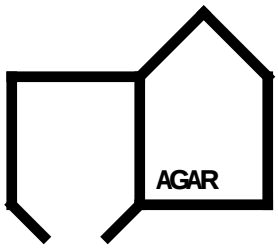

The Australian Group on Antimicrobial Resistance
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Staphylococcus aureus Programme 2006 (SAP 2006) Community Survey MRSA Epidemiology and Typing Report

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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) 2006 *Staphylococcus aureus* Surveillance Programme (SAP 2006)

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Staphylococcus aureus Programme 2006 (SAP 2006) Community Survey MRSA Epidemiology and Typing Report

1. Overview

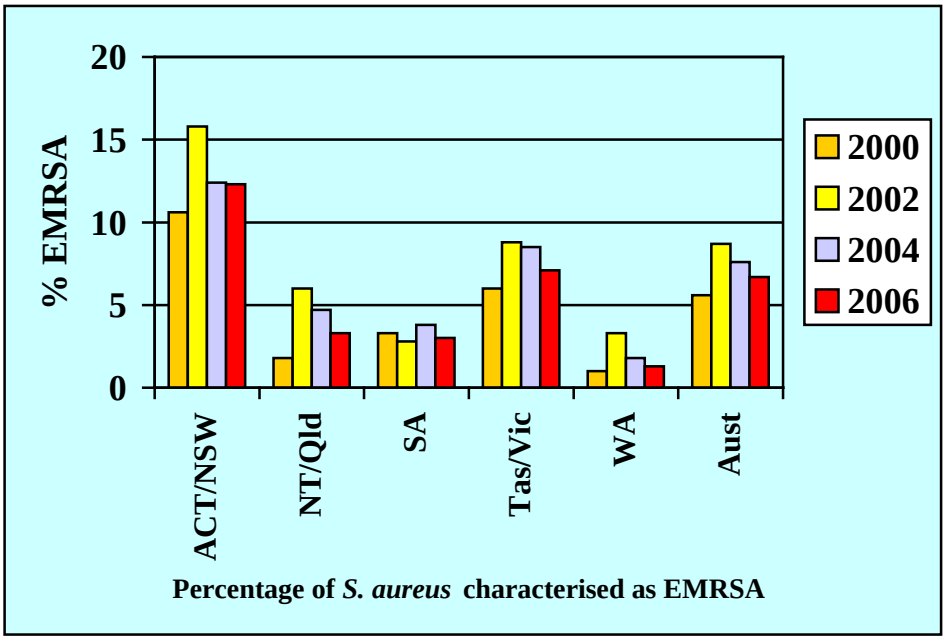
Of the 476 S. aureus classified as MRSA in the SAP 2006 Community Survey, molecular typing was performed on 462 (97.1%) isolates. Although the percentage of S. aureus characterized as "hospital-associated MRSA" or "Epidemic MRSA (EMRSA)" was lower in this survey (6.7%) when compared to the 2004 survey (7.6%), ST22-MRSA-IV (EMRSA-15) has emerged as a major MRSA clone in most Australian communities surveyed, accounting for 18.4% of all community MRSA infections. Of particular concern has been the rapid emergence of this clone in the Victorian/Tasmanian community (0% in 2002 to 17.3% in 2006). Community-associated MRSA (cMRSA) accounted for 56.7% of MRSA and 8.8% of all S. aureus. Since 2000 there has been an 87% increase in the number of S. aureus characterized as cMRSA. As in previous surveys, although MRSA was multiclonal (25 clones) 90.2% of strains could be characterized into eight clones. ST93-MRSA-IV (Queensland cMRSA), a Panton Valentine leucocidin (PVL)-positive clone, has become the most frequently isolated cMRSA clone in the Australian community accounting for 33.2% of all cMRSA and 18.8% of all MRSA infections. Overall 51.5% of cMRSA were PVL positive, a 13% increase when compared to the 2004 survey. This increase in PVL-positive MRSA is not only due to the expansion of the ST93-MRSA-IV clone but also due to the introduction of several international cMRSA clones including ST30-MRSA-IV (WSPP MRSA), ST8-MRSA-IV (USA300) ST59-MRSA-V_T (Taiwan cMRSA) and ST80-MRSA-IV (European cMRSA). Several variants of these clones were characterized in this survey. A ST22-MRSA-IV (EMRSA-15) carrying the PVL determinant was also identified. For this clone, which is able to survive and spread in the Australian community, to acquire the PVL determinant is a major public health concern.

2. Summary

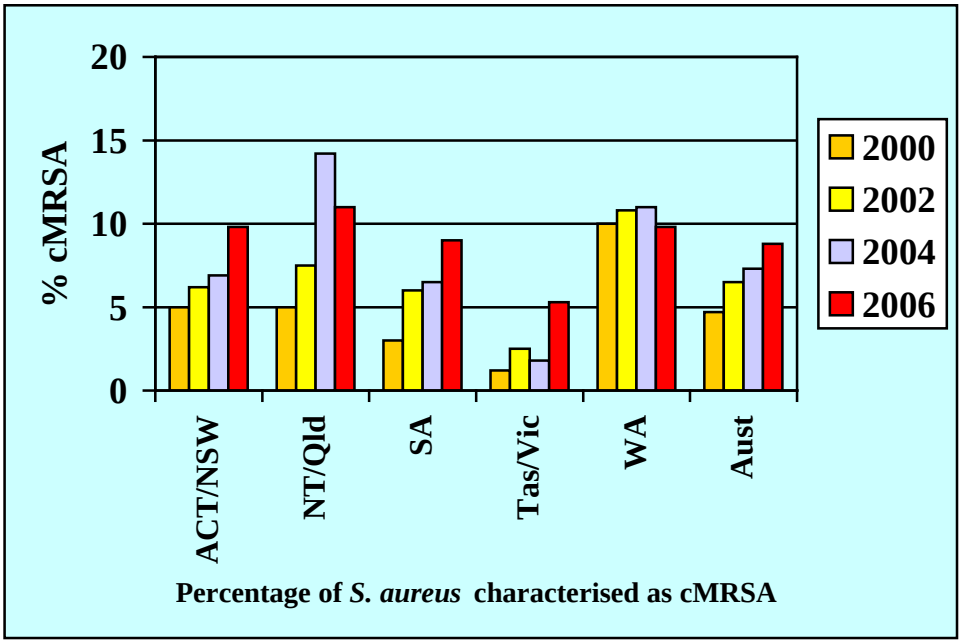
The Australian Group for Antimicrobial Resistance (AGAR) biennial community *Staphylococcus aureus* surveillance programme commenced in 2000. In the 2006 programme (SAP 2006) up to 100 clinically significant consecutive isolates of *S. aureus* from different patients were collected by each of 30 institutions located across Australia. Isolates were collected from non-hospitalised patients included nursing homes, long-term care facilities and hospice patients. Day surgery and dialysis patients were excluded. All methicillin-resistant *S. aureus* (MRSA) isolates were referred to the Western Australian (WA) Gram-positive Bacteria Typing and Research Unit (GPBTRU) for clone characterization and Panton-Valentine leucocidin (PVL) toxin determination.
The molecular characterization of the MRSA isolates is designed to provide a "snapshot" of MRSA clones circulating in the Australian community.

Of the 476 (16.0%) *S. aureus* classified as MRSA in SAP 2006, 462 (97.1%) were referred to the WA GPBTRU. Overall 56.7% and 43.3% of MRSA were characterized as Community-associated (cMRSA) and Hospital-associated/ Epidemic MRSA (EMRSA) respectively.

Throughout Australia the percentage of *S. aureus* characterized as EMRSA was 6.7% ranging from 1.3% in WA to 12.3% in the ACT/NSW region.

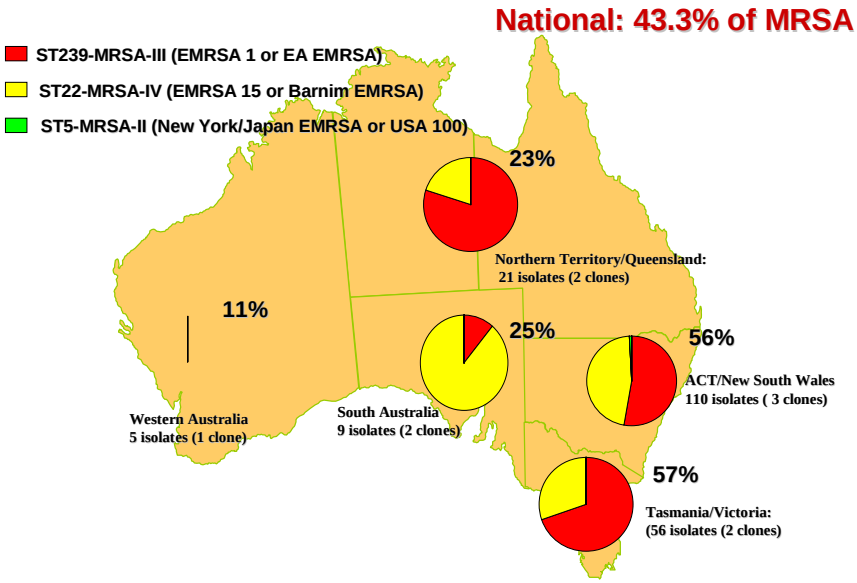


The percentage of *S. aureus* characterized as cMRSA was 8.8% ranging from 5.3% in the Tas/Vic region to 11.0% in the NT/Qld region.



2.1. EMRSA

Three EMRSA clones were identified in the Australian community; 57.0% were ST239-MRSA-III (Aus-2/3 EMRSA), 42.5% ST22-MRSA-IV (UK EMRSA-15) and 0.5% ST5-MRSA-II (New York/Japan EMRSA).



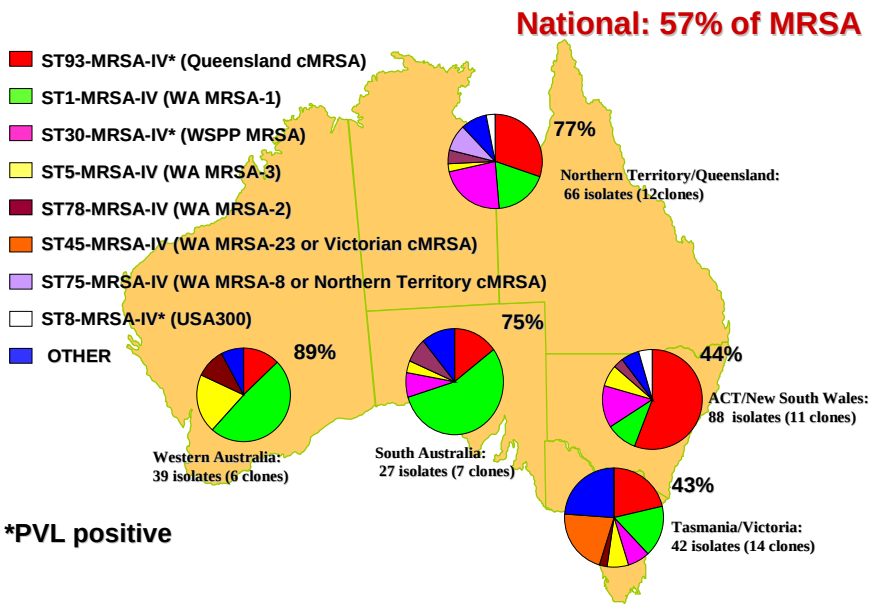
Aus2/3 EMRSA was isolated in most Australian regions, accounting for 39.8% and 29.3% of MRSA in the Tas/Vic and ACT/NSW regions. Aus2/3 EMRSA however was not isolated in the WA community. Over the four community surveys the percentage of isolates characterized as Aus-2/3 has decreased throughout Australia. UK EMRSA-15, which was initially reported in Australia in 1997, accounted for 18.4% of all MRSA isolated in Australia, ranging from 4.7% in the NT/Qld region to 25.8% in the ACT/NSW region. The percentage of MRSA characterized as UK EMRSA-15 has increased in all Australian regions over the four surveys noticeably in the Tas/Vic region.

2.2. cMRSA

Twenty five community MRSA clones were identified by pulsed-field gel electrophoresis (corresponding to 22 MLST/SCC*mec* clones) of which 90.2% were:

- ST93-MRSA-IV (33.2%)
- ST1-MRSA-IV (23.7%)
- ST30-MRSA-IV (12.2%)
- ST5-MRSA-IV (7.6%)
- ST78-MRSA-IV (5.0%)
- ST45-MRSA-IV (3.4%)
- ST75-MRSA-IV (2.7%)
- ST8-MRSA-IV (2.3%)

In contrast to previous community surveys, ST93-MRSA-IV (PVL-positive Queensland clone), which was isolated in all regions, was the predominant cMRSA clone isolated in Australia.

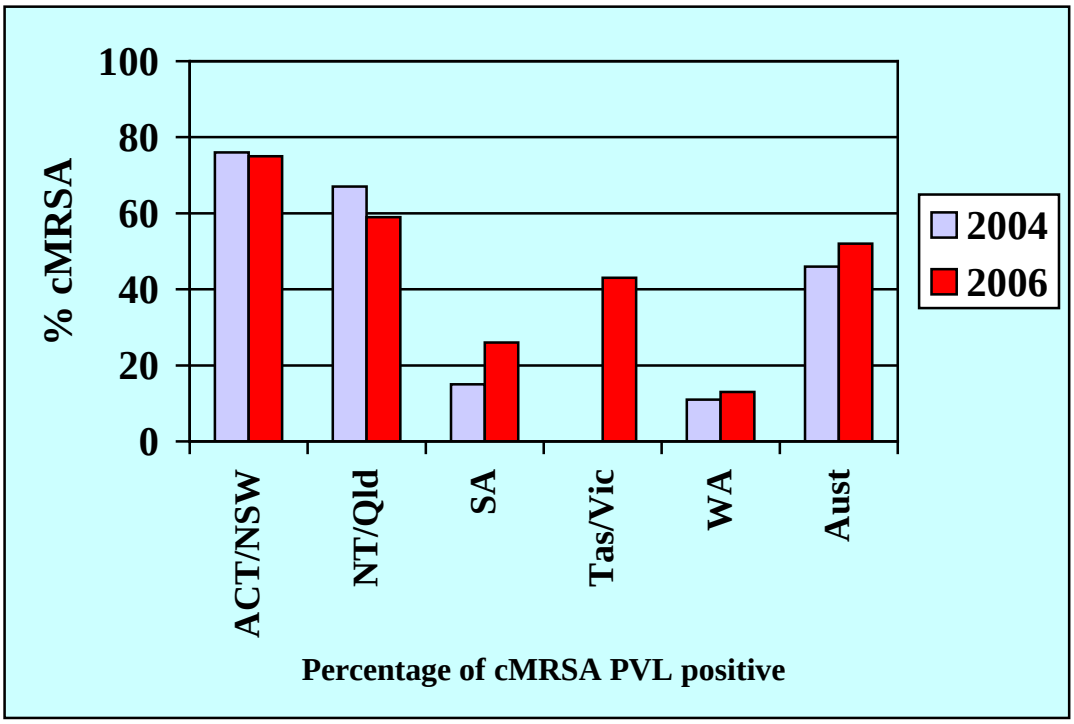


2.3. Panton-Valentine Leucocidin (PVL) Toxin

cMRSA

Overall 52% (n=135) of cMRSA (8 clones) were PVL positive:

- ST93-MRSA-IV (Qld cMRSA) – 87 isolates
- The following recognised international clones:
  - ST30-MRSA-IV (WSPP) – 31 isolates
  - ST30slv-MRSA-IV – 1 isolate
  - ST8-MRSA-IV (USA300) – 6 isolates
  - ST80-MRSA-IV (European cMRSA) – 2 isolates
  - 59-MRSA-V_T (Taiwan cMRSA) – 2 isolates
  - ST338-MRSA-IV (slv of ST59-MRSA-V_T) – 1 isolate.
- Five isolates of ST1-MRSA-IV. It is possible that these are USA400 strains however further molecular studies are required to confirm



Although PVL positive cMRSA were also isolated throughout Australia, the percentage of cMRSA that were positive varied from 13% in WA to 59% and 75% in NT/Qld and ACT/NSW respectively. In the previous community survey (SAP 2004), 46% of cMRSA were PVL positive ranging from 0% in Tas/Vic to 76% in ACT/NSW. Apart from the Tas/Vic region (0 to 43%, P=0.0096) the percentage of cMRSA that were PVL positive did not significantly vary within regions between the two surveys.

2.4. EMRSA

A PVL-positive ST22-MRSA-IV (EMRSA-15) was identified by PCR in the Vic/Tas region. This result was confirmed by array hybridisation. The detection of PVL in a prevalent hospital-associated epidemic strain is a cause of serious concern because of the potential increased virulence associated with PVL-positive strains and the rapid expansion of EMRSA-15 in both the hospital and community setting.

3. SAP 2006 Protocol

3.1. Commencement Date

1st July 2006

3.2. Isolates

Approximately 100 consecutive isolates of *Staphylococcus aureus* from 100 different patients at each site were tested by 30 laboratories located across Australia (total number of isolates = 2,979). Isolates were collected from outpatients only and excluded dialysis and day surgery patients.

3.3. Participating Laboratories

Australian Capital Territory (1)
- The Canberra Hospital

New South Wales (8)
- Concord Hospital
- Douglass Hanly Moir Pathology
- John Hunter Hospital
- Nepean Hospital
- Royal Prince Alfred Hospital
- Royal North Shore Hospital
- South West Area Pathology Services
- Westmead Hospital

Northern Territory (1)
- Royal Darwin Hospital

Queensland (5)
- Pathology Queensland Gold Coast Hospital
- Pathology Queensland Prince Charles Hospital
- Pathology Queensland Princess Alexandra Hospital
- Pathology Queensland Royal Brisbane Hospital
- Sullivan Nicolaides Pathology

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

Tasmania (2)
- Launceston General Hospital
- Royal Hobart Hospital

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

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

3.4. Methicillin Susceptibility Testing

Vitek2® AST-P545 susceptibility card according to the manufacturer's guidelines.

3.5. Epidemiological Typing

Performed by the Western Australian Gram-positive Bacteria Typing and Research Unit

- 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

The Gram-positive Bacteria Typing and Research Unit employs the international MRSA nomenclature system described by *Enright et al*. (1). This system provides a universally standardised MRSA nomenclature allowing MRSA clones to be readily compared between laboratories and countries. It is based upon the combination of the sequences of seven housekeeping genes combined to define a sequence type (ST) using multilocus sequence typing (MLST), and the 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-MRSA-IV (previously known as EMRSA-15).

Multi Locus 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 (.saureus.mlst.net). As there are many alleles for each loci, isolates are highly unlikely to have identical ST by chance, and therefore isolates with the same ST or STs that differ at no more than two alleles are considered to belong to the same clonal complex (CC) and be members of the same clone. Isolates that are found to have a one or two house keeping gene(s) that have not previously been reported may be referred to as single (slv) or double locus variants (dlv) of a previously described sequence type (eg ST30slv).

Staphylococcal Cassette Chromosome *mec* (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.

Six SCC*mec* types have been identified globally. Types I, II, III and VI are associated with "health-care-associated MRSA" while Types IV and V are normally associated with "community associated MRSA".

In this report MRSA are identified as either "epidemic" or "community" and are assigned an MLST/SCC*mec* type. The previous nomenclature that was applied to EMRSA and cMRSA clones is also reported.

3.7. Panton-Valentine Leucocidin (PVL) Toxin

cMRSA 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 cMRSA studied in Europe and USA (3). In Australia, it was initially reported that cMRSA infrequently carry the genes encoding PVL (4). However, two cMRSA clones now frequently isolated in Australia are PVL positive; ST30-MRSA-IV and ST93-MRSA-IV. These clones were originally reported in Auckland, New Zealand and Queensland, Australia respectively. ST30-MRSA-IV was first noted in Australia in 1997 in the Polynesian population living in the eastern Australian states and the Australian Capital Territory (5). ST93-MRSA-IV 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 several regions of Australia especially on the east coast (7).

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

1. ST8-MRSA-IV (USA300)
2. ST80-MRSA-IV (European cMRSA)
3. ST59-MRSA-V_T (Taiwan cMRSA)
4. ST1-MRSA-IV (USA400)

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

4. Methods

4.1. Epidemiological Typing Methods

Antibiogram

Participating laboratories performed antimicrobial susceptibility tests using the Vitek2® AST-P545 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, imipenem, and nitrofurantoin. Penicillin susceptible strains were tested for β-lactamase production using nitrocefin. A cefoxitin disc diffusion test was used to confirm methicillin-resistance. Mupirocin and cefoxitin were tested by disc diffusion using the CLSI or CDS methods. The MIC of tigecycline and mupirocin-resistant isolates was determined by Etest® (AB Biodisk, Solna, Sweden).

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^{o}C (16).

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

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

Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)

Electrophoresis of chromosomal DNA was performed as previously described (18) using the CHEF DR III System (Bio-Rad Laboratories Pty Ltd). Chromosomal patterns were examined visually, scanned with a Fluor-S Multimager and digitally analysed using Multi-Analyst/PC (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 ://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)

4.2. Identification of EMRSA Clones

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

Antibiogram
Resistogram
CHEF
Coagulase PCR-RFLP on selected isolates

ST22-MRSA-IV (UK EMRSA-15)

Antibiogram
Urea Slope
CHEF
Coagulase PCR-RFLP on selected isolates

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

Antibiogram
Urea Slope
Coagulase PCR/RFLP
CHEF

4.3. Identification of cMRSA Clones

ST30-MRSA-IV (Western Samoan Phage Pattern MRSA - WSPP MRSA)

Antibiogram
CHEF
Coagulase PCR-RFLP on selected isolates

ST93-MRSA-IV (Queensland MRSA)

Antibiogram
CHEF
Coagulase PCR-RFLP on selected isolates

ST8-MRSA-IV (USA300 MRSA)

Antibiogram
CHEF
Coagulase PCR-RFLP on selected isolates

ST59-MRSA-V_T (Taiwan MRSA)

Antibiogram
CHEF
Coagulase PCR-RFLP on selected isolates

ST80-MRSA-IV (European MRSA)

Antibiogram
CHEF
Coagulase PCR-RFLP on selected isolates

"WA MRSA"

ST1-MRSA-IV (WA-1)
ST78-MRSA-IV (WA-2)
ST5-MRSA-IV (WA-3)
ST45-MRSA-V (WA-4)
ST8-MRSA-IV (WA-5)
ST75-MRSA-IV (WA-8)
ST59-MRSA-IV (WA-15)
ST45-MRSA-IV (WA-23)

Antibiogram
CHEF
Coagulase PCR-RFLP on selected isolates

ST584 MRSA-IV (WA-13)
ST5-MRSA-V (WA-35)
ST583-MRSA-IV (WA-17)
ST45-MRSA-V (WA-23)
ST5-MRSA-V
ST7-MRSA-V
ST8-MRSA-IV
ST12-MRSA-IV (WA-69)
ST20-MRSA-IV
ST30slv-MRSA-IV
ST72-MRSA-V
ST338-MRSA-V
ST361-MRSA-IV

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

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

The presence of the PVL determinants was detected by PCR using previously published primers (23).

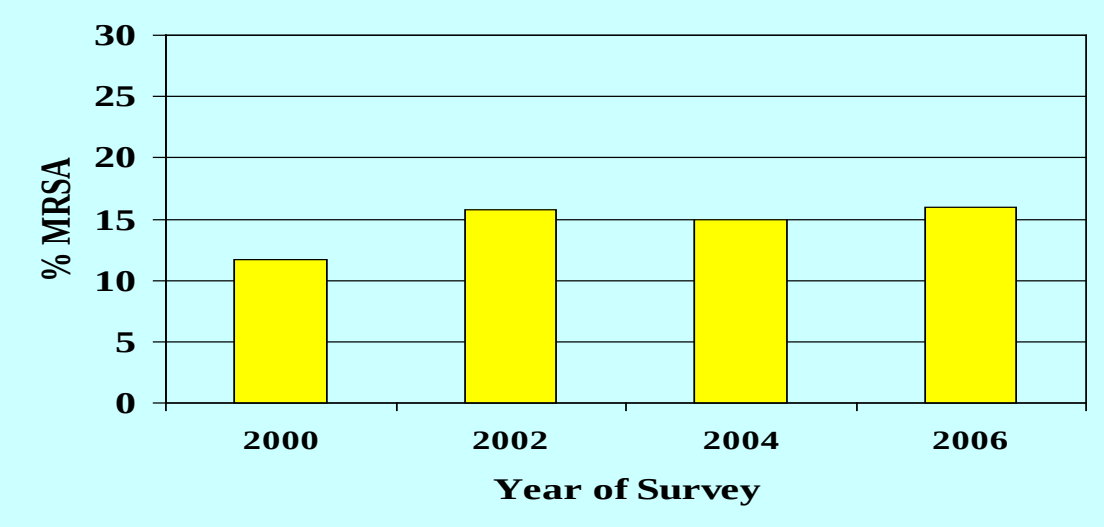
5. Results

In SAP 2006, 476 (16.0%) *Staphylococcus aureus* were classified as MRSA.

5.1. AGAR Community SAP 2000 – 2006

Percentage of *Staphylococcus aureus* Identified as MRSA

SAP	Laboratories (n)	*S aureus* (n)	MRSA (n)	MRSA (%)
2000	25	2,498	293	11.7
2002	24	2,386	378	15.8
2004	27	2,652	395	14.9
2006	30	2,979	476	16.0

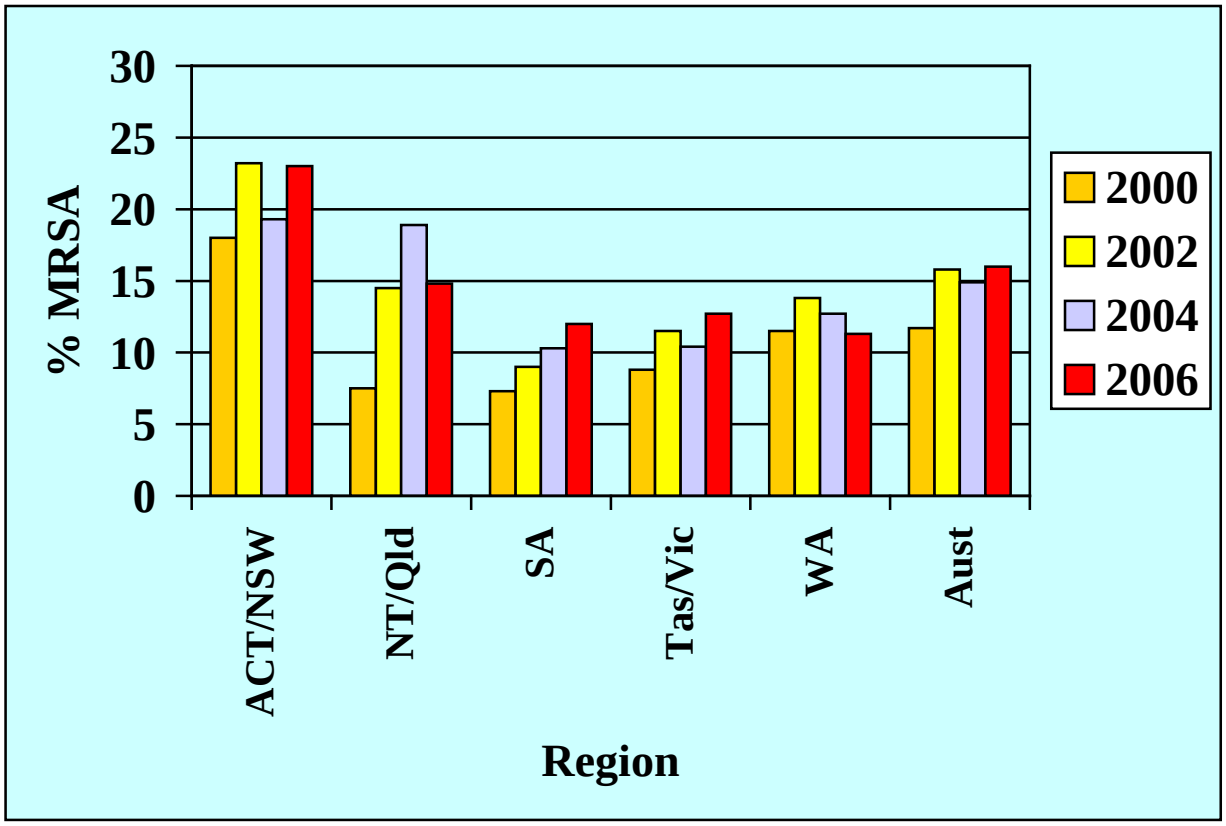


Percentage figures relate to the total number of *Staphylococcus aureus* isolates

Regional Distribution of MRSA

Region	2000	2002	2004	2006
ACT/NSW	144 (18.0%)	183 (23.2%)	173 (19.3%)	206 (23.0%)
NT/Qld	30 (7.5%)	58 (14.5%)	68 (18.9%)	89 (14.8%)
SA	29 (7.3%)	36 (9.0%)	41 (10.3%)	36 (12.0%)
Tas/Vic	44 (8.8%)	46 (11.5%)	62 (10.4%)	100 (12.7%)
WA	46 (11.5%)	55 (13.8%)	51 (12.7%)	45 (11.3%)
Total	293 (11.7%)	378 (15.8%)	395 (14.9%)	476 (16.0%)

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 2006 Epidemiological Typing of MRSA

Of the 476 MRSA identified in SAP 2006, 462 were referred to the GPBTU for epidemiological typing

Typing Tests Performed

Test	N
Cefoxitin Susceptibility Testing	**464**
Coagulase Gene PCR-RFLP Assay	**227**
Resistogram	**121**
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	**464**
Urease Reaction	**464**
Multi Locus Sequencing Typing (MLST)	**16**
SCC*mec* PCR	**16**
Panton-Valentine Leucocidin PCR	**464**

Regional Distribution of EMRSA and cMRSA

Region	EMRSA (%)	cMRSA (%)	Total MRSA
ACT/NSW	**110 (55.6)**	**88 (44.4)**	**198**
NT/Qld	**20 (23.3)**	**66 (76.7)**	**86**
SA	**9 (25.0)**	**27 (75.0)**	**36**
Tas/Vic	**56 (57.1)**	**42 (42.9)**	**98**
WA	**5 (11.4)**	**39 (88.6)**	**44**
TOTAL	**200 (43.3)**	**262 (56.7)**	**462**

Percentage figures relate to the total number of MRSA isolates

SAP 2000 – 2006: Regional Distribution of EMRSA and cMRSA

	2000 (n = 257)[a]		2002 (n = 363)[b]		2004 (n = 395)		2006 (n = 462)[c]	
Region	**Epidemic (%)**	**Community (%)**	**Epidemic (%)**	**Community (%)**	**Epidemic (%)**	**Community (%)**	**Epidemic (%)**	**Community (%)**
ACT/NSW	**85 (68.0)**	**40 (32.0)**	**125 (71.8)**	**49 (28.2)**	**111 (64.2)**	**62 (35.8)**	**110 (55.6)**	**88 (44.4)**
NT/Qld	**7 (25.9)**	**20 (74.1)**	**24 (44.4)**	**30 (55.6)**	**17 (25.0)**	**51 (75.0)**	**20 (23.3)**	**66 (76.7)**
SA	**13 (52.0)**	**12 (48.0)**	**11 (31.4)**	**24 (68.6)**	**15 (36.6)**	**26 (63.4)**	**9 (25.0)**	**27 (75.0)**
Tas/Vic	**30 (83.3)**	**6 (16.7)**	**35 (77.8)**	**10 (22.2)**	**51 (82.3)**	**11 (17.7)**	**56 (57.1)**	**42 (42.9)**
WA	**4 (9.1)**	**40 (90.9)**	**13 (23.6)**	**42 (76.4)**	**7 (13.4)**	**44 (86.3)**	**5 (11.4)**	**39 (88.6)**
TOTAL	**139 (54.1)**	**118 (45.9)**	**208 (57.3)**	**155 (42.7)**	**201 (50.9)**	**194 (49.1)**	**200 (43.3)**	**262 (56.7)**

Percentage figures relate to the total number of MRSA isolates

[a]In SAP 2000, 257 of the 293 MRSA were fully characterised
[b]In SAP 2002, 363 of the 378 MRSA were fully characterised
[c]In SAP 2006, 462 of the 476 MRSA were fully characterised

SAP 2000 – 2006: Regional Distribution of EMRSA and cMRSA as a Proportion of *Staphylococcus aureus*

	2000			2002			2004			2006		
Region	**Total**	**Epidemic (%)**	**Community (%)**	**Total**	**Epidemic (%)**	**Community (%)**	**Total**	**Epidemic (%)**	**Community (%)**	**Total**	**Epidemic (%)**	**Community (%)**
ACT/NSW	**800**	**85 (10.6)**	**40 (5.0)**	**789**	**125 (15.8)**	**49 (6.2)**	**895**	**111 (12.4)**	**62 (6.9)**	**895**	**110 (12.3)**	**88 (9.8)**
NT/Qld	**399**	**7 (1.8)**	**20 (5.0)**	**400**	**24 (6.0)**	**30 (7.5)**	**359**	**17 (4.7)**	**51 (14.2)**	**600**	**20 (3.3)**	**66 (11.0)**
SA	**399**	**13 (3.3)**	**12 (3.0)**	**400**	**11 (2.8)**	**24 (6.0)**	**399**	**15 (3.8)**	**26 (6.5)**	**299**	**9 (3.0)**	**27 (9.0)**
Tas/Vic	**500**	**30 (6.0)**	**6 (1.2)**	**399**	**35 (8.8)**	**10 (2.5)**	**599**	**51 (8.5)**	**11 (1.8)**	**788**	**56 (7.1)**	**42 (5.3)**
WA	**400**	**4 (1.0)**	**40 (10.0)**	**398**	**13 (3.3)**	**42 (10.8)**	**400**	**7 (1.8)**	**44 (11.0)**	**397**	**5 (1.3)**	**39 (9.8)**
TOTAL	**2498**	**139 (5.6)**	**118 (4.7)**	**2386**	**208 (8.7)**	**155 (6.5)**	**2,652**	**201 (7.6)**	**194 (7.3)**	**2,979**	**200 (6.7)**	**262 (8.8)**

SAP 2006: EMRSA by AGAR Laboratory

LAB	ST239-MRSA-III Aus-2 EMRSA	ST239-MRSA-III Aus-3 EMRSA	ST22-MRSA-IV UK-EMRSA 15	ST5-MRSA-I1 NY/Japan MRSA	TOTAL
ACT/NSW (110)					
1	1	1			2
2	3		12		15
3	9		7		16
4	8		8		16
5	9	1	5		15
6	13		4		17
7	2		7		9
8	8		3	1	12
9	3		5		8
NT/Qld (20)					
10	2				2
11	2	1	1		4
12	2				2
13			1		1
28	3		1		4
30	3	3	1		7
SA (9)					
14	1		7		8
15			1		1
16					0
Tas/Vic (56)					
18		2	1		3
19	5	6	6		17
20		3	2		5
21					0
22		3	1		4
23		12	1		13
31	1	4	2		7
32	2	1	4		7
WA (5)					
24			1		1
25			2		2
26			1		1
27			1		1
TOTAL	77	37	85	1	200

SAP 2006: cMRSA by AGAR Laboratory

CC	1		5				7	8			12	20	30		45		59			72	78	80	S	S		
ST SCC*mec*	1 IV WA1	1 V	5 IV WA3	584 IV WA13	5 V WA35	5 V	7 V	8 IV WA5	8 IV USA 300	8 IV	12 IV WA69	20 V	30 IV WSPP	30 slv IV	45 V WA4	45 IV WA23	59 IV WA15	59 V Taiwan	338 V	72 V	78 IV WA2	80 IV Eur	93 IV QLD	75 IV WA8	361 IV	TOTAL
ACT /NSW (88)																										
1																							**3**			**3**
2	**3**							**1**					**2**										**1**		**1**	**8**
3	**1**		**1**										**1**										**13**			**16**
4	**1**																						**3**			**4**
5			**1**										**4**										**3**			**8**
6	**2**								**2**				**5**										**8**			**17**
7			**2**			**1**					**1**												**5**			**9**
8	**1**								**2**												**2**		**2**			**7**
9	**1**		**2**												**1**						**1**		**11**			**16**
NT/Qld (66)																										
10	**3**		**1**						**1**				**5**										**3**	**5**		**18**
11	**4**											**1**	**4**	**1**							**3**		**4**			**17**
12	**2**									**1**			**2**										**4**	**1**		**10**
13	**2**												**2**										**4**			**8**
28		**1**	**1**										**2**										**1**			**5**
30	**1**							**2**	**1**														**4**			**8**
SA (27)																										
14	**6**												**2**		**2**								**1**			**11**
15	**5**																						**1**			**6**
16	**4**		**1**	**1**																	**2**		**2**			**10**

CC	**1**		**5**				**7**	**8**			**12**	**20**	**30**		**45**		**59**			**72**	**78**	**80**	**S**	**S**		
ST SCC*mec*	1 IV WA1	1 V	5 IV WA3	584 IV WA13	5 V WA35	5 V	7 V	8 IV WA5	8 IV USA 300	8 IV	12 IV WA69	20 V	30 IV WSPP	30 slv IV	45 V WA4	45 IV WA23	59 IV WA15	59 V Taiwan	338 V	72 V	78 IV WA2	80 IV Eur	93 IV QLD	75 IV WA8	361 IV	TOTAL
TAS/Vic (42)																										
18																							**2**			**2**
19	**1**		**2**															**1**					**2**			**6**
20	**1**					**1**										**1**							**1**			**4**
21	**3**				**1**		**1**						**1**				**1**	**1**			**1**					**9**
22													**1**			**2**							**1**			**4**
23	**1**		**1**													**1**										**3**
31	**1**												**1**			**5**			**1**			**2**	**3**			**13**
32																				**1**						**1**
WA (39)																										
24	**4**		**1**																		**2**		**2**			**9**
25	**5**		**1**																		**1**			**1**		**8**
26	**5**		**5**												**1**						**1**		**1**			**13**
27	**5**		**1**												**1**								**2**			**9**
TOT	**62**	**1**	**20**	**1**	**1**	**2**	**1**	**3**	**6**	**1**	**1**	**1**	**32**	**1**	**5**	**9**	**1**	**2**	**1**	**1**	**13**	**2**	**87**	**7**	**1**	**262**

5.3. EMRSA

Certain strains of MRSA are known to spread easily between and within hospitals and are designated epidemic MRSA (EMRSA) or healthcare associated MRSA.

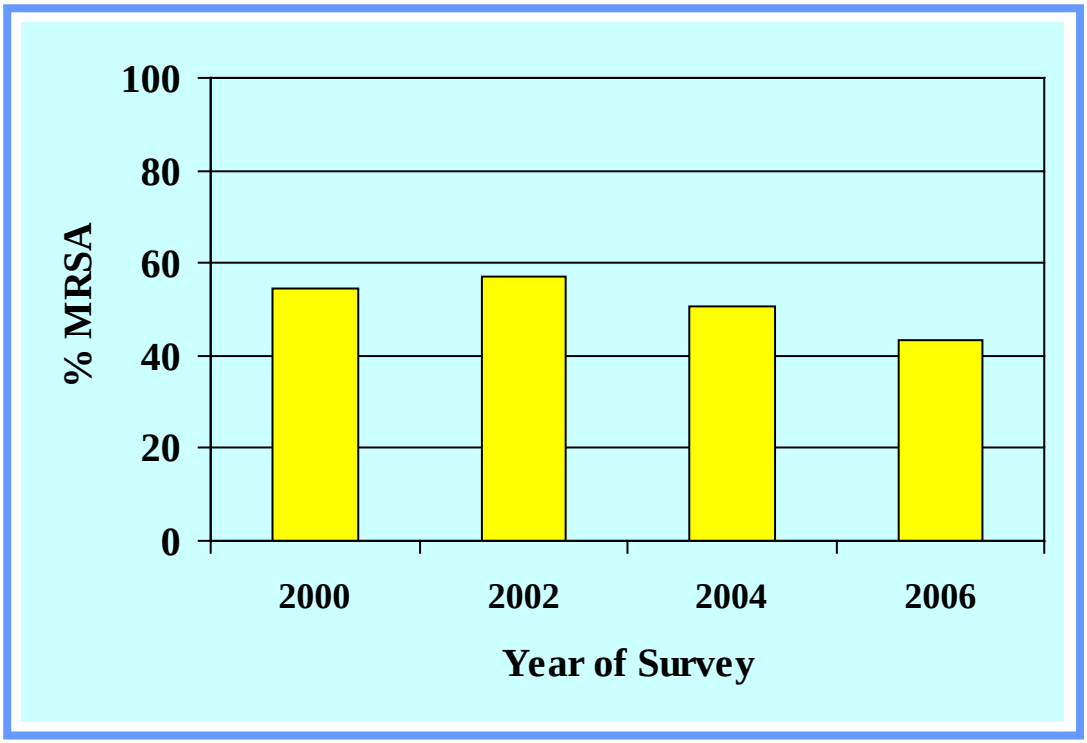
SAP 2006 EMRSA

In SAP 2006 three international EMRSA clones (200 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST239-MRSA-III	Aus -2 and Aus -3 EMRSA	114 (57.0)
ST22-MRSA-IV	UK EMRSA-15	85 (42.5)
ST5-MRSA-II	New York/Japan MRSA	1 (0.5)
TOTAL		200

Percentage figures relate to epidemic MRSA isolates

SAP 2000 – 2006: Percentage of MRSA Identified as EMRSA



ST239-MRSA-III

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

Phenotypic Characteristics

Antibiogram:

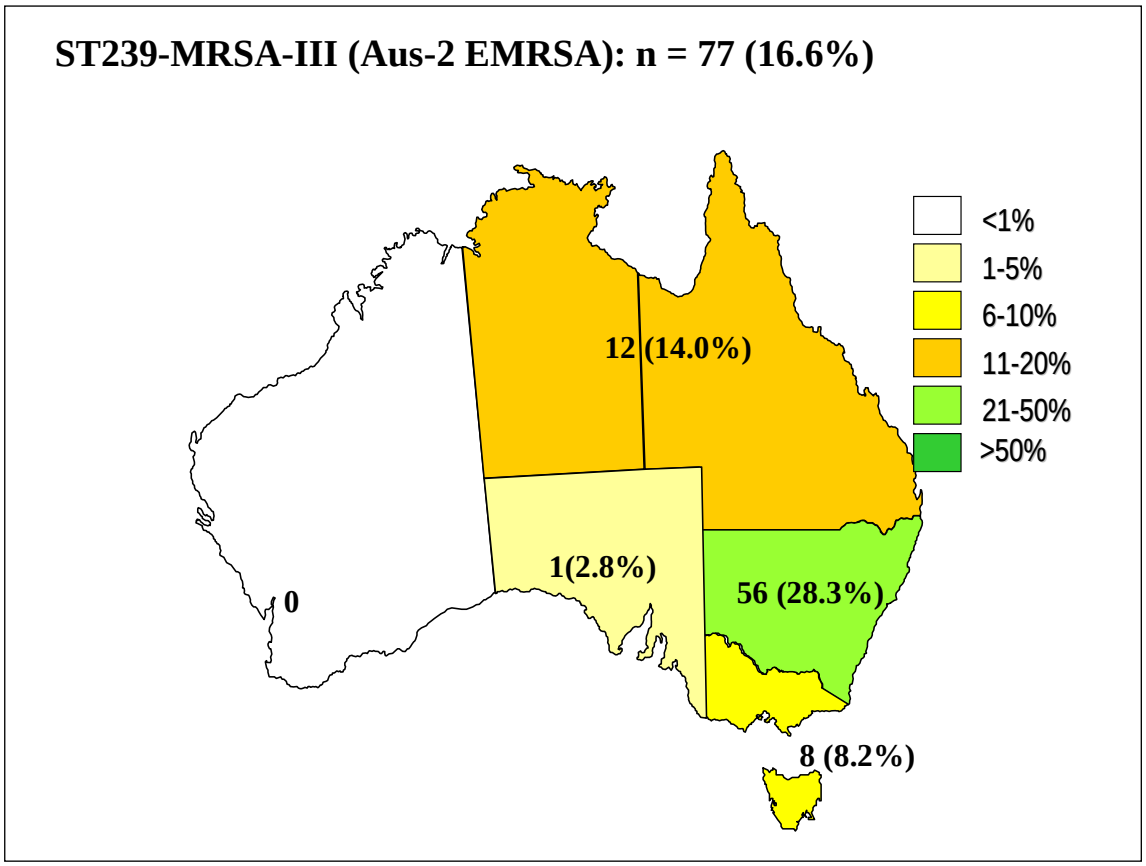
	Aus-2 EMRSA (n = 77)	Aus-3 EMRSA (n = 37)
Erythromycin^{R}	**99%**	**100%**
Tetracycline^{R}	**99%**	**92%**
Cotrimoxazole^{R}	**96%**	**100%**
Gentamicin^{R}	**95%**	**92%**
Ciprofloxacin^{R}	**94%**	**97%**
Fusidic Acid^{R}	**1%**	**3%**
Rifampicin^{R}	**1%**	**11%**
Mupirocin^{R}	**1%**	**0%**

Resistogram:

	Aus-2 EMRSA (n = 77)	Aus-3 EMRSA (n = 37)
Mercuric Acetate^{R}	**<1%**	**>99%**
Mercuric Chloride^{R}	**<1%**	**>99%**

Aus-2 EMRSA

Epidemiology

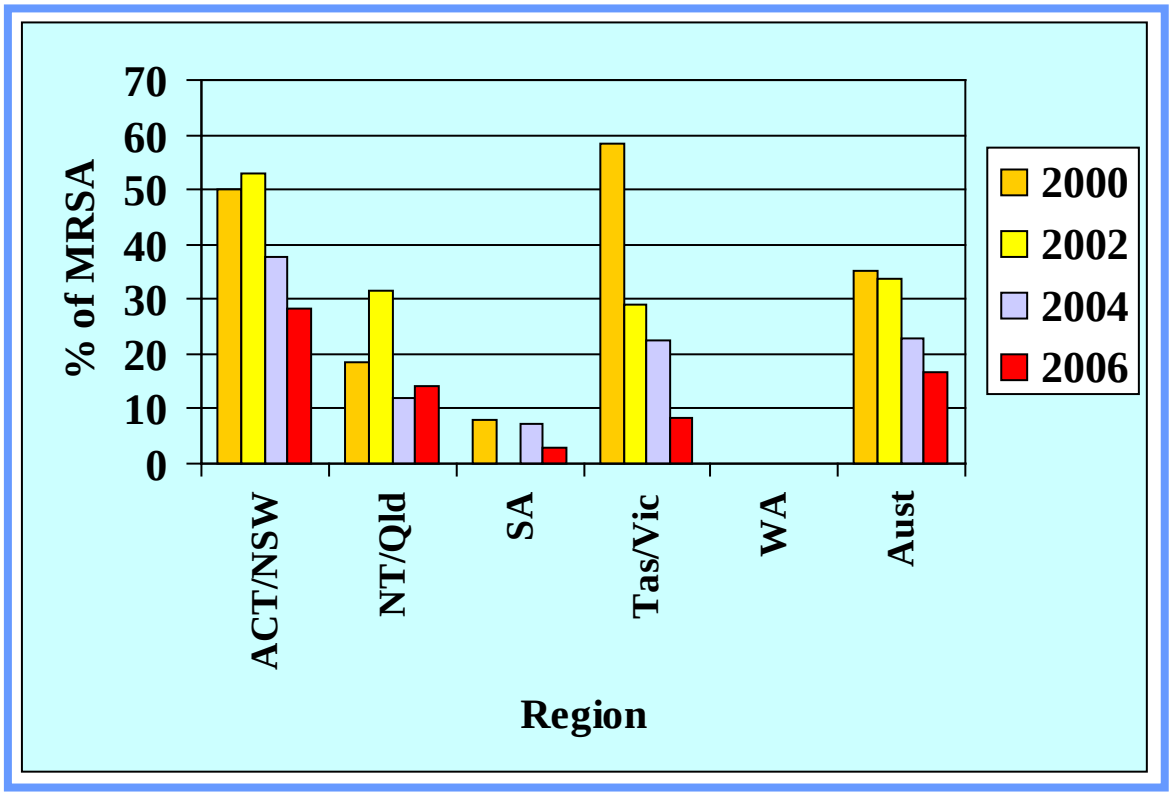


SAP 2000 – 2006: Regional Distribution of ST239-MRSA-III (Aus-2 EMRSA)

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	62 (49.6%)	93 (53.4%)	65 (37.6%)	56 (28.3%)
NT/Qld	5 (18.5%)	17 (31.5%)	8 (11.8%)	12 (14.0%)
SA	2 (8.0%)	0	3 (7.3%)	1 (2.8%)
Tas/Vic	21 (58.3%)	13 (28.9%)	14 (22.6%)	8 (8.2%)
WA	0	0	0	0
Total	90 (35.0%)	123 (33.9%)	90 (22.8%)	77 (16.6%)

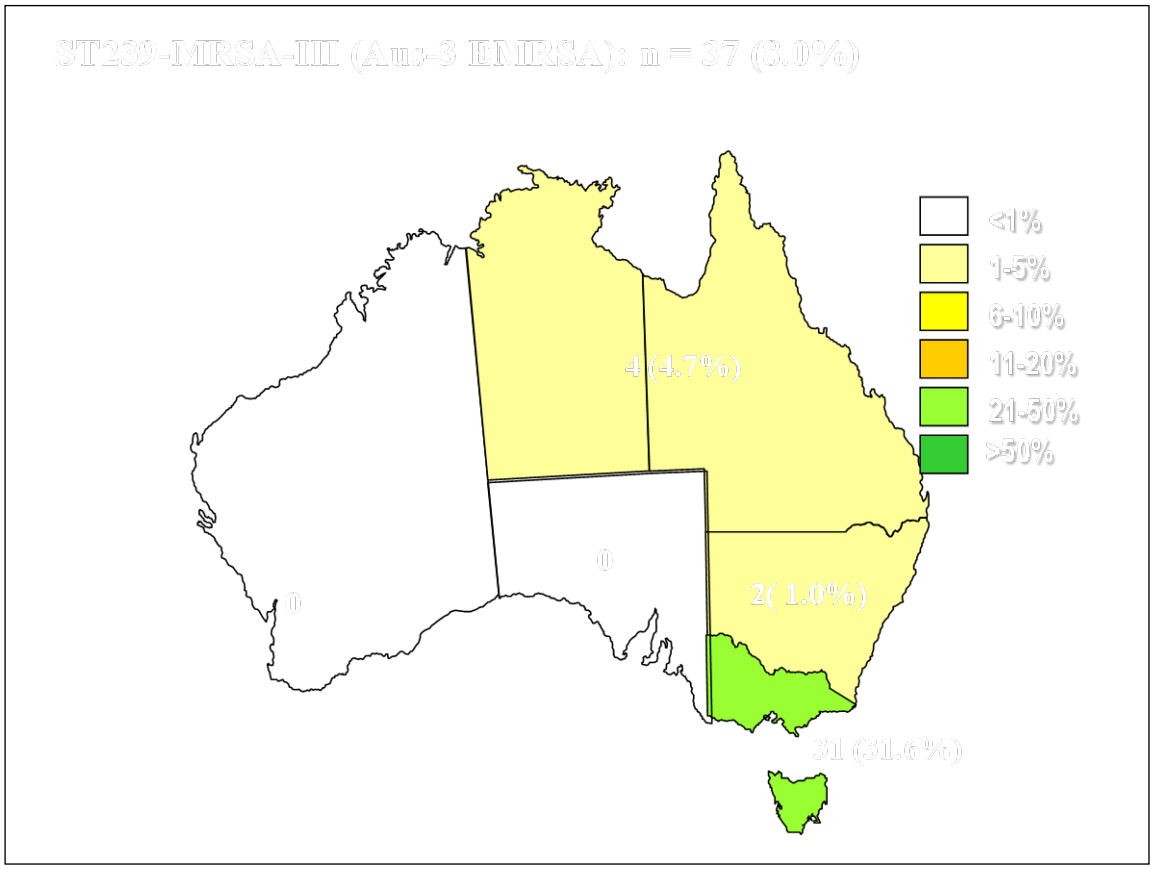
Percentage figures relate to total MRSA isolates

SAP 2000 – 2006: Regional Distribution of ST239-MRSA-III (Aus-2 EMRSA)



Aus-3 EMRSA

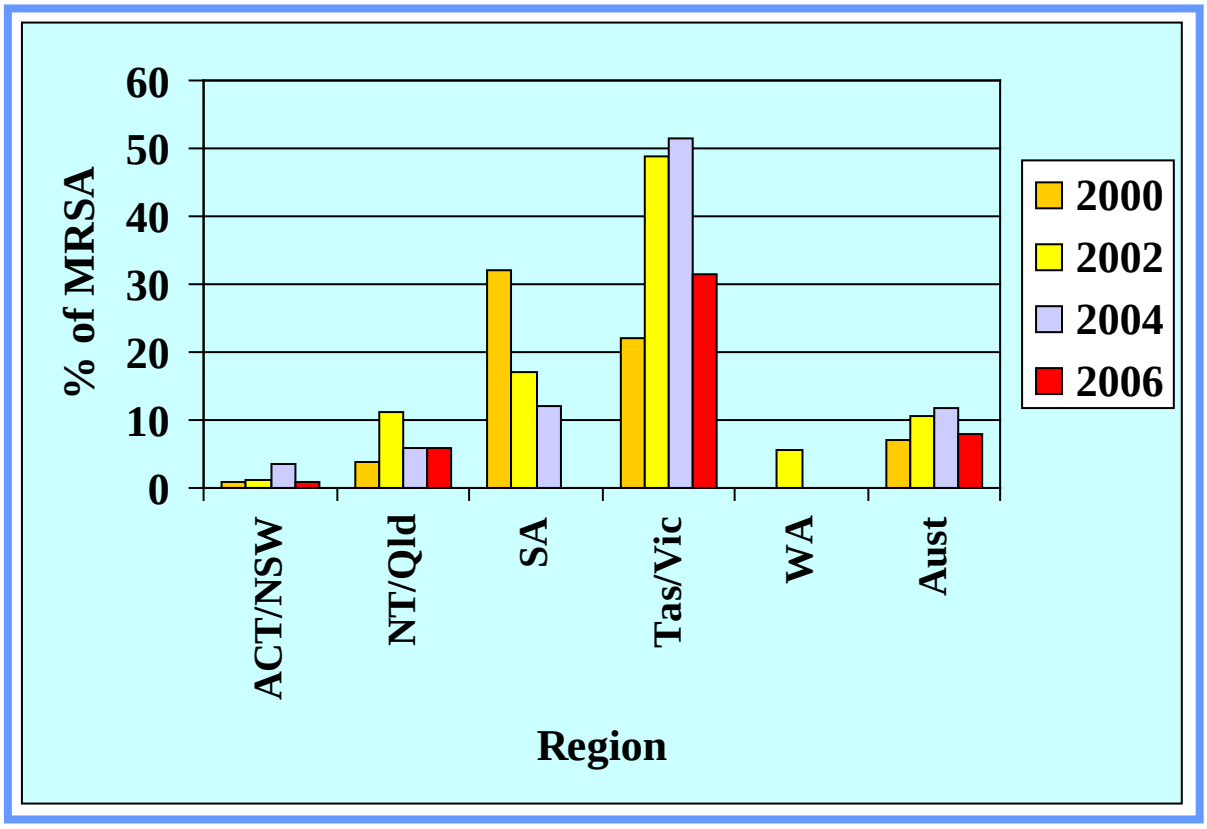
Epidemiology



Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	1 (0.8%)	2 (1.1%)	6 (3.5%)	2 (1.0%)
NT/Qld	1 (3.7%)	6 (11.1%)	4 (5.9%)	4 (4.7%)
SA	8 (32.0%)	6 (17.1%)	5 (12.2%)	0
Tas/Vic	8 (22.2%)	22 (48.9%)	32 (51.6%)	31 (31.6%)
WA	0	3 (5.5%)	0	0
Total	18 (7.0%)	39 (10.7%)	47 (11.9%)	37 (8.0%)

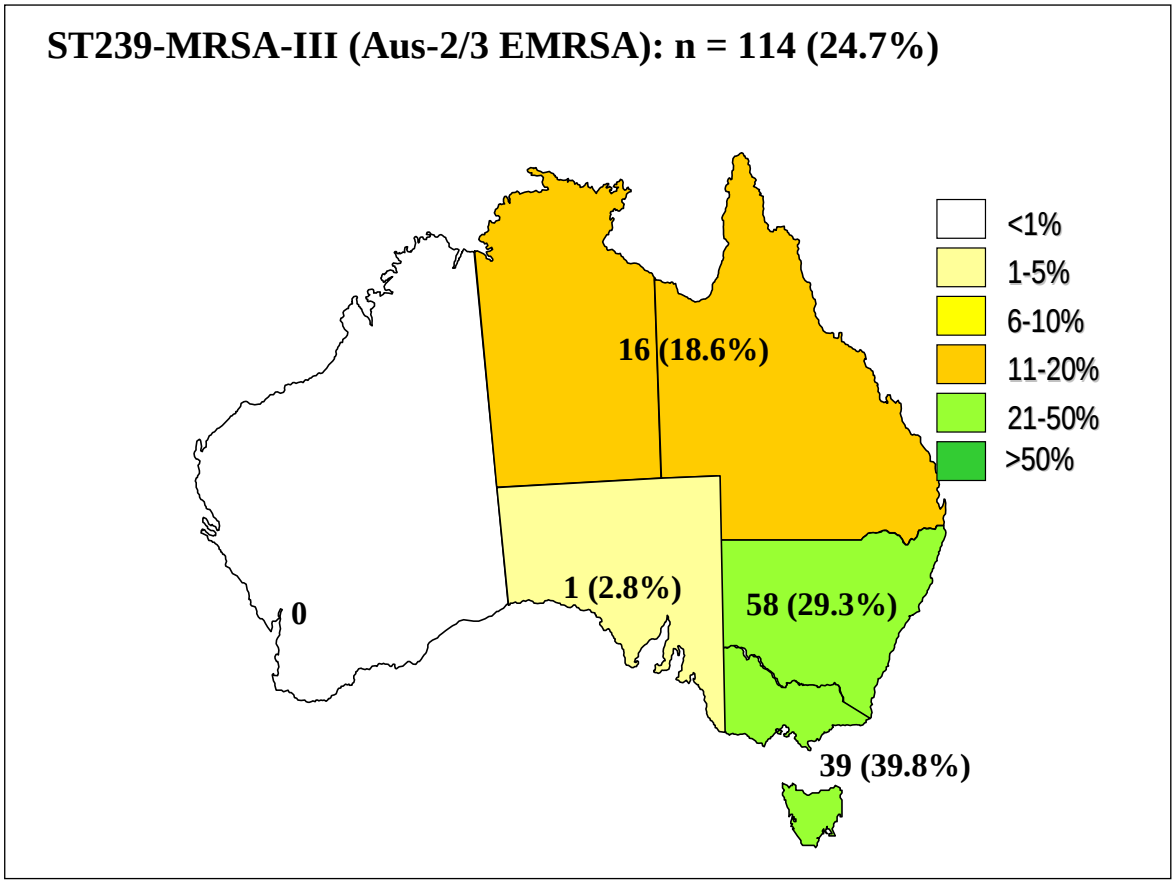
Percentage figures relate to total MRSA isolates

SAP 2000 – 2006: Regional Distribution of ST239-MRSA-III (Aus-3 EMRA)



Aus-2 and Aus-3 EMRSA

Epidemiology

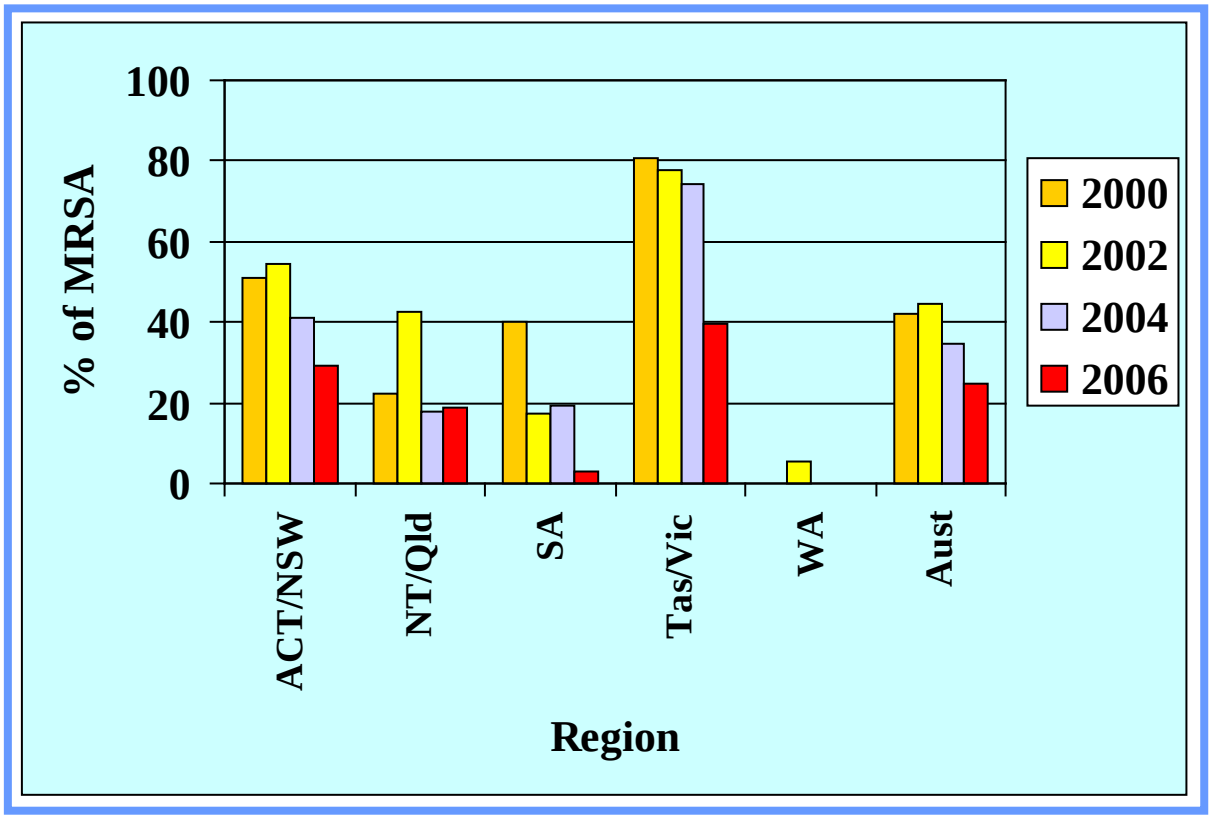


SAP 2000 – 2006: Regional Distribution of ST239-MRSA-III (Aus-2 and Aus-3 EMRSA)

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	63 (50.4%)	95 (54.6%)	71 (41.0%)	58 (29.3%)
NT/Qld	6 (22.2%)	23 (42.6%)	12 (17.7%)	16 (18.6%)
SA	10 (40.0%)	6 (17.1%)	8 (19.5%)	1 (2.8%)
Tas/Vic	29 (80.6%)	35 (77.8%)	46 (74.2%)	39 (39.8%)
WA	0	3 (5.5%)	0	0
Total	108 (42.0%)	162 (44.6%)	137 (34.7%)	114 (24.7%)

Percentage figures relate to total MRSA isolates

SAP 2000 – 2006: Regional Distribution of ST239-MRSA-III (Aus-2 and Aus-3 EMRSA)



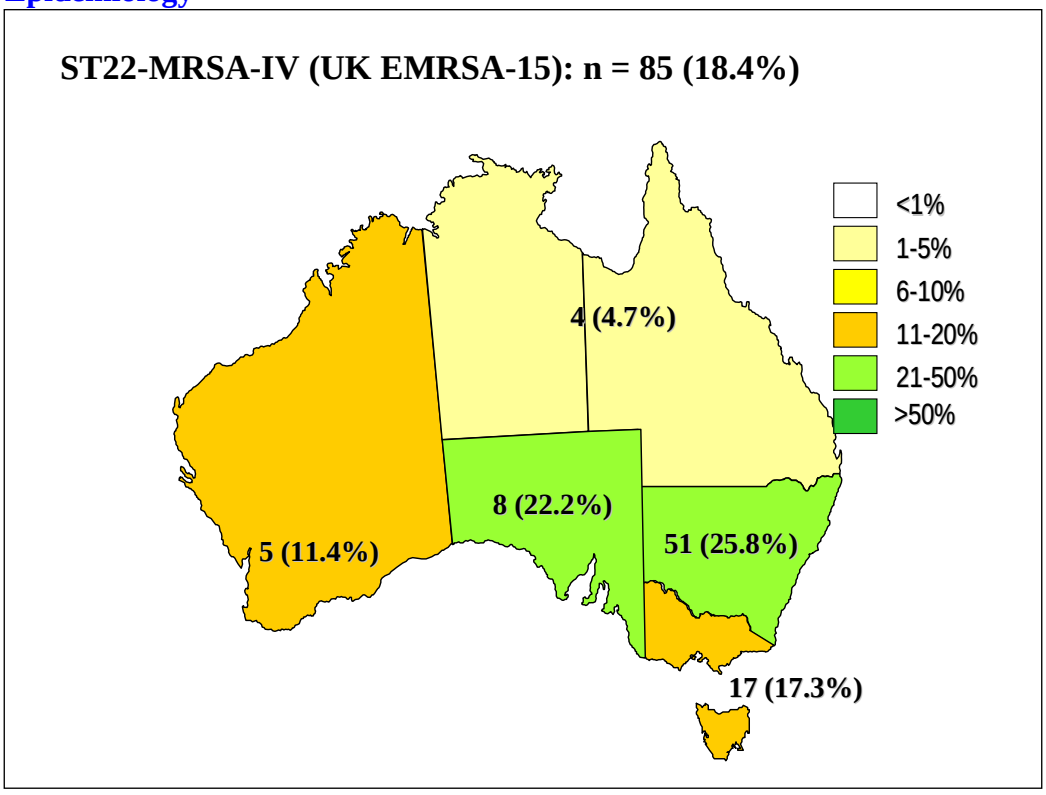
ST22-MRSA-IV

Also known as "UK EMRSA-15" or the "German Barnim" strain, ST22-MRSA-IV has become a major EMRSA clone in many parts of the world including Australia, United Kingdom, New Zealand, several European countries and recently Singapore. First identified in the Midlands and South-East England in the early 1990s it accounts for over half of UK isolates sent to the Laboratory of Hospital Infection in Colindale for typing. It is non-multiresistant (typically resistant to ciprofloxacin and erythromycin only) and is staphylococcal enterotoxin C, G and I positive. In New Zealand and Australia, ST22-MRSA-IV is frequently isolated from patients in long term care facilities and is associated with pre-employment screening of health staff from the United Kingdom.

Phenotypic Characteristics

Antibiogram:	Ciprofloxacin^{R}	98%
	Erythromycin^{R}	53%
	Tetracycline^{R}	2%
	Rifampicin^{R}	2%
	Gentamicin^{R}	2%
	Trimethoprim^{R}	1%
	Mupirocin^{R}	1%
	Fusidic Acid^{R}	0%
Urease:	Negative	

Epidemiology

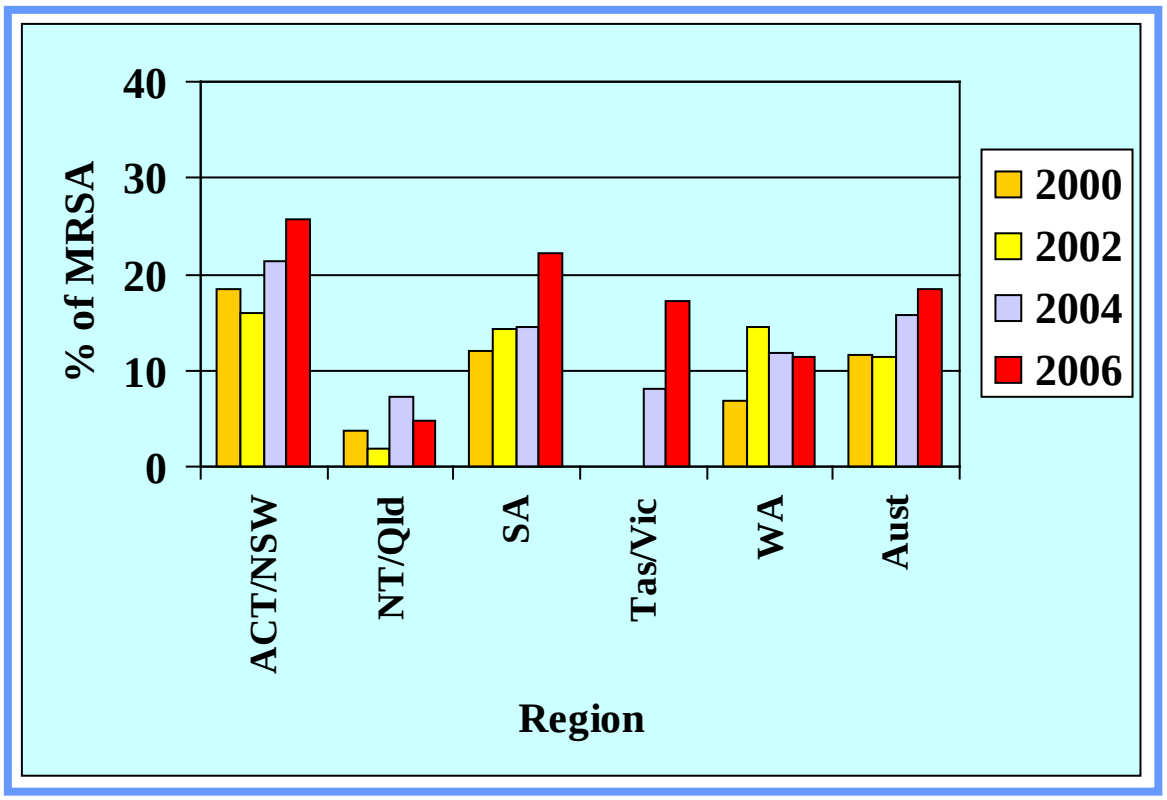


SAP 2000 – 2006: Regional Distribution of ST22-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	23 (18.4%)	28 (16.1%)	37 (21.4%)	51 (25.8%)
NT/Qld	1 (3.7%)	1 (1.9%)	5 (7.3%)	4 (4.7%)
SA	3 (12.0%)	6 (14.6%)	8 (19.5%)	8 (22.2%)
Tas/Vic	0	0	5 (8.1%)	17 (17.3%)
WA	3 (6.8%)	8 (14.5%)	6 (11.8%)	5 (11.4%)
Total	30 (11.7%)	42 (11.6%)	62 (15.7%)	85 (18.4%)

Percentage figures relate to total MRSA isolates

SAP 2000 – 2006: Regional Distribution of ST22-MRSA-IV



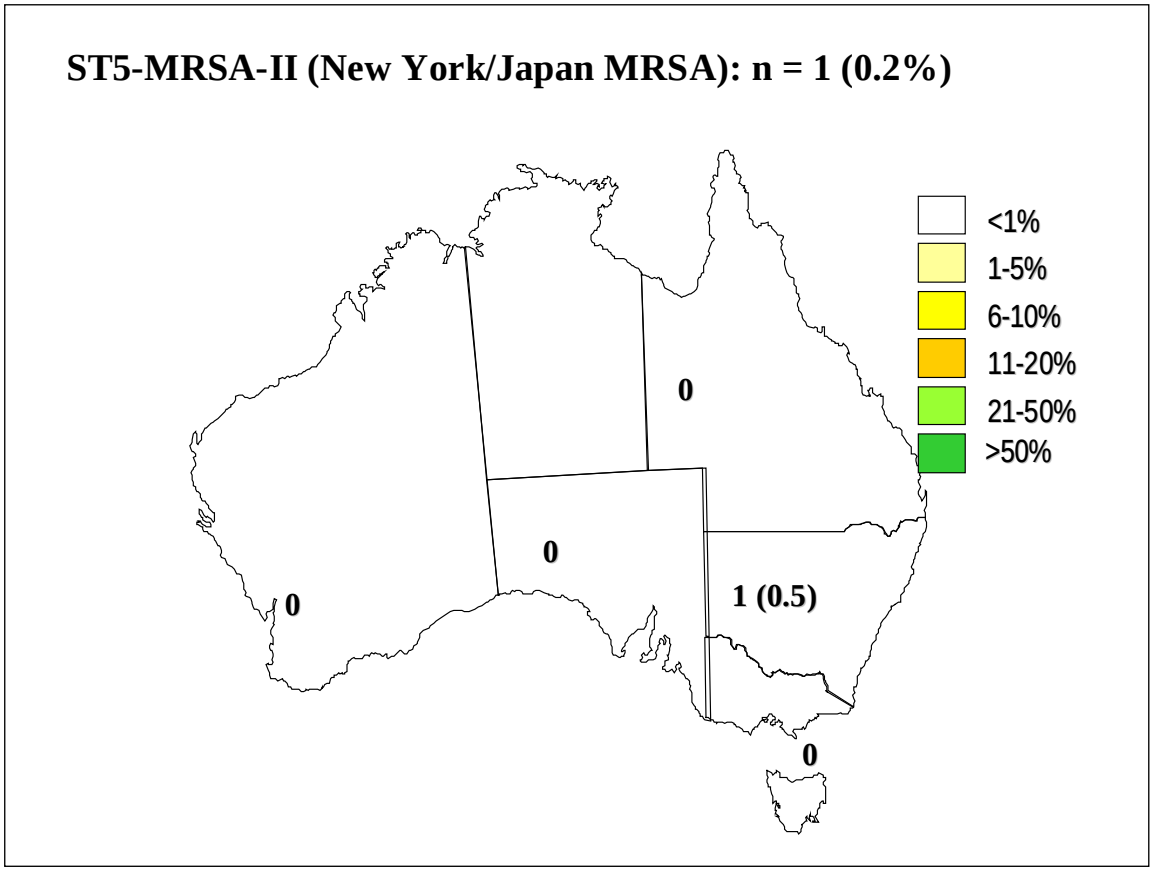
ST5-MRSA-II

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

Phenotypic Characteristics

Antibiogram:	Erythromycin^{R}	100%
	Ciprofloxacin^{R}	100%
	Trimethoprim^{R}	0%
	Mupirocin^{S}	0%
	Fusidic Acid^{S}	0%
	Tetracycline^{S}	0%
	Rifampicin^{S}	100%
	Gentamicin^{S}	0%
Urease:	Positive	

Epidemiology



Summary of EMRSA Isolated in AGAR SAPs 2000 – 2006

Clone	Alternative Name	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ST239-MRSA-III	Aus-2, -3 EMRSA	108 (77.7%)	162 (77.9%)	137 (68.2%)	114 (57.0%)
ST22-MRSA-IV	UK EMRSA-15	30 (21.6%)	42 (20.2%)	62 (30.8%)	85 (42.5%)
ST5-MRSA-II	New York/Japan	0	0	0	1[e] (0.5%)
ST36-MRSA-II	UK EMRSA-16	0	1[b] (0.5%)	2[d] (1.0%)	0
ST8-MRSA-II	Irish-1 EMRSA	0	3[c] (1.4%)	0	0
ST8-MRSA-VI	Irish-2 EMRSA	1[a] (0.7%)	0	0	0
Total		139	208	201	200

Percentage figures relate to the epidemic MRSA isolates

[a]Isolated in WA
[b]Isolated in WA
[c]Isolated in NSW/ACT region (n=2) and WA (n= 1)
[d]Isolated in SA (n-1) and WA (n=1)
[e]Isolated in ACT/NSW (n=1)

5.4. cMRSA

cMRSA 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 SCC*mec* types IV and V, which lack transposons, integrated plasmids and other antibiotic resistance genes. Although they have been introduced into teaching hospitals they rarely cause outbreaks. In the 1990s, non-multiresistant MRSA were isolated on the eastern seaboard in suburban/regional areas of south-east Queensland, Sydney and Canberra (5). They were frequently isolated in people of Pacific Island descent and were subsequently identified as "Western Samoan Phage Pattern MRSA" (WSPP MRSA). WSPP MRSA has previously been reported in New Zealand and several Pacific islands. In 2000, a non-multiresistant MRSA was identified as a cause of community acquired infection in the Caucasian population living in Ipswich Queensland and was subsequently identified as "Queensland MRSA" (6). Although both strains initially caused skin infections they have now been associated with serious invasive disease and have been shown to be PVL positive.

SAP 2006 cMRSA

In SAP 2006, 25 community MRSA clones (22 MLST clone types) were identified:

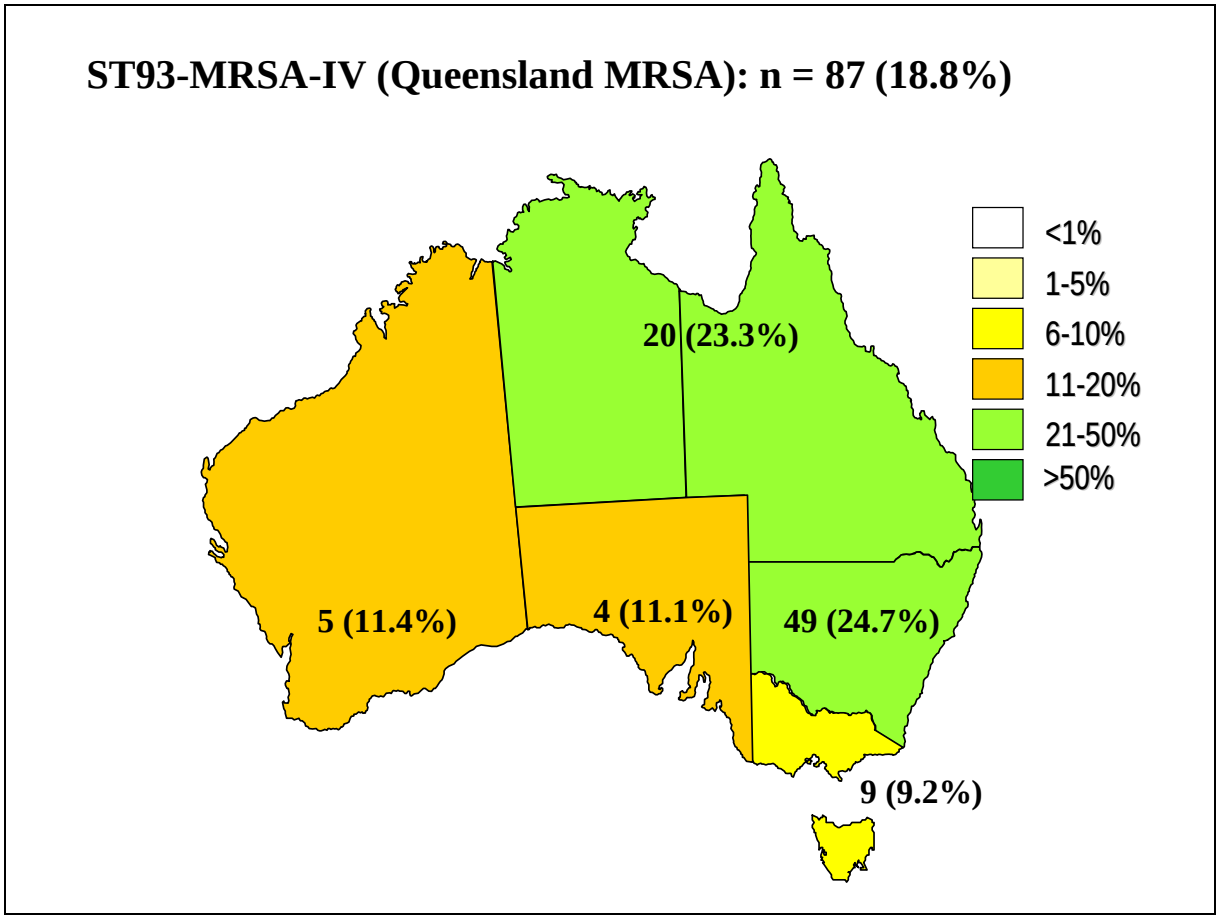
Clone	CC	Alternative Name	n (% of cMRSA)
ST93-MRSA-IV	Singleton	Queensland cMRSA	87 (33.2%)
ST1-MRSA-IV	1	WA MRSA -1	62 (23.7%)
ST30-MRSA-IV	30	WSPP MRSA	32 (12.2%)
ST5-MRSA-IV	5	WA MRSA-3	20 (7.6%)
ST78-MRSA-IV	78	WA MRSA-2	13 (5.0%)
ST45-MRSA-IV	45	WA MRSA-23	9 (3.4%)
ST75-MRSA-IV	Singleton	WA MRSA-8	7 (2.7%)
ST8-MRSA-IV	8	USA300 MRSA	6 (2.3%)
ST45-MRSA-V	45	WA MRSA-4	5 (1.9%)
ST8-MRSA-IV	8	WA MRSA- 5	3 (1.1%)
ST59-MRSA-V_T	59	Taiwan cMRSA	2 (0.8%)
ST80-MRSA-IV	80	European cMRSA	2 (0.8%)
ST5-MRSA-V	5	Novel	2 (0.8%)
ST361-MRSA-IV	S	Novel	1 (0.4%)
ST1-MRSA-V	1	Novel	1 (0.4%)
ST5-MRSA-V	5	WA MRSA-35	1 (0.4%)
ST7-MRSA-V	7	Novel	1 (0.4%)
ST8-MRSA-IV	8	Novel	1 (0.4%)
ST584-MRSA-IV	9	WA MRSA-13	1 (0.4%)
ST12-MRSA-IV	12	WA MRSA-69	1 (0.4%)
ST20-MRSA-V	20	Novel	1 (0.4%)
ST30slv-MRSA-IV	30	Novel	1 (0.4%)
ST338-MRSA-V	59	Novel	1 (0.4%)
ST59-MRSA-IV	59	WA MRSA-15	1 (0.4%)
ST72-MRSA-V	72	Novel	1 (0.4%)
Total			262

Major cMRSA Clones

ST93-MRSA-IV

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

Epidemiology

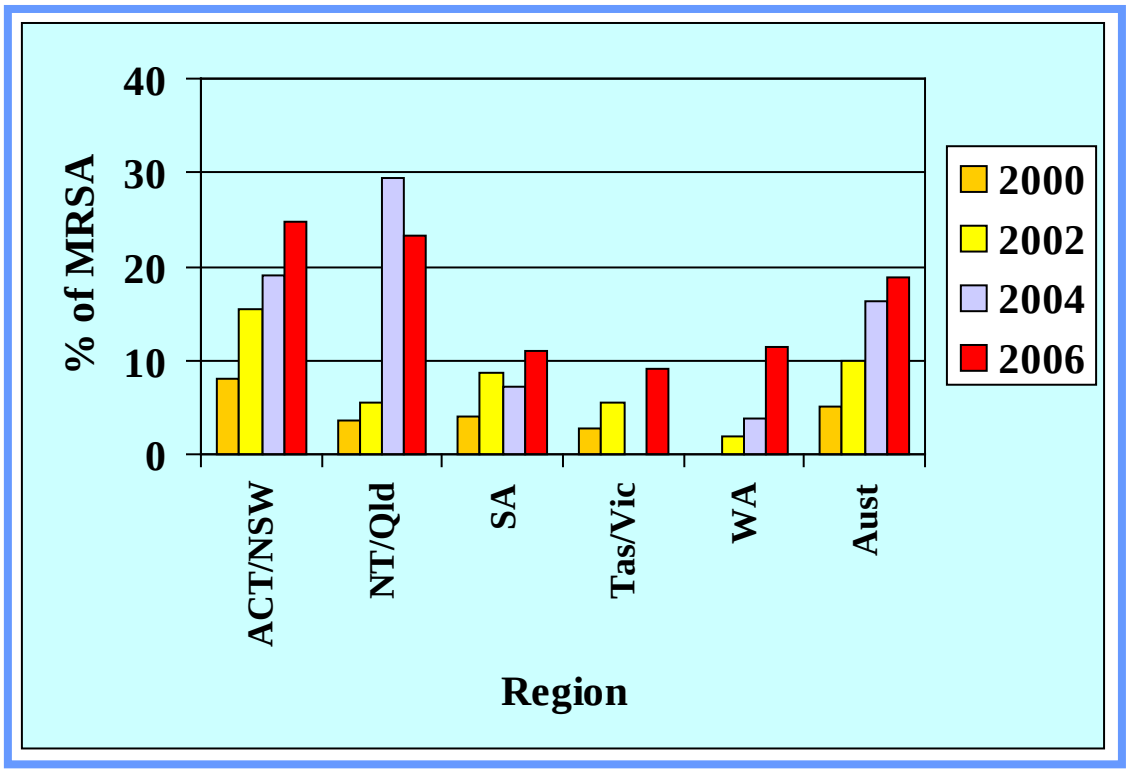


SAP 2000 to SAP 2006 Regional Distribution of ST93-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	10 (8.0%)	27 (15.5%)	33 (19.1%)	49 (24.7%)
NT/Qld	1 (3.7%)	3 (5.6%)	20 (29.4%)	20 (23.3%)
SA	1 (4.0%)	3 (8.6%)	3 (7.3%)	4 (11.1%)
Tas/Vic	1 (2.8%)	2 (5.4%)	0	9 (9.2%)
WA	0	1 (1.8%)	2 (3.9%)	5 (11.4%)
Total	13 (5.1%)	36 (9.9%)	58 (14.7%)	87 (18.8%)

Percentage figures relate to total MRSA isolates

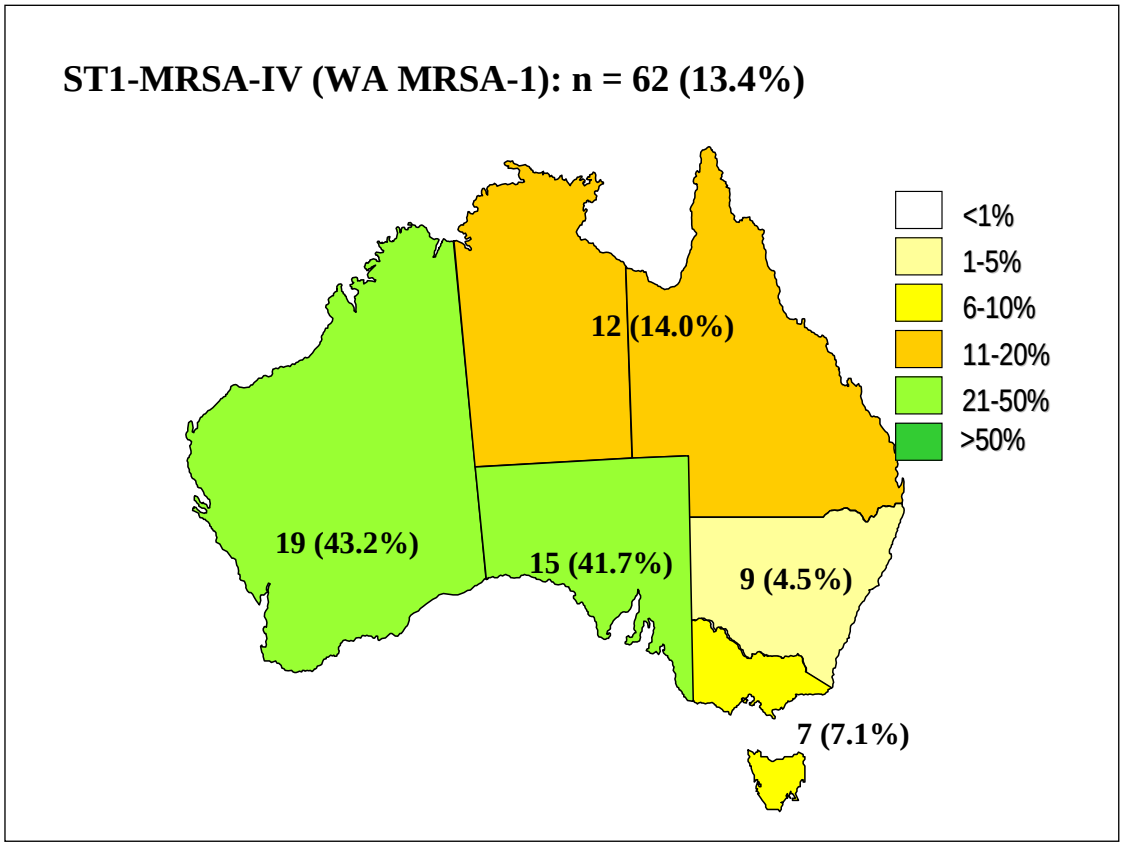
SAP 2000 to SAP2006 Regional Distribution of ST93-MRSA-IV



ST1-MRSA-IV

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

Epidemiology

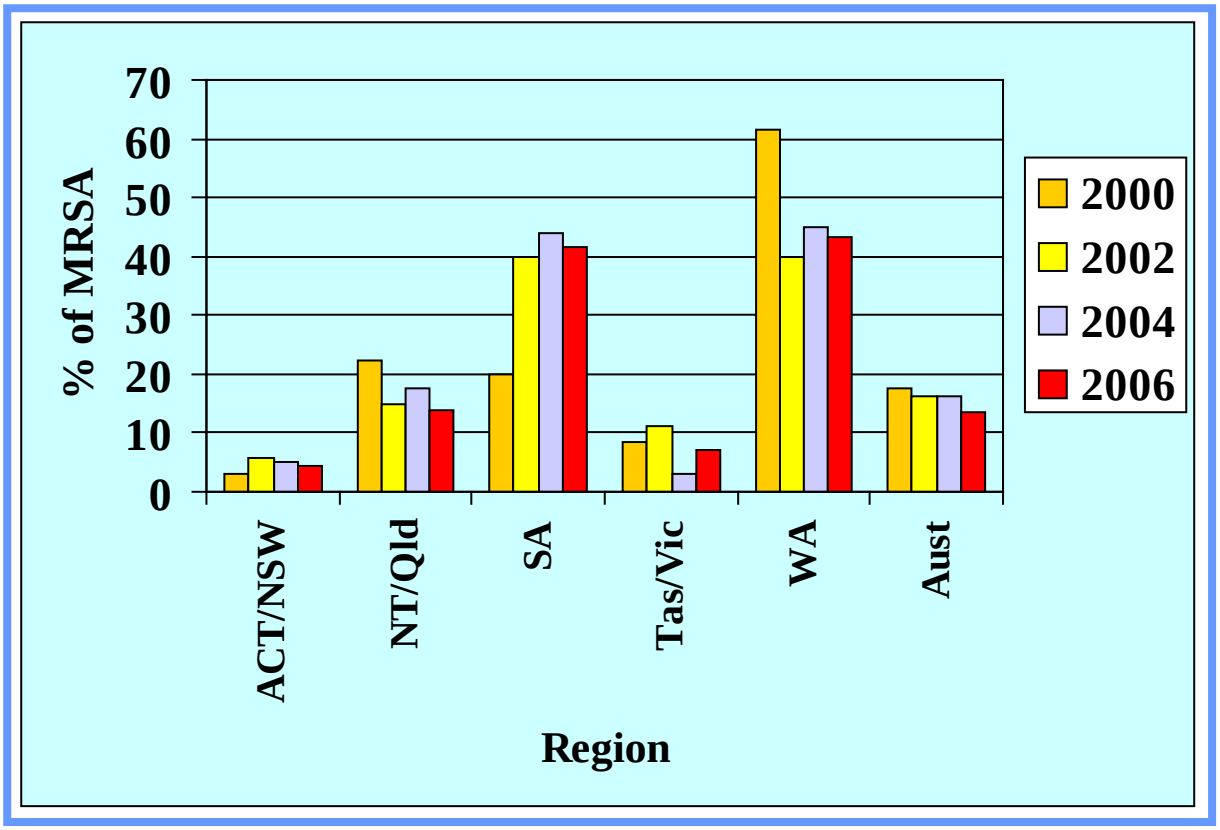


SAP 2000 to SAP 2006 Regional Distribution of ST1-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	4 (3.2%)	10 (5.7%)	9 (5.2%)	9 (4.5%)
NT/Qld	6 (22.2%)	8 (14.8%)	12 (17.6%)	12 (14.0%)
SA	5 (20.0%)	14 (40%)	18 (43.9%)	15 (41.7%)
Tas/Vic	3 (8.3%)	5 (11.1%)	2 (3.2%)	7 (7.1%)
WA	27 (61.4%)	22 (40%)	23 (45.1%)	19 (43.2%)
Total	45 (17.5%)	59 (16.3%)	64 (16.2%)	62 (13.4%)

Percentage figures relate to total MRSA isolates

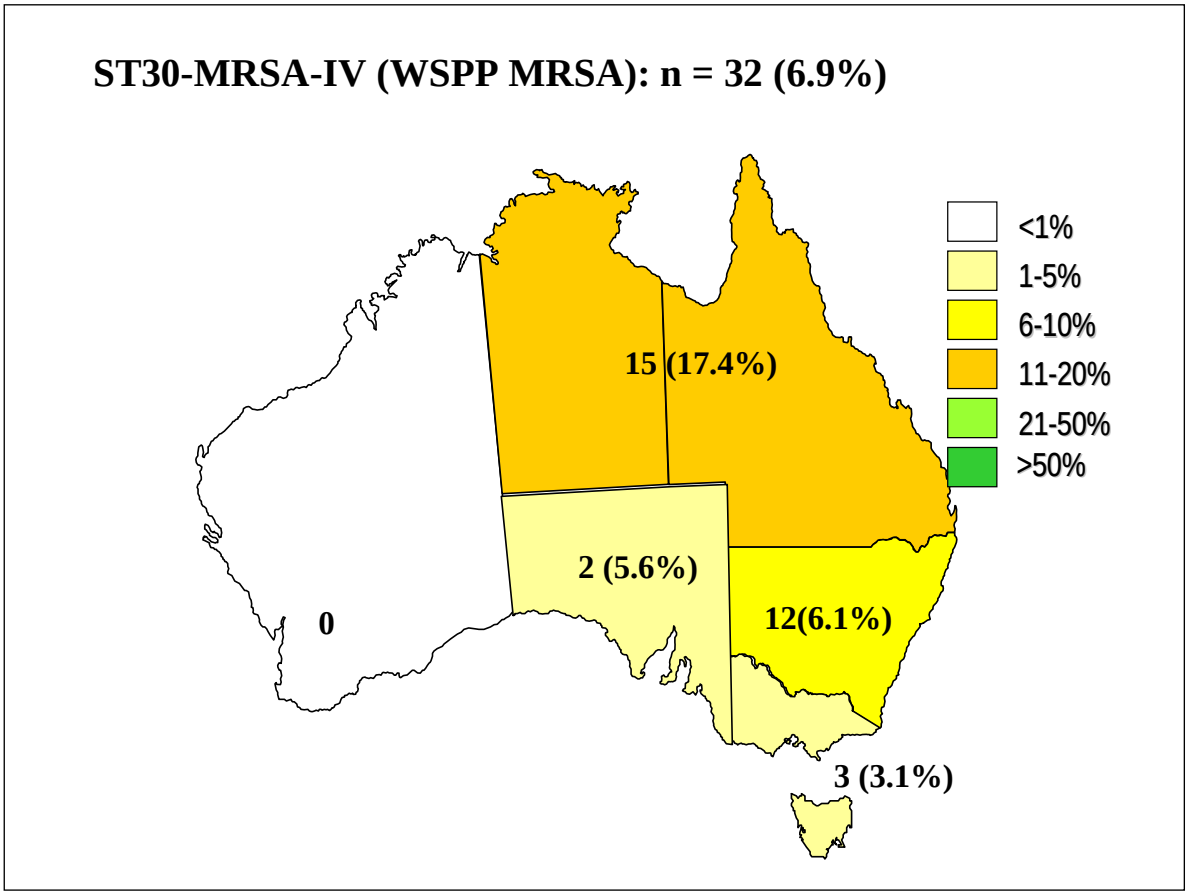
SAP 2000 to SAP 2006 Regional Distribution of ST1-MRSA-IV



ST30-MRSA-IV

Also known as "WSPP MRSA", ST30-MRSA-IV was originally described in Polynesians living in New Zealand and the Pacific islands and is PVL positive.

Epidemiology

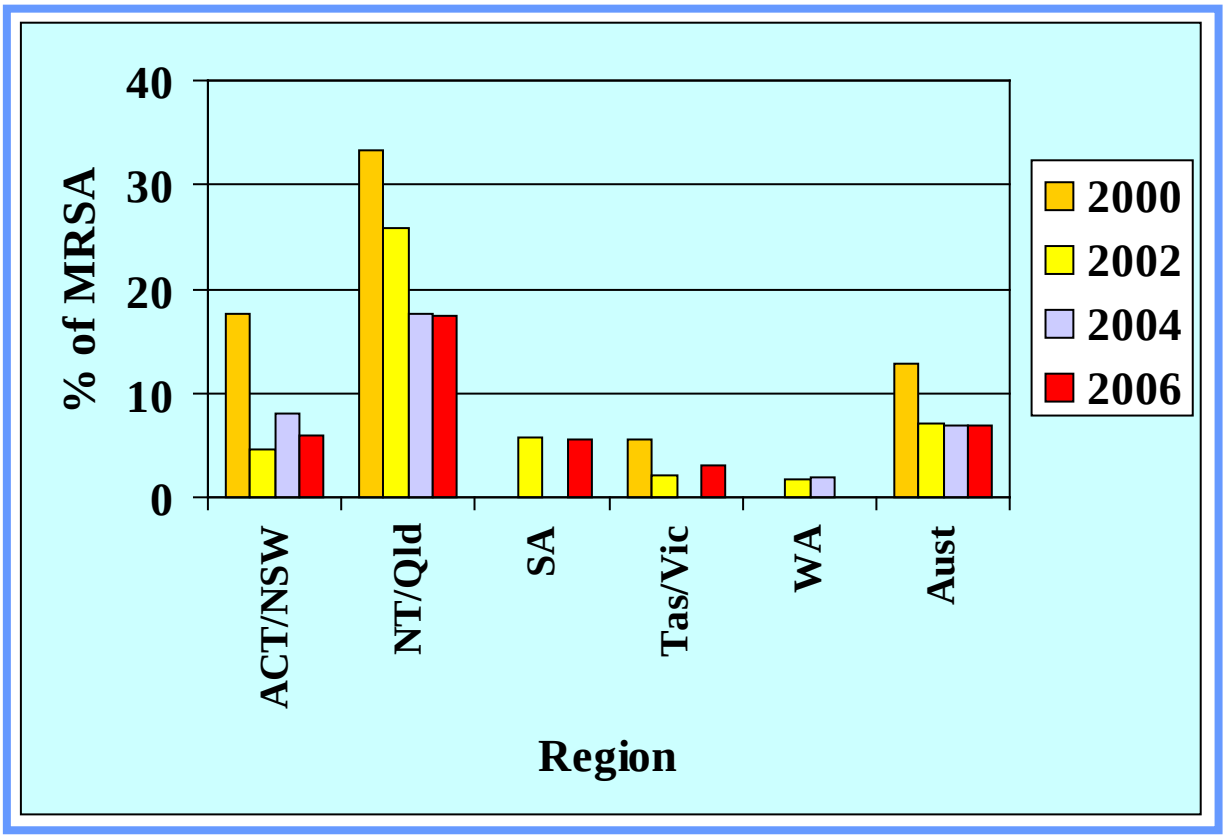


SAP 2000 to SAP 2006 Regional Distribution of ST30-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	22 (17.6%)	8 (4.6%)	13 (7.5%)	12 (6.1%)
NT/Qld	9 (33.3%)	14 (25.9%)	12 (17.6%)	15 (17.4%)
SA	0	2 (5.7%)	0	2 (5.6%)
Tas/Vic	2 (5.6%)	1 (2.2%)	0	3 (3.1%)
WA	0	1 (1.8%)	1 (2.0%)	0
Total	33 (12.8%)	26 (7.2%)	26 (6.6%)	32 (6.9%)

Percentage figures relate to total MRSA isolates

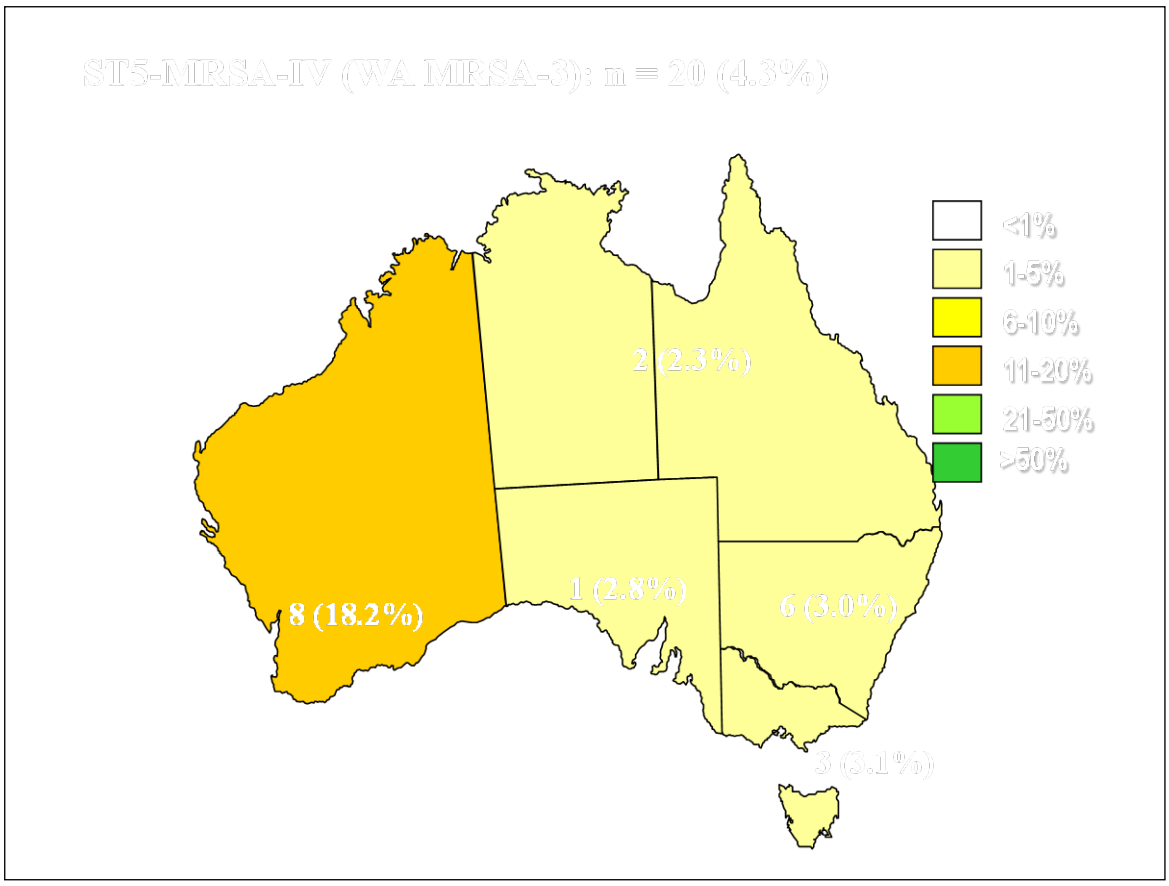
SAP 2000 to SAP 2006 Regional Distribution of ST30-MRSA-IV



ST5-MRSA-IV

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

Epidemiology

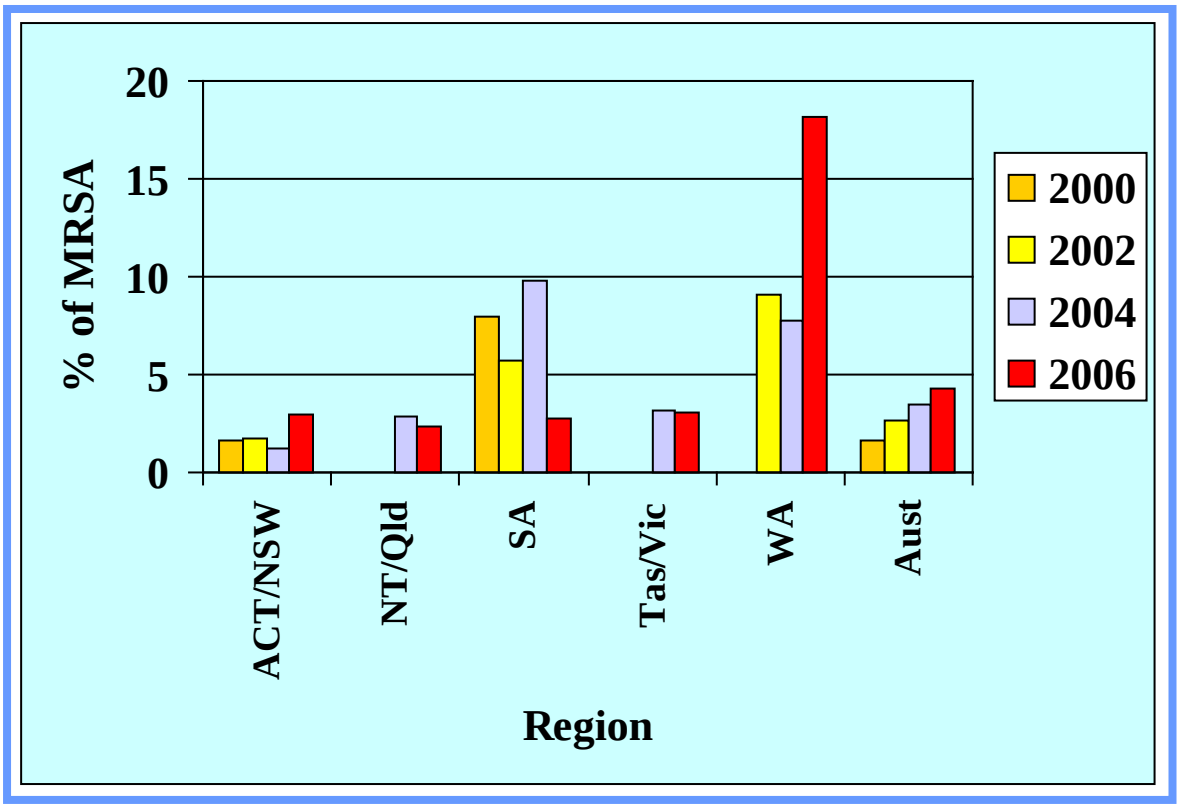


SAP 2000 to SAP 2006 Regional Distribution of ST5-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	2 (1.6%)	3 (1.7%)	2 (1.2%)	6 (3.0%)
NT/Qld	0	0	2 (2.9%)	2 (2.3%)
SA	2 (8%)	2 (5.7%)	4 (9.8%)	1 (2.8%)
Tas/Vic	0	0	2 (3.2%)	3 (3.1%)
WA	0	5 (9.1%)	4 (7.8%)	8 (18.2%)
Total	4 (1.6%)	10 (2.8%)	14 (3.5%)	20 (4.3%)

Percentage figures relate to total MRSA isolates

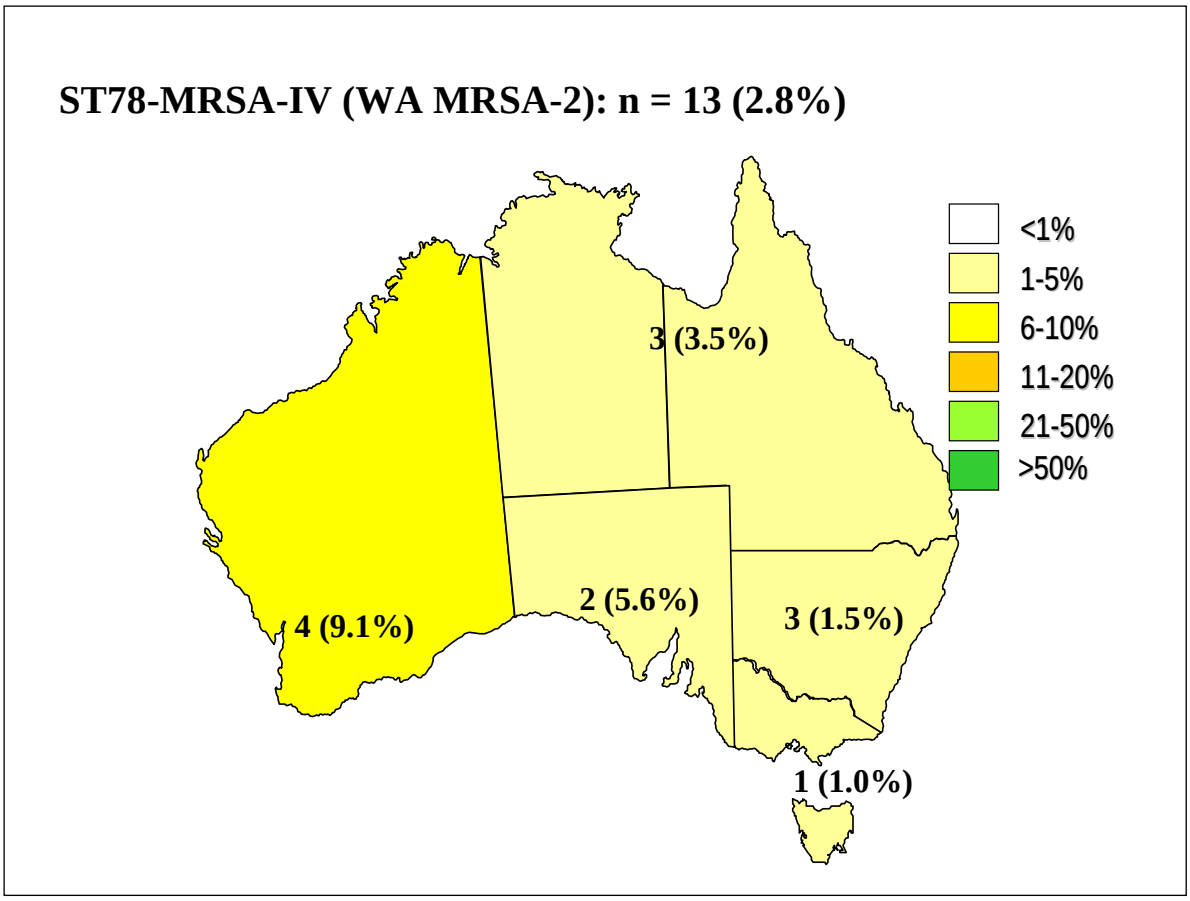
SAP 2000 to SAP 2006 Regional Distribution of ST5-MRSA-IV



ST78-MRSA-IV

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

Epidemiology

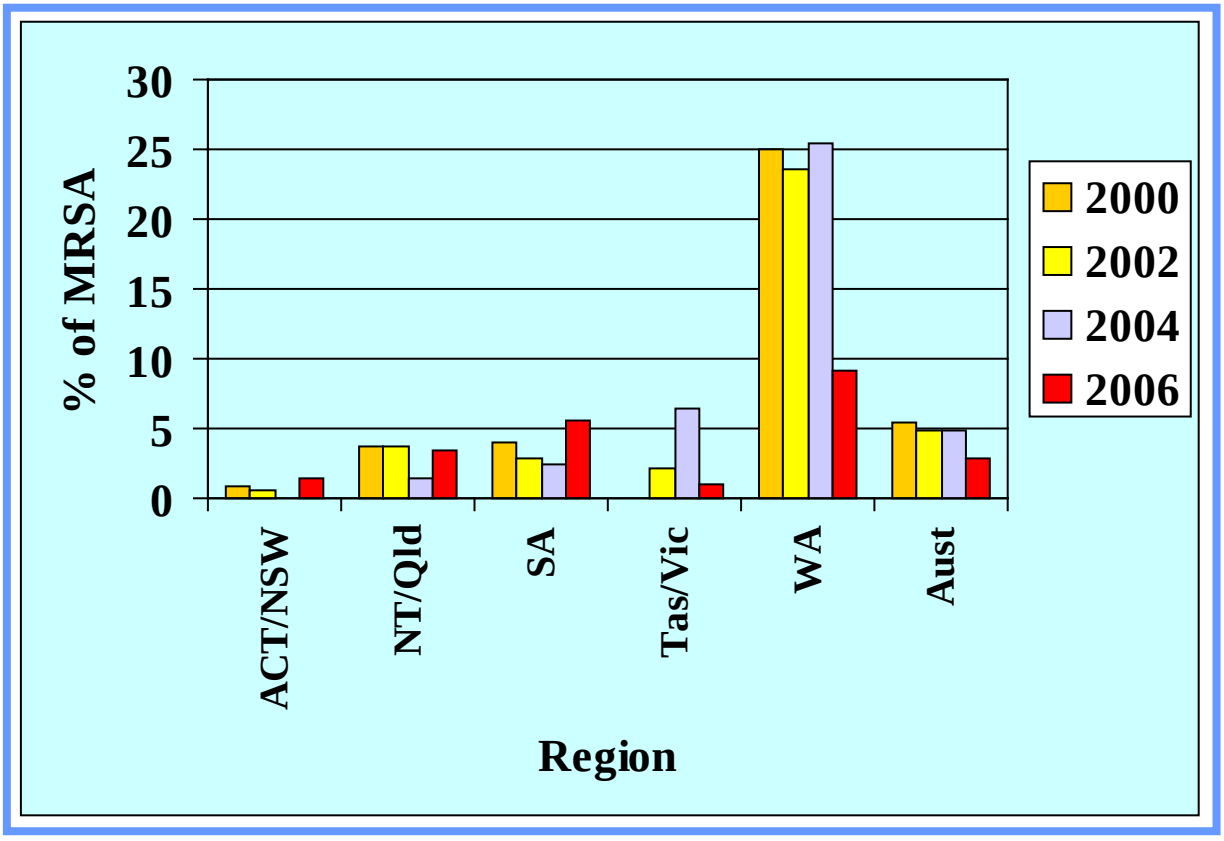


SAP 2000 to SAP 2006 Regional Distribution of ST78-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006
ACT/NSW	1 (0.8%)	1 (0.6%)	0	3 (1.5%)
NT/Qld	1 (3.7%)	2 (3.7%)	1 (1.5%)	3 (3.5%)
SA	1 (4.0%)	1 (2.9%)	1 (2.4%)	2 (5.6%)
Tas/Vic	0	1 (2.2%)	4 (6.5%)	1 (1.0%)
WA	11 (25.0%)	13 (23.6%)	13 (25.5%)	4 (9.1%)
Total	14 (5.4%)	18 (5.0%)	19 (4.8)	13 (2.8%)

Percentage figures relate to total MRSA isolates

SAP 2000 to SAP 2006 Regional Distribution of ST78-MRSA-IV



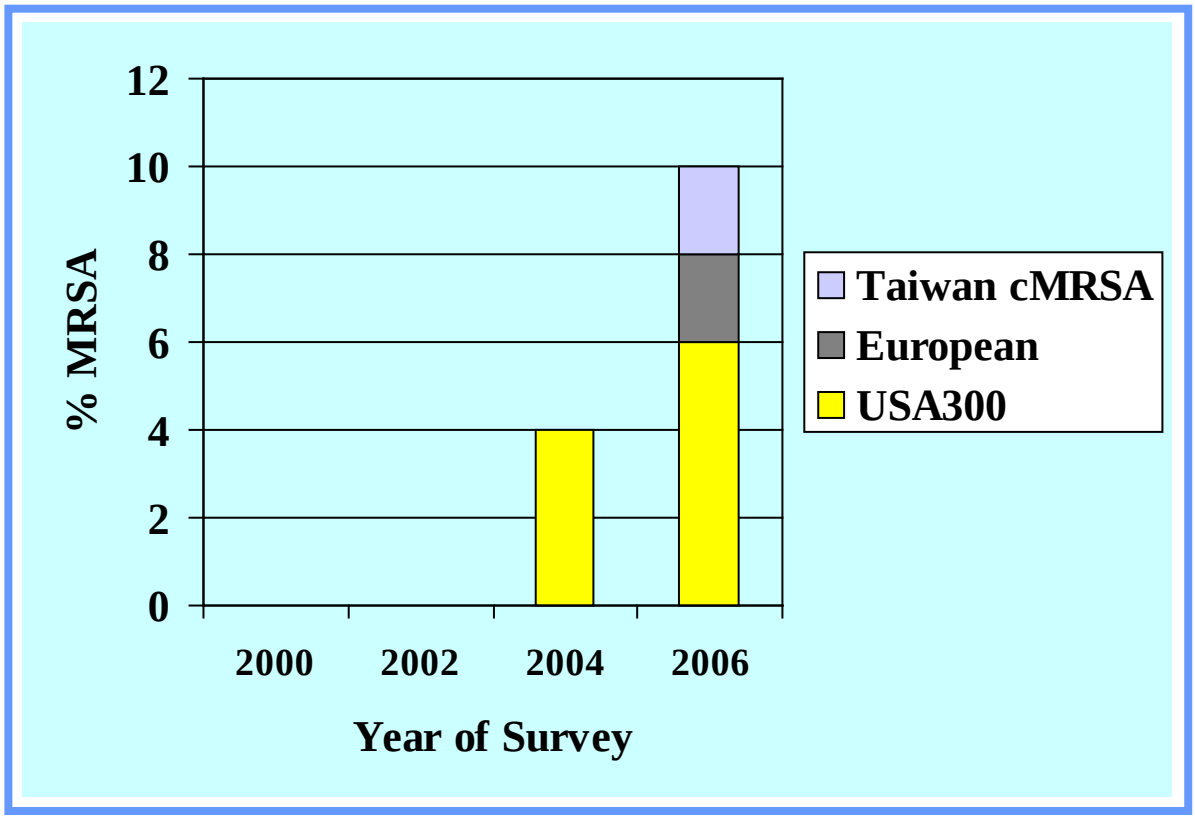
International cMRSA Clones

In SAP 2006, three international cMRSA clones were characterized. All were Panton Valentine leucocidin (PVL) positive.

CLONE	ALTERNATIVE NAME	n (%)
ST8-MRSA-IV	USA300	6 (2.3)
ST80-MRSA-IV	European cMRSA	2 (0.8)
ST59-MRSA-V_T	Taiwan cMRSA	2 (0.8)
TOTAL		10

Percentage figures relate to cMRSA isolates

SAP 2000 – 2006: Number of MRSA Identified as International cMRSA



SAP 2000 – 2006: Number of MRSA Identified as International cMRSA

CLONE	SAP 2004			SAP 2006		
	USA300	European	Taiwan	USA300	European	Taiwan
ACT/NSW	3	0	0	4	0	0
NT/Qld	1	0	0	2	0	0
SA	0	0	0	0	0	0
Tas/Vic	0	0	0	0	2	2
WA	0	0	0	0	0	0
Total	4	0	0	6	2	2

Minor cMRSA CLONES

Clone	Clonal Complex	CHEF	2000 (n = 9)	2002 (n = 6)	2004 (n = 13)	2006 (n=38)
ST75-MRSA-IV	S	WA MRSA-8	2 (NT/Qld)	1 (NT/Qld)	1 (NT/Qld)	6 (NT/Qld) 1 (WA)
ST8-MRSA-IV	8	WA MRSA-5	0	1 (ACT/NSW)	1 (ACT/NSW)	1 (ACT/NSW) 2 (NT/Qld)
ST45-MRSA-V	45	WA MRSA-4	3 (2 WA) (1 SA)	1 (SA)	0	1 (ACT/NSW) 2 (SA) 2 (WA)
ST45-MRSA-IV	45	WA MRSA-23	0	0	2 (Tas/Vic)	9 (Tas/Vic)
ST583-MRSA-IV	80	WA MRSA-17	1 (ACT/NSW)	1 (Tas/Vic)	1 (ACT/NSW)	0
ST59-MRSA-IV	59	WA MRSA-15	0	0	2 (1 NT/Qld) (1 WA)	1 (Tas/Vic)
ST584-MRSA-IV	9	WA MRSA-13	0	0	2 (1 ACT/NSW) (1 Tas/Vic)	1 (SA)
STnovel-MRSA-IV	Singleton	Novel	1 (NT/Qld)	1 (NT/Qld)	0	0
ST152-MRSA-V	Singleton	Novel	0	1 (SA)	0	0
ST8-MRSA-V	8	Novel	2 (SA)	0	0	0
ST1-MRSA-V	1	Novel	0	0	0	1 (NT/Qld)

Clone	Clonal Complex	CHEF	2000 (n = 9)	2002 (n = 6)	2004 (n = 13)	2006 (n=38)
ST5-MRSA-V	5	WA MRSA-35	0	0	0	1 (Tas/Vic)
ST5-MRSA-V	5	Novel	0	0	0	1 (Tas/Vic) 1 (ACT/NSW)
ST7-MRSA-V	7	Novel	0	0	0	1 (Tas/Vic)
ST8-MRSA-IV	8	Novel	0	0	0	1 (NT/Qld)
ST30slv-MRSA-IV	30	Novel	0	0	0	1 (NT/Qld)
ST338-MRSA-V	59	Novel	0	0	0	1 (Tas/Vic)
ST72-MRSA-V	72	Novel	0	0	0	1 (Tas/Vic)
ST20-MRSA-V	20	Novel	0	0	0	1 (NT/Qld)
ST12-MRSA-IV	12	WA MRSA-69	0	0	0	1 (ACT/NSW)
ST361-MRSA-IV	Unique	Novel	0	0	0	1 (ACT/NSW)

5.5. Panton-Valentine Leucocidin (PVL) Toxin

cMRSA

Clone	Alternative Name	Positive	Negative	Total
ST93-MRSA-IV	Queensland MRSA	87	0	87
ST30-MRSA-IV	WSPP MRSA	31	1	32
ST8-MRSA-IV	USA300	6	0	6
ST1-MRSA-IV	WA MRSA -1	5	57	62
ST59-MRSA-V_T	Taiwan cMRSA	2	0	2
ST80-MRSA-IV	European cMRSA	2	0	2
ST338-MRSA-V	Novel	1	0	1
ST30slv-MRSA-IV	Novel	1	0	1
ST78-MRSA-IV	WA MRSA – 2	0	13	13
ST5-MRSA-IV	WA MRSA – 3	0	20	20
ST584-MRSA-IV	WA MRSA – 13	0	1	1
ST59-MRSA-IV	WA MRSA – 15	0	1	1
ST45-MRSA-IV	WA MRSA – 23	0	9	9
ST8-MRSA-IV	WA MRSA – 5	0	3	3
ST75-MRSA-IV	WA MRSA – 8	0	7	7
ST45-MRSA-V	WA MRSA-4	0	5	5
ST5-MRSA-V	WA MRSA-35	0	1	1
ST12-MRSA-IV	WA MRSA-69	0	1	1
ST1-MRSA-V	Novel	0	1	1
ST20-MRSA-V	Novel	0	1	1
ST361-MRSA-IV	Novel	0	1	1
ST5-MRSA-V	Novel	0	2	2
ST72-MRSA-V	Novel	0	1	1
ST7-MRSA-V	Novel	0	1	1
ST8-MRSA-IV	Novel	0	1	1
Total		135 (51.5%)	127 (48.5%)	262

Epidemic MRSA

Clone	Alternative Name	Positive	Negative	Total
ST22-MRSA-IV	UK EMRSA 15	1	84	85
ST239-MRSA-III	AUS-2 EMRSA	0	77	77
ST239-MRSA-III	AUS-3 EMRSA	0	37	37
ST5-MRSA-II	New York/Japan EMRSA	0	1	1
Total		1 (0.5%)	199 (99.5%)	200

Panton-Valentine Leucocidin (PVL) Toxin: Regional Distribution

cMRSA

CC	1		5				7	8			12	20	30		45		59			72	78	80	S	S		
	1 IV WA1	1 V	5 IV WA3	584 IV WA13	5 V WA35	5 V	7 V	8 IV WA5	8 IV USA 300	8 IV	12 IV WA69	20 V	30 IV WSPP	30 slv IV	45 V WA4	45 IV WA23	59 IV WA15	59 V Taiwan	338 V	72 V	78 IV WA2	80 IV Eur	93 IV QLD	75 IV WA8	361 IV	TOTAL (%)
ACT/NSW (88)	**2 (22)**		**0**	**0**		**0**		**0**	**4 (100)**		**0**		**11 (92)**		**0**						**0**		**49 (100)**		**0**	**66 (75)**
NT/ Qld (66)	**1 (8)**	**0**	**0**	**0**				**0**	**2 (100)**	**0**		**0**	**15 (100)**	**1 (100)**							**0**		**20 (100)**	**0**		**39 (59)**
SA (36)	**1**		**0**	**0**									**2 (100)**		**0**						**0**		**4 (100)**			**7 (19)**
Tas/Vic (42)	**1 (7)**		**0**	**0**	**0**	**0**	**0**						**3 (100)**			**0**	**0**	**2 (100)**	**1 (100)**	**0**	**0**	**2 (100)**	**9 (100)**			**18 (43)**
WA (39)	**0**		**0**	**0**											**0**						**0**		**5 (100)**	**0**		**5 (13)**
Total (262)	**5 (8)**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**6 (100)**	**0**	**0**	**0**	**31 (97)**	**1 (100)**	**0**	**0**	**0**	**2 (100)**	**1 (100)**	**0**	**0**	**2 (100)**	**87 (100)**	**0**	**0**	**135 (52)**

Epidemic MRSA

A single isolate of ST22-MRSA-IV (UK EMRSA-15) isolated from Victoria/Tasmania was PVL positive.

5.6. cMRSA Antibiogram

CC	1		5				7	8			12	20	30		45		59			72	78	80	S	S		
	1 IV WA1	1 V	5 IV WA3	584 IV WA13	5 V WA35	5 V	7 V	8 IV WA5	ST8 V USA 300	8 IV	12 IV WA69	20 V	30 IV WSPP	30 slv IV	45 V WA4	45 IV WA23	59 IV WA15	59 V Taiwan	338 V	72 V	78 IV WA2	80 IV Eur	93 IV QLD	75 IV WA8	361 IV	TOTAL (%)
Oxacillin only: 167 (63.7%)																										
Ox^R	31		12			2				1	1	1	28	1	3						2	2	78	5		**167 (63.7)**
One non beta lactam antibiotic: 62 (23.7%)																										
Ox^R Em^R	5		8	1				1	1						1		1		1		8		9	2		**38 (14.5)**
Ox^R Cp^R															1	9										**10 (3.8)**
Ox^R FA^R	7																									**7 (2.7)**
Ox^R Gm^R	1							1																		**2 (0.8)**
Ox^R Tc^R					1															1					1	**3 (1.1)**
Ox^R Mp^R													2													**2 (0.8)**
Two non beta lactam antibiotics: 18 (6.9%)																										
Ox^R Em^R FA^R	9																									**9 (3.4)**
Ox^R Cp^R FA^R	1																									**1 (0.4)**
Ox^R Em^R Cp^R									1																	**1 (0.4)**
Ox^R Em^R Mp^R																					1					**1 (0.4)**
Ox^R Em^R Gm^R	1																									**1 (0.4)**

CC	1		5				7	8			12	20	30		45		59			72	78	80	S	S		
	1 IV WA1	1 V	5 IV WA3	584 IV WA13	5 V WA35	5 V	7 V	8 IV WA5	ST8 V USA 300	8 IV	12 IV WA69	20 V	30 IV WSPP	30 slv IV	45 V WA4	45 IV WA23	59 IV WA15	59 V Taiwan	338 V	72 V	78 IV WA2	80 IV Eur	93 IV QLD	75 IV WA8	361 IV	TOTAL (%)
Ox^R Gm^R Mp^R	1																									**1 (0.4)**
Ox^R Cp^R Tc^R									1																	**1 (0.4)**
Ox^R Gm^R Tc^R									1																	**1 (0.4)**
Ox^R Em^R Tc^R													1					1								**2 (0.8)**
Three non beta lactam antibiotics: 12 (4.6%)																										
Ox^R Em^R Cp^R FA^R	1																									**1 (0.4)**
Ox^R Em^R Tc^R Tm^R																		1								**1 (0.4)**
Ox^R Em^R Gm^R Rf^R	1																				1					**2 (0.8)**
Ox^R Em^R Gm^R Mp^R	1																									**1 (0.4)**
Ox^R Em^R FA^R Mp^R	2																									**2 (0.8)**
Ox^R Em^R Tc^R FA^R	1	1																								**2 (0.8)**
Ox^R Em^R Gm^R Tm^R							1																			**1 (0.4)**
Ox^R Em^R Cp^R Tm^R								1	1																	**2 (0.8)**
Four non beta lactam antibiotics: 3 (1.1%)																										
Ox^R Em^R Gm^R Tc^R Cp^R									1																	**1 (0.4)**

CC	**1**		**5**				**7**	**8**			**12**	**20**	**30**		**45**		**59**			**72**	**78**	**80**	**S**	**S**		
	1 IV WA1	1 V	5 IV WA3	584 IV WA13	5 V WA35	5 V	7 V	8 IV WA5	ST8 V USA 300	8 IV	12 IV WA69	20 V	30 IV WSPP	30 slv IV	45 V WA4	45 IV WA23	59 IV WA15	59 V Taiwan	338 V	72 V	78 IV WA2	80 IV Eur	93 IV QLD	75 IV WA8	361 IV	TOTAL (%)
Ox^R Em^R Rf^R FA^R Mp^R																					1					**1 (0.4)**
Ox^R Tm^R Gm^R Tc^R Cp^R													1													**1 (0.4)**
Total	**62**	**1**	**20**	**1**	**1**	**2**	**1**	**3**	**6**	**1**	**1**	**1**	**32**	**1**	**5**	**9**	**1**	**2**	**1**	**1**	**13**	**2**	**87**	**7**	**1**	**262**

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

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