

The Australian Group on Antimicrobial Resistance

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***Staphylococcus aureus* Programme 2009 (SAP 2009)
Hospital-onset 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) 2009
Staphylococcus aureus Surveillance Programme (SAP 2009)**

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***Staphylococcus aureus* Programme 2009 (SAP 2009)**

Hospital-onset Survey

MRSA Epidemiology and Typing Report

1.0. Overview

Of the 916 S. aureus classified as MRSA in the SAP 2009 Hospital-onset Survey, molecular typing was performed on 899 (98.1%) isolates. The percentage of S. aureus characterized as “Healthcare-Associated MRSA (HA-MRSA)” clones was similar in this survey (22.3%) when compared to the 2007 survey (24.6%). Although four HA-MRSA clones were characterized, 99.2% of HA-MRSA were classified as either ST239-III (Aus-2/3 EMRSA) or ST22-IV (EMRSA-15). Apart from in Western Australia, Aus-2/3 remains the prominent HA-MRSA clone in Australian hospitals but decreased significantly from 19.8% to 14.1% of all S. aureus (2005 to 2009, $P < 0.002$). Over the three surveys EMRSA-15 increased significantly in several regions particularly in the Victorian/Tasmanian hospitals (5.8% of MRSA in 2005 to 30.8% in 2009). Community-Associated MRSA clones (CA-MRSA) increased markedly from 6.5% in 2005 to 10.6% of all S. aureus in 2009 ($P < 0.002$). As in the previous surveys CA-MRSA were multiclonal (28 clones) however 87.9% of isolates could be characterized into six clones. Although ST1-IV was the most frequently isolated CA-MRSA clone in most regions of Australia (31.7% of CA-MRSA), approximately 27% of CA-MRSA were characterized as either ST93-IV (Queensland CA-MRSA) or ST30-IV (WSPP CA-MRSA). These two clones are Pantone Valentine leucocidin (PVL) positive. Overall 28.3% of CA-MRSA were PVL positive, a much lower proportion than seen in outpatient/community surveys.

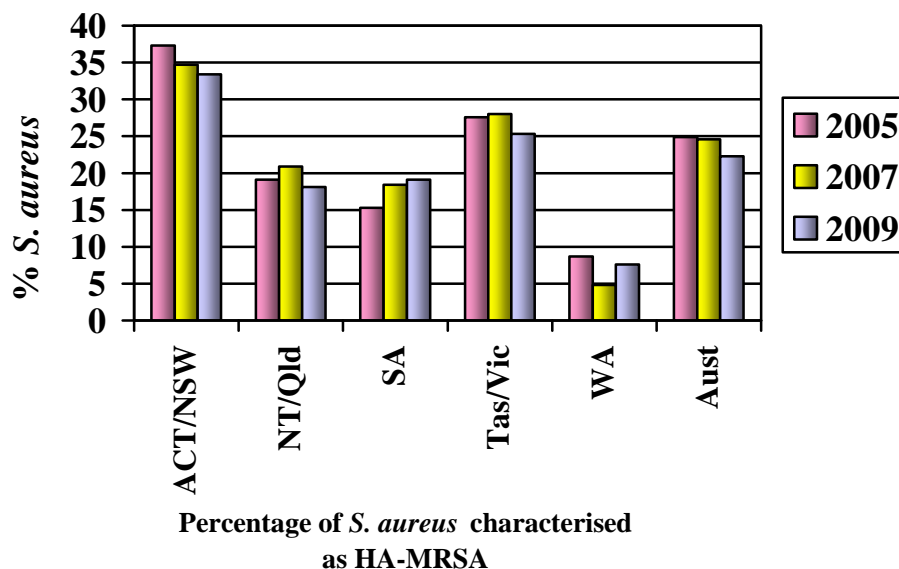
2.0. Summary

The Australian Group for Antimicrobial Resistance (AGAR) biennial hospital-onset *Staphylococcus aureus* surveillance programme commenced in 2005. In the 2009 programme (SAP 2009) up to 100 clinically significant consecutive isolates of *S. aureus* from different patients were collected by each of 30 institutions located across Australia. Isolates were collected from hospitalised patients (>48 hours at the time of specimen collection). All 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 Pantone-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.

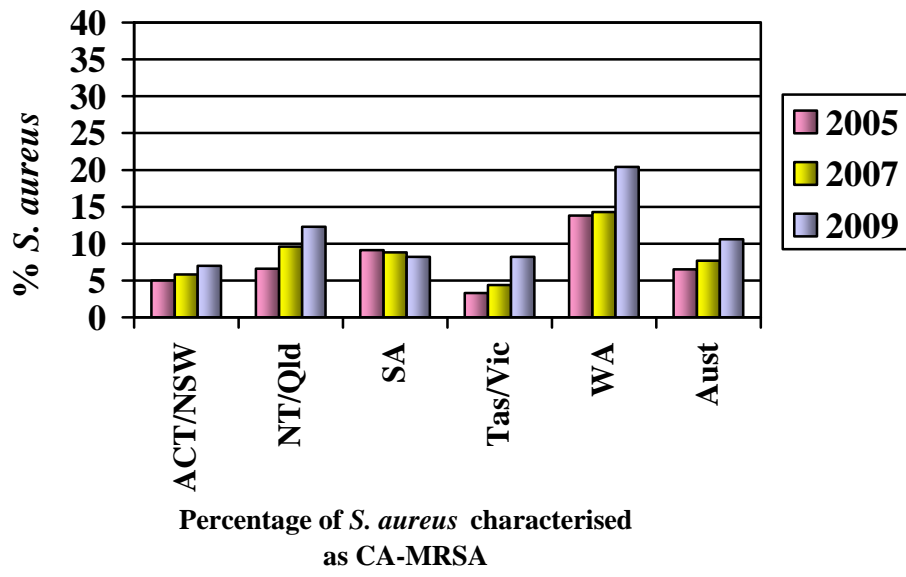
Of the 916 (33.6%) *S. aureus* classified as MRSA in SAP 2009, 899 (98.1%) were referred to the **ACCESS** Typing and Research. Overall 67.7% and 32.3% of MRSA were characterized as “healthcare-associated MRSA” (HA-MRSA) strains and “community-associated MRSA” (CA-MRSA) strains respectively.

Throughout Australia the percentage of *S. aureus* characterized as HA-MRSA was 22.3% ranging from 7.6% in WA to 33.4% in the ACT/NSW region. The proportion

of *S. aureus* characterized as HA-MRSA decreased in all but one region over the three surveys and decreased significantly nationally (P=0.02). Within HA-MRSA the proportion of ST239-III decreased even more markedly while it was only partially replaced by ST22-IV (see below).

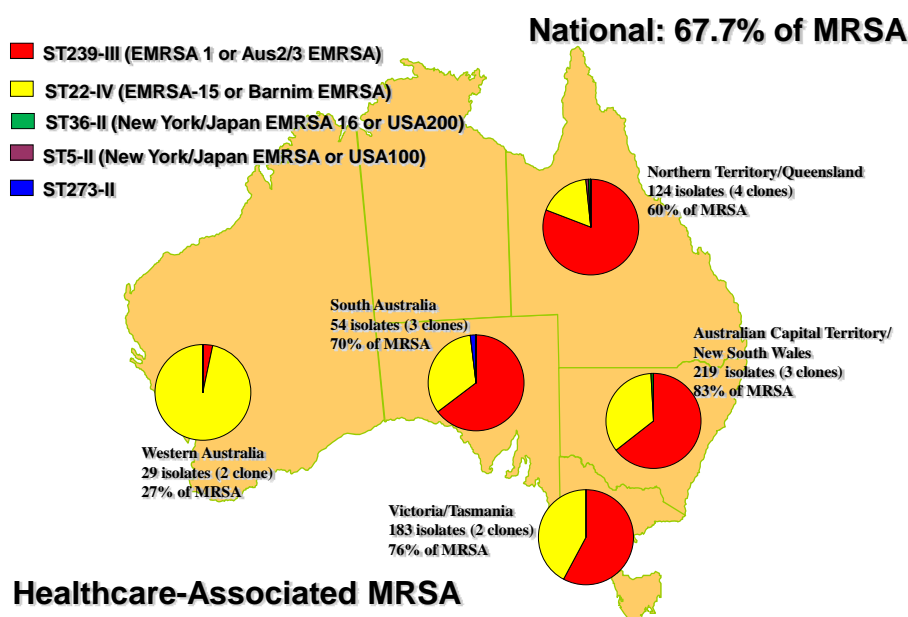


Overall 10.6% of *S. aureus* were characterized as CA-MRSA ranging from 8.2% in the Tas/Vic and SA regions to 20.4% in WA. CA-MRSA increased significantly as a proportion of *S. aureus* over the three surveys (P < 0.002). There continues to be a marked heterogeneity of strains constituting CA-MRSA seen 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).



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

Four HA-MRSA clones were identified: 63.1% were ST239-III (Aus-2/3 EMRSA), 36.1% ST22-IV (EMRSA-15), and three isolates of ST36-II (EMRSA-16 or USA200), and single isolates of ST5-II (New York Japan EMRSA or USA100) and ST273-II [a single locus variant of ST5]

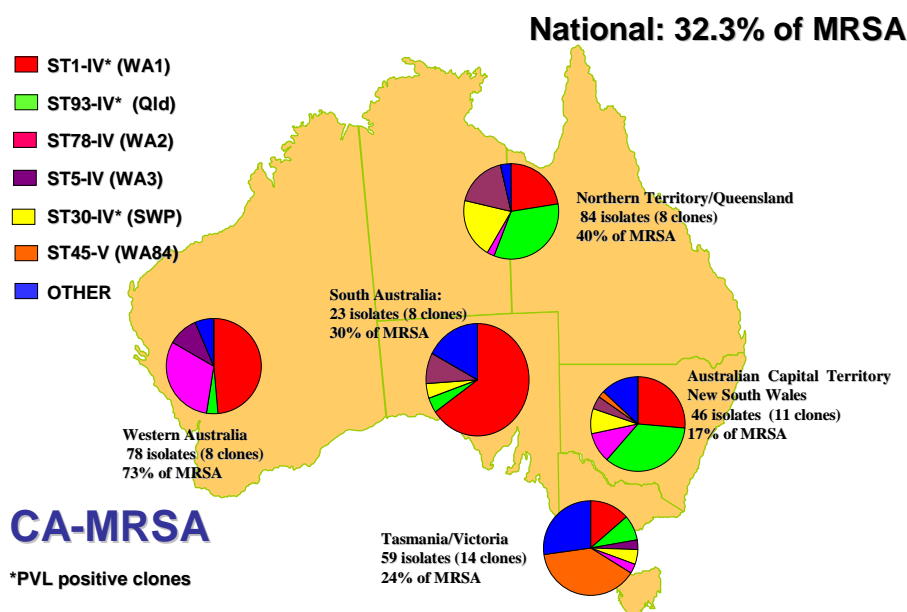


ST239-III (Aus-2/3 EMRSA) was isolated in all regions, accounting for 53.6% MRSA in the ACT/NSW region. As a consequence of the state's MRSA prevention policy the percentage of MRSA identified as ST239-III in WA remained low accounting for only 0.9% of MRSA. Overall 42.7% of MRSA were identified as Aus-2/3 EMRSA compared to 63.1% and 57.0% in SAP 2007 and SAP 2005 respectively. ST22-IV (EMRSA-15), which was initially reported in Australia in 1997, accounted for 24.5% of all MRSA isolated in Australia (18.5% in SAP 2007), ranging from 10.6% in the NT/Qld region to 31.8% in the Tas/Vic region. The percentage of MRSA characterized as EMRSA-15 has increased in three Australian regions over the three surveys noticeably in the Tas/Vic region (5.8% to 31.8% of MRSA).

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

Twenty eight community MRSA clones were identified by pulsed-field gel electrophoresis (corresponding to 20 MLST/SCC*mec* clones) of which 87.9% were:

- ST1-IV [WA MRSA-1] (31.7% of CA-MRSA)
- ST93-IV [Queensland CA-MRSA] (18.3%)
- ST5-IV [WA MRSA-3] (10.0%)
- ST78-IV [WA MRSA-2] (11.4%)
- ST30-IV [WSPP MRSA] (8.6%)
- ST45-V [WA MRSA-84 or Victorian CA-MRSA] (8.3%)



2.3. Panton Valentine Leucocidin (PVL) Toxin

HA-MRSA Clones

One PVL positive ST22-IV was isolated.

CA-MRSA Clones

82 CA-MRSA (5 clones) were PVL positive:

- ST93-IV (Queensland CA-MRSA) – 53 isolates (100% PVL positive)
- ST30-IV [WSPP MRSA] – 23 isolates (92% PVL positive)
- ST1-IV [WA MRSA-1] – 4 isolates (4.3% PVL positive)
- ST59-V_T [Taiwan CA-MRSA] – 1 isolate
- ST59-IV [WA MRSA-15] – 1 isolate

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

Overall 28.3% of CA-MRSA were identified as PVL positive.

3.0. SAP 2009 Protocol

3.1. Commencement Date

1st July 2009

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 30 laboratories located across Australia (total number of isolates = 2,728).

3.3. Participating Laboratories

Australian Capital Territory (1)

The Canberra Hospital

Science

New South Wales (7) Hospital

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)

Princess Alexandra Hospital

Royal Brisbane and Women's Hospital

Sullivan Nicolaides Pathology

Pathology Queensland, Cairns Base Hospital

Pathology Queensland, Gold Coast Hospital

Pathology Queensland, Prince Charles Hospital

Northern Territory (1)

II

Hospital

Royal Darwin Hospital

South Australia (3)

Flinders Medical Centre

Institute of Medical Veterinary

Women's and Children's

Tasmania (2)

Royal Hobart Hospital

Launceston General Hospital

Victoria (6)

Alfred Hospital

Gribbles Pathology

Royal Children's Hospital

St Vincent's Hospital

Austin Health

Monash Medical Centre

Western Australia (4)

PathWest-WA Fremantle
Hospital

PathWest-WA Queen Elizabeth

PathWest-WA Royal Perth

Saint John of God Pathology

3.4. Methicillin Susceptibility Testing

Vitek2[®] AST-P579 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 *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).

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). 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.

Staphylococcal Cassette Chromosome *mec* (*SCCmec*)

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

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

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

3.7. Panton-Valentine Leucocidin (PVL) Toxin

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

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

1. ST8-IV [2B] (USA300)
2. ST80-IV [2B] (European CA-MRSA)
3. ST59-V_T[5C2&5] (Taiwan CA-MRSA)
4. ST1-IV [2B] (USA400)

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

4.0. Methods

4.1. Epidemiological Typing Methods

Antibiogram

Participating laboratories performed antimicrobial susceptibility tests using the Vitek2[®] AST-P579 card (BioMerieux, Durham, NC). Antimicrobials tested were benzylpenicillin, oxacillin, cefazolin, vancomycin, rifampicin, fusidic acid, gentamicin, erythromycin, clindamycin, tetracycline, trimethoprim/sulphamethoxazole (cotrimoxazole), ciprofloxacin, quinupristin/dalfopristin (Synercid[®]), teicoplanin, linezolid, nitrofurantoin, mupirocin and chloramphenicol. 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 (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 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).

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 (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

ST22-IV (EMRSA-15)

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

ST36-II (EMRSA-16 or USA200)

- Antibiogram
- Urea broth
- CHEF

ST5-II (New York/Japan MRSA or USA100)

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

ST273-II (ST5slv – New York/Japan MRSA or USA100 slv)

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

4.3. Identification of CA-MRSA Clones

ST30-IV (Western Samoan MRSA - WSPP MRSA)

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

ST93-IV (Queensland CA-MRSA)

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

ST59-V_T (Taiwan CA-MRSA)

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

“WA MRSA”

ST1-IV (WA-1)
ST78-IV (WA-2)

Antibiogram
Urea Broth
CHEF
Coagulase PCR-RFLP on selected isolates

ST5-IV (WA-3)
ST5-IV (WA-71)
ST5-V (WA-35)
ST5-V (WA-81)
ST8-IV (WA-5)
ST8-V (WA77)
ST45-V (WA-4)
ST45-V (WA-84)
ST59-IV (WA-15)
ST59-IV (WA-55)
ST73-IV (WA-65)
ST188-IV (WA-78)
ST188-IV (WA-38)
ST573-V (WA-10)
ST835-V (WA-40)
ST953-IV (WA-54)

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

ST1-V (unique)
ST5-IV (unique)
ST5-V (unique)
ST7-V (unique)
ST72-IV (WA-44)
ST59-V (unique)
ST1756-V (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).

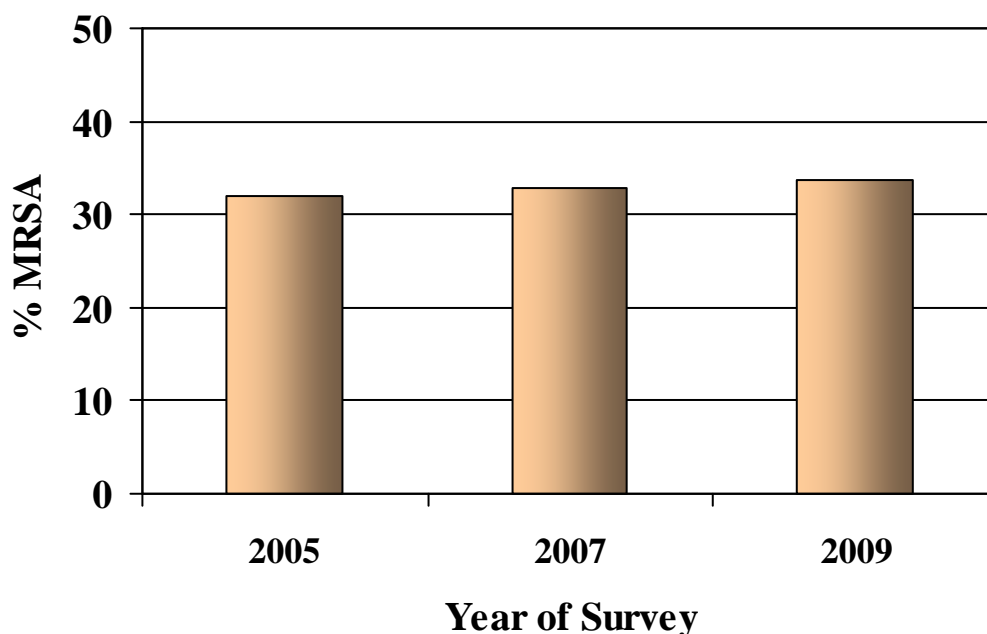
5.0. Results

In SAP 2009, 916 (33.6%) *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 – 2009

Percentage of *Staphylococcus aureus* Identified as MRSA

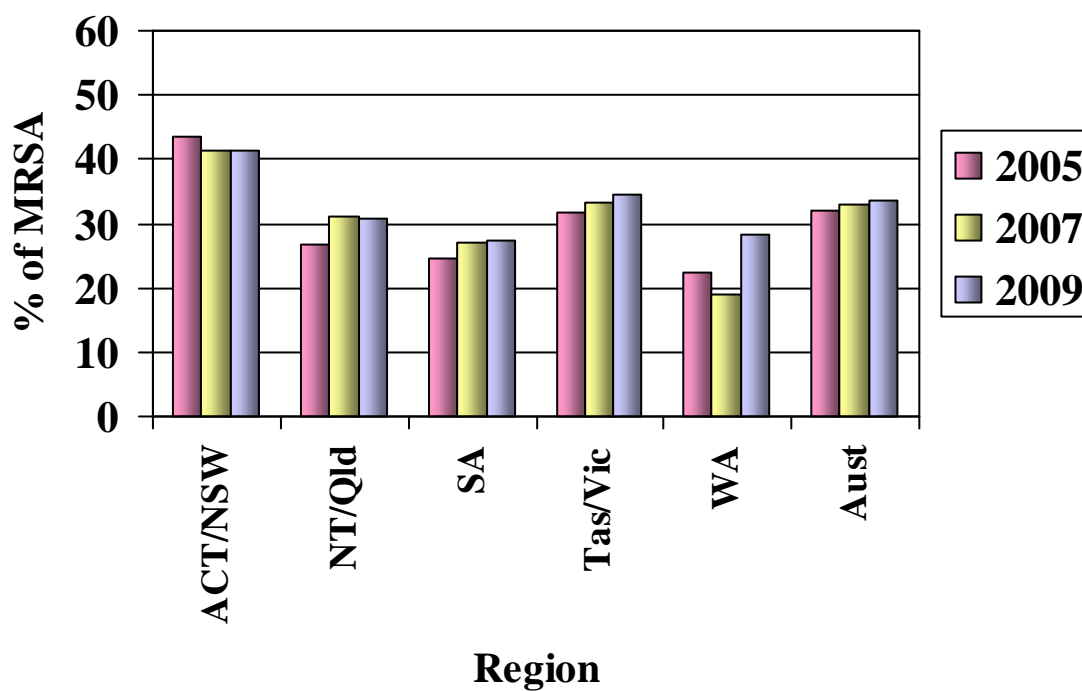
SAP	Laboratories (n)	<i>S aureus</i> (n)	MRSA (n)	MRSA (%)
2005	32	2,908	928	31.9%
2007	31	2,705	889	32.9%
2009	30	2,728	916	33.6%



Regional Distribution of MRSA

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

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 2009 Epidemiological Typing of MRSA

Of the 916 MRSA identified in SAP 2009, 899 (98.1%) were referred to the *ACCESS* Typing and Research for epidemiological typing.

Typing Tests Performed

Test	N
Cefoxitin Susceptibility Testing	930
Coagulase Gene PCR-RFLP Assay	110
Resistogram	387
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	905
Urease Reaction	920
Multilocus Sequencing Typing (MLST)	19
SCC <i>mec</i> PCR	28
Panton-Valentine leucocidin PCR	906

Regional Distribution of HA-MRSA and CA-MRSA Clones

Region	HA-MRSA (%)	CA-MRSA (%)	Total MRSA
ACT/NSW	219 (82.6)	46 (17.4)	265
Qld/NT	124 (59.6)	84 (40.4)	208
SA	54 (70.1)	23 (29.9)	77
Tas/Vic	183 (75.6)	59 (24.4)	242
WA	29 (27.1)	78 (72.9)	107
TOTAL	609 (67.7)	290 (32.3)	899

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

SAP 2005 - SAP 2009 Regional Distribution of HA-MRSA and CA-MRSA Clones

SAP 2009: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

	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	308 (88.3)	41 (11.7)	280 (85.6)	47 (14.4)	219 (82.6)	46 (17.4)
NT/Qld	108 (74.5)	37 (25.5)	143 (68.4)	66 (31.6)	124 (59.6)	84 (40.4)
SA	52 (62.7)	31 (37.3)	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	699 (79.3)	182 (20.7)	665 (76.1)	209 (23.9)	609 (67.7)	290 (32.3)

Percentage figures relate to the total number of MRSA isolates characterized

SAP 2005 - SAP 2009: Regional Distribution of HA-MRSA and CA-MRSA Clones as a Proportion of *Staphylococcus aureus*

Region	SAP 2005			SAP 2007		
	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)
ACT/NSW	825	308 (37.3)	41 (5.0)	806	280 (34.7)	47 (5.8)
NT/Qld	564	108 (19.1)	37 (6.6)	684	143 (20.9)	66 (9.6)
SA	340	52 (15.3)	31 (9.1)	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	2,808	699 (24.9)	182 (6.5)	2,705	665 (24.6)	209 (7.7)

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

Region	SAP 2009		
	Total	HA-MRSA (%)	CA-MRSA (%)
ACT/NSW	655	219 (33.4)	46 (7.0)
NT/Qld	685	124 (18.1)	84 (12.3)
SA	282	54 (19.1)	23 (8.2)
Tas/Vic	723	183 (25.3)	59 (8.2)
WA	383	29 (7.6)	78 (20.4)
TOTAL	2,728	609 (22.3)	290 (10.6)

SAP 2009: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

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

SAP 2009: HA-MRSA Clones by AGAR Laboratory

LAB	ST239-III Aus 2 EMRSA	ST239-III Aus 3 EMRSA	ST22-IV EMRSA-15	ST36-II EMRSA-16	ST5-II NY/Japan MRSA	ST273-II NY/Japan MRSA slv	TOTAL
ACT/NSW (219)							
1	9		7	1			17
2	24		14				38
3	8		4				12
4	14	1	19				34
5	25		9				34
6	32		8	1			41
7			1				1
8	28	1	13				42
NT/Qld (124)							
10	10		3				13
11	6		4				10
12	21		1				22
13	2		7	1			10
28	30	1	5				36
29	10		3				13
30	12	5	2		1		20
SA (54)							
14	13	3	6				22
15	15	4	12			1	32
16							0
Tas/Vic (183)							
18	2	1	7				10
19	5	24	9				38
20	2	8	4				14
21							0
22	3	25	13				41
23	1	24	14				39
31	2	6	10				18
32	1	2	20				23
WA (29)							
24	1		3				4
25			11				11
26			8				8
27			6				6
TOTAL	276	105	223	3	1	1	609

SAP 2009 CA-MRSA Clones by AGAR Laboratory

CC	1					5								7	8		30	45		59				72	88	97	S	Total		
	1 IV	1 V	188 IV	188 IV	573 V	5 IV	5 IV	5 IV	5 V	5 V	5 V	73 IV	835 V	1756 V	7 V	8 IV	8 V	30 IV	45 V	45 V	59 IV	59 IV	59 V	59 V	72 IV	78 IV	953 IV		93 IV	
	WA 1		WA 78	WA 38	WA 10	WA 3		WA 71		WA 35	WA 81	WA 65	WA 40			WA 5	WA 77	WSPP	WA 4	WA 84	WA 15	WA 55	Tw		WA 44	WA 2	WA 54	Qld		
ACT/NSW (46)																														
1	3					1												1									2		1	8
2	1												1					1		1									2	6
3	1							1										1					1					6	10	
4	2		1			1												1								1	1	1	7	
5	2																	1											3	
6	1							1																		2		3	7	
7																													0	
8	2																											3	5	
NT/Qld (84)																														
10	11					3												5										7	26	
11	2					2												1										2	7	
12	2																	3								1	8	14		
13	1					1											1	1			1							1	6	
28	1	1																1								1	1	5		
29	1					9												4										2	16	
30	1																	2										7	10	
SA (23)																														
14	2										1								1				1						5	
15	9											1																	10	
16	4					2												1										1	8	
Tas/Vic (59)																														
18	2								1																				3	
19									1	1					1														3	
20									2									1		7								1	11	
21	2					1			1						1														5	
22	1															1				5						1	2	10		
23	1				1			1	3									1		5								1	13	
31	2											1		1				1		5									10	
32						1														1						1	1	4		

SAP 2009: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

CC	1					5								7	8		30	45		59				72	88	97	S	Total		
	1 IV	1 V	188 IV	188 IV	573 V	5 IV	5 IV	5 IV	5 V	5 V	5 V	73 IV	835 V	1756 V	7 V	8 IV	8 V	30 IV	45 V	45 V	59 IV	59 IV	59 V	59 V	72 IV	78 IV	953 IV		93 IV	
	WA 1		WA 78	WA 38	WA 10	WA 3		WA 71		WA 35	WA 81	WA 65	WA 40			WA 5	WA 77	WSPP	WA 4	WA 84	WA 15	WA 55	Tw		WA 44	WA 2	WA 54	Qld		
WA (78)																														
24	10			1																							4		1	16
25	12					1																				1	7			21
26	9					5						2										1					6		2	25
27	7					2																					7			16
Total	92	1	1	1	1	29	2	1	8	1	1	4	1	1	2	1	1	25	1	24	1	1	1	1	1	33	1	53	290	

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].

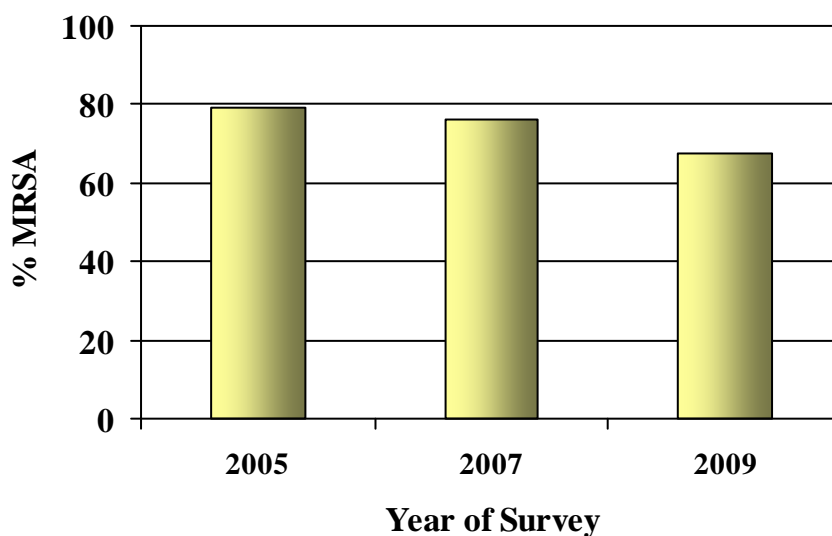
SAP 2009 HA-MRSA Clones

In SAP 2009 four international HA-MRSA clones (609 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST239-III	Aus -2 and Aus -3 EMRSA or EA MRSA	384 (63.1%)
ST22-IV	EMRSA-15	220 (36.1%)
ST36-II	EMRSA-16 or USA200	3 (0.5%)
ST5-II	New York Japan MRSA or USA100	2 (0.3%)
ST273-II	New York Japan MRSA single locus variant (slv)	
TOTAL		609

Percentage figures in parenthesis relate to HA-MRSA isolates

SAP 2005 - 2009: Percentage of MRSA Identified as HA-MRSA



ST239-III

In Australia ST239-III 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 evolved from the “Eastern Australian EMRSA” clone described in the 1980s. ST239-III 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 = 278)	Aus-3 EMRSA (n = 106)
Erythromycin ^R	99%	98%
Tetracycline ^R	99%	98%
Cotrimoxazole ^R	92%	100%
Gentamicin ^R	97%	96%
Ciprofloxacin ^R	97%	100%
Fusidic Acid ^R	2%	2%
Rifampicin ^R	4%	13%
High Level Mupirocin ^R	0	1%

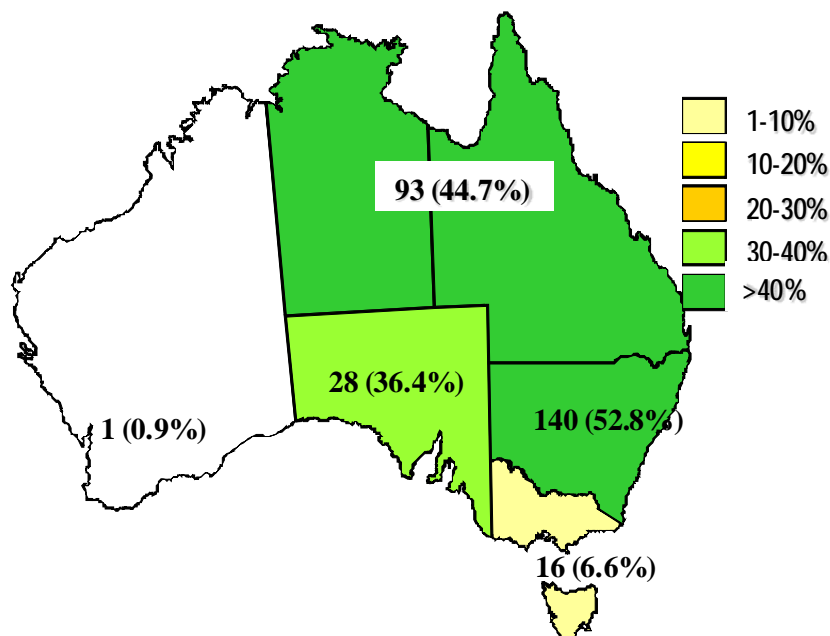
Resistogram

	Aus-2 EMRSA (n = 278)	Aus-3 EMRSA (n = 106)
Mercuric Acetate ^R	0	93%
Mercuric Chloride ^R	0	93%

Aus-2 EMRSA

Epidemiology

ST239-III (Aus-2 EMRSA): n = 278 (30.9%)



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

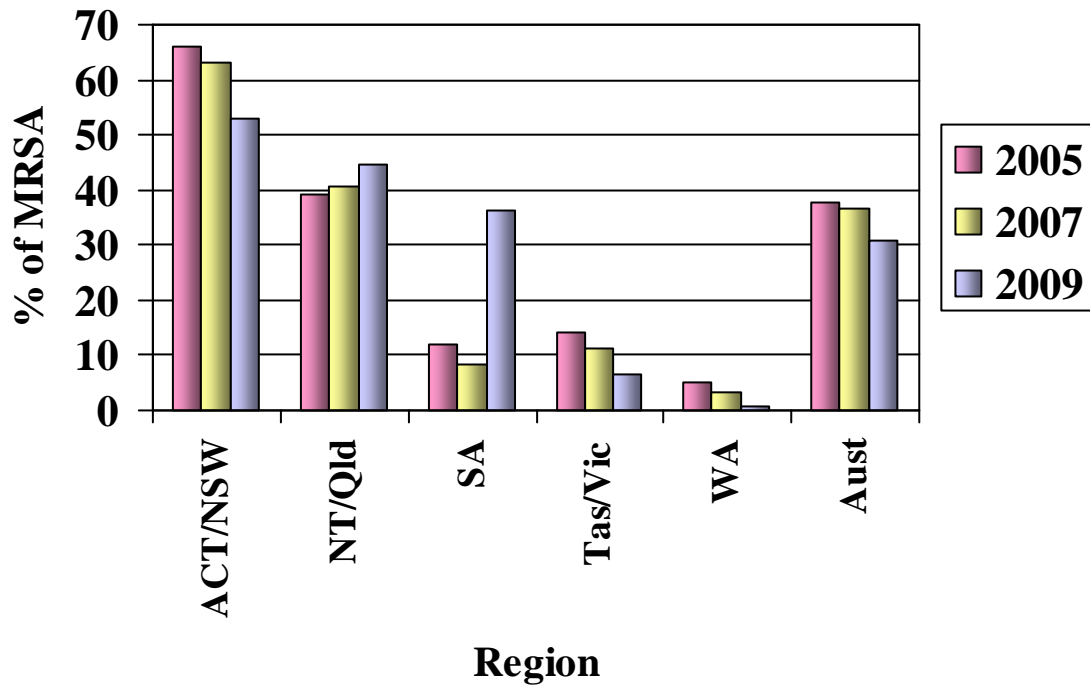
SAP 2005 - 2009: Regional Distribution of ST239-III (Aus-2 EMRSA)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	230 (65.9%)	206 (63.0%)	140 (52.8%)
Qld/NT	57 (39.3%)	85 (40.7%)	93 (44.7%)
SA	10 (12.0%)	6 (8.5%)	28 (36.4%)
Tas/Vic	32 (14.3%)	23 (11.1%)	16 (6.6%)
WA	4 (5.0%)	2 (3.3%)	1 (0.9%)
TOTAL	333 (37.8%)	322 (36.8%)	278 (30.9%)

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

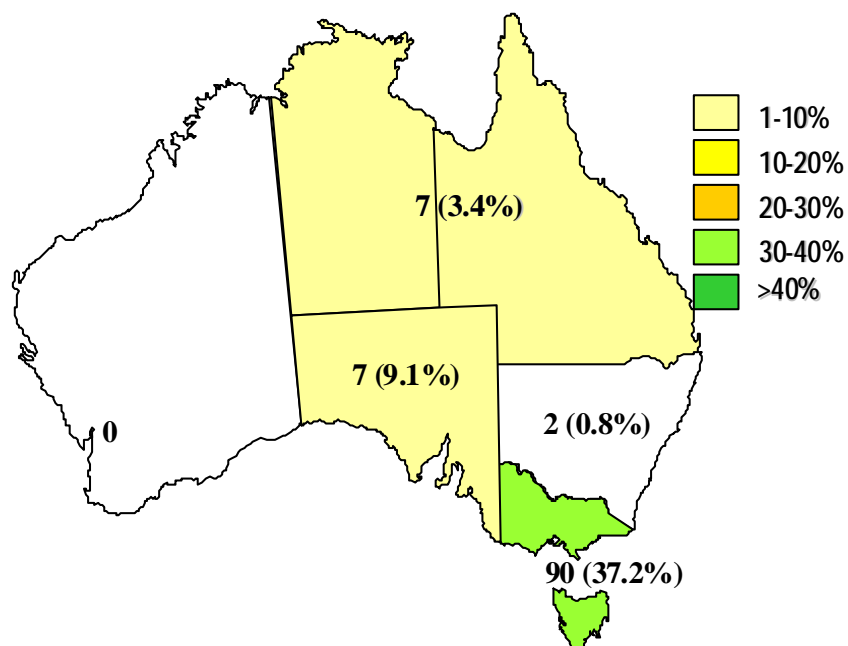
SAP 2005 - 2009: Regional Distribution of ST239-III (Aus-2 EMRSA)



Aus-3 EMRSA

Epidemiology

ST239-III (Aus-3 EMRSA): n =106 (11.8%)



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

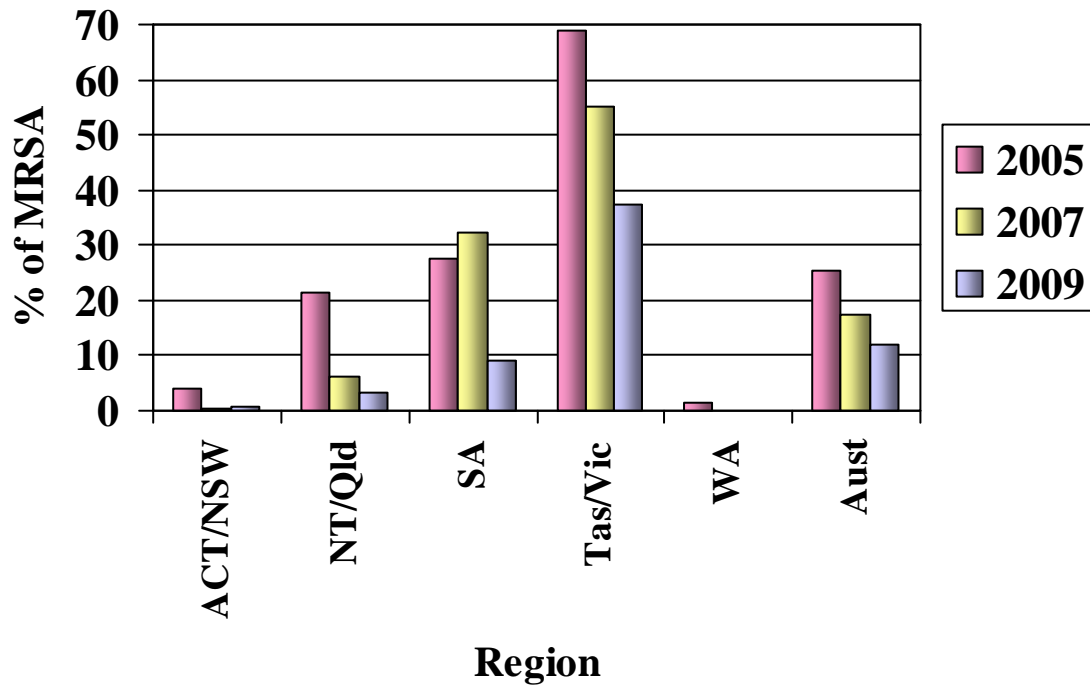
SAP 2005 - 2009: Regional Distribution of ST239-III (Aus-3 EMRSA)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	14 (4.0%)	1 (0.3%)	2 (0.8%)
Qld/NT	31 (21.4%)	13 (6.2%)	7 (3.4%)
SA	23 (27.7%)	23 (32.4%)	7 (9.1%)
Tas/Vic	154 (68.8%)	114 (55.1%)	90 (37.2%)
WA	1 (1.3%)	0	0
TOTAL	223 (25.3%)	151 (17.3%)	106 (11.8%)

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

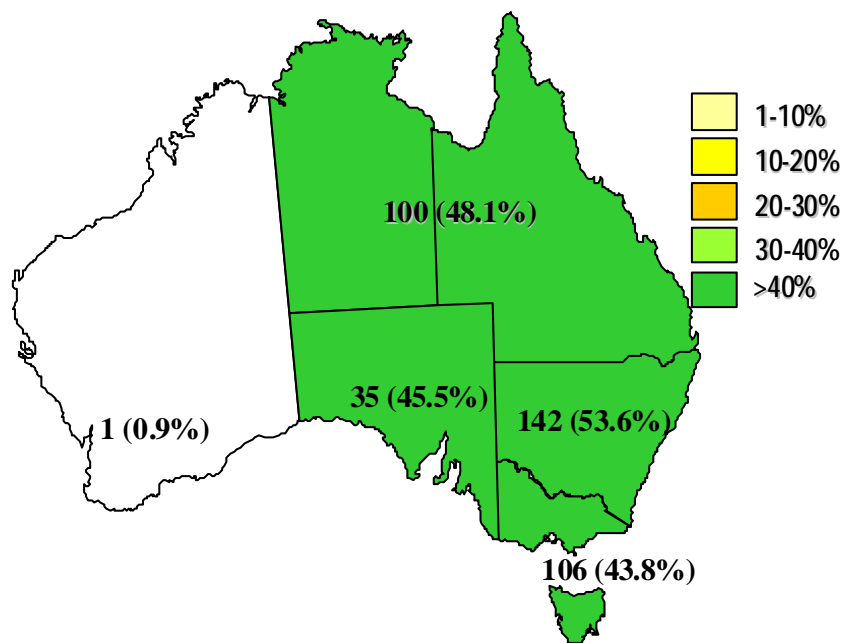
SAP 2005 - 2009: Regional Distribution of ST239-III (Aus-3 EMRSA)



Aus-2 and Aus-3 EMRSA (ST239-III)

Epidemiology

ST239-III (Aus-2 and Aus-3 EMRSA): n = 384 (42.7%)



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

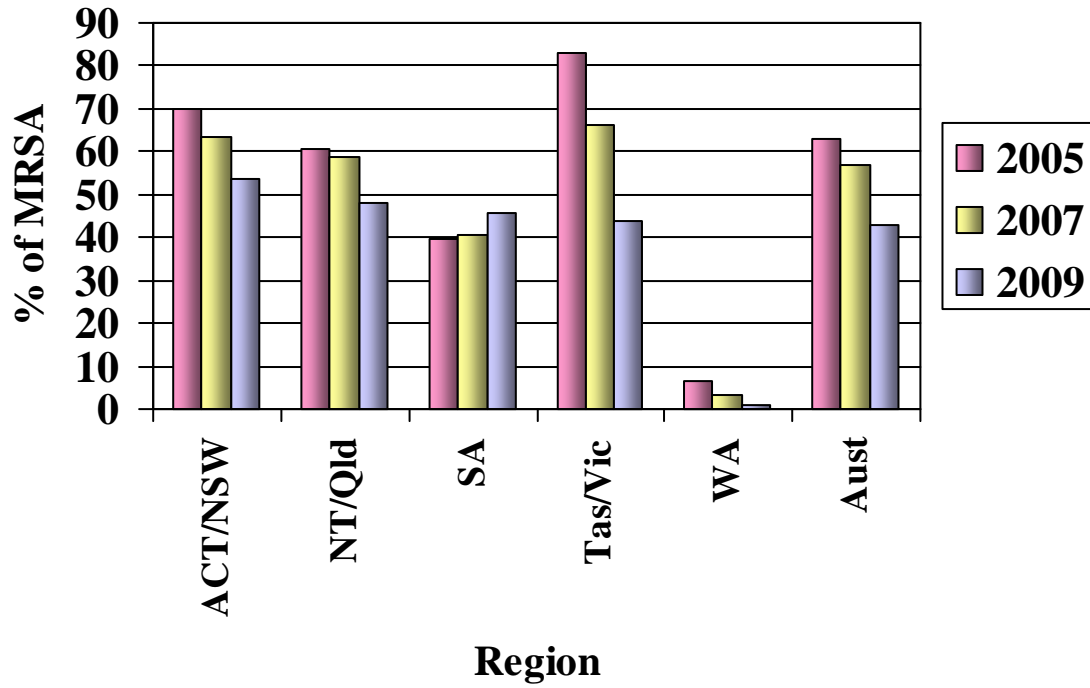
SAP 2005 - 2009: Regional Distribution of ST239-III (Aus-2 and Aus-3 EMRSA)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	244 (69.9%)	207 (63.3%)	142 (53.6%)
Qld/NT	88 (60.7%)	123 (58.8%)	100 (48.1%)
SA	33 (39.8%)	29 (40.8%)	35 (45.5%)
Tas/Vic	186 (83.0%)	137 (66.2%)	106 (43.8%)
WA	5 (6.3%)	2 (3.3%)	1 (0.9%)
TOTAL	556 (63.1%)	498 (57.0%)	384 (42.7%)

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

SAP 2005 - 2009: Regional Distribution of ST239-III (Aus-2 and Aus-3 EMRSA)



ST22-IV (EMRSA-15)

Also known as “EMRSA-15” or the “German Barnim” strain, ST22- IV 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 is frequently isolated from patients in long term care facilities and is associated with pre-employment screening of health staff from the UK.

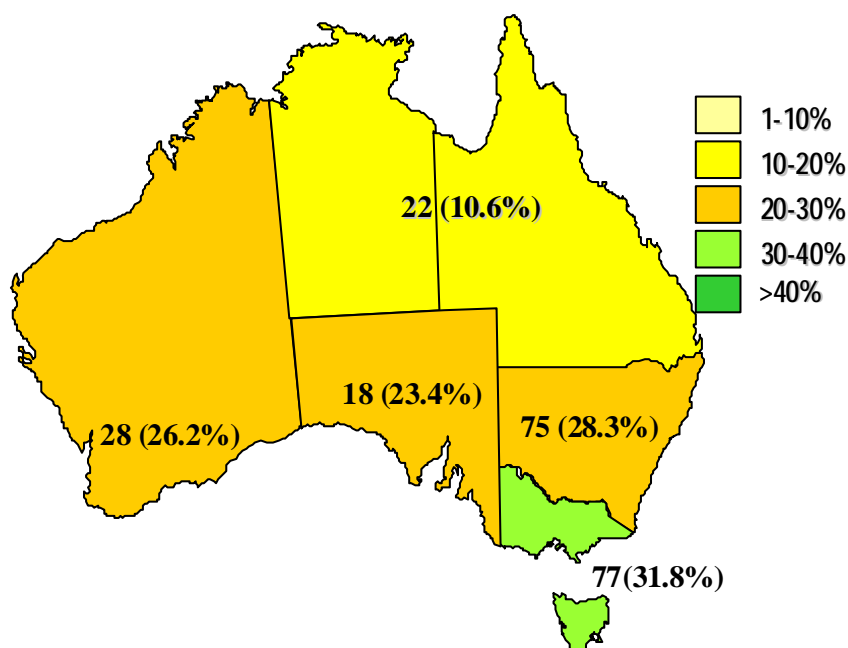
Phenotypic Characteristics

Antibiogram:	Ciprofloxacin ^R	100%
	Erythromycin ^R	68%
	Tetracycline ^R	1%
	Rifampicin ^R	1%
	Gentamicin ^R	1%
	Cotrimoxazole ^R	1%
	High Level Mupirocin ^R	0
	Fusidic Acid ^R	0

Urease: Negative

Epidemiology

ST22-IV (EMRSA-15): n = 220 (24.5%)



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

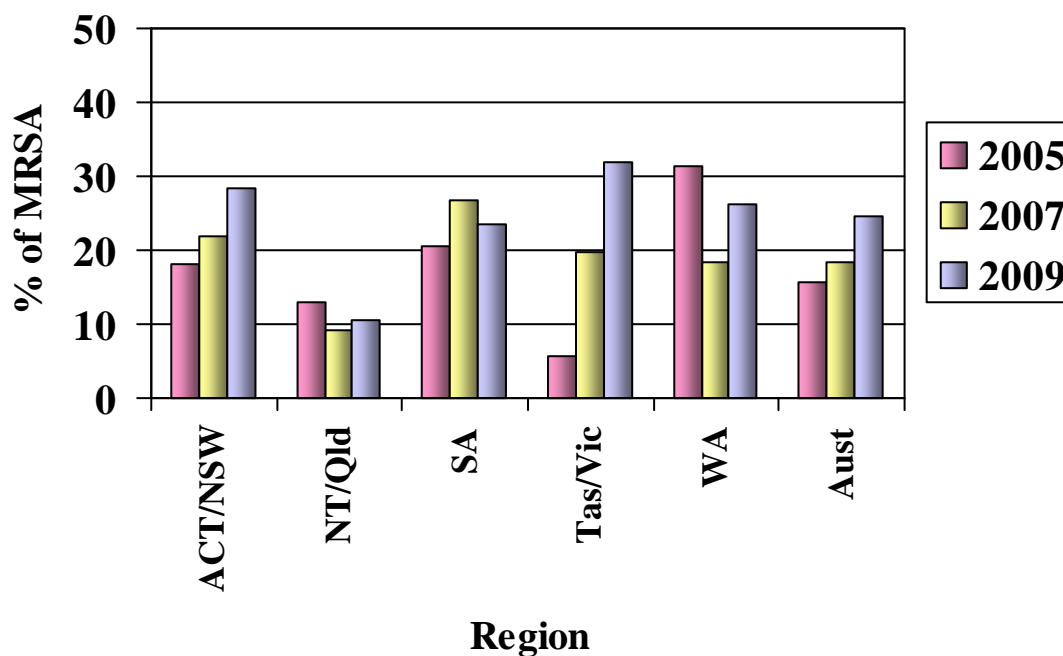
SAP 2005 - 2009: Regional Distribution of ST22-IV (EMRSA-15)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	63 (18.1%)	72 (22.0%)	75 (28.3%)
Qld/NT	19 (13.1%)	19 (9.1%)	22 (10.6%)
SA	17 (20.5%)	19 (26.8%)	18 (23.4%)
Tas/Vic	13 (5.8%)	41 (19.8%)	77 (31.8%)
WA	25 (31.3%)	11 (18.3%)	28 (26.2%)
TOTAL	137 (15.6%)	162 (18.5%)	220 (24.5%)

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

SAP 2005 - 2009: Regional Distribution of ST22-IV (EMRSA-15)



ST36-II (EMRSA-16)

Also known as “EMRSA-16” or “USA200”, ST36-II was first identified in a single hospital outbreak in London in 1991-2. It now accounts for almost a quarter of UK isolates sent to the Laboratory of Hospital Infection in Colindale for typing. ST36-II has been isolated in several European countries including Denmark, Finland, Sweden and Turkey, and in the USA. ST36-II is resistant to ciprofloxacin, erythromycin and variably resistant to the aminoglycosides. It carries staphylococcal enterotoxin A, G and I and TSST-1.

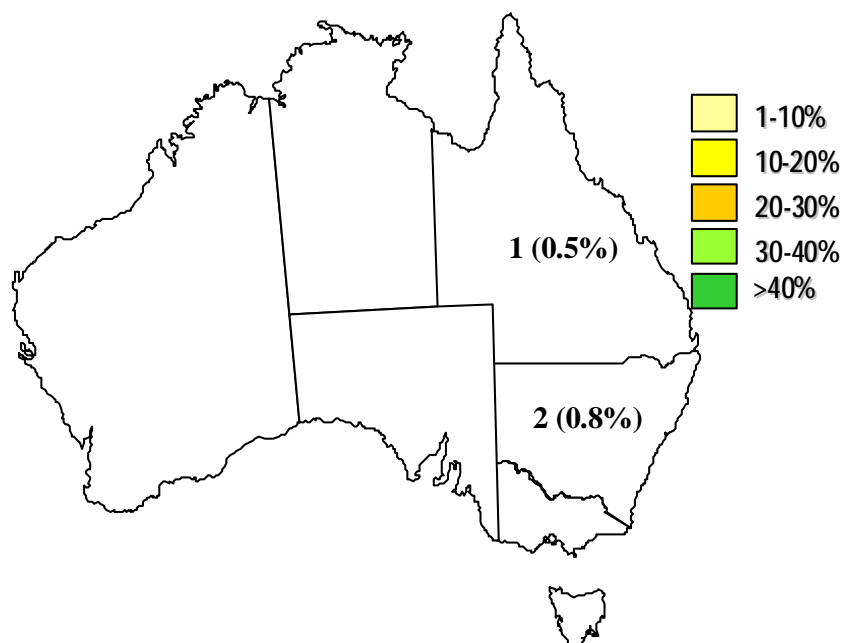
Phenotypic Characteristics

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 (EMRSA-16): n = 3 (0.3%)



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

ST5-II (New York Japan MRSA)

Also known as “New York Japan MRSA”, ST5-II is a major HA-MRSA of the USA and Japan and forms part of clonal complex 5.

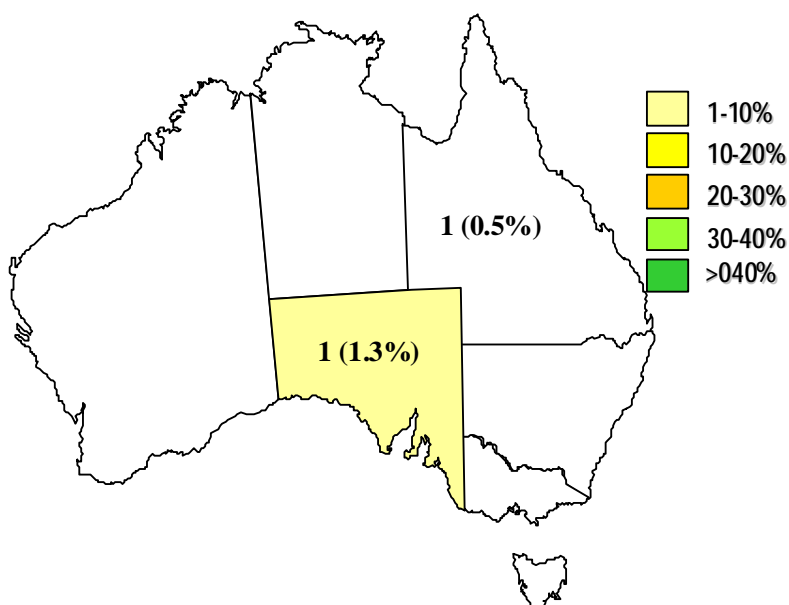
Phenotypic Characteristics

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

Urease: Positive

Epidemiology

ST5-II (New York Japan MRSA): n = 2 (0.2%)



Percentage figures in parenthesis relate to the total number of MRSA isolates characterized including ST273 (ST5slv)-II

Summary of HA-MRSA Isolated in AGAR SAP 2005 - 2009

Clone	Alternative Name	SAP 2005	SAP 2007	SAP 2009
ST239-III	Aus-2, -3 EMRSA	556 (63.1%)	498 (57.0%)	384 (42.7%)
ST22-IV	EMRSA-15	137 (15.6%)	162 (18.5%)	220 (24.5%)
ST36-II	EMRSA-16	2 ^a (0.2%)	1 ^b (0.1%)	3 ⁱ (0.3%)
ST247-I	EMRSA 17	2 ^c (0.2%)	1 ^d (0.1%)	0
ST8-VI	Irish-2 EMRSA	0	1 ^e (0.1%)	0
ST5-II	New York Japan	2 ^f (0.2%)	1 ^g (0.1%)	2 ^j (0.2%)
ST228-I	Southern German EMRSA	0	1 ^h (0.1%)	0
Total		699 (79.3%)	665 (76.1%)	607 (67.5%)

Percentage figures relate to the total number of MRSA characterized

^aIsolated in SA (n=1) and Vic/Tas (n=1)

^bIsolated in Qld/NT

^cIsolated in WA (n=1) and NSW/ACT (n=1)

^dIsolated in NSW/ACT

^eIsolated in WA

^fIsolated in SA (n=1) and Qld/NT (n=1)

^gIsolated in Vic/Tas

^hIsolated in WA

ⁱIsolated in NSW/ACT (n=2) and Qld/NT (n=1)

^jIsolated in Qld/NT (n=1) and SA (n=1)

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 -lactams antibiotics. “WA MRSA” has acquired the community associated *SCCmec* types IV and V, which usually lack transposons, integrated plasmids and other antibiotic resistance genes. Although they have been introduced into teaching hospitals 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 “Western Samoan MRSA” (WSPP MRSA). WSPP MRSA has previously been reported in New Zealand and several Pacific islands. In 2000 a non-multiresistant MRSA was identified as a cause of community acquired infection in the Caucasian population living in Ipswich Queensland and was subsequently identified as “Queensland MRSA” (6). Although both strains initially caused skin infections they have now been associated with serious invasive disease and have been shown to be PVL positive.

SAP 2009 CA-MRSA Clones

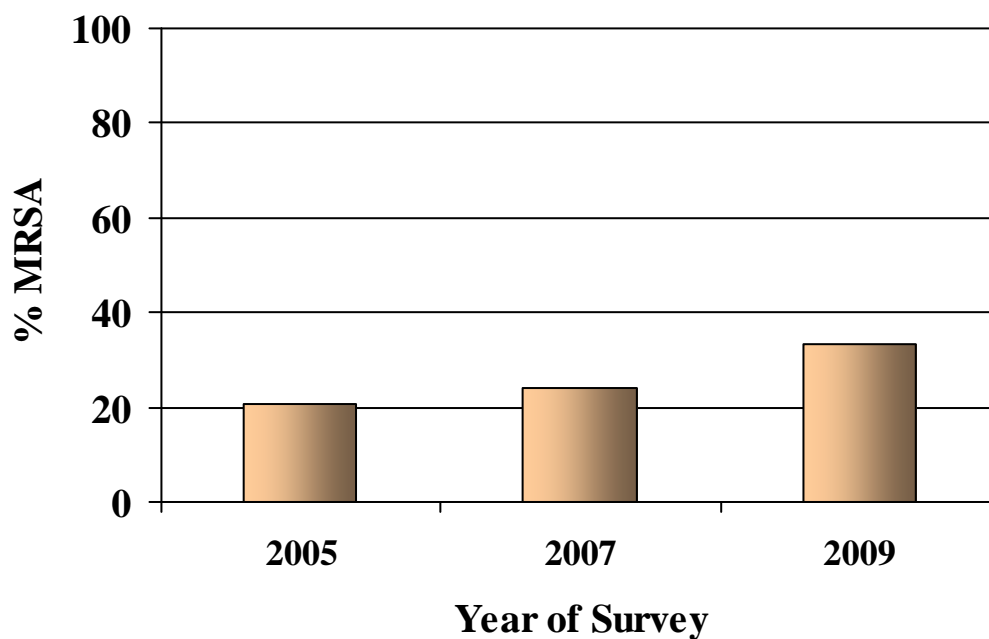
In SAP 2009 28 community MRSA clones (twenty MLST/*SCCmec* clone types) were identified.

Clone	CC	Alternative Name	n (%)
ST1-IV	1	WA MRSA-1	92 (31.8%)
ST93-IV	Singleton	Queensland MRSA	53 (18.3%)
ST78-IV	88	WA MRSA-2	33 (11.4%)
ST5-IV	5	WA MRSA-3	29 (10.0%)
ST30-IV	30	WSPP MRSA	25 (8.6%)
ST45-V	45	WA MRSA-84 (Victorian CA-MRSA)	24 (8.3%)
ST5-V	5		8 (2.8%)
ST73-IV	5	WA MRSA-65	4 (1.4%)
ST5-IV	5		2 (0.7%)
ST7-V	7		2 (0.7%)
ST1-V	1		1 (0.3%)
ST188-IV	1	WA MRSA-78	1 (0.3%)
ST188-IV	1	WA MRSA-38	1 (0.3%)
ST573-V	1	WA MRSA-10	1 (0.3%)
ST5-IV	5	WA MRSA-71	1 (0.3%)

Clone	CC	Alternative Name	n (%)
ST5-V	5	WA MRSA-35	1 (0.3%)
ST5-V	5	WA MRSA-81	1 (0.3%)
ST835-V	5	WA MRSA-40	1 (0.3%)
ST1756-V	5		1 (0.3%)
ST8-IV	8	WA MRSA – 5	1 (0.3%)
ST8-V	8	WA MRSA – 77	1 (0.3%)
ST45-V	45	WA MRSA-4	1 (0.3%)
ST59-IV	59	WA MRSA-15	1 (0.3%)
ST59-IV	59	WA MRSA-55	1 (0.3%)
ST59-V _T	59	Taiwan CA-MRSA	1 (0.3%)
ST59-V	59		1 (0.3%)
ST72-IV	72	WA MRSA-44	1 (0.3%)
ST953-IV	97	WA MRSA-54	1 (0.3%)

Percentage figures in parenthesis relate to community MRSA isolates

SAP 2005 - 2009: Percentage of MRSA Identified as CA-MRSA

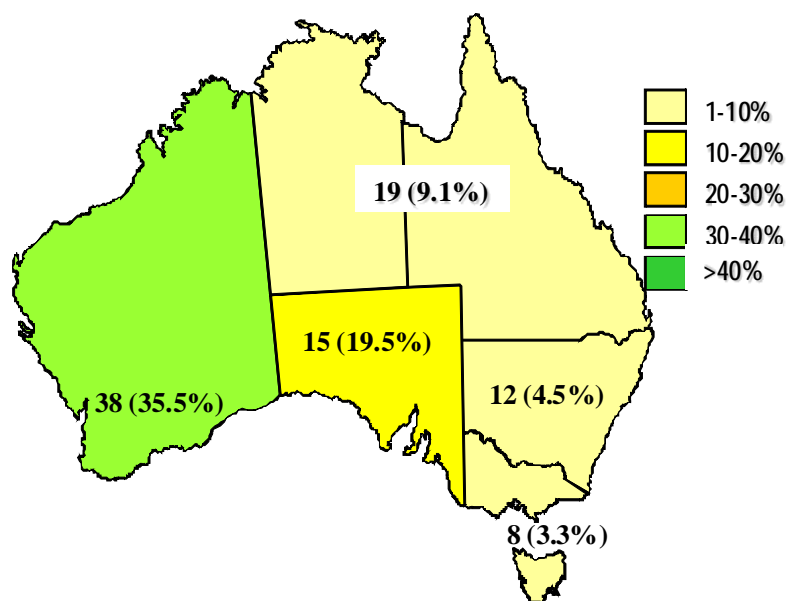


ST1-IV

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

Epidemiology

ST1-IV (WA MRSA-1): n = 92 (10.2%)



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

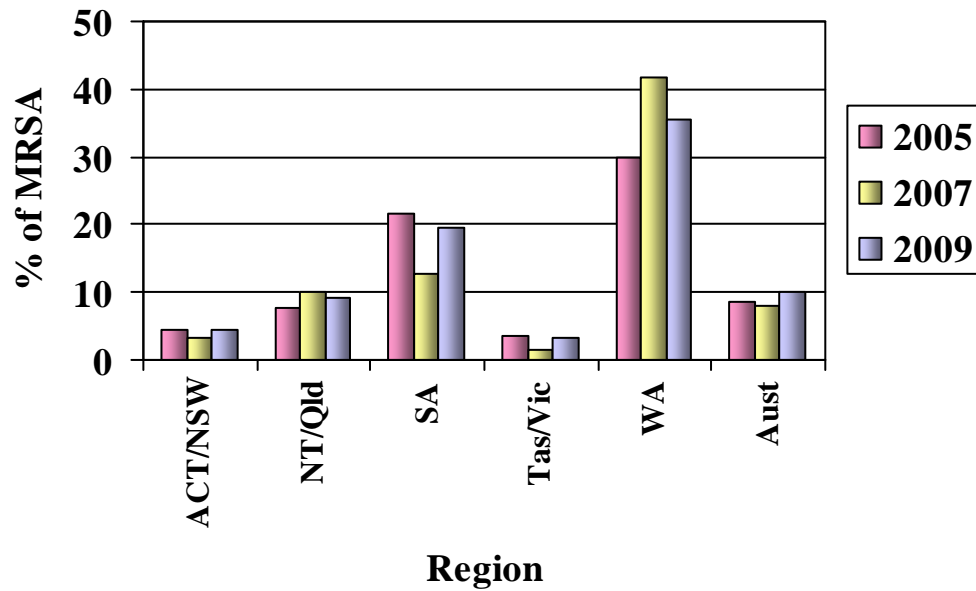
SAP 2005 - 2009: Regional Distribution of ST1-IV (WA MRSA-1)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	15 (4.3%)	11 (3.4%)	12 (4.5%)
Qld/NT	11 (7.6%)	21 (10.0%)	19 (9.1%)
SA	18 (21.7%)	9 (12.7%)	15 (19.5%)
Tas/Vic	8 (3.6%)	3 (1.5%)	8 (3.3%)
WA	24 (30.0%)	25 (41.7%)	38 (35.5%)
TOTAL	76 (8.6%)	69 (7.9%)	92 (10.2%)

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

SAP 2005 - 2009: Regional Distribution of ST1-IV (WA MRSA-1)

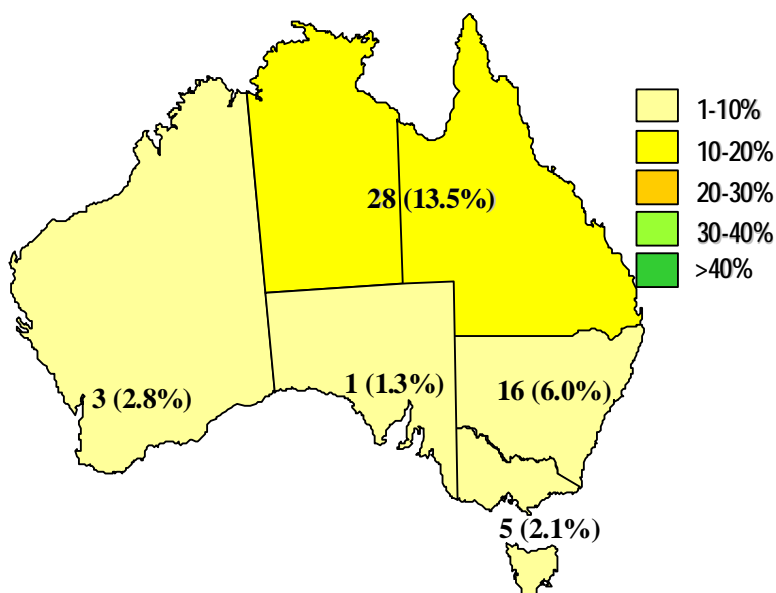


ST93-IV

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

Epidemiology

ST93-IV (QLD MRSA): n = 53 (5.9%)



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

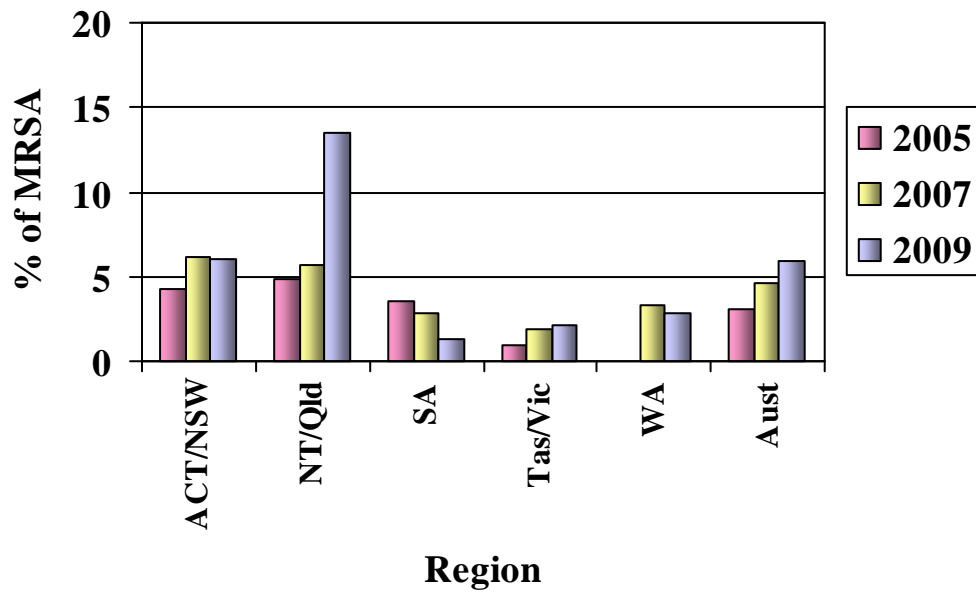
SAP 2005 - 2009: Regional Distribution of ST93-IV (Qld CA-MRSA)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	15 (4.3%)	20 (6.1%)	16 (6.0%)
Qld/NT	7 (4.8%)	12 (5.7%)	28 (13.5%)
SA	3 (3.6%)	2 (2.8%)	1 (1.3%)
Tas/Vic	2 (0.9%)	4 (1.9%)	5 (2.1%)
WA	0	2 (3.3%)	3 (2.8%)
TOTAL	27 (3.1%)	40 (4.6%)	53 (5.9%)

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

SAP 2005 - 2009: Regional Distribution of ST93-IV (Qld CA-MRSA)

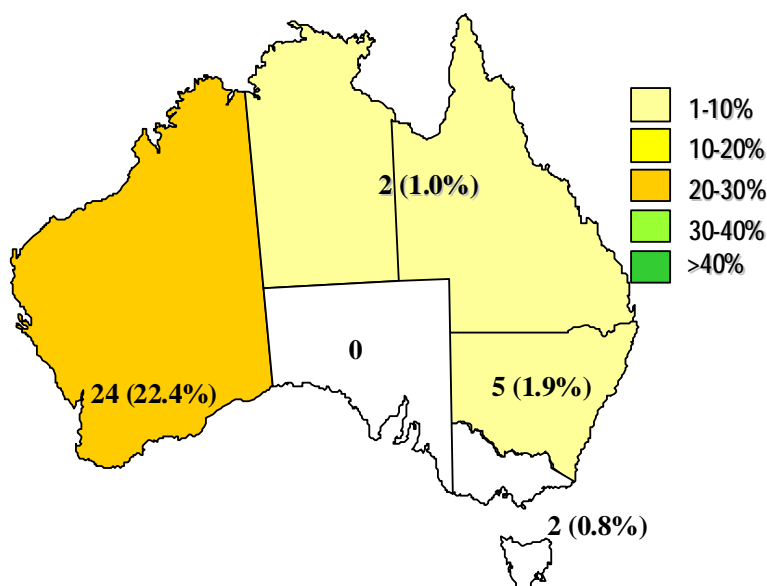


ST78-IV

Also known as “WA MRSA-2”, ST78-IV forms part of clonal complex 88 and is PVL negative.

Epidemiology

ST78-IV (WA MRSA-2): n = 33 (3.7%)



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

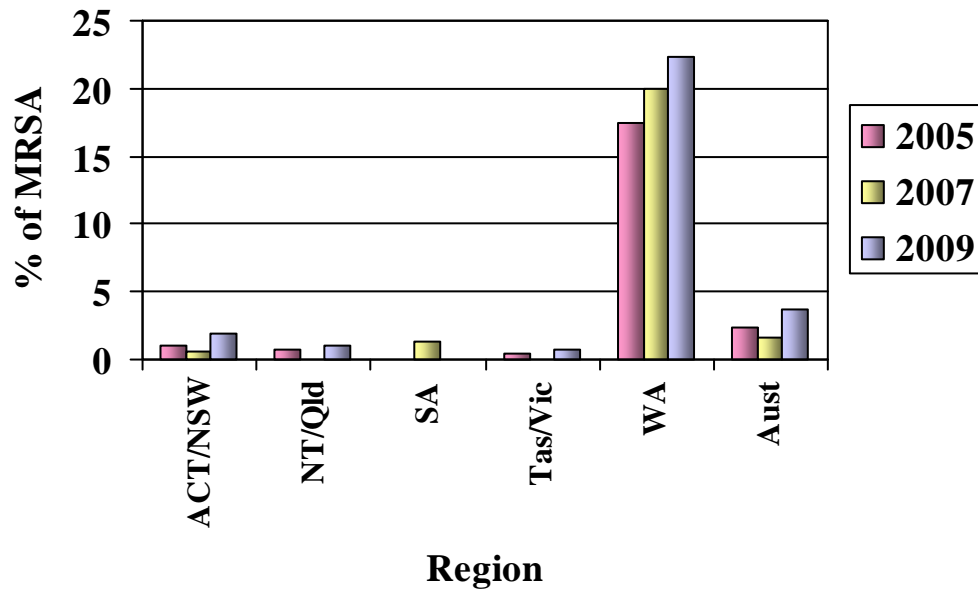
SAP 2005 - 2009: Regional Distribution of ST78-IV (WA MRSA-2)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures.

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	4 (1.1%)	2 (0.6%)	5 (1.9%)
Qld/NT	1 (0.7%)	0	2 (1.0%)
SA	0	1 (1.4%)	0
Tas/Vic	1 (0.4%)	0	2 (0.8%)
WA	14 (17.5%)	12 (20.0%)	24 (22.4%)
TOTAL	20 (2.3%)	15 (1.7%)	33 (3.7%)

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

SAP 2005 - 2009: Regional Distribution of ST78-IV (WA MRSA-2)

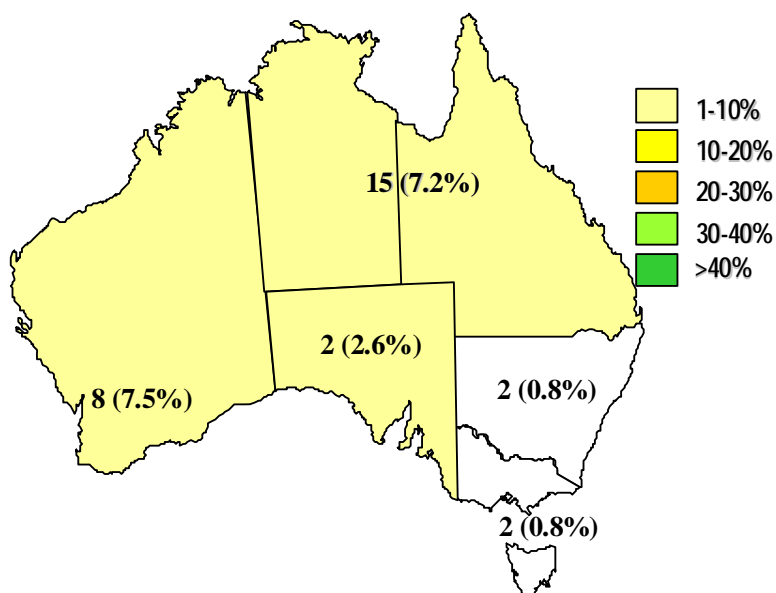


ST5-IV

Also known as “WA MRSA-3”, ST5-IV forms part of clonal complex 5 and is PVL negative.

Epidemiology

ST5-IV (WA MRSA-3): n = 29 (3.2%)



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

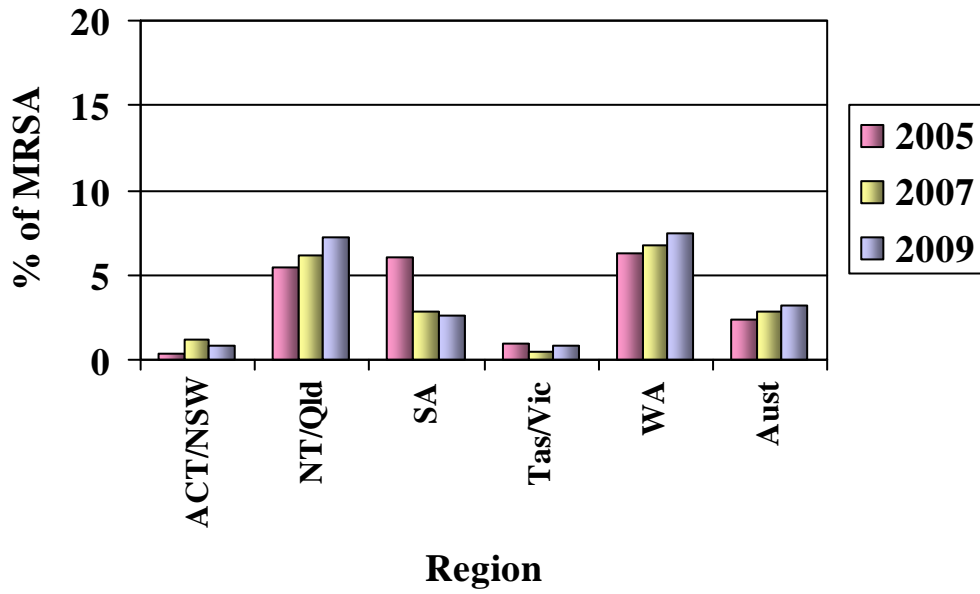
SAP 2005 - 2009: Regional Distribution of ST5-IV (WA MRSA-3)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	1 (0.3%)	4 (1.2%)	2 (0.8%)
Qld/NT	8 (5.5%)	13 (6.2%)	15 (7.2%)
SA	5 (6.0%)	2 (2.8%)	2 (2.6%)
Tas/Vic	2 (0.9%)	1 (0.5%)	2 (0.8%)
WA	5 (6.3%)	4 (6.7%)	8 (7.5%)
TOTAL	21 (2.4%)	24 (2.8%)	29 (3.2%)

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

SAP 2005 - 2009: Regional Distribution of ST5-IV (WA MRSA-3)

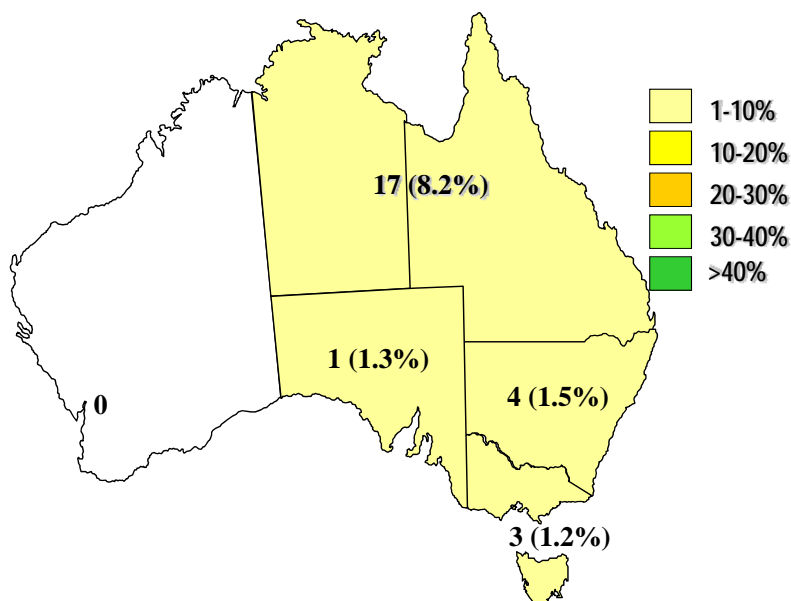


ST30-IV

Also known as “WSPP MRSA”, ST30-IV 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 (WSPP MRSA): n = 25 (2.8%)



Percentage figures in parenthesis relate to total MRSA isolates characterized

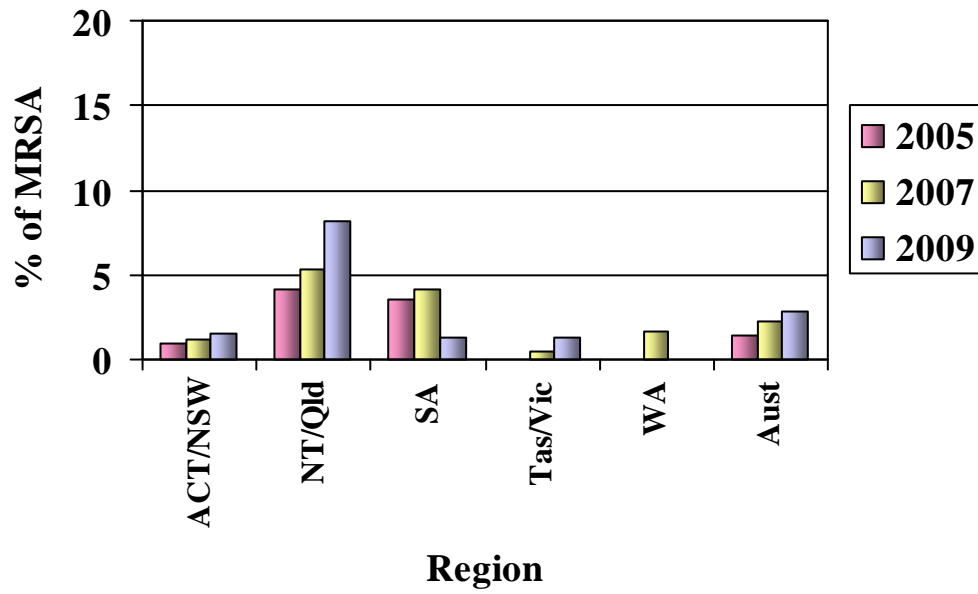
SAP 2005 - 2009: Regional Distribution of ST30-IV (WSPP CA-MRSA)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures.

Region	SAP 2005	SAP 2007	SAP 2009
ACT/NSW	3 (0.9%)	4 (1.2%)	4 (1.5%)
Qld/NT	6 (4.1%)	11 (5.3%)	17 (8.2%)
SA	3 (3.6%)	3 (4.2%)	1 (1.3%)
Tas/Vic	0	1 (0.5%)	3 (1.2%)
WA	0	1 (1.7%)	0
TOTAL	12 (1.4%)	20 (2.3%)	25 (2.8%)

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

SAP 2005 - 2009: Regional Distribution of ST30-IV (WSPP CA-MRSA)

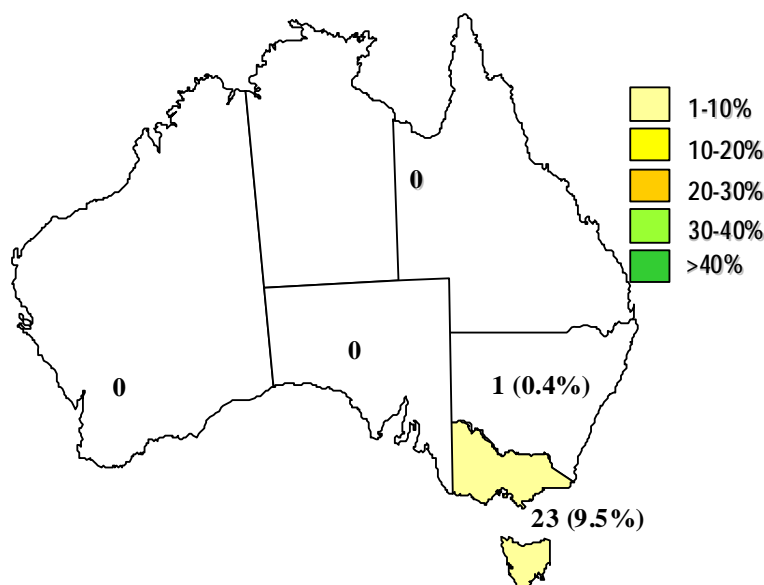


ST45-V

Also known as “WA MRSA-84” or “Victorian CA-MRSA”, ST45-V forms part of clonal complex 45 and is PVL negative.

Epidemiology

ST45-V (WA MRSA-84 or Victorian CA-MRSA): n = 24 (2.7%)



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

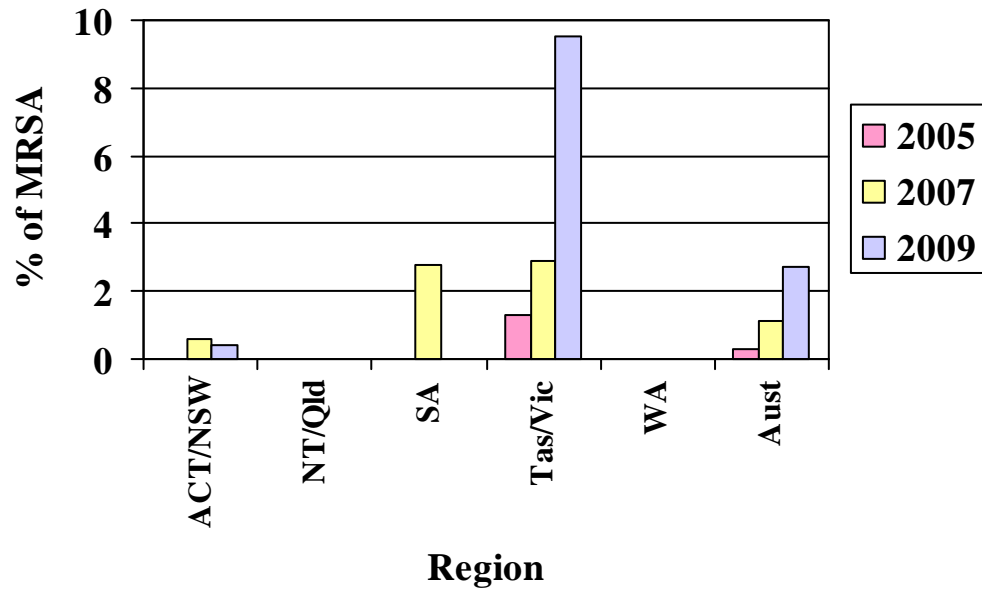
SAP 2005 - 2009: Regional Distribution of ST45-IV (WA MRSA-84 or Victorian CA-MRSA)

In SAP 2005 MRSA from NT were not characterized and are therefore not included in the 2005 NT/Qld figures.

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

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

SAP 2005 - 2009: Regional Distribution of ST45-IV (WA MRSA-84 or Victorian CA-MRSA)



International CA-MRSA Clones

In SAP 2009 the PVL positive international Taiwan CA-MRSA clone was identified.

CLONE	ALTERNATIVE NAME	n (%)
ST59-V_T	Taiwan CA-MRSA	1 (0.1%)

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
ST239-III	Aus -2 and Aus -3 EMRSA or EA MRSA	0	384	384
ST22-IV	EMRSA-15	1	219	220
ST36-II	EMRSA-16 or USA200	0	3	3
ST5-II	New York Japan MRSA or USA100	0	2	2
ST273-II	New York Japan slv			
Total		1	608	609

CA-MRSA Clones

Clone	Alternative Name	Positive	Negative	Total
ST1-IV	WA MRSA-1	4	88	92
ST93-IV	Queensland MRSA	53	0	53
ST78-IV	WA MRSA-2	0	33	33
ST5-IV	WA MRSA-3	0	29	29
ST30-IV	WSPP MRSA	23	2	25
ST45-V	WA MRSA – 84 (Victorian CA-MRSA)	0	24	24
ST5-V		0	8	8
ST73-IV	WA MRSA-65	0	4	4
ST5-IV		0	2	2
ST7-V		0	2	2
ST1-V		0	1	1
ST188-IV	WA MRSA-78	0	1	1
ST188-IV	WA MRSA-38	0	1	1
ST573-V	WA MRSA-10	0	1	1
ST5-IV	WA MRSA-71	0	1	1
ST5-V	WA MRSA-35	0	1	1
ST5-V	WA MRSA-81	0	1	1
ST835-V	WA MRSA-40	0	1	1
ST1756-V		0	1	1
ST8-IV	WA MRSA-5	0	1	1
ST8-V	WA MRSA-77	0	1	1
ST45-V	WA MRSA-4	0	1	1
ST59-IV	WA MRSA-15	0	1	1
ST59-IV	WA MRSA-55	1	0	1
ST59-V _T	Taiwan CA-MRSA	1	0	1
ST59-V		0	1	1
ST72-IV	WA MRSA-44	0	1	1
ST953-IV	WA MRSA-54	0	1	1
TOTAL		82	208	290

5.6. CA-MRSA Antibiogram

	1 IV WA 1	1 V	188 IV WA 78	188 IV WA 38	573 V WA 10	5 IV WA 3	5 IV	5 IV WA 71	5 V	5 V WA 35	5 V WA 81	73 IV WA 65	835 V WA 40	1756 V	7 V	8 IV WA 5	8 V WA 77	30 IV WSPP
Ox ^R	59					15	2		4		1	2				1	1	22
One non beta lactam antibiotic																		
Ox ^R Em ^R	7					11			2			2						
Ox ^R Cp ^R	1								1									2
Ox ^R FA ^R	6					1												
Ox ^R Te ^R		1							1									
Ox ^R Gn ^R	3												1					
Two non beta lactam antibiotics																		
Ox ^R Em ^R FA ^R	11																	
Ox ^R Em ^R Cp ^R	2							1		1				1				
Ox ^R Em ^R Mp ^R						1												
Ox ^R Em ^R Gn ^R					1													
Ox ^R Em ^R Te ^R	1																	
Ox ^R Te ^R FA ^R	1																	
Ox ^R Gn ^R Mp ^R						1												
Ox ^R Te ^R Cp ^R																		
Ox ^R Em ^R Rf ^R																		
Three non beta lactam antibiotics																		
Ox ^R Em ^R Gn ^R FA ^R	1																	
Ox ^R Em ^R Gn ^R Cot ^R															2			
Ox ^R Em ^R Cp ^R Te ^R																		1
Ox ^R Gn ^R Cp ^R Te ^R																		
Four non beta lactam antibiotics																		
Ox ^R Gn ^R Em ^R Cp ^R Cot ^R				1														

SAP 2009: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

	1 IV WA 1	1 V	188 IV WA 78	188 IV WA 38	573 V WA 10	5 IV WA 3	5 IV	5 IV WA 71	5 V	5 V WA 35	5 V WA 81	73 IV WA 65	835 V WA 40	1756 V	7 V	8 IV WA 5	8 V WA 77	30 IV WSPP
Five non beta lactam antibiotics																		
Ox ^R Gn ^R Em ^R Cp ^R Cot ^R Te ^R			1															
Total	92	1	1	1	1	29	2	1	8	1	1	4	1	1	2	1	1	25

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	45 V	45 V	59 IV	59 IV	59 V _T	59 V	72 IV	78 IV	953 IV	93 IV
	WA 4	WA 84	WA 15	WA 55	Tw		WA 44	WA 2	WA 54	Qld
Ox ^R	1						1	2	1	44
One non beta lactam antibiotic										
Ox ^R Em ^R			1					29		9
Ox ^R Cp ^R		14								
Ox ^R FA ^R										
Ox ^R Te ^R						1				
Ox ^R Gn ^R										
Two non beta lactam antibiotics										
Ox ^R Em ^R FA ^R										
Ox ^R Em ^R Cp ^R		1								
Ox ^R Em ^R Mp ^R										
Ox ^R Em ^R Gn ^R										
Ox ^R Em ^R Te ^R				1	1			1		
Ox ^R Te ^R FA ^R										
Ox ^R Gn ^R Mp ^R										
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		7								
Ox ^R Gn ^R Cp ^R Te ^R		1								
Four non beta lactam antibiotics										
Ox ^R Gn ^R Em ^R Cp ^R Cot ^R										

SAP 2009: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

	45 V	45 V	59 IV	59 IV	59 V _T	59 V	72 IV	78 IV	953 IV	93 IV
	WA 4	WA 84	WA 15	WA 55	Tw		WA 44	WA 2	WA 54	Qld
Five non beta lactam antibiotics										
Ox ^R Gr ^R Em ^R Cp ^R Cot ^R Te ^R										
Total	1	24	1	1	1	1	1	33	1	53

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Pathology Queensland Gold Coast Hospital, QLD
Pathology Queensland Prince Charles Hospital, QLD
Pathology Queensland Princess Alexandra Hospital, QLD
PathWest Fremantle Hospital, WA
PathWest QEII Hospital, WA
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