**28 (13.5)**	**183 (75.6)**	**59 (24.4)**
WA	**31 (38.8)**	**49 (61.2)**	**15 (25.0)**	**45 (75.0)**	**29 (27.1)**	**78 (72.9)**
TOTAL	**705 (78.9)**	**189 (21.1)**	**665 (76.1)**	**209 (23.9)**	**609 (67.7)**	**290 (32.3)**

Percentage figures relate to the total number of MRSA isolates characterized

	SAP 2011 (n = 703)	
Region	**HA-MRSA (%)**	**CA-MRSA (%)**
ACT/NSW	**179 (78.2)**	**50 (21.8)**
NT/Qld	**84 (46.9)**	**95 (53.1)**
SA	**29 (52.7)**	**26 (47.3)**
Tas/Vic	**121 (69.5)**	**53 (30.5)**
WA	**15 (22.7)**	**51 (77.3)**
TOTAL	**428 (60.9)**	**275 (39.1)**

Percentage figures relate to the total number of MRSA isolates characterized

SAP 2005 - SAP 2011: Regional Distribution of HA-MRSA and CA-MRSA Clones as a Proportion of *Staphylococcus aureus*

	SAP 2005			SAP 2007		
Region	**Total**	**HA-MRSA (%)**	**CA-MRSA (%)**	**Total**	**HA-MRSA (%)**	**CA-MRSA (%)**
ACT/NSW	**825**	**309 (37.5)**	**40 (4.8)**	**806**	**280 (34.7)**	**47 (5.8)**
NT/Qld	**664**	**114 (17.2)**	**44 (6.6)**	**684**	**143 (20.9)**	**66 (9.6)**
SA	**340**	**51 (15.0)**	**32 (9.4)**	**261**	**48 (18.4)**	**23 (8.8)**
Tas/Vic	**724**	**200 (27.6)**	**24 (3.3)**	**639**	**179 (28.0)**	**28 (4.4)**
WA	**355**	**31 (8.7)**	**49 (13.8)**	**315**	**15 (4.8)**	**45 (14.3)**
TOTAL	**2,908**	**705 (24.2)**	**189 (6.5)**	**2,705**	**665 (24.6)**	**209 (7.7)**

Percentage figures relate to the total number of *S. aureus*

	SAP 2009			SAP 2011		
Region	**Total**	**HA-MRSA (%)**	**CA-MRSA (%)**	**Total**	**HA-MRSA (%)**	**CA-MRSA (%)**
ACT/NSW	**655**	**219 (33.4)**	**46 (7.0)**	**639**	**179 (28.0)**	**50 (7.8)**
NT/Qld	**685**	**124 (18.1)**	**84 (12.3)**	**591**	**84 (14.2)**	**95 (16.1)**
SA	**282**	**54 (19.1)**	**23 (8.2)**	**254**	**29 (11.4)**	**26 (10.2)**
Tas/Vic	**723**	**183 (25.3)**	**59 (8.2)**	**541**	**121 (22.4)**	**53 (9.8)**
WA	**383**	**29 (7.6)**	**78 (20.4)**	**332**	**15 (4.5)**	**51 (15.4)**
TOTAL	**2,728**	**609 (22.3)**	**290 (10.6)**	**2,357**	**428 (18.2)**	**275 (11.7)**

Percentage figures relate to the total number of *S. aureus*

SAP 2011 HA-MRSA Clones by AGAR Laboratory

LAB	ST239-III Aus 2/3 EMRSA	ST22-IV EMRSA-15	ST36-II EMRSA-16	ST5-I1 NY/Japan MRSA	TOTAL
ACT/NSW (179)					
1	3	7			10
2	11	9		1	21
3	2	5			7
4	12	15			27
5	9	18			27
6	27	19			46
7	2	1			3
8	16	18	2	2	38
NT/Qld (84)					
10	16				16
11	9	5			14
12	10	3			13
13	2	6			8
28	7	8			15
29	2	1			3
30	10	5			15
SA (29)					
14	4	12			16
15	6	6			12
16		1			1
Tas/Vic (121)					
18		6			6
19	19	17			36
21	2	2			4
22	11	6			17
23	16	3			19
31	15	7			22
32		17			17
WA (15)					
24		4			4
25		3			3
26		5			5
27		3			3
TOTAL	211	212	2	3	428

SAP 2011 CA-MRSA Clones by AGAR Laboratory

CC	1					5										7	8	30
	1 IV WA 1	1 V	188 IV WA 38	573 V WA 10	772 V Bengal Bay	5 IV WA 3	5 V WA 14	575 IV WA 25	835 IV WA 48	5 V WA 35	73 IV WA 65	5 V WA 90	5 V WA 108	5 V WA 109	1756 V	7 V	8 IV USA 300	30 IV SWP
ACT/NSW (50)																		
1	2																	
2																		
3	1					1												1
4						5											1	
5	4			1							1							1
6	2					3											1	
7						1												
8	2																	1
NT/Qld (95)																		
10	10					1					1							2
11	2					3												2
12	2	1				1										1	1	3
13	2						1										2	2
28	3					1					1							2
29	1				1	6					2			1				4
30		1				1												
SA (25)																		
14	3					1												
15						2					2						1	
16	2																	
Tas/Vic (53)																		
18																		
19	1		1					1										
21																		2
22	1									1								
23												1	1		1		1	
31	1				2	2					1						1	
32	3										1							
WA (51)																		
24	8								1									
25	4					2						1						
26	9					4			1		1							1
27									1									
Total	63	2	1	1	3	34	1	1	3	1	10	2	1	1	1	1	8	21

SAP 2011 CA-MRSA Clones by AGAR Laboratory cont

CC	45						59		72	75		88	97	S	Total
	45 V WA 4	45 V	45 IV WA 23	45 IV WA 75	45 V WA 84	1970 V WA 106	59 IV WA 15	59 IV WA 55	72 IV WA 44	75 IV WA 8	1304 IV WA 72	78 IV WA 2	953 IV WA 54	93 IV Qld	
ACT/NSW (50)															
1					**1**							**1**		**1**	**5**
2									**1**						**1**
3														**2**	**5**
4									**1**			**1**		**1**	**9**
5					**1**	**1**								**5**	**14**
6					**1**									**3**	**10**
7															**1**
8								**1**						**1**	**5**
NT/Qld (95)															
10										**1**		**2**		**17**	**34**
11							**1**					**1**		**2**	**11**
12							**1**							**2**	**12**
13												**1**			**8**
28														**1**	**8**
29											**1**			**4**	**20**
30															**2**
SA (26)															
14	**2**	**2**			**1**							**1**			**10**
15	**1**				**1**							**1**	**1**	**3**	**12**
16														**2**	**4**
Tas/Vic (53)															
18															**0**
19					**2**									**1**	**6**
21					**1**					**1**					**4**
22					**6**									**1**	**9**
23				**1**	**7**							**4**			**16**
31			**1**		**4**							**1**		**1**	**14**
32															**4**
WA (51)															
24												**4**		**2**	**15**
25				**2**								**4**			**13**
26												**2**		**2**	**20**
27												**2**			**3**
Total	**3**	**2**	**1**	**3**	**25**	**1**	**2**	**1**	**2**	**2**	**1**	**25**	**1**	**51**	**275**

5.3. HA-MRSA Clones

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

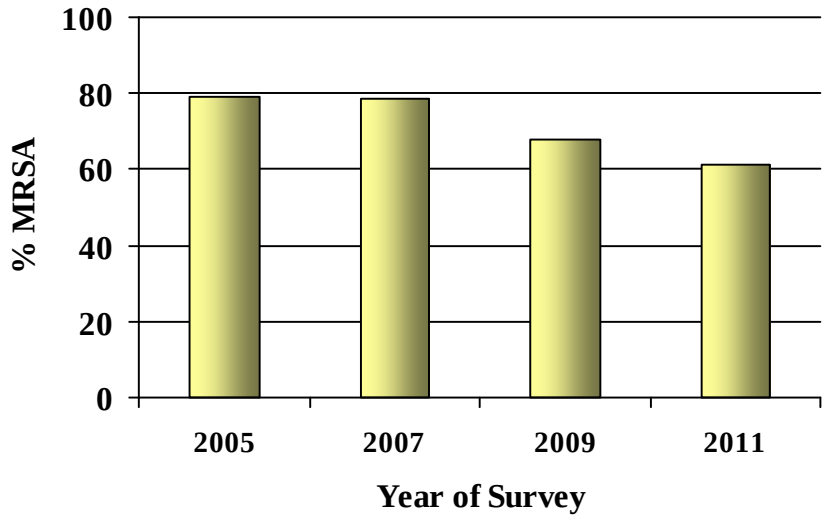
SAP 2011 HA-MRSA Clones

In SAP 2011 four international HA-MRSA clones (428 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST22-IV [2B]	EMRSA-15	212 (49.5%)
ST239-III [3A]	Aus -2 and Aus -3 EMRSA or EA MRSA	211(49.3%)
ST5-II [2A]	New York Japan MRSA or USA100	3 (0.7%)
ST36-II [2A]	EMRSA-16 or USA200	2 (0.5%)
TOTAL		428

Percentage figures in parenthesis relate to HA-MRSA isolates

SAP 2005 - 2011: Percentage of MRSA Identified as HA-MRSA



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

Also known as "EMRSA-15" or the "German Barnim" strain, ST22-IV [2B] has become a major HA-MRSA clone in many parts of the world including Australia, United Kingdom (UK), New Zealand, several European countries and Singapore. First identified in the Midlands and South-East England in the early 1990s it accounts for over half of UK isolates sent to the Laboratory of Hospital Infection in Colindale for typing. It is 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 UK.

Phenotypic Characteristics

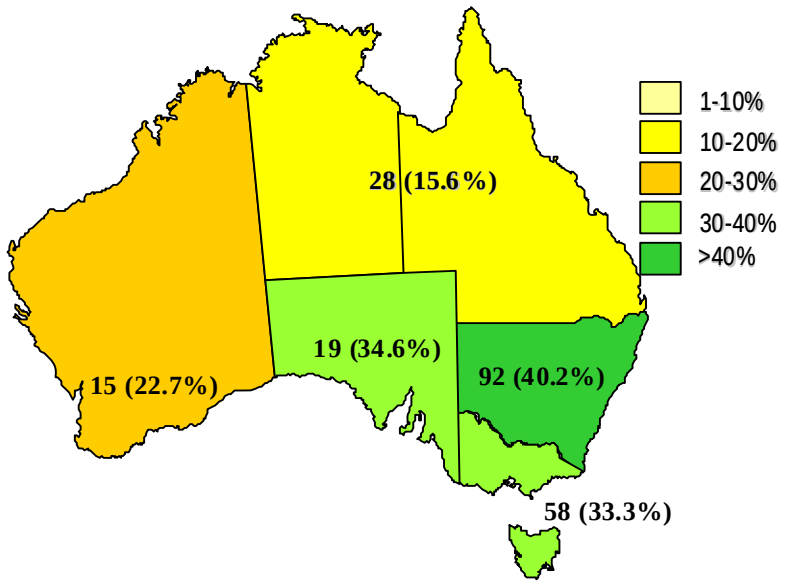
Antibiogram:

Ciprofloxacin^{R}	99%
Erythromycin^{R}	66%
Cotrimoxazole^{R}	3%
Gentamicin^{R}	2%
High Level Mupirocin^{R}	2%
Tetracycline^{R}	2%
Rifampicin^{R}	1%
Fusidic Acid^{R}	1%

Urease: Negative

Epidemiology

ST22-IV [2B] (EMRSA-15): n = 212 (30.2%)



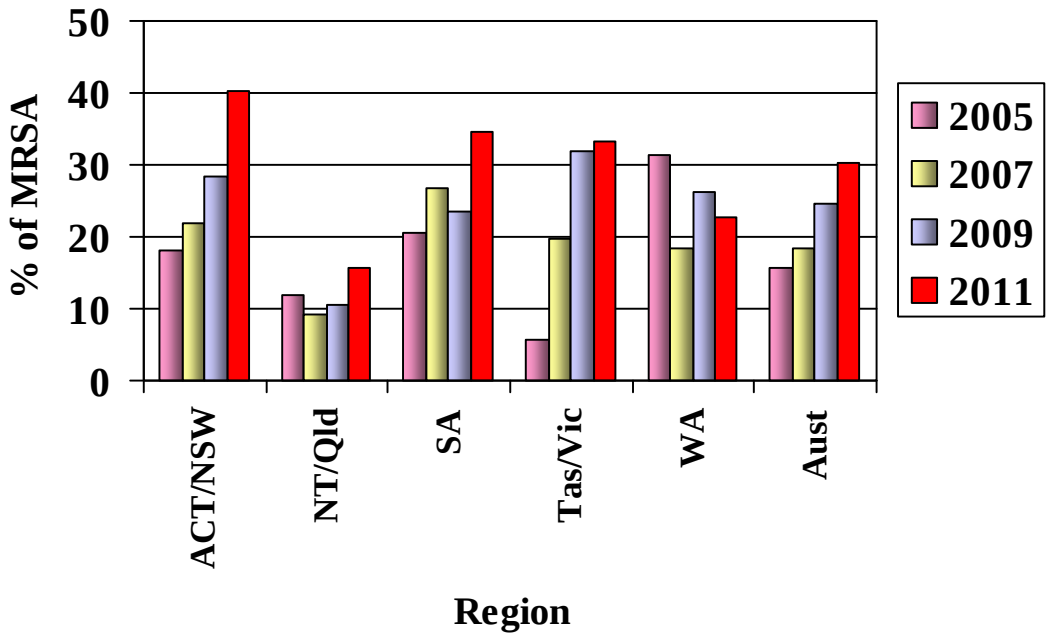
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST22-IV [2B] (EMRSA-15)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	63 (18.1%)	72 (22.0%)	75 (28.3%)	92 (40.2%)
Qld/NT	19 (12.0%)	19 (9.1%)	22 (10.6%)	28 (15.6%)
SA	17 (20.5%)	19 (26.8%)	18 (23.4%)	19 (34.5%)
Tas/Vic	13 (5.8%)	41 (19.8%)	77 (31.8%)	58 (33.3%)
WA	25 (31.3%)	11 (18.3%)	28 (26.2%)	15 (22.7%)
TOTAL	137 (15.3%)	162 (18.5%)	220 (24.5%)	212 (30.2%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST22-IV [2B] (EMRSA-15)



ST239-III [3A]

In Australia ST239-III [3A] has been classified into two subclones: Aus-2 and Aus-3 EMRSA. This classification is based on the mercuric acetate and phenylmercuric chloride resistogram and CHEF pattern. ST239-III [3A] evolved from the "Eastern Australian EMRSA" clone described in the 1980s. ST239-III [3A] has emerged as one of the most commonly encountered and internationally disseminated multidrug-resistant HA-MRSA clones. It is also known as "EMRSA-1", the "Portuguese/Brazilian" clone or the "Vienna" clone.

Phenotypic Characteristics

	Aus-2 EMRSA (n = 152)	**Aus-3 EMRSA (n = 59)**
Erythromycin^{R}	99%	92%
Tetracycline^{R}	100%	100%
Cotrimoxazole^{R}	93%	100%
Gentamicin^{R}	94%	93%
Ciprofloxacin^{R}	95%	100%
Fusidic Acid^{R}	2%	0%
Rifampicin^{R}	3%	10%
High Level Mupirocin^{R}	2%	3%

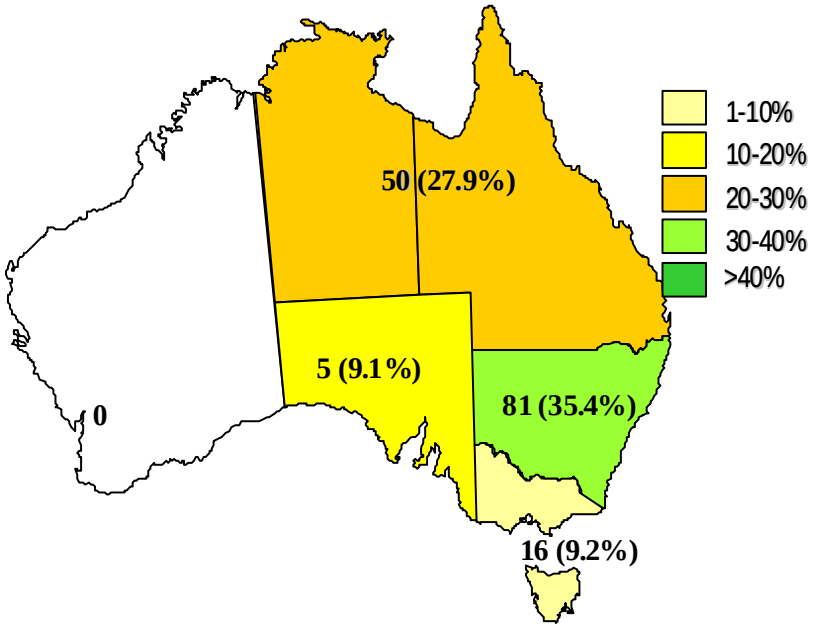
Resistogram

	Aus-2 EMRSA (n = 152)	**Aus-3 EMRSA (n = 59)**
Mercuric Acetate^{R}	0%	100%
Mercuric Chloride^{R}	0%	100%

Aus-2 EMRSA

Epidemiology

ST239-III [3A] (Aus-2 EMRSA): n = 152 (21.6%)



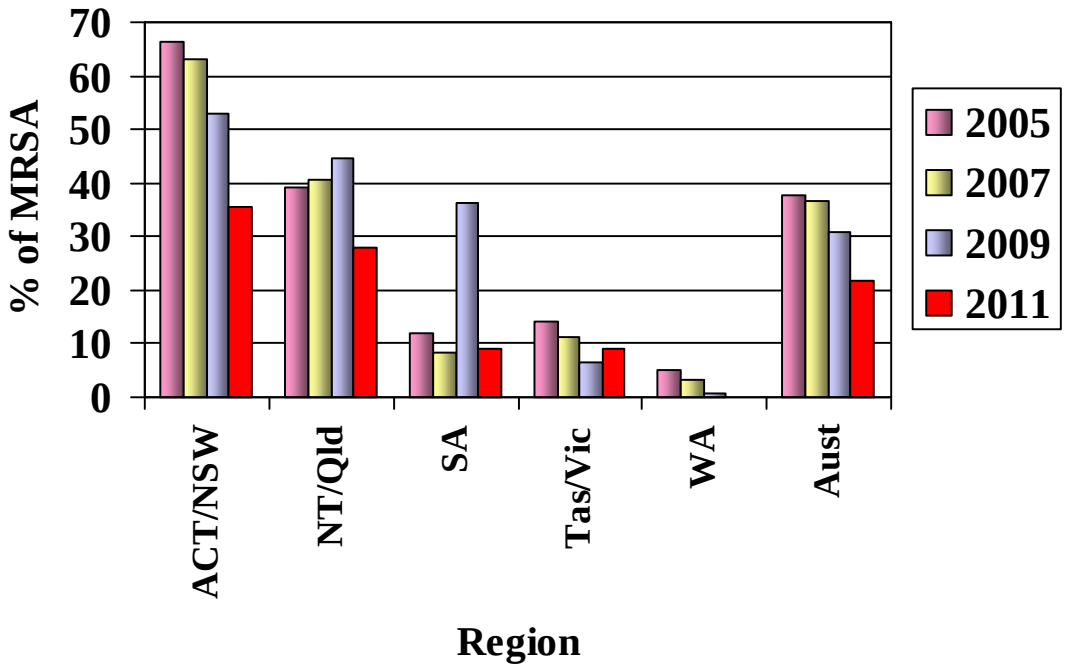
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST239-III [3A] (Aus-2 EMRSA)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	231 (66.2%)	206 (63.0%)	140 (52.8%)	81 (35.4%)
Qld/NT	62 (39.2%)	85 (40.7%)	93 (44.7%)	50 (27.9%)
SA	10 (12.0%)	6 (8.5%)	28 (36.4%)	5 (9.1%)
Tas/Vic	32 (14.3%)	23 (11.1%)	16 (6.6%)	16 (9.2%)
WA	4 (5.0%)	2 (3.3%)	1 (0.9%)	0
TOTAL	339 (37.9%)	322 (36.8%)	278 (30.9%)	152 (21.6%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

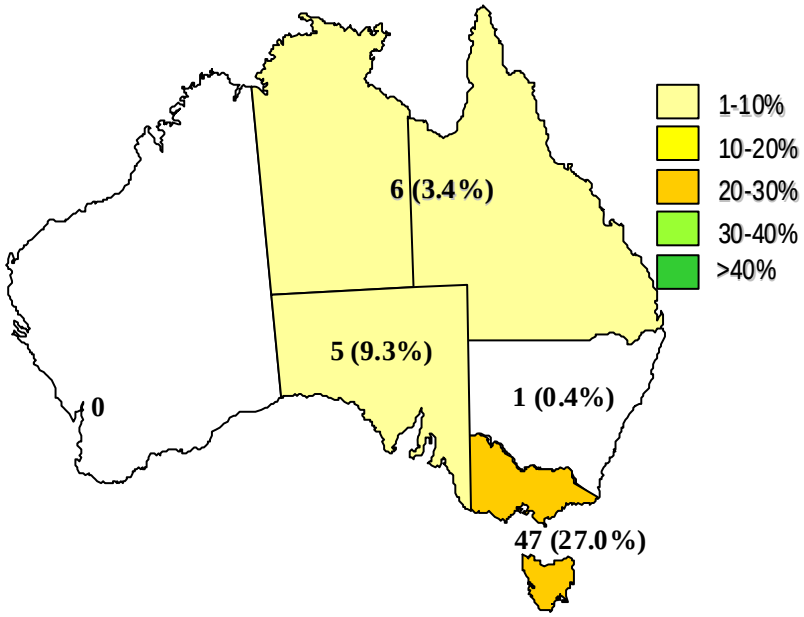
SAP 2005 - 2011: Regional Distribution of ST239-III [3A] (Aus-2 EMRSA)



Aus-3 EMRSA

Epidemiology

ST239-III [3A] (Aus-3 EMRSA): n = 59 (8.4%)



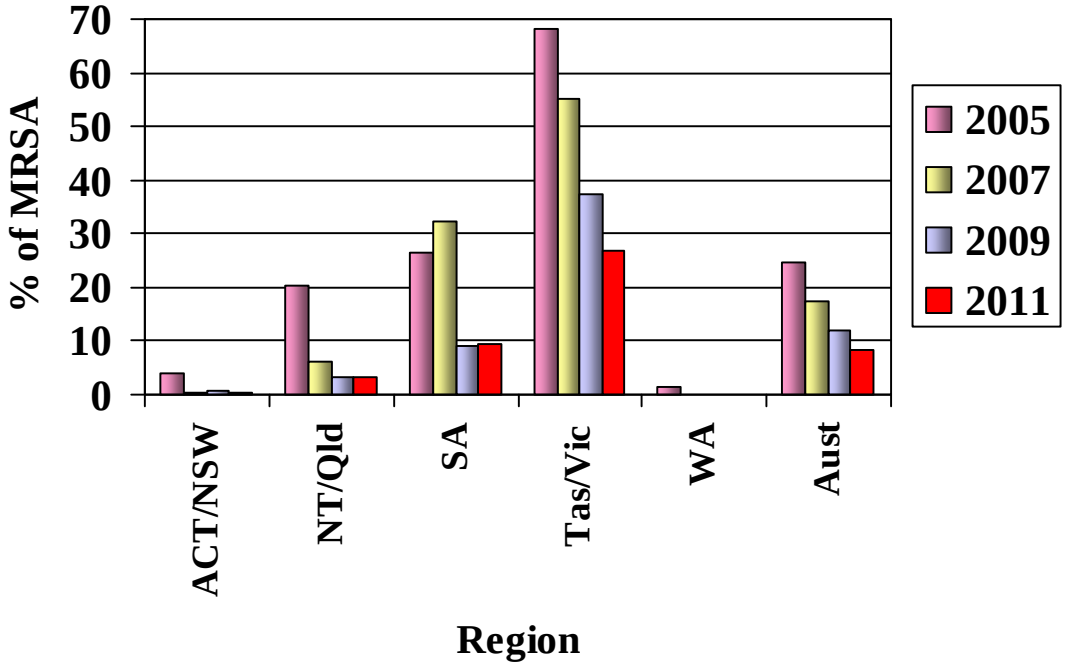
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST239-III [3A] (Aus-3 EMRSA)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	14 (4.0%)	1 (0.3%)	2 (0.8%)	1 (0.4%)
Qld/NT	32 (20.3%)	13 (6.2%)	7 (3.4%)	6 (3.4%)
SA	22 (26.5%)	23 (32.4%)	7 (9.1%)	5 (9.1%)
Tas/Vic	153 (68.3%)	114 (55.1%)	90 (37.2%)	47 (27.0%)
WA	1 (1.3%)	0	0	0
TOTAL	222 (24.8%)	151 (17.3%)	106 (11.8%)	59 (8.4%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

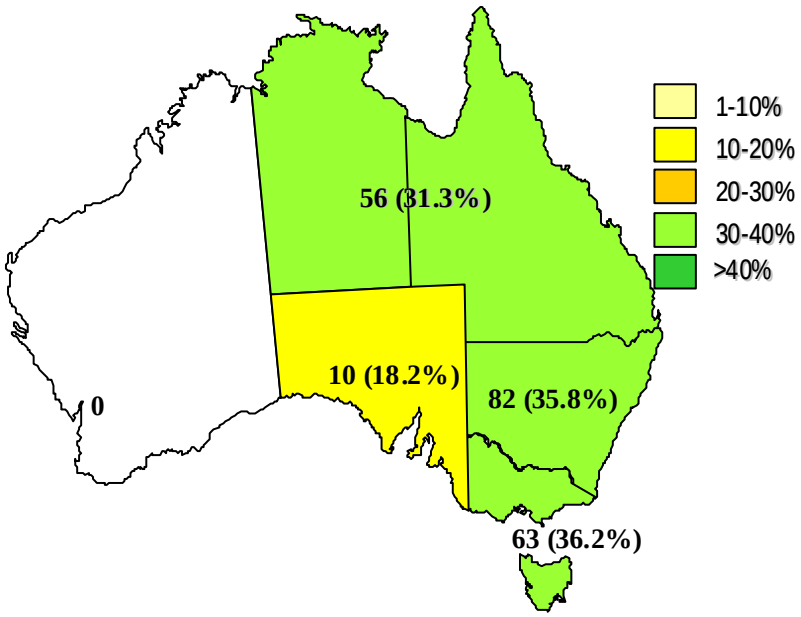
SAP 2005 - 2011: Regional Distribution of ST239-III [3A] (Aus-3 EMRSA)



Aus-2 and Aus-3 EMRSA (ST239-III [3A])

Epidemiology

ST239-III [3A] (Aus-2 and Aus-3 EMRSA): n = 211 (30.0%)



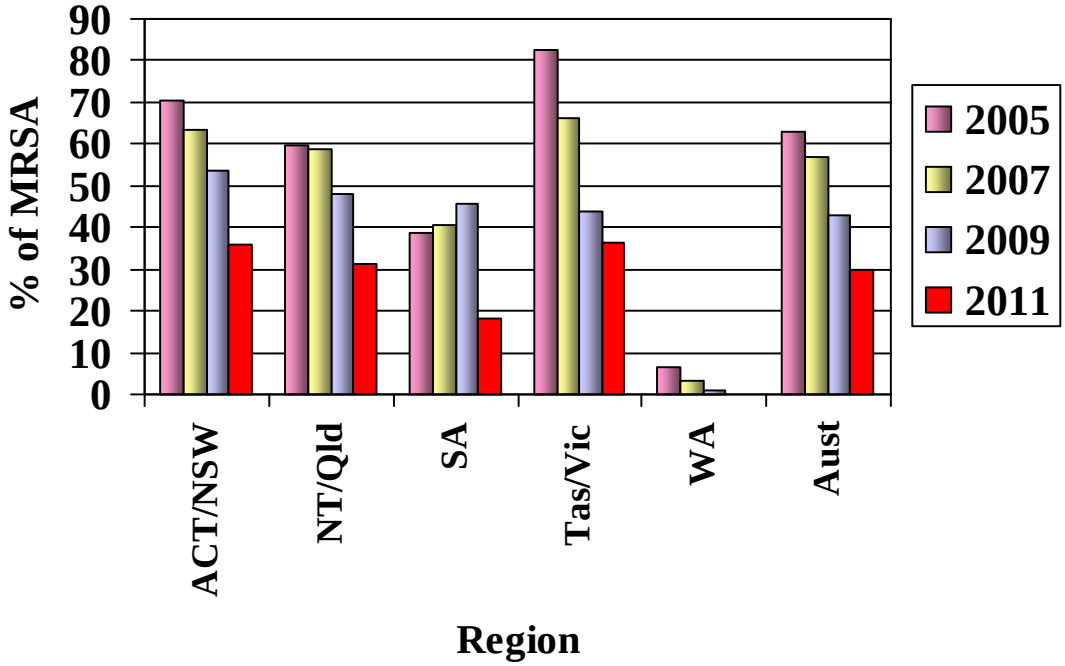
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 20011: Regional Distribution of ST239-III [3A] (Aus-2 and Aus-3 EMRSA)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	245 (70.2%)	207 (63.3%)	142 (53.6%)	82 (35.8%)
Qld/NT	94 (59.5%)	123 (58.8%)	100 (48.1%)	56 (31.3%)
SA	32 (38.6%)	29 (40.8%)	35 (45.5%)	10 (18.2%)
Tas/Vic	185 (82.6%)	137 (66.2%)	106 (43.8%)	63 (36.2%)
WA	5 (6.3%)	2 (3.3%)	1 (0.9%)	0
TOTAL	561 (62.8%)	498 (57.0%)	384 (42.7%)	211 (30.0%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST239-III [3A] (Aus-2 and Aus-3 EMRSA)



ST5-II [2A] (New York Japan MRSA)

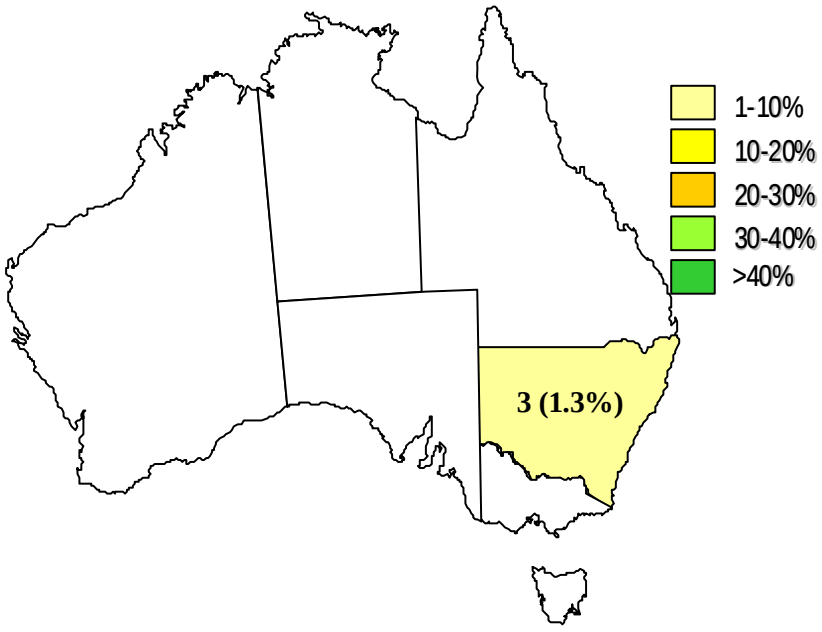
Also known as "New York Japan MRSA", ST5-II [2A] is a major HA-MRSA of the USA and Japan and forms part of clonal complex 5.

Phenotypic Characteristics

Antibiogram:	Ciprofloxacin^{R}	100%
	Erythromycin^{R}	100%
	Tetracycline^{R}	100%
	Gentamicin^{R}	66%
	Rifampicin^{R}	0
	Cotrimoxazole^{R}	0
	High Level Mupirocin^{R}	0
	Fusidic Acid^{R}	0
Urease:	Positive	

Epidemiology

ST5-II [2A] (New York Japan MRSA): n = 3 (0.4%)



Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

ST36-II [2A] (EMRSA-16)

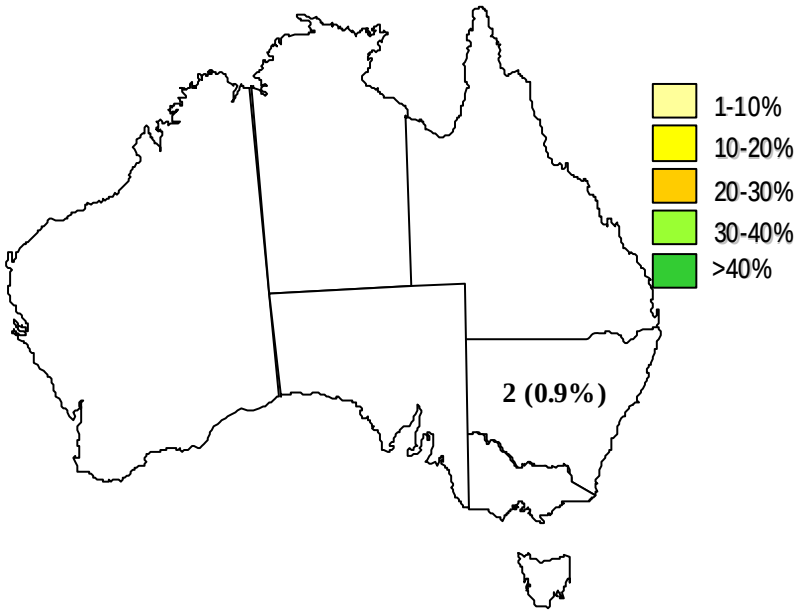
Also known as "EMRSA-16" or "USA200", ST36-II [2A] was first identified in a single hospital outbreak in London in 1991-2. ST36-II [2A] has been isolated in several European countries including Denmark, Finland, Sweden and Turkey, and in the USA. ST36-II [2A] is resistant to ciprofloxacin, erythromycin and variably resistant to the aminoglycosides. It carries staphylococcal enterotoxin A, G and I and TSST-1.

Phenotypic Characteristics

Antibiogram:	Ciprofloxacin^{R}	100%
	Erythromycin^{R}	100%
	Tetracycline^{R}	0
	Rifampicin^{R}	0
	Gentamicin^{R}	0
	Cotrimoxazole^{R}	0
	High Level Mupirocin^{R}	0
	Fusidic Acid^{R}	0
Urease:	Positive	

Epidemiology

ST36-II [2A] (EMRSA-16): n = 2 (0.3%)



Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

Summary of HA-MRSA Isolated in AGAR SAP 2005 - 2011

Clone	Alternative Name	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ST239-III [3A]	**Aus-2, -3 EMRSA**	**561 (62.8%)**	**498 (57.0%)**	**384 (42.7%)**	**211 (30.1%)**
ST239-novel		**1 (0.1)**			
ST22-IV [2B]	**EMRSA-15**	**137[a] (15.3%)**	**162 (18.5%)**	**220 (24.5%)**	**212 (30.0%)**
ST36-II [2A]	**EMRSA-16**	**2[b] (0.2%)**	**1[c] (0.1%)**	**3[j] (0.3%)**	**2[l] (0.3%)**
ST247-I [1B]	**EMRSA 17**	**2[d] (0.2%)**	**1[e] (0.1%)**	**0**	**0**
ST8-VI [4B]	**Irish-2 EMRSA**	**0**	**1[f] (0.1%)**	**0**	**0**
ST5-II [2A]	**New York Japan**	**2[g] (0.2%)**	**1[h] (0.1%)**	**2[k] (0.2%)**	**3[m] (0.4%)**
ST228-I [1B]	**Southern German EMRSA**	**0**	**1[i] (0.1%)**	**0**	**0**
Total		**705 (79.3%)**	**665 (76.1%)**	**607 (67.5%)**	**428 (60.9%)**

Percentage figures relate to the total number of MRSA characterized

[a]Isolated in Tas/Vic
[b]Isolated in SA (n=1) and Tas/Vic (n=1)
[c]Isolated in Qld/NT
[d]Isolated in WA (n=1) and ACT/NSW (n=1)
[e]Isolated in ACT/NSW
[f]Isolated in WA
[g]Isolated in SA (n=1) and Qld/NT (n=1)
[h]Isolated in Tas/Vic
[i]Isolated in WA
[j]Isolated in ACT/NSW (n=2) and Qld/NT (n=1)
[k]Isolated in Qld/NT (n=1) and SA (n=1)
[l]Isolated in ACT/NSW (n=2)
[m]Isolated in ACT/NSW (n=3)

5.4. CA-MRSA Clones

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-lactam antibiotics. "WA MRSA" has acquired the community associated SCC*mec* types IV [2B] and V [5C2], which usually lack transposons, integrated plasmids and other antibiotic resistance genes. Although they have been introduced into teaching hospital outbreaks have rarely been reported. 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 Western Pacific MRSA" (SWP MRSA). SWP MRSA has previously been reported in New Zealand and several Pacific islands. In 2000 a non-multiresistrant 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 2011 CA-MRSA Clones

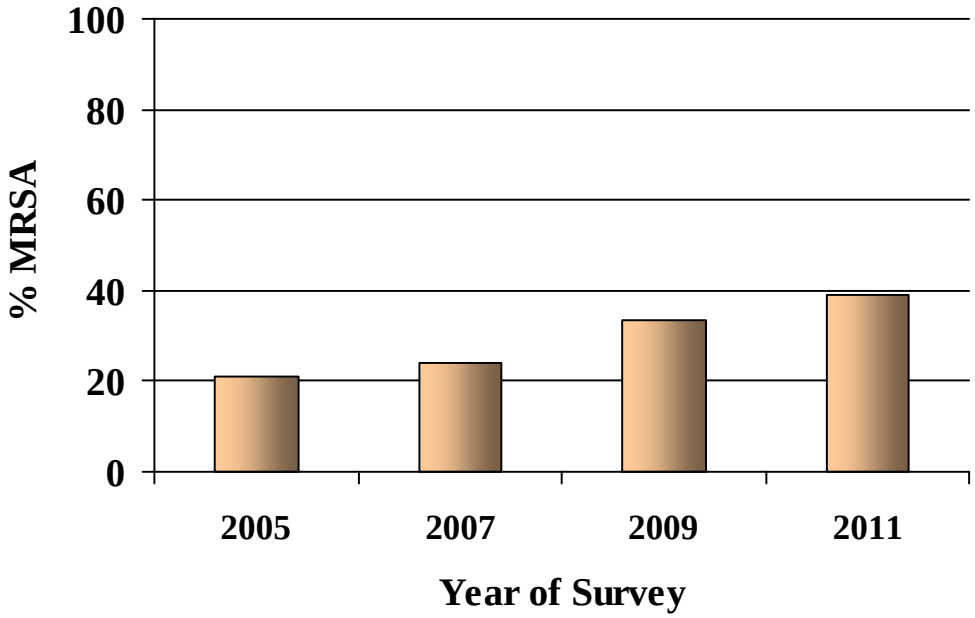
In SAP 2011 32 community MRSA clones (twenty fiveMLST/SCC*mec* clone types) were identified.

Clone	CC	Alternative Name	n (%)
ST1-IV [2B]	**1**	**WA MRSA-1**	**63 (22.9%)**
ST93-IV [2B]	**Singleton**	**Queensland MRSA**	**51 (18.6%)**
ST5-IV [2B]	**5**	**WA MRSA-3**	**34 (12.4%)**
ST78-IV [2B]	**88**	**WA MRSA-2**	**25 (9.1%)**
ST45-V [5C2]	**45**	**WA MRSA-84 (Victorian CA-MRSA)**	**25 (9.1%)**
ST30-IV [2B]	**30**	**SWP MRSA**	**21 (7.6%)**
ST73-IV [2B]	**5**	**WA MRSA-65**	**10 (3.6%)**
ST8-IV [2B]	**8**	**USA300**	**8 (2.9%)**
ST772-V [5C2]	**1**	**Bengal Bay**	**3 (1.1%)**
ST835-IV [2B]	**5**	**WA MRSA-48**	**3 (1.1%)**
ST45-V [5C2]	**45**	**WA MRSA-4**	**3 (1.1%)**
ST45-IV [2B]	**45**	**WA MRSA-75**	**3 (1.1%)**
ST1-V [5C2]	**1**		**2 (0.7%)**

Clone	CC	Alternative Name	n (%)
ST5-V [5C2]	**5**	**WA MRSA-90**	**2 (0.7%)**
ST59-IV [2B]	**59**	**WA MRSA-15**	**2 (0.7%)**
ST72-IV [2B]	**72**	**WA MRSA-44**	**2 (0.7%)**
ST75-IV [2B]	**75**	**WA MRSA-8**	**2 (0.7%)**
ST45-V [5C2]	**45**		**2 (0.7%)**
ST188-IV [2B]	**1**	**WA MRSA-38**	**1 (0.4%)**
ST573-V [5C2]	**1**	**WA MRSA-10**	**1 (0.4%)**
ST5-V [5C2]	**5**	**WA MRSA-14**	**1 (0.4%)**
ST575-IV [2B]	**5**	**WA MRSA-25**	**1 (0.4%)**
ST5-V [5C2]	**5**	**WA MRSA-35**	**1 (0.4%)**
ST5-V [5C2]	**5**	**WA MRSA-108**	**1 (0.4%)**
ST5-V [5C2]	**5**	**WA MRSA-109**	**1 (0.4%)**
ST1756-V [5C2]	**5**		**1 (0.4%)**
ST7-V [5C2]	**7**		**1 (0.4%)**
ST45-IV [2B]	**45**	**WA MRSA-23**	**1 (0.4%)**
ST1970-V [5C2]	**45**	**WA MRSA-106**	**1 (0.4%)**
ST59-IV [2B]	**59**	**WA MRSA-55**	**1 (0.4%)**
ST1304-IV [2B]	**75**	**WA MRSA-72**	**1 (0.4%)**
ST953-IV [2B]	**97**	**WA MRSA-54**	**1 (0.4%)**
TOTAL			**275**

Percentage figures in parenthesis relate to community MRSA isolates

SAP 2005 - 2011: Percentage of MRSA Identified as CA-MRSA

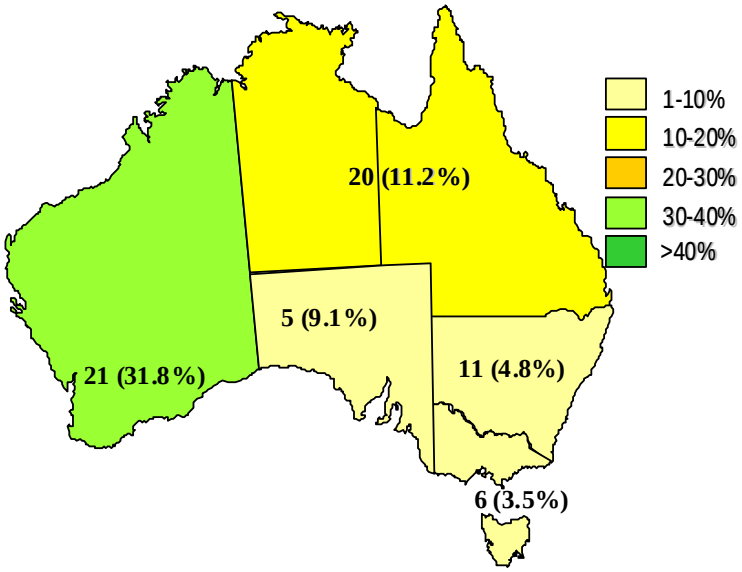


ST1-IV [2B]

Also known as "WA MRSA-1", ST1-IV [2B] forms part of clonal complex 1. Although normally PVL-negative, PVL-positive "USA400" MRSA-like strains are isolated in Australia.

Epidemiology

ST1-IV [2B] (WA MRSA-1): n = 63 (9.0%)



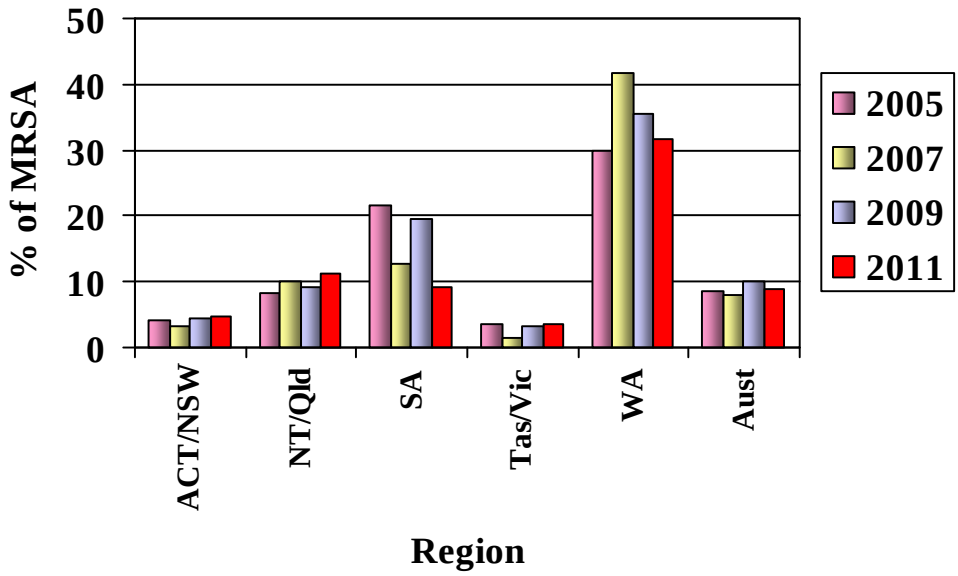
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST1-IV [2B] (WA MRSA-1)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	14 (4.0%)	11 (3.4%)	12 (4.5%)	11 (4.8%)
Qld/NT	13 (8.2%)	21 (10.0%)	19 (9.1%)	20 (11.2%)
SA	18 (21.7%)	9 (12.7%)	15 (19.5%)	5 (9.1%)
Tas/Vic	8 (3.6%)	3 (1.5%)	8 (3.3%)	6 (3.5%)
WA	24 (30.0%)	25 (41.7%)	38 (35.5%)	21 (31.8%)
TOTAL	77 (8.6%)	69 (7.9%)	92 (10.2%)	63 (9.0%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST1-IV [2B] (WA MRSA-1)

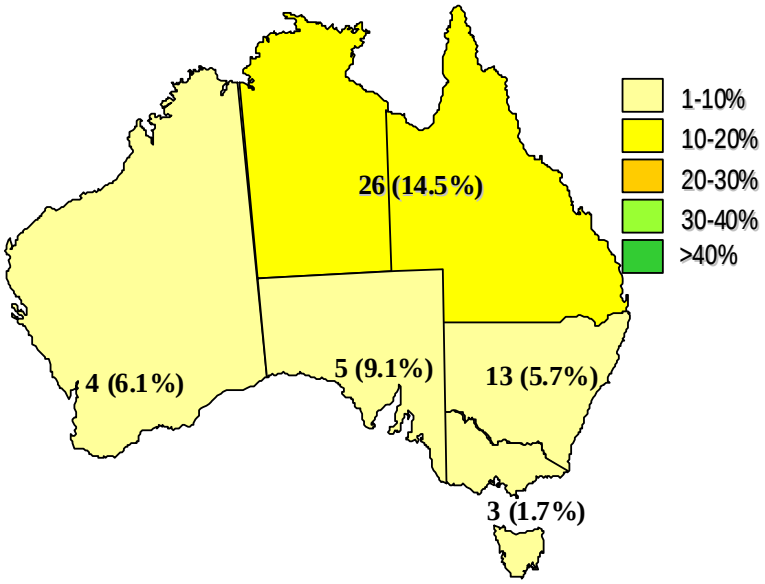


ST93-IV [2B]

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.

Epidemiology

ST93-IV [2B] (QLD MRSA): n = 51 (7.3%)



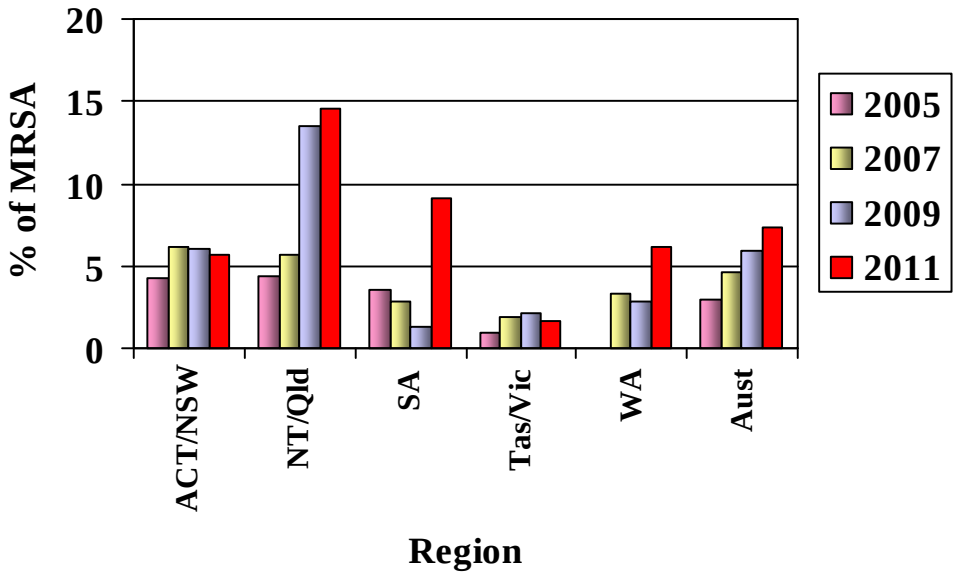
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST93-IV [2B] (Qld CA-MRSA)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	15 (4.3%)	20 (6.1%)	16 (6.0%)	13 (5.7%)
Qld/NT	7 (4.4%)	12 (5.7%)	28 (13.5%)	26 (14.5%)
SA	3 (3.6%)	2 (2.8%)	1 (1.3%)	5 (9.1%)
Tas/Vic	2 (0.9%)	4 (1.9%)	5 (2.1%)	3 (1.7%)
WA	0	2 (3.3%)	3 (2.8%)	4 (6.1%)
TOTAL	27 (3.0%)	40 (4.6%)	53 (5.9%)	51 (7.3%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST93-IV [2B] (Qld CA-MRSA)

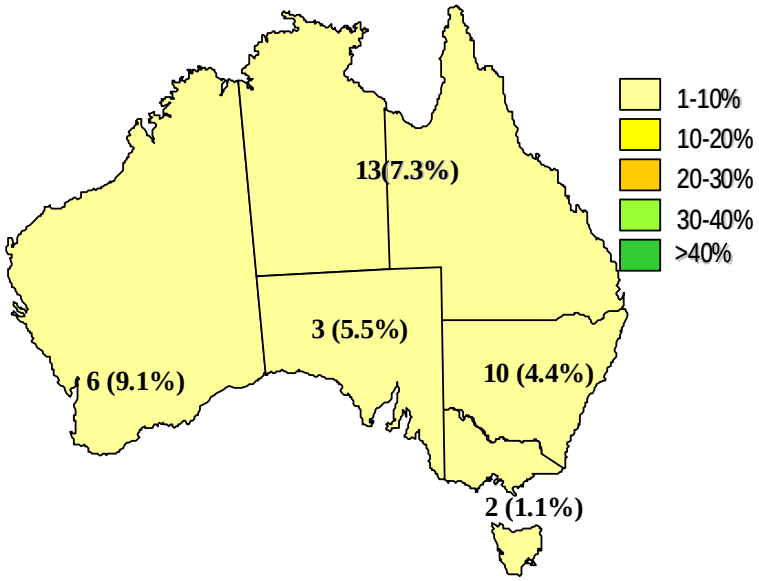


ST5-IV [2B]

Also known as "WA MRSA-3", ST5-IV [2B] forms part of clonal complex 5 and is PVL negative.

Epidemiology

ST5-IV [2B] (WA MRSA-3): n = 34 (4.8%)



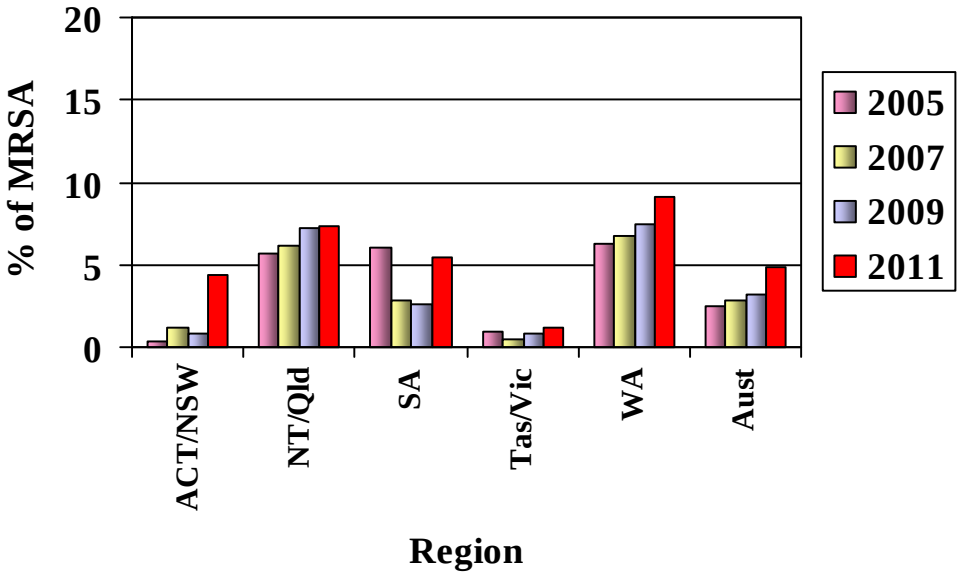
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST5-IV [2B] (WA MRSA-3)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	1 (0.3%)	4 (1.2%)	2 (0.8%)	10 (4.4%)
Qld/NT	9 (5.7%)	13 (6.2%)	15 (7.2%)	13 (7.3%)
SA	5 (6.0%)	2 (2.8%)	2 (2.6%)	3 (5.5%)
Tas/Vic	2 (0.9%)	1 (0.5%)	2 (0.8%)	2 (1.1%)
WA	5 (6.3%)	4 (6.7%)	8 (7.5%)	6 (9.1%)
TOTAL	22 (2.5%)	24 (2.8%)	29 (3.2%)	34 (4.8%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2009: Regional Distribution of ST5-IV [2B] (WA MRSA-3)

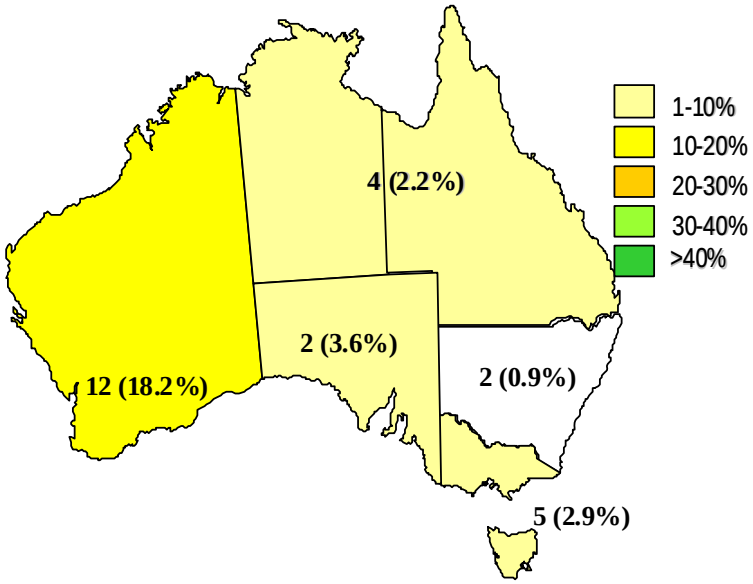


ST78-IV [2B]

Also known as "WA MRSA-2", ST78-IV [2B] forms part of clonal complex 88 and is PVL negative.

Epidemiology

ST78-IV [2B] (WA MRSA-2): n = 25 (3.6%)



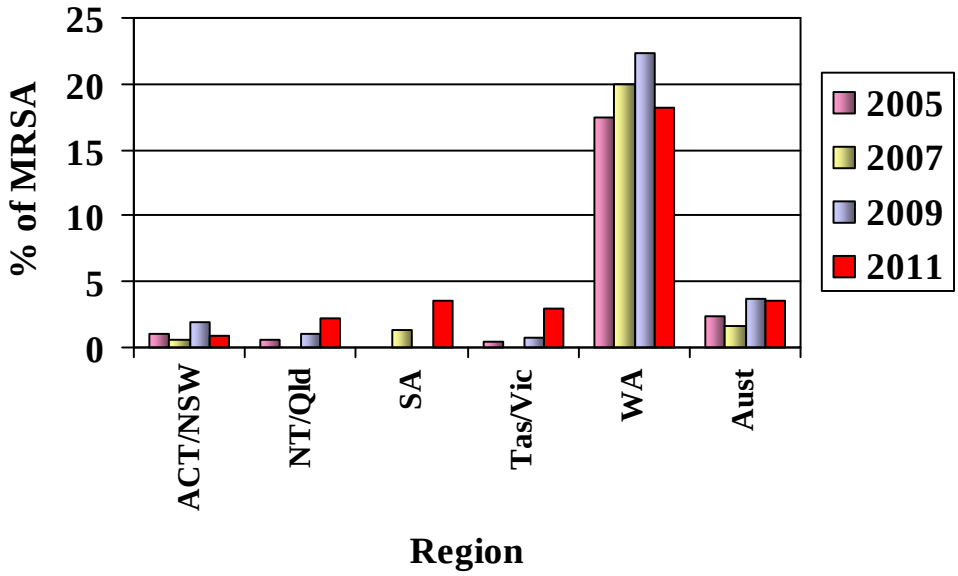
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST78-IV [2B] (WA MRSA-2)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	4 (1.1%)	2 (0.6%)	5 (1.9%)	2 (0.9%)
Qld/NT	1 (0.6%)	0	2 (1.0%)	4 (2.2%)
SA	0	1 (1.4%)	0	2 (3.6%)
Tas/Vic	1 (0.4%)	0	2 (0.8%)	5 (2.9%)
WA	14 (17.5%)	12 (20.0%)	24 (22.4%)	12 (18.2%)
TOTAL	20 (2.3%)	15 (1.7%)	33 (3.7%)	25 (3.6%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST78-IV [2B] (WA MRSA-2)

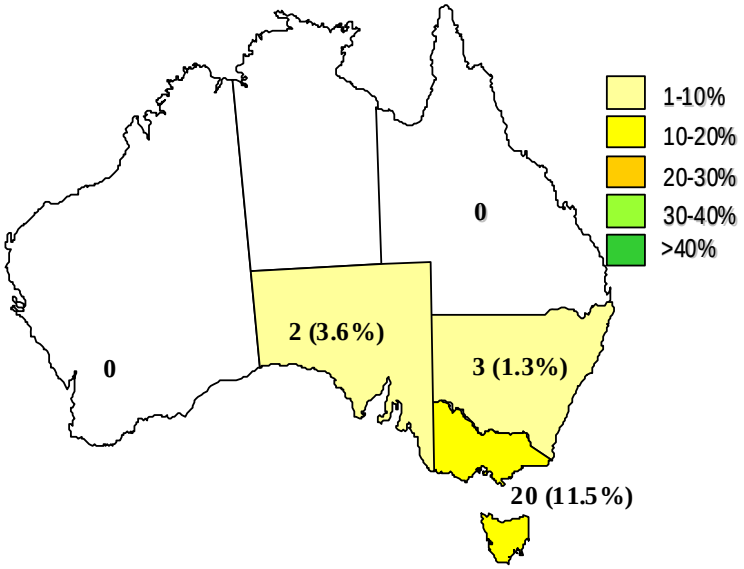


ST45-V [5C2]

Also known as "WA MRSA-84" or "Victorian CA-MRSA", ST45-V [5C2] forms part of clonal complex 45 and is PVL negative.

Epidemiology

ST45-V [5C2] (WA MRSA-84 or Victorian CA-MRSA): n = 25 (3.6%)



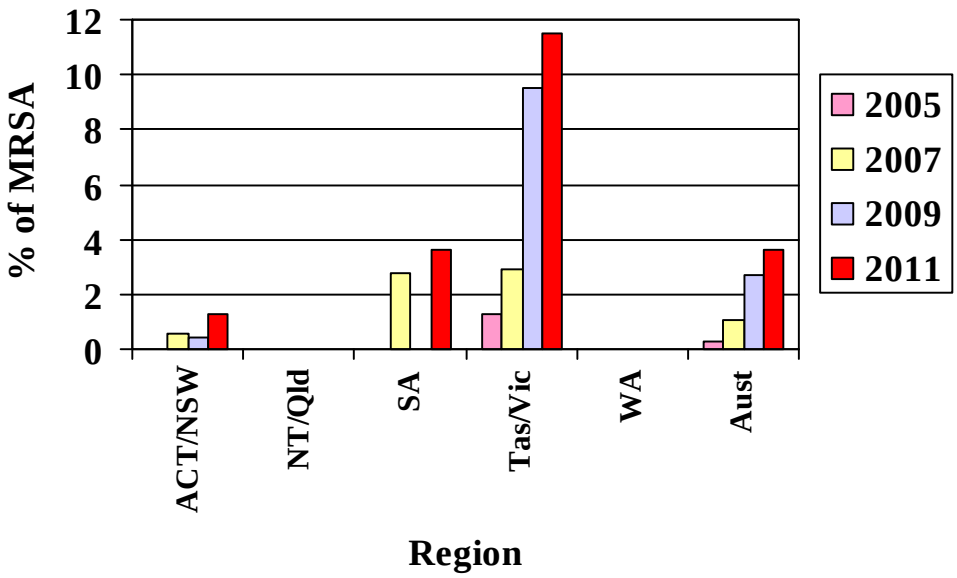
Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST45-V [5C2] (WA MRSA-84 or Victorian CA-MRSA)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	0	2 (0.6%)	1 (0.4%)	3 (1.3%)
Qld/NT	0	0	0	0
SA	0	2 (2.8%)	0	2 (3.6%)
Tas/Vic	3 (1.3%)	6 (2.9%)	23 (9.5%)	20 (11.5%)
WA	0	0	0	0
TOTAL	3 (0.3%)	10 (1.1%)	24 (2.7%)	25 (3.6%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST45-V [5C2] (WA MRSA-84 or Victorian CA-MRSA)

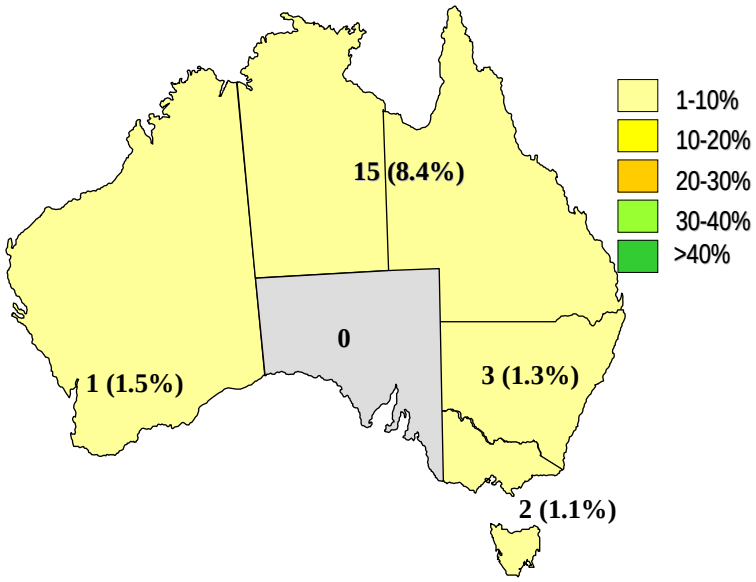


ST30-IV [2B]

Also known as "SWP MRSA", ST30-IV [2B] was originally described in Polynesians living in New Zealand and the Pacific islands. This clone forms part of clonal complex 30 and is PVL positive.

Epidemiology

ST30-IV [2B] (SWP MRSA): n = 21 (3.0%)



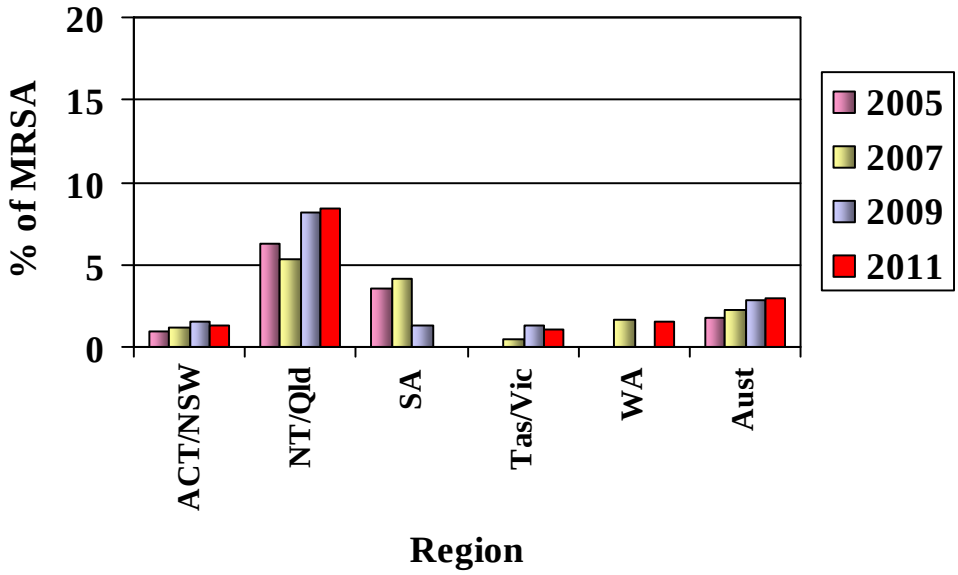
Percentage figures in parenthesis relate to total MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST30-IV [2B] (SWP CA-MRSA)

Region	SAP 2005	SAP 2007	SAP 2009	SAP 2011
ACT/NSW	3 (0.9%)	4 (1.2%)	4 (1.5%)	3 (1.3%)
Qld/NT	10 (6.3%)	11 (5.3%)	17 (8.2%)	15 (8.4%)
SA	3 (3.6%)	3 (4.2%)	1 (1.3%)	0
Tas/Vic	0	1 (0.5%)	3 (1.2%)	2 (1.1%)
WA	0	1 (1.7%)	0	1 (1.5%)
TOTAL	16 (1.8%)	20 (2.3%)	25 (2.8%)	21 (3.0%)

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

SAP 2005 - 2011: Regional Distribution of ST30-IV [2B] (SWP CA-MRSA)



International CA-MRSA Clones

In SAP 2011 two PVL positive international CA-MRSA clone were identified.

CLONE	ALTERNATIVE NAME	n (%)
ST8-IV [2B]	**USA300**	**8 (1.1%)**
ST772-V [5C2]	**Bengal Bay CA-MRSA**	**3 (0.4%)**

Percentage figures in parenthesis relate to the total number of MRSA isolates characterized

5.5. Panton Valentine Leucocidin (PVL) Toxin

HA-MRSA Clones

Clone	Alternative Name	Positive	Negative	Total
ST22-IV [2B]	EMRSA-15	8	204	212
ST239-III [3A]	Aus -2 and Aus -3 EMRSA or EA MRSA	0	211	211
ST5-II [2A]	New York Japan MRSA or USA100	0	3	3
ST36-II [2A]	EMRSA-16 or USA200	0	2	2
Total		8	420	428

CA-MRSA Clones

Clone	Alternative Name	Positive	Negative	Total
ST1-IV [2B]	WA MRSA-1	3	60	63
ST93-IV [2B]	Queensland MRSA	51	0	51
ST5-IV [2B]	WA MRSA-3	2	32	34
ST78-IV [2B]	WA MRSA-2	0	25	25
ST45-V [5C2]	WA MRSA-84 (Victorian CA-MRSA)	0	25	25
ST30-IV [2B]	SWP MRSA	18	3	21
ST73-IV [2B]	WA MRSA-65	0	10	10
ST8-IV [2B]	USA300	8	0	8
ST772-V [5C2]	Bengal Bay CA-MRSA	3	0	3
ST835-IV [2B]	WA MRSA-48	0	3	3
ST45-V [5C2]	WA MRSA-4	0	3	3
ST45-IV [2B]	WA MRSA-75	0	3	3
ST1-V [5C2]		0	2	2
ST5-V [5C2]	WA MRSA-90	0	2	2
ST59-IV [2B]	WA MRSA-15	0	2	2
ST72-IV [2B]	WA MRSA-44	0	2	2
ST75-IV [2B]	WA MRSA-8	0	2	2
ST45-V [5C2]&4		0	2	2
ST188-IV [2B]	WA MRSA-38	0	1	1
ST573-V [5C2]	WA MRSA-10	1	0	1
ST5-IV [2B]	WA MRSA-14	0	1	1
ST575-IV [2B]	WA MRSA-25	0	1	1
ST5-V [5C2]	WA MRSA-35	0	1	1
ST5-V [5C2]	WA MRSA-108	0	1	1

SAP 2011: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

Clone	Alternative Name	Positive	Negative	Total
ST5-V [5C2]	**WA MRSA-109**	**0**	**1**	**1**
ST1756-V [5C2]		**0**	**1**	**1**
ST7-V [5C2]		**0**	**1**	**1**
ST45-IV [2B]	**WA MRSA-23**	**0**	**1**	**1**
ST1970-V [5C2]	**WA MRSA-106**	**0**	**1**	**1**
ST59-IV [2B]	**WA MRSA-55**	**1**	**0**	**1**
ST1304-1V [2B]	**WA MRSA-72**	**0**	**1**	**1**
ST953-IV [2B]	**WA MRSA-54**	**0**	**1**	**1**
TOTAL		**87**	**188**	**275**

5.6. CA-MRSA Antibiogram

	1 IV WA 1	1 V	188 IV WA 38	573 V WA 10	772 V Bengal Bay	5 IV WA 3	5 V WA 14	575 IV WA 25	835 IV WA 48	5 V WA 35	73 V WA 65	5 V WA 90	5 V WA 108	5 V WA 109	1756 V
Ox^R	**37**					**23**	**1**	**1**	**1**		**7**		**1**		
One non beta lactam antibiotic															
Ox^R Em^R	**10**					**9**								**1**	
Ox^R Cp^R	**1**					**1**			**2**		**1**				
Ox^R FA^R	**4**										**2**				
Ox^R Te^R	**1**														
Ox^R Gn^R	**1**														
Ox^R Cot^R	**1**														
Two non beta lactam antibiotics															
Ox^R Em^R FA^R	**5**														
Ox^R Em^R Cp^R												**1**			**1**
Ox^R Em^R Mp^R						**1**									
Ox^R Em^R Gn^R															
Ox^R Em^R Te^R															
Ox^R Te^R FA^R		**2**													
Ox^R Gn^R Cp^R															
Ox^R Te^R Cp^R															
Ox^R Em^R Rf^R															
Three non beta lactam antibiotics															
Ox^R Mp^R Gn^R FA^R	**1**														
Ox^R Cot^R Gn^R Cot^R				**1**											
Ox^R Em^R Mp^R FA^R															

	1 IV WA 1	**1 V**	**188 IV WA 38**	**573 V WA 10**	**772 V Bengal Bay**	**5 IV WA 3**	**5 V WA 14**	**575 IV WA 25**	**835 IV WA 48**	**5 V WA 35**	**73 V WA 65**	**5 V WA 90**	**5 V WA 108**	**5 V WA 109**	**1756 V**
Ox^R Em^R Cp^R Cot^R												**1**			
Ox^R Em^R Cp^R Te^R															
Ox^R Er^R Gn^R Mp^R	**2**														
Four non beta lactam antibiotics															
Ox^R Gn^R Em^R Cp^R Cot^R			**1**		**3**										
Ox^R Gn^R Te^R Cp^R Cot^R										**1**					
Ox^R Te^R Em^R Cp^R FA^R															
Five non beta lactam antibiotics															
Ox^R Gn^R Em^R Cp^R Cot^R Te^R															
Total	**63**	**2**	**1**	**1**	**3**	**34**	**1**	**1**	**3**	**1**	**10**	**2**	**1**	**1**	**1**

CA-MRSA Antibiogram cont

	7 V	8 IV USA 300	30 IV SWP	45 V WA 4	45 V	45 IV WA 23	45 IV WA 75	45 V WA 84	1970 V WA 106	59 IV WA 15	59 IV WA 55	72 IV WA 44	75 IV WA 8	1304 IV WA 72	78 IV WA 2	953 IV WA 54	93 IV Qld
Ox^R		**1**	**18**	**3**					**1**			**1**	**2**		**1**	**1**	**41**
One non beta lactam antibiotic																	
Ox^R Em^R		**1**	**1**				**1**			**2**	**1**	**1**			**22**		**10**
Ox^R Cp^R			**2**				**2**	**9**									
Ox^R FA^R																	
Ox^R Te^R																	
Ox^R Gn^R																	
Two non beta lactam antibiotics																	
Ox^R Em^R FA^R															**1**		
Ox^R Em^R Cp^R		**5**						**5**									
Ox^R Em^R Mp^R														**1**			
Ox^R Em^R Gn^R																	
Ox^R Em^R Te^R																	
Ox^R Em^R Cot^R					**2**												
Ox^R Te^R FA^R																	
Ox^R Gn^R Cp^R								**2**									
Ox^R Te^R Cp^R						**1**											
Ox^R Em^R Rf^R															**1**		
Three non beta lactam antibiotics																	
Ox^R Em^R Gn^R FA^R																	
Ox^R Em^R Gn^R Cot^R																	
Ox^R Em^R Cp^R Te^R								**6**									
Ox^R Em^R Mp^R FA^R								**1**									
Ox^R Em^R Cp^R Cot^R																	

	7 V	**8 IV USA 300**	**30 IV SWP**	**45 V WA 4**	**45 V**	**45 IV WA 23**	**45 IV WA 75**	**45 V WA 84**	**1970 V WA 106**	**59 IV WA 15**	**59 IV WA 55**	**72 IV WA 44**	**75 IV WA 8**	**1304 IV WA 72**	**78 IV WA 2**	**953 IV WA 54**	**93 IV Qld**
Ox^R Gn^R Cp^R Te^R																	
Ox^R Gn^R Cp^R Mp^R		**1**															
Four non beta lactam antibiotics																	
Ox^R Gn^R Em^R Cp^R Cot^R																	
Ox^R Te^R Em^R Cp^R FA^R								**2**									
Five non beta lactam antibiotics																	
Ox^R Gn^R Em^R Cp^R Cot^R Te^R	**1**																
Total	**1**	**8**	**21**	**3**	**2**	**1**	**3**	**25**	**1**	**2**	**1**	**2**	**2**	**1**	**25**	**1**	**51**

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Royal Perth Hospital, WA
Yung Lee

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