

The Australian Group on Antimicrobial Resistance

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***Staphylococcus aureus* Programme 2005 (SAP 2005)
Hospital 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) 2005
Staphylococcus aureus Surveillance Programme (SAP 2005)**

Contents

- 1.0 Summary
- 2.0 Commencement Date
- 3.0 Isolates
- 4.0 Participating Laboratories
- 5.0 Methicillin Susceptibility Testing
- 6.0 Epidemiological Typing
 - 6.1 MRSA Nomenclature
 - 6.2 Multilocus Sequence Typing (MLST)
 - 6.3 Staphylococcal Cassette Chromosome *mec* (SCC*mec*)
- 7.0 Panton-Valentine Leucocidin (PVL) Toxin
- 8.0 Methods
 - 8.1 Epidemiological Typing Methods
 - 8.1.1 Antibiogram
 - 8.1.2 Resistogram
 - 8.1.3 Urease
 - 8.1.4 Coagulase Gene PCR-RFLP Assay
 - 8.1.5 Contour-clamped Homogeneous Electric Field Electrophoresis
 - 8.1.6 Chromosomal DNA Preparation
 - 8.1.7 Multi Locus Sequence Typing (MLST)
 - 8.1.8 Staphylococcal Cassette Chromosome *mec* (SCC*mec*)
 - 8.2 Identification of EMRSA Clones
 - 8.2.1 ST239-MRSA-III (Aus-2 and Aus-3 EMRSA)
 - 8.2.2 ST22-MRSA-IV (EMRSA-15)
 - 8.2.3 ST36-MRSA-II (EMRSA-16 or USA200)
 - 8.2.4 ST247-MRSA-I (EMRSA-17)
 - 8.2.5 ST5-MRSA-II (New York/Japan MRSA or USA100)
 - 8.3 Identification of cMRSA Clones
 - 8.3.1 ST30-MRSA-IV (Western Samoan Phage Pattern MRSA – WSPP MRSA)
 - 8.3.2 ST93-MRSA-IV (Queensland MRSA)
 - 8.3.3 ST8-MRSA-IV (WA MRSA-12 or USA300)
 - 8.3.3 WA MRSA
 - 8.4 Detection of Panton-Valentine Leucocidin (PVL) Toxin Genes
- 9.0 SAP05 Results
 - 9.1 Typing Tests Performed
 - 9.2 Regional Distribution of MRSA
 - 9.2.1 Regional Distribution of MRSA as a Proportion of *S aureus*
 - 9.2.2 Regional Distribution of EMRSA and cMRSA as a Proportion of

	MRSA
9.2.3	Regional Distribution of EMRSA and cMRSA as a Proportion of <i>S aureus</i>
9.3	EMRSA Clones by Institution
9.4	cMRSA Clones by Institution
9.5.	EMRSA Clones
9.5.1	ST239-MRSA-III
9.5.1.1	ST239-MRSA-III Phenotypic Characteristics
9.5.1.2	ST239-MRSA-III Epidemiology
9.5.1.2.1	Aus-2 EMRSA
9.5.1.2.2	Aus-3 EMRSA
9.5.1.2.3	Aus-2 and Aus-3 EMRSA
9.5.2	ST22-MRSA-IV
9.5.2.1	ST22-MRSA-IV Phenotypic Characteristics
9.5.2.2	ST22-MRSA-IV Epidemiology
9.4.3.3	AGAR Community SAPs 2000 – 2004: Regional
9.5.3	ST36-MRSA-II
9.5.3.1	ST36-MRSA-II Phenotypic Characteristics
9.5.3.2	ST36-MRSA-II Epidemiology
9.5.4	ST247-MRSA-I
9.5.4.1	ST247-MRSA-I Phenotypic Characteristics
9.5.4.2	ST247-MRSA-I Epidemiology
9.5.5	ST5-MRSA-II
9.5.5.1	ST5-MRSA-II Phenotypic Characteristics
9.5.5.2	ST5-MRSA-II Epidemiology
9.5.6	Summary of EMRSA Characterised
9.6	cMRSA
9.6.1	ST1-MRSA-IV
9.6.1.1	ST1-MRSA-IV Epidemiology
9.6.2	ST93-MRSA-IV
9.6.2.1	ST93-MRSA-IV Epidemiology
9.6.3	ST5-MRSA-IV
9.6.3.1	ST5-MRSA-IV Epidemiology
9.6.4	ST78-MRSA-IV
9.6.4.1	ST78-MRSA-IV Epidemiology
9.6.5	ST30-MRSA-IV
9.6.5.1	ST30-MRSA-IV Epidemiology
9.6.6	Summary of cMRSA Characterised
9.7	Panton-Valentine Leucocidin (PVL) Toxin
9.7.1	Panton-Valentine Leucocidin (PVL) Toxin: Regional Distribution
9.8	Community MRSA Antibigram
10.0	References
11.0	Acknowledgments

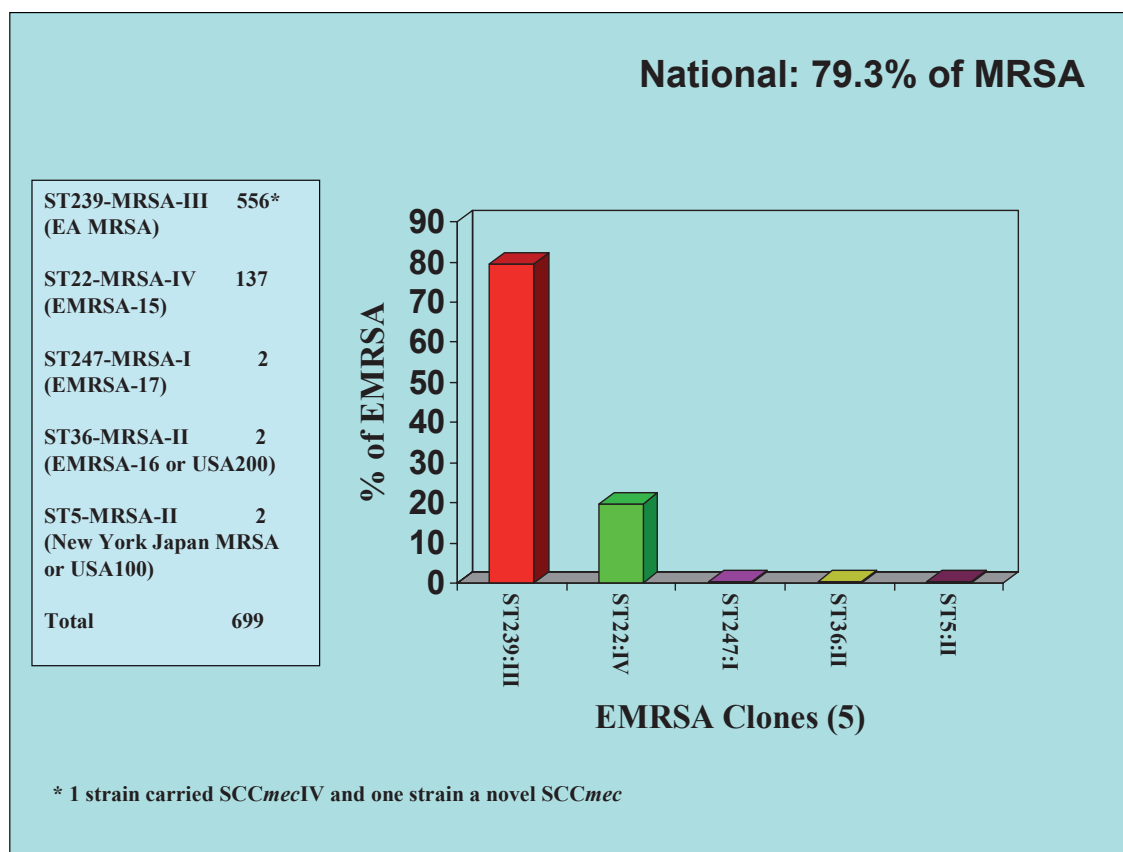
Staphylococcus aureus Programme 2005 (SAP 2005) Hospital Survey MRSA Epidemiology and Typing Report

1.0 Summary

From the AGAR SAP 2005, 881 MRSA were forwarded to the Gram-positive Bacteria Typing and Research Unit for epidemiological typing.

Epidemic MRSA (EMRSA)

699 (79.3%) MRSA were classified as Epidemic MRSA (EMRSA) or healthcare associated MRSA.



These strains were classified into five international clones:

- ST239-MRSA-III (also known as Aus-2/3 EMRSA, EA MRSA, EMRSA-1, Portuguese/Brazilian clone or the Vienna clone).
- ST22-MRSA-IV (also known as EMRSA-15 or the German Barnim strain).
- ST36-MRSA-II (also known as EMRSA-16 or USA200).
- ST247-MRSA-I (also known as EMRSA-17)

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

In this survey ST239-MRSA-III, a multiresistant EMRSA, was the predominant MRSA isolated (n = 556). 63.1% of MRSA and 79.5% of EMRSA were identified as ST239-MRSA-III. Although ranging from 39.8% to 83.0% of MRSA in the central and eastern regions of Australia, only 6.3% of MRSA isolated in WA were characterised as ST239-MRSA-III. This difference can be attributed to the MRSA management policy introduced into WA in the early 1980s.

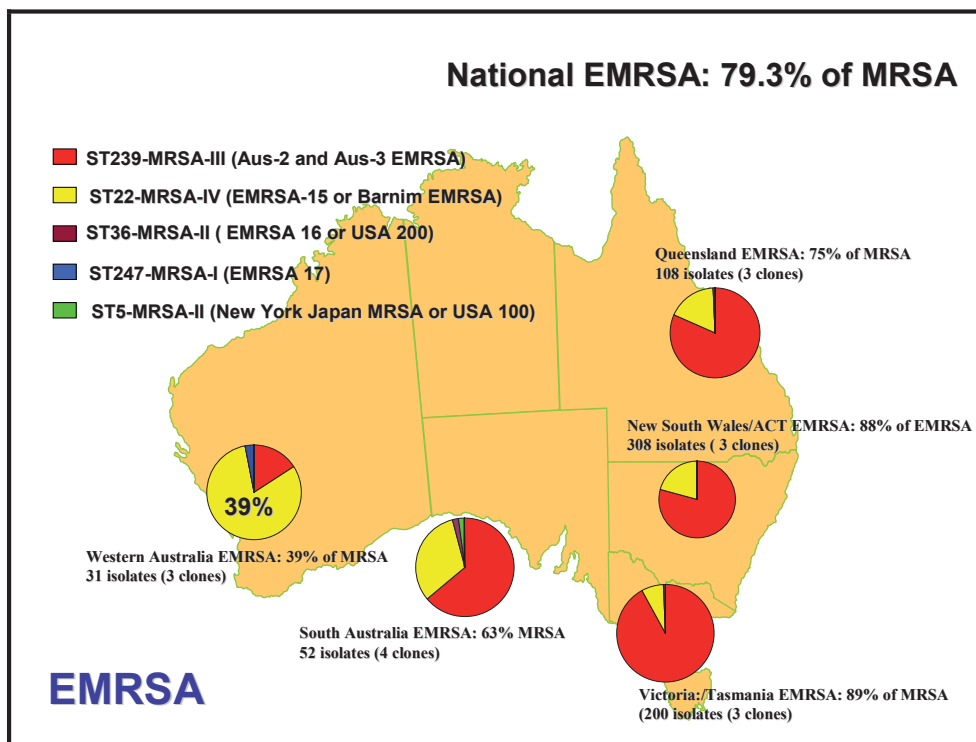
Based on their susceptibility to mercuric chloride and phenylmercuric acetate, ST239-MRSA-III was classified into two subclones, Aus-2 EMRSA and Aus-3 EMRSA. Aus-2 EMRSA was predominant in Qld and the ACT/NSW region and Aus-3 EMRSA was predominant in SA and the Tas/Vic region.

ST22-MRSA-IV, a non multiresistant EMRSA, was first documented in Australia in 1997 in Perth where it was detected in pre-employment screening of healthcare workers from the United Kingdom, Ireland and eastern Australia (19). This clone has now become established throughout Australia. Overall 15.6% of MRSA and 19.6% of EMRSA were identified as ST22-MRSA-IV. Rates varied from 5.8% of MRSA in the Tas/Vic region to 31.3% in WA.

ST36-MRSA-II, a non multiresistant EMRSA, was first reported in the United Kingdom. In this survey two strains were identified; one from SA and the other from Tas/Vic region.

ST247-MRSA-I, a multiresistant EMRSA, was first reported in the United Kingdom. In this survey two strains were identified; one from WA and the other from the ACT/NSW region.

ST5-MRSA-II, a non multiresistant EMRSA, was first reported in the United States of America. In this survey two strains were identified; one from SA and the other Qld.

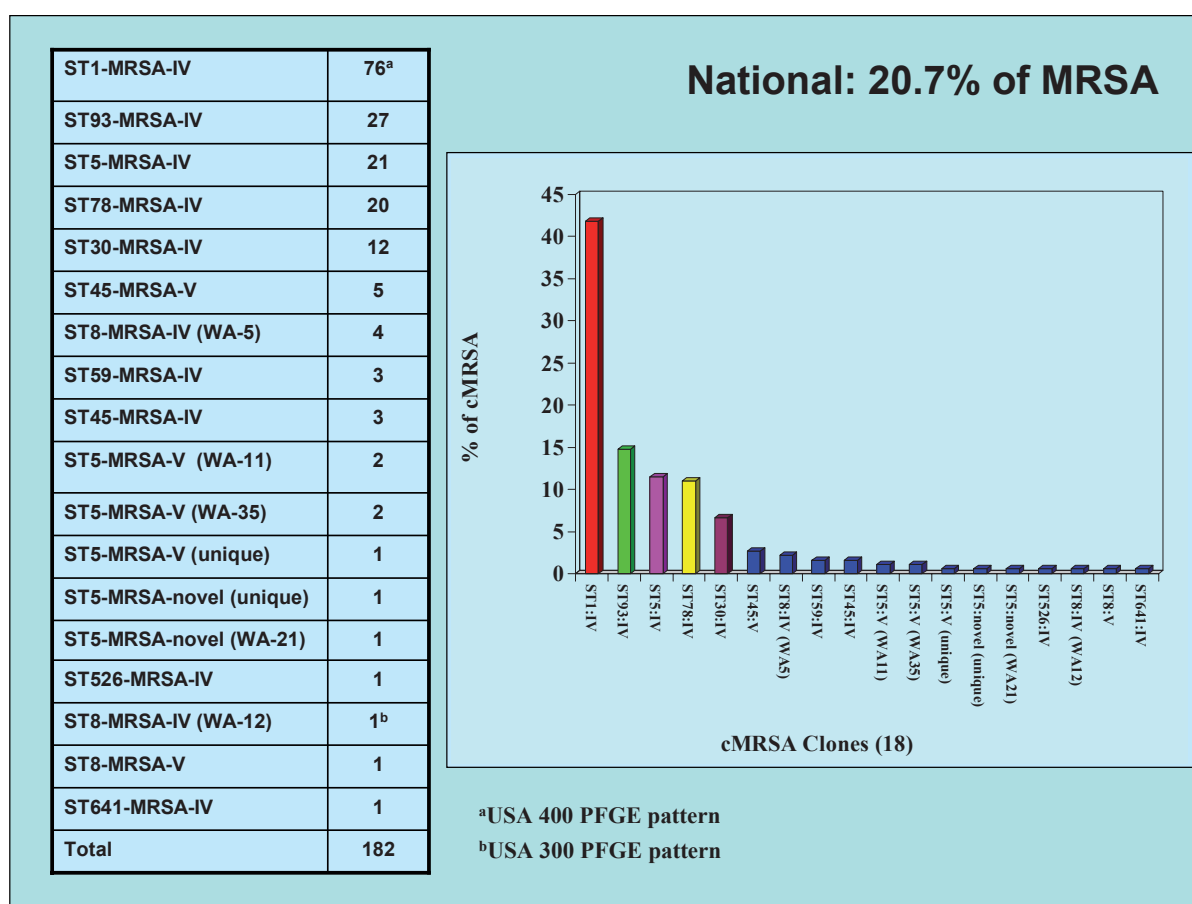


Community MRSA (cMRSA)

182 (21.7%) MRSA were classified as community MRSA. Epidemiological typing has shown these strains have emerged from diverse genetic backgrounds. The fifteen MLST clones identified were grouped into 7 clonal complexes and one singleton. *SCCmec* types IV and V, and one novel *SCCmec* type were identified.

- Clonal Complex 1
ST1-MRSA-IV (WA MRSA-1)
- Clonal Complex 5
ST5-MRSA-IV (WA MRSA-3)
ST5-MRSA-V (WA MRSA-11, -35, novel)
ST5-MRSA-novel (WA MRSA-21, novel)
ST526-MRSA-IV (WA MRSA-39)
ST641-MRSA-IV (novel)
- Clonal Complex 8
ST8-MRSA-IV (WA MRSA -5 and -12)
ST8-MRSA-V (novel)
- Clonal Complex 45
ST45-MRSA-IV (WA MRSA-23)
ST45-MRSA-V (WA MRSA-4)

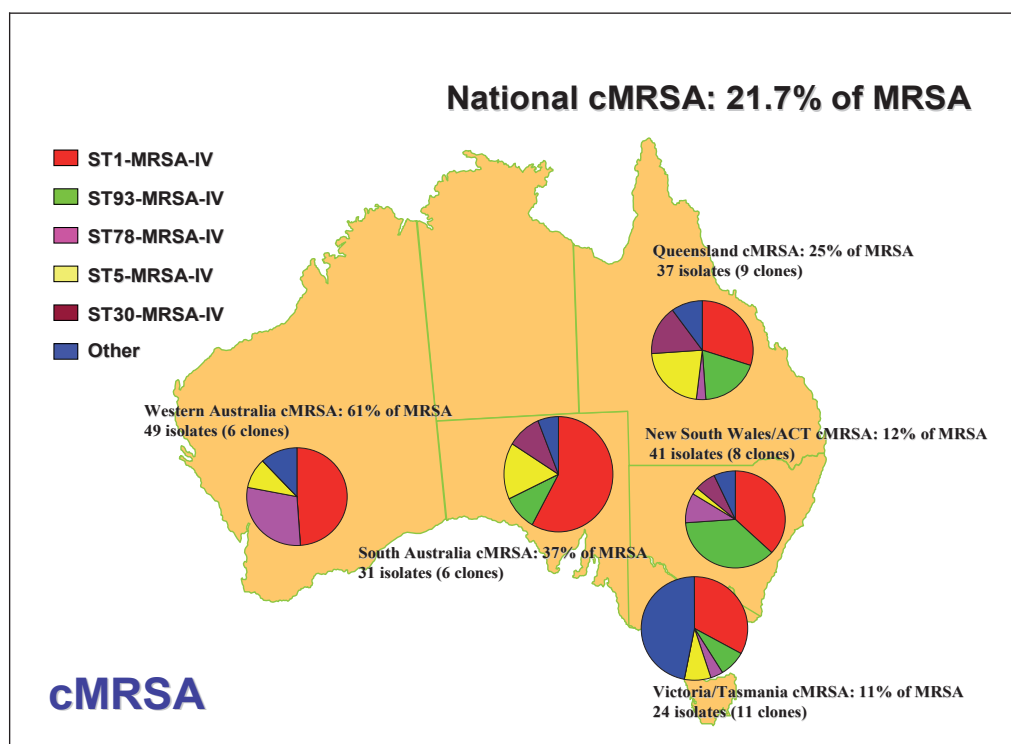
- Clonal Complex 59
ST59-MRSA-IV (WA MRSA-15)
- Clonal Complex 30
ST30-MRSA-IV (WSPP MRSA)
- Clonal Complex 78
ST78-MRSA-IV (WA MRSA-2)
- Singleton
ST93-MRSA-IV (Queensland MRSA)



85.7% (n=156) of cMRSA were classified into five major community clones:

- ST1-MRSA-IV (n = 76)
Isolated throughout Australia ranging from 3.6% in the Tas/Vic region to 30.0% of MRSA in WA. 3.9% (n=3) of strains were PVL positive.
- ST93-MRSA-IV (n = 27)
Isolated in most regions of Australia ranging from 0.9% in the Tas/Vic region to 4.8% of MRSA in Qld (not isolated in WA). 96.3% (n=26) of strains were PVL positive.

- ST5-MRSA-IV (n = 21)
Isolated throughout Australia ranging from 0.3% in the ACT/NSW region to 6.3% of MRSA in WA. All strains were PVL negative
- ST78-MRSA-IV (n = 20)
Isolated in most regions of Australia ranging from 0.9% in the ACT/NSW region to 17.5% of MRSA in WA (not isolated in SA). All strains were PVL negative.
- ST30-MRSA-IV (n = 12)
Isolated in most regions of Australia ranging from 0.9% in the ACT/NSW region to 4.1% of MRSA in Qld (not isolated in the WA and Tas/Vic region). 91.7% (n=11) of strains were PVL positive.



In addition to the three mentioned PVL positive clones (ST1-MRSA-IV, ST93-MRSA-IV and ST30-MRSA-IV), ST8-MRSA-IV (WA MRSA-12) was also PVL positive. This strain could not be differentiated from USA300 - the major PVL positive MRSA clone isolated in the United States of America. Overall 22.5% of cMRSA isolated were PVL positive.

53.8% (n=98) of cMRSA were resistant to the beta lactam antibiotics only. 84 strains (46.2%) were resistant to at least one non beta lactam antibiotic including:

- 33.5% (n=61) resistant to one non beta lactam antibiotic
- 8.2% (n=15) resistant to two non beta lactam antibiotics
- 3.3% (n=6) resistant to three non beta lactam antibiotics

1.1% (n=2) resistant to four non beta lactam antibiotics

The emergence of PVL-positive multiresistant cMRSA infections in Australian hospitals is a major public health concern which may require the modification of guidelines for the treatment and control of hospital associated infections due to *Staphylococcus aureus*.

2.0 Commencement Date

1st November 2005

3.0 Isolates

Approximately 100 consecutive clinical isolates of *Staphylococcus aureus* from 100 different patients at each site were tested by 32 laboratories located across Australia (total number of isolates = 2,908). Isolates were collected from inpatients only (hospital stay >48 hours at the time of collection).

4.0 Participating Laboratories

Australian Capital Territory (1)

The Canberra Hospital

South Australia (4)

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

New South Wales (8)

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

Tasmania (2)

Royal Hobart Hospital
Launceston General Hospital

Queensland (6)

Princess Alexandra Hospital
Royal Brisbane and Women's Hospital
Sullivan Nicolaides Pathology
Cairns Base Hospital
Gold Coast Hospital
Prince Charles Hospital

Victoria (6)

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

Northern Territory (1)

Royal Darwin Hospital

Western Australia (4)

PathWest Fremantle Hospital
PathWest Queen Elizabeth II
PathWest Royal Perth Hospital
Saint John of God Pathology

5.0 Methicillin Susceptibility Testing

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

6.0 Epidemiological Typing

Performed by the 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.

6.1 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 *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-MRSA-IV (previously known as EMRSA-15).

6.2 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.

6.3 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 *SCCmec*s 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.

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.

7.0 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). However, in Australia, it has been reported that cMRSA infrequently carry the genes encoding PVL (4). However, two cMRSA clones 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).

PVL genes have been shown to be transmitted by a temperate phage indicating that the PVL determinants are transferable (8).

8.0 Methods

8.1 Epidemiological Typing Methods

8.1.1 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 mupirocin resistant isolates was determined by Etest® (AB Biodisk, Solna, Sweden).

8.1.2 Resistogram

Disk Diffusion (9, 10)

mercuric chloride (HgCl₂) (0.4μM)
phenylmercuric acetate (PMA) (5 mM)

8.1.3 Urease

Christensen's Urea broth incubated for 24hrs at 37°C (11).

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

Coagulase gene restriction fragment length polymorphism typing was performed as previously described (12).

8.1.5 Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)

Electrophoresis of chromosomal DNA was performed as previously described (13) 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.* (14) and using a dendrogram similarity of 80% or greater to assign strain relatedness. *S aureus* NCTC 8325 was used as the size marker.

8.1.6 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).

8.1.7 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.

8.1.8 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 (15,16,17)

8.2 Identification of EMRSA Clones

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

Antibiogram
Resistogram
CHEF

8.2.2 ST22-MRSA-IV (EMRSA-15)

Antibiogram
Urea Broth
Coagulase PCR-RFLP

8.2.3 ST36-MRSA-II (EMRSA-16 or USA200)

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

8.2.4 ST247-MRSA-I (EMRSA-17)

Antibiogram
Urea Broth
Coagulase PCR-RFLP

CHEF

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

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

8.3 Identification of cMRSA Clones

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

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

8.3.2 ST93-MRSA-IV (Queensland MRSA)

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

8.3.3 ST8-MRSA-IV (WA MRSA-12 or USA300)

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

8.3.4 “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)

Antibiogram
Urea Broth
Coagulase PCR-RFLP
CHEF

ST5-MRSA-V (WA-11)
ST59-MRSA-IV (WA-15)
ST5-MRSA-novel (WA-21)
ST45-MRSA-V (WA-23)
ST5-MRSA-V (WA-35)
ST526-MRSA-V (WA-39)
ST8-MRSA-V (unique)
ST641-MRSA-IV (unique)
ST5-MRSA-novel (unique)
ST5-MRSA-V (unique)

Antibiogram
Urea Broth
Coagulase PCR/RFLP
CHEF
Multilocus Sequence Typing
SCC_{mec} PCR

8.4 Detection of Panton-Valentine Leucocidin (PVL) Toxin Genes

The presence of the PVL determinants was detected by PCR using previously published primers (22).

9.0 SAP05 Results

881 *Staphylococcus aureus* from SAP05 were referred to the GPBTRU for epidemiological typing.

NOTE: MRSA isolates from the Northern Territory were not available for epidemiological typing.

9.1 Typing Tests Performed

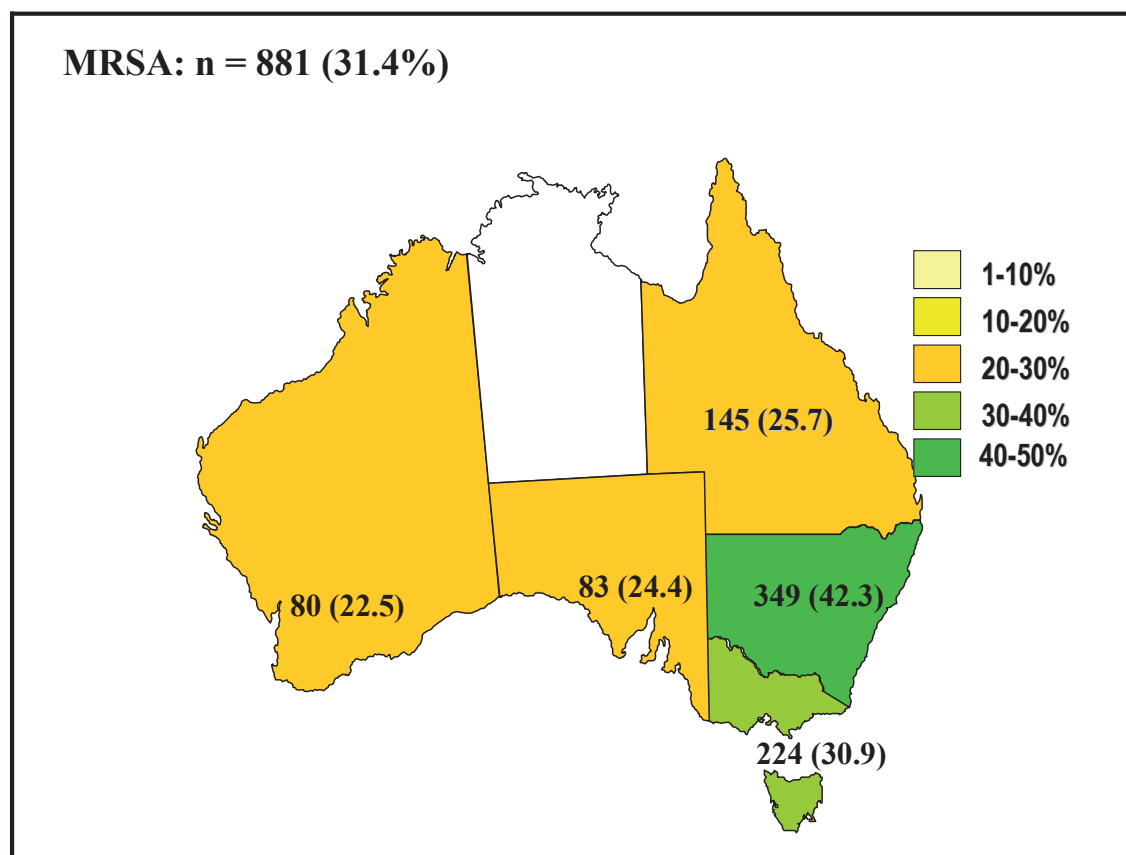
Test	N
Cefoxitin Susceptibility Testing	923
Coagulase Gene PCR-RFLP Assay	395
Resistogram	571
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	889
Urease Reaction	923
Multilocus Sequencing Typing (MLST)	22
SCC _{mec} PCR	22
Panton-Valentine leucocidin PCR	187

9.2 Regional Distribution of MRSA

9.2.1 Regional Distribution of MRSA as a Proportion of *S aureus*

Region	<i>S aureus</i>	MRSA
Australian Capital Territory (ACT)/New South Wales (NSW)	825	349 (42.3%)
Queensland (Qld)	564	145 (25.7%)
South Australia (SA)	340	83 (24.4%)
Tasmania (Tas) /Victoria (Vic)	724	224 (30.9%)
Western Australia (WA)	355	80 (22.5%)
Total	2,808	881 (31.4%)

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



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

9.2.2 Regional Distribution of EMRSA and cMRSA as a Proportion of MRSA

Region	Total MRSA	EMRSA (%)	cMRSA (%)
ACT/NSW	349	308 (88.3)	41 (11.7)
Qld	145	108 (74.5)	37 (25.5)
SA	83	52 (62.7)	31 (37.3)
Tas/Vic	224	200 (89.3)	24 (10.7)
WA	80	31 (38.8)	49 (61.2)
TOTAL	881	699 (79.3)	182 (20.7)

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

9.2.3 Regional Distribution of EMRSA and cMRSA as a Proportion of *S aureus*

Region	Total <i>S aureus</i>	Epidemic (%)	Community (%)
ACT/NSW	825	308 (37.3)	41 (5.0)
Qld	564	108 (19.1)	37 (6.6)
SA	340	52 (15.3)	31 (9.1)
Tas/Vic	724	200 (27.6)	24 (3.3)
WA	355	31 (8.7)	49 (13.8)
TOTAL	2,808	699 (24.9)	182 (6.5)

Percentage figures in parenthesis relate to the total number of *S aureus* isolates

9.3 EMRSA Clones by Institution

LAB	ST239-MRSA-III Aus 2 EMRSA	ST239-MRSA-III Aus 3 EMRSA	ST22-MRSA-IV UK EMRSA 15	ST36-MRSA-II UK EMRSA 16	ST2471-MRSA-1 UK EMRSA 17	ST5-MRSA-II NY/Japan MRSA	TOTAL
ACT/NSW (308)							
1	25		3				28
2	32		15				47
3	14	1	9				24
4	32	2	9				43
5	44	5	3				52
6	36		7				43
7	6	2	1				9
8	25	3	13				41
9	16	1	3		1		21
Qld (108)							
11	7	3	5				15
12	7	2	1				10
13	14	1	6		1		22
28	12	5	1				18
29	7		3				10
30	10	20	3				33
SA (52)							
14	7	9	4			1	21
15	2	11	10	1			24
16	1		2				3
17		3	1				4
Tas/Vic (200)							
18	4						4
19	8	33	1				42
20		1					1
21	2	5					7
22	3	30	2				35

SAP 2005: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

LAB	ST239-MRSA-III Aus 2 EMRSA	ST239-MRSA-III Aus 3 EMRSA	ST22-MRSA-IV UK EMRSA 15	ST36-MRSA-II UK EMRSA 16	ST2471-MRSA-1 UK EMRSA 17	ST5-MRSA-II NY/Japan MRSA	TOTAL
23	9	37	1				47
31	4	24	3	1			32
32	2	24	6				32
WA (31)							
24	1						1
25	3		8				11
26		1	9		1		11
27			8				8
TOTAL	333	223	137	2	2	2	699

9.4 cMRSA Clones by Institution

LAB	ST1 MRSA IV (WA1)	ST78 MRSA IV (WA2)	ST5 MRSA IV (WA3)	ST45 MRSA V (WA4)	ST8 MRSA IV (WA5)	ST5 MRSA V (WA11)	ST8 MRSA IV (WA12)	ST93 MRSA IV (QLD)	ST30 MRSA IV (WSPP)	ST59 MRSA IV (WA15)	ST5 MRSA novel (WA21)	ST45 MRSA IV (WA23)	ST5 MRSA V (WA35)	ST526 MRSA V (WA39)	ST8 MRSA V	ST641 MRSA IV	ST5 MRSA nov	ST5 MRSA V	TOTAL
ACT/NSW (41)																			
1								2											2
2						1													1
3	3	1	1					1	1										7
4	1	1																	2
5	1							2	1										4
6	4							4											8
7	1																		1
8	1							1					1						3
9	4	2						5	1		1								13
QLD (37)																			
11	1	1						2											4
12	2		1					4						1					8
13	2		2																4
28	2				1				1	1									5
29	2		5					1	5										13
30	2						1												3
SA (31)																			
14	6		1	1															8
15	3		1												1				5
16	8		2						2										12
17	1		1					3	1										6
Tas/Vic (24)																			
18																			0
19	1		1									1							3
20	4				1														5
21	2							1											3

SAP 2005: HOSPITAL MRSA EPIDEMIOLOGY AND TYPING REPORT

LAB	ST1 MRSA IV (WA1)	ST78 MRSA IV (WA2)	ST5 MRSA IV (WA3)	ST45 MRSA V (WA4)	ST8 MRSA IV (WA5)	ST5 MRSA V (WA11)	ST8 MRSA IV (WA12)	ST93 MRSA IV (QLD)	ST30 MRSA IV (WSP)	ST59 MRSA IV (WA15)	ST5 MRSA novel (WA21)	ST45 MRSA IV (WA23)	ST5 MRSA V (WA35)	ST526 MRSA V (WA39)	ST8 MRSA V	ST641 MRSA IV	ST5 MRSA nov	ST5 MRSA V	TOTAL
22		1	1		1					2			1						6
23	1											1					1	1	4
31												1				1			2
32								1											1
WA (49)																			
24	4	3	2		1														10
25	8	4		3															15
26	6	2	2	1															11
27	6	5	1			1													13
Σ	76	20	21	5	4	2	1	27	12	3	1	3	2	1	1	1	1	1	182

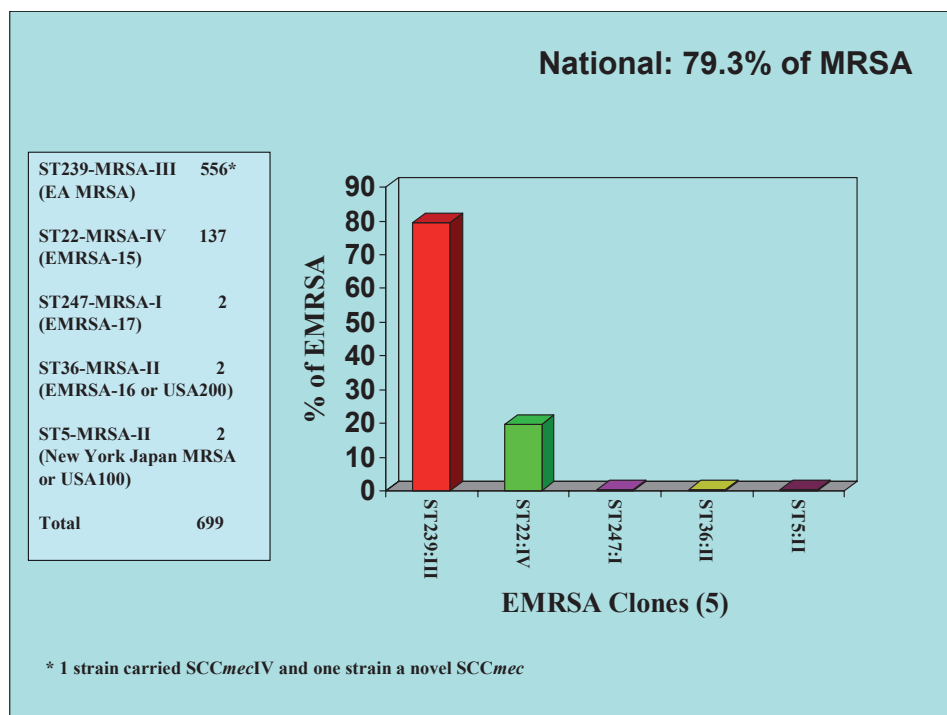
9.5 EMRSA CLONES

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

In SAP 2005 five international EMRSA clones (699 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST239-MRSA-III	Aus -2 and Aus -3 EMRSA or EA MRSA	556 (79.5)
ST22-MRSA-IV	EMRSA-15	137 (19.6)
ST36-MRSA-II	EMRSA-16 or USA200	2 (0.3)
ST247-MRSA-I	EMRSA-17	2 (0.3)
ST5-MRSA-II	New York Japan MRSA or USA100	2 (0.3)
TOTAL		699

Percentage figures in parenthesis relate to epidemic MRSA isolates



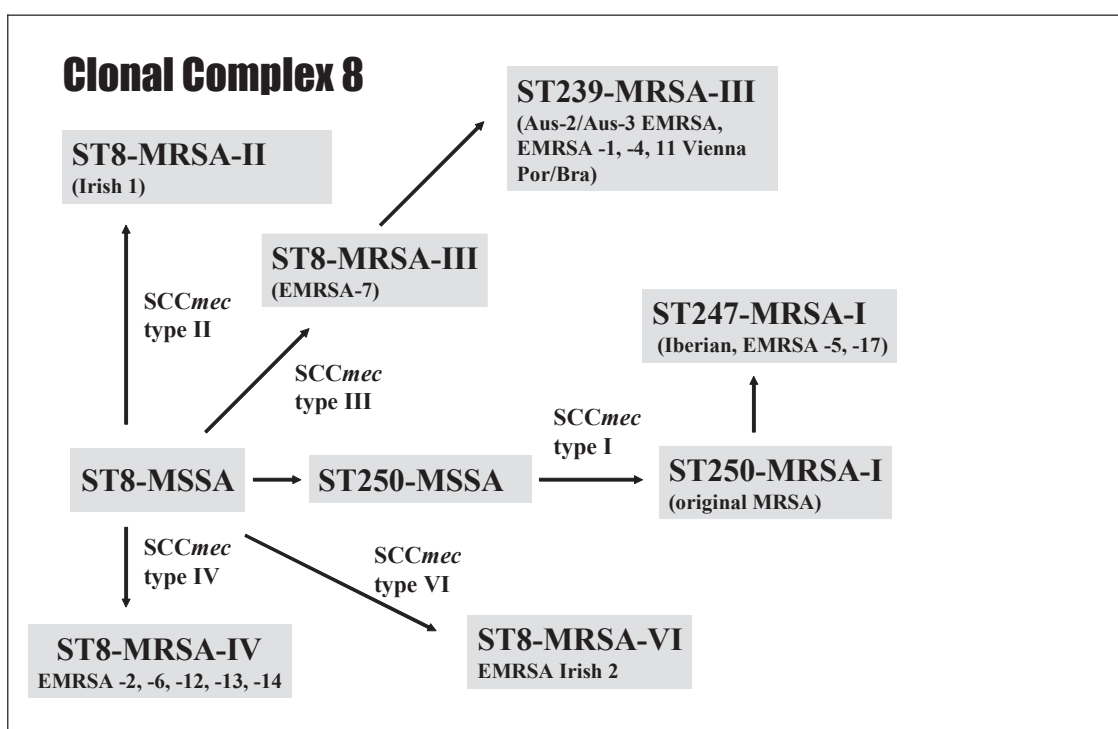
Percentage figures relate to epidemic MRSA isolates

9.5.1 ST239-MRSA-III

In Australia ST239-MRSA-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. 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 “EMRSA-1”, the “Portuguese/Brazilian” clone or the “Vienna” clone. SCC*mec* type III is a health care associated SCC*mec* which has several antibiotic resistance genes, transposons and integrated plasmids. Hence ST239-MRSA-III is typically resistant to multiple antibiotics including erythromycin, tetracycline, trimethoprim, ciprofloxacin and gentamicin.

ST239 belongs to clonal complex 8. Within this clonal complex there are three other major EMRSA clones: ST8-MRSA-II (Irish-1 EMRSA), ST8-MRSA-IV (EMRSA – 2, –6, –12, –13 and –14) and ST247-MRSA-I (Iberian or EMRSA-17). The original MRSA clone ST250-MRSA-I, and ST8-MRSA-VI (Irish-2 EMRSA) are also located within this clonal complex.

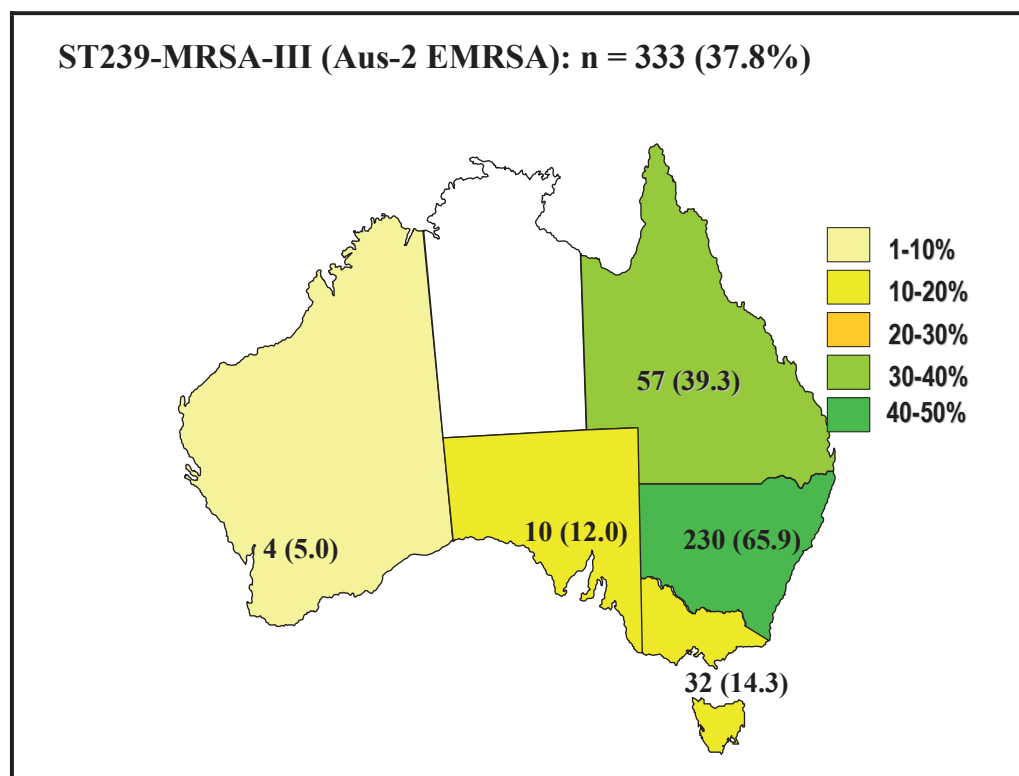


9.5.1.1 ST239-MRSA-III Phenotypic Characteristics

Antibiogram:	Aus-2 EMRSA (n = 333)	Aus-3 EMRSA (n = 223)
Erythromycin ^R	99%	99%
Tetracycline ^R	97%	90%
Trimethoprim ^R	95%	98%
Gentamicin ^R	94%	98%
Ciprofloxacin ^R	94%	99%
Fusidic Acid ^R	1%	8%
Rifampicin ^R	3%	15%
Mupirocin ^R	2%	0%
Resistogram:		
Mercuric Acetate ^R	< 1%	> 99%
Mercuric Chloride ^R	< 1%	> 99%
Urease:	Positive	Positive

9.5.1.2 ST239-MRSA-III Epidemiology

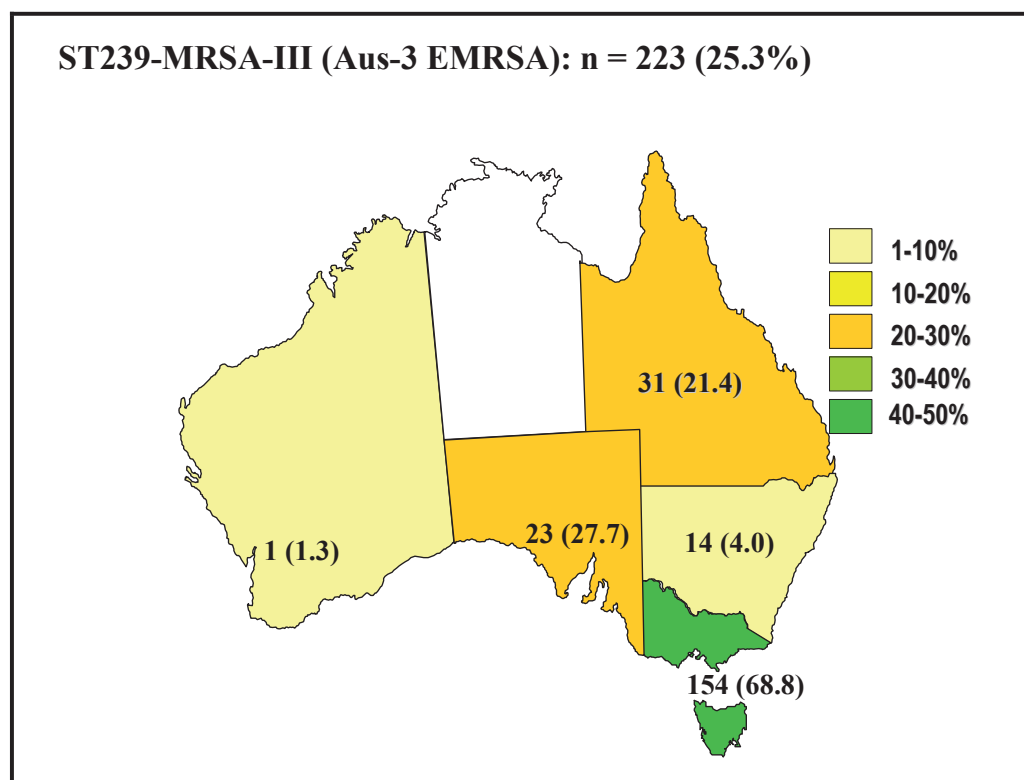
9.5.1.2.1 Aus-2 EMRSA



Percentage figures in parenthesis relate to total MRSA isolates

333 (37.8%) MRSA isolated in SAP 2005 were characterised as Aus-2 EMRSA which accounted for 47.6% of EMRSA. Although reported throughout Australia, Aus-2 EMRSA was the dominant MRSA in the ACT/NSW region.

9.5.1.2.2 Aus-3 EMRSA



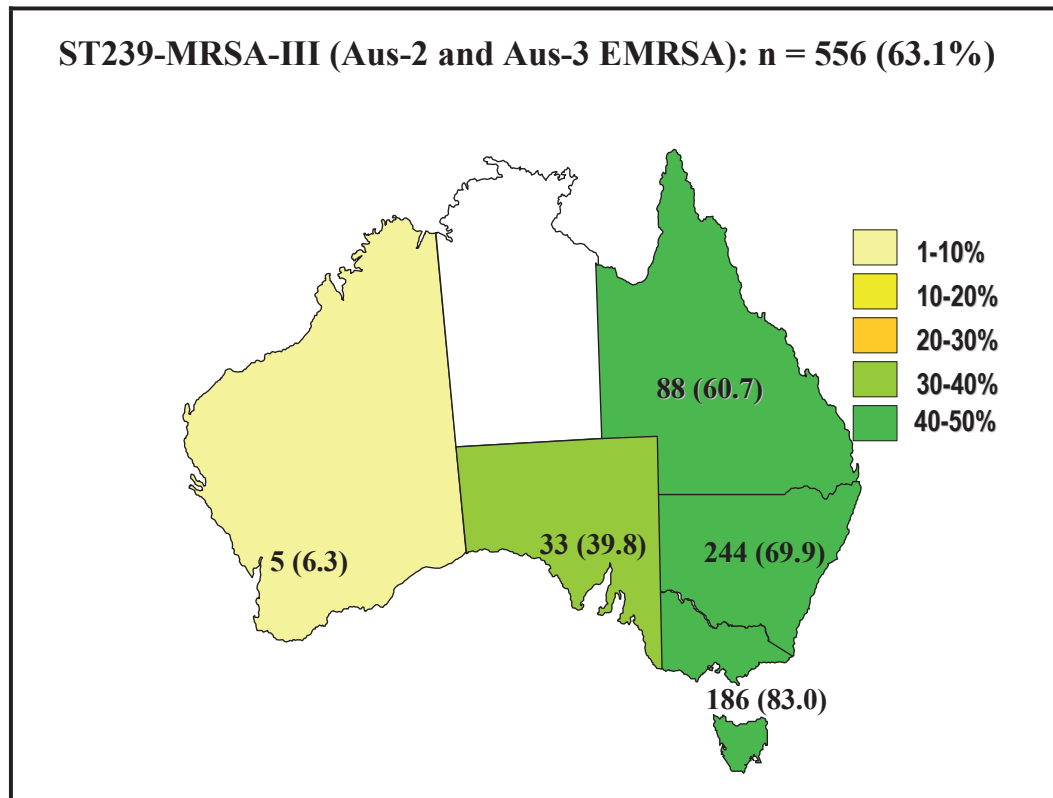
Percentage figures in parenthesis relate to total MRSA isolates

223 (25.3%) MRSA isolated in SAP 2005 were characterised as Aus-3 EMRSA which accounted for 31.9% of EMRSA. Although reported throughout Australia, Aus-3 EMRSA was the dominant MRSA clone isolated in the Tas/Vic region.

9.5.1.2.3 Aus-2 and Aus-3 EMRSA

556 (63.1%) MRSA isolated in SAP 2005 were characterised as ST239-MRSA-III (either Aus-2 or Aus-3) which accounted for 79.5% of EMRSA isolated.

ST239-MRSA-III was the dominant MRSA clone in most regions of Australia including Qld, NSW/ACT, Tas/Vic and SA. In WA however only 6.3% of MRSA were characterized as ST239-MRSA-III.

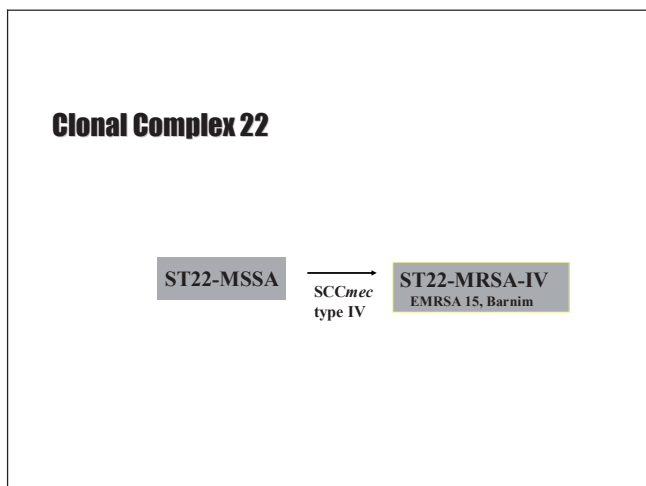


Percentage figures in parenthesis relate to total MRSA isolates

9.5.2 ST22-MRSA-IV

Also known as “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 (UK), 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.

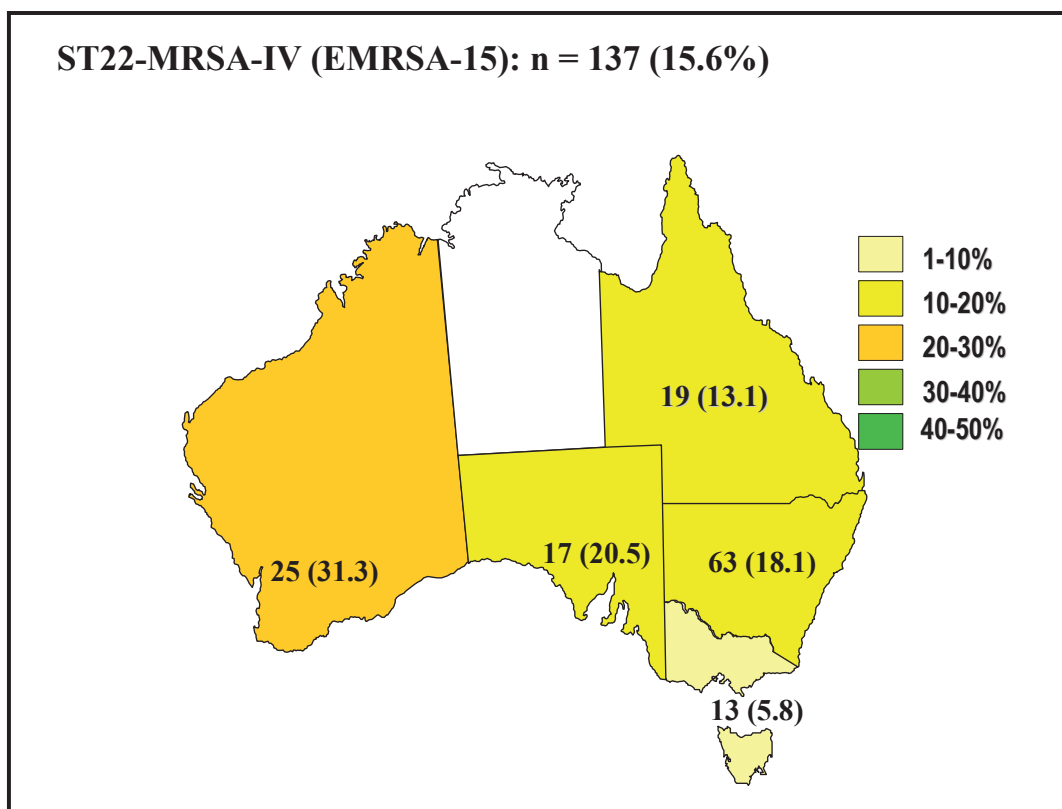
ST22 belongs to clonal complex 22. Although it is considered to be a health care associated MRSA it has acquired the type IV community *SCC_{mec}* which lacks transposons, integrated plasmids and other antibiotic resistance genes. Clonal complex 22 has a single epidemic clone that is believed to have evolved from ST22 MSSA.



9.5.2.1 ST22-MRSA-IV Phenotypic Characteristics

Antibiogram:	Erythromycin ^R (72%) Fusidic Acid ^R (0%) Trimethoprim ^R (1%) Mupirocin ^R (3%)	Ciprofloxacin ^R (100%) Tetracycline ^R (<1%) Rifampicin ^R (0%) Gentamicin ^R (2%)
Urease:	Negative	

9.5.2.2 ST22-MRSA-IV Epidemiology



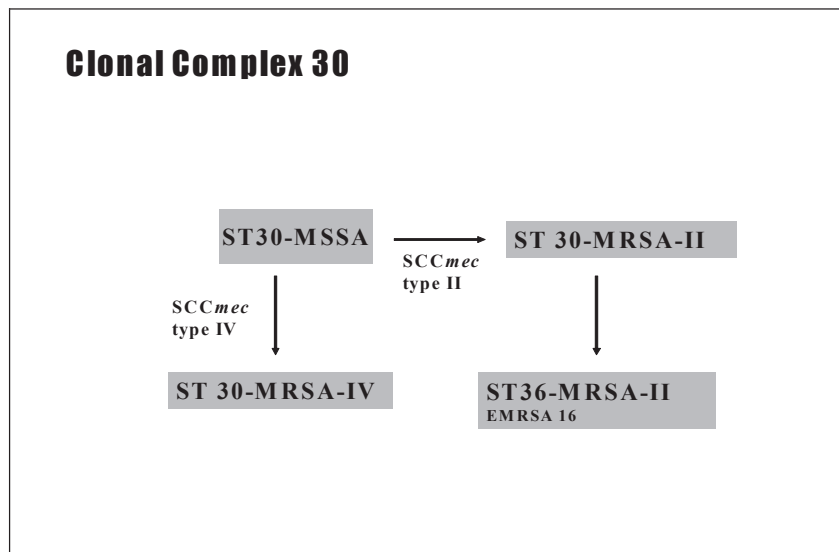
Percentage figures in parenthesis relate to total MRSA isolates

137 (15.6%) MRSA isolated in SAP 2005 were characterised as ST22-MRSA-IV which accounted for 19.6% of EMRSA isolated. This clone was identified throughout Australia.

9.5.3 ST36-MRSA-II

Also known as “EMRSA-16” or “USA200”, ST36-MRSA-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-MRSA-II has been isolated in several European countries including Denmark, Finland, Sweden and Turkey, and in the USA. ST36-MRSA-II is resistant to ciprofloxacin, erythromycin and variably resistant to the aminoglycosides. It carries staphylococcal enterotoxin A, G and I and TSST-1.

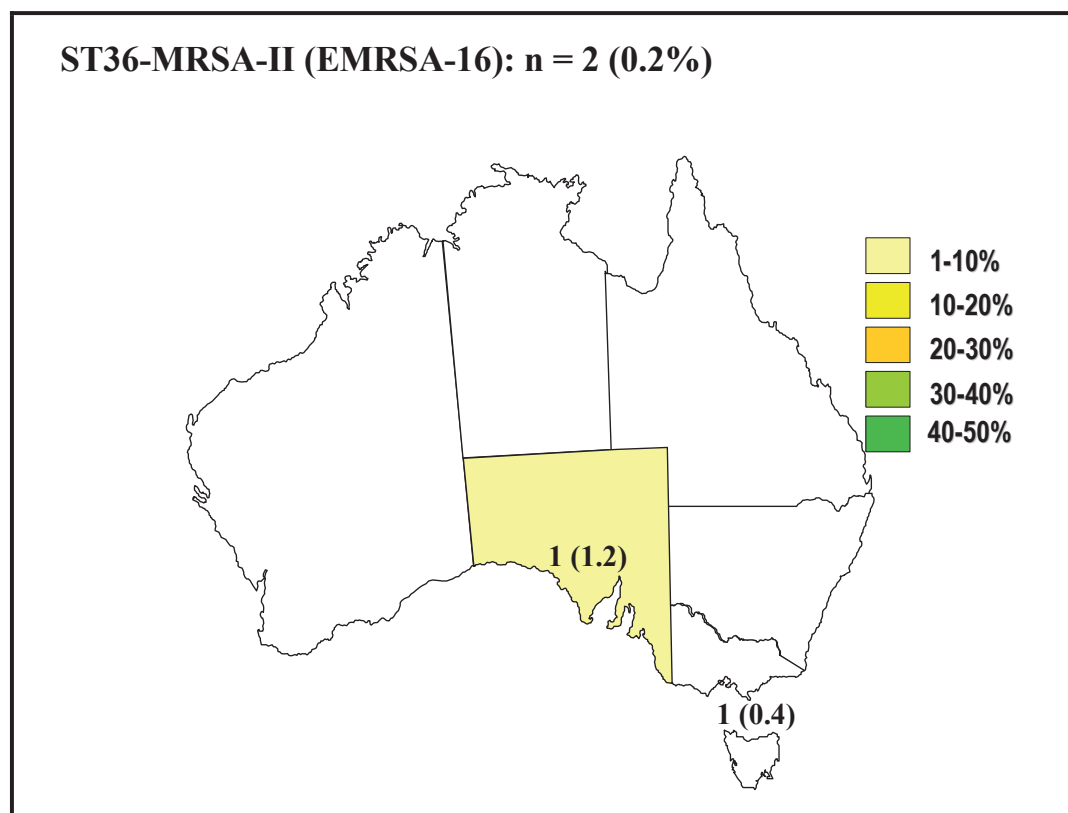
ST36 belongs to clonal complex 30 and is thought to have evolved from ST30-MRSA-II. ST36-MRSA-II is the only EMRSA in this complex. SCCmec type II is a health care associated SCCmec which carries *aadD*, the gene for tobramycin and kanamycin resistance, and *Tn554* which carries the erythromycin resistance gene *ermA*.



9.5.3.1 ST36-MRSA-II Phenotypic Characteristics

Antibiogram:	Erythromycin ^R Mupirocin ^R Fusidic Acid ^S Trimethoprim ^S	Ciprofloxacin ^R (Gentamicin ^R) Tetracycline ^S Rifampicin ^S
Urease:	Positive	

9.5.3.2 Epidemiology



Percentage figures in parenthesis relate to total MRSA isolates

Two isolates of ST36-MRSA-II were reported in SAP 2005: single isolates in SA and the Vic/Tas region.

9.5.4 ST247-MRSA-I

Also known as “EMRSA-17”, ST247-MRSA-I was first reported in an extensive outbreak in a hospital on the south coast of England in 2000. Multiresistant, the strain was phenotypically similar to a strain seen in several hospitals in that region since 1996. The strain is urease positive and typically resistant to multiple antibiotics including methicillin, ciprofloxacin, erythromycin, fusidic acid, rifampicin, gentamicin, kanamycin, neomycin, streptomycin and tetracycline, with or without high- or low-level mupirocin resistance. Borderline resistance to teicoplanin has also been reported. The strain usually carries the toxin *sea* gene and may carry *seg*, *sei* and *tst*.

ST247 belongs to clonal complex 8 and is thought to have evolved from the original MRSA clone “ST250-MRSA-I” first isolated in the early 1960s. SCC_{mec} type I is a health care associated which has several antibiotic resistance genes, transposons and integrated plasmids.

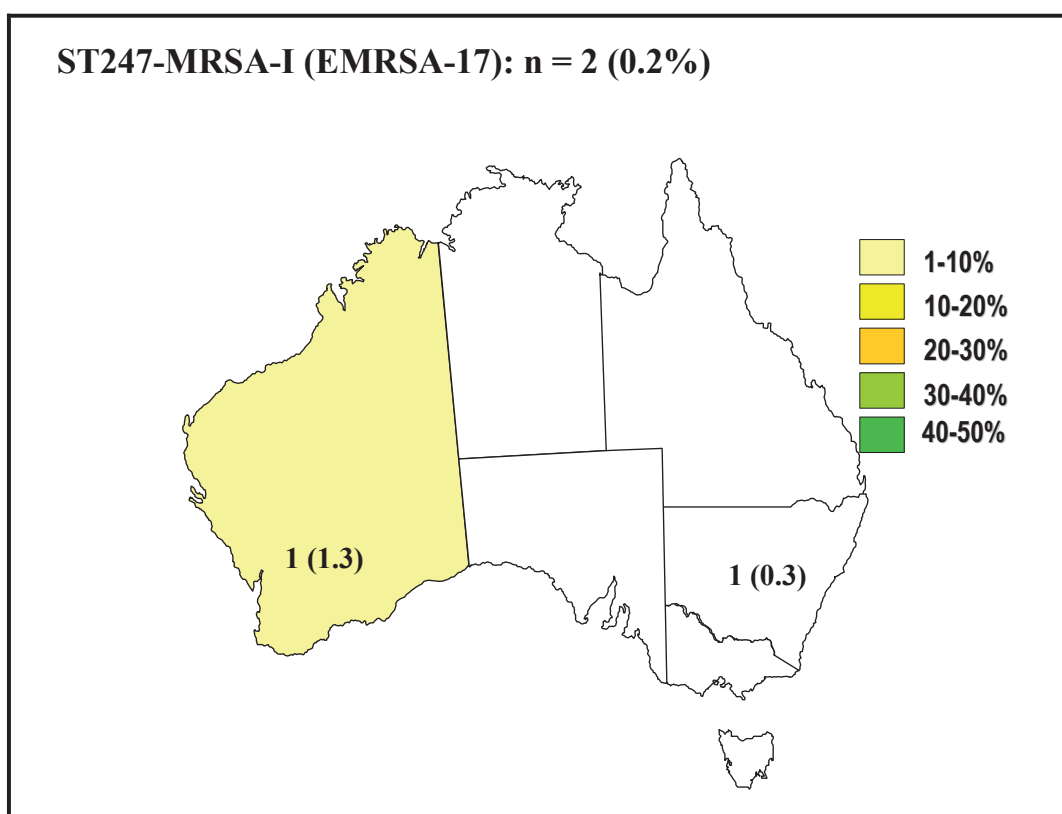
9.5.4.1 ST247-MRA-I Phenotypic Characteristics

Antibiogram: Erythromycin^R Ciprofloxacin^R
 Mupirocin^R Gentamicin^R
 Tetracycline^R Rifampicin^R
 (Fusidic Acid^R)

 Trimethoprim^S

Urease: Positive

9.5.4.2 ST247-MRSA-I Epidemiology

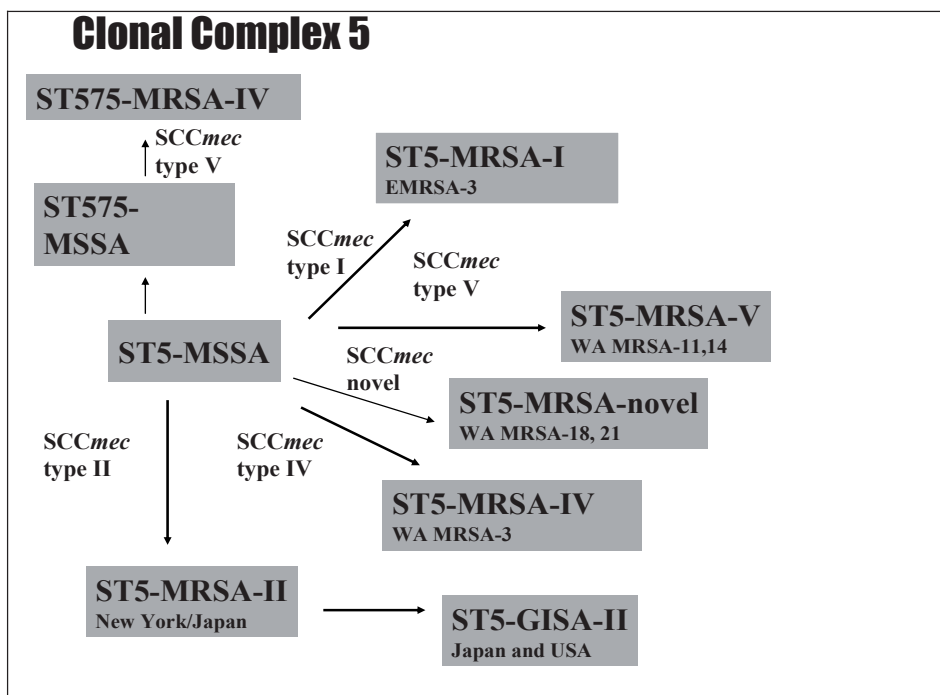


Percentage figures in parenthesis relate to total MRSA isolates

Two isolates of ST247-MRSA-I were reported in SAP 2005: single isolates in WA and in the ACT/NSW region.

9.5.5 ST5-MRSA-II

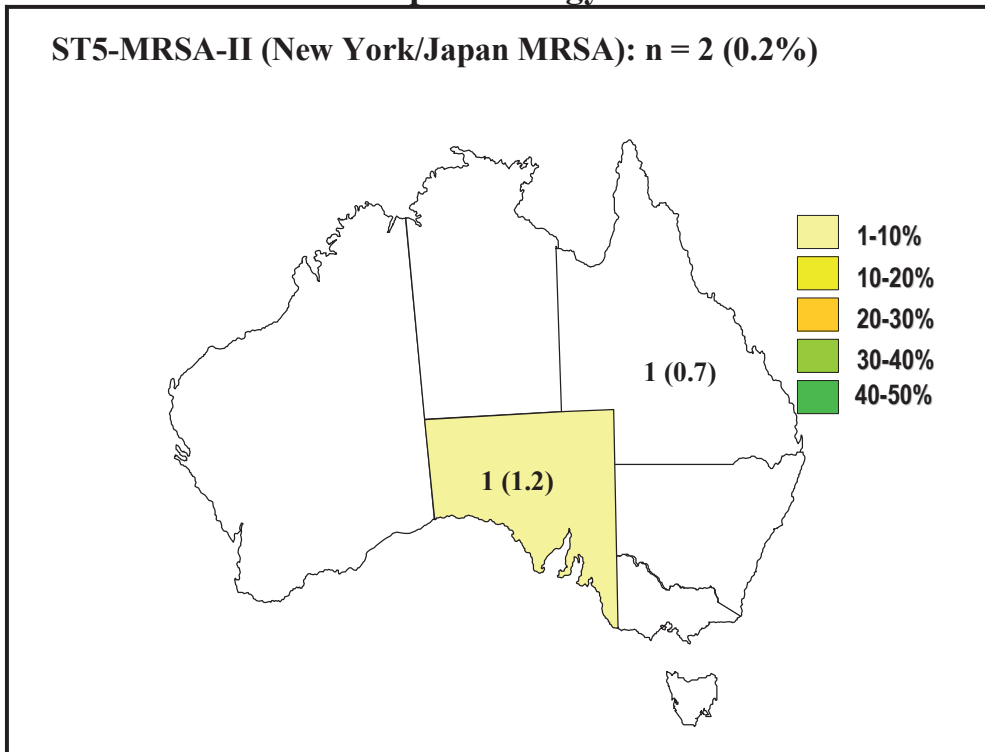
Also known as “New York/Japan MRSA” or “USA100 MRSA”, ST5-MRSA-II belongs to clonal complex 8. This clonal complex has two EMRSA clones, ST5-MRSA-II, and ST5MRSA-I also known as “EMRSA-3”. The original hVISA, ST5-GISA-II, is thought to have evolved from the New York/Japan EMRSA clone.



9.5.5.1 ST5-MRSA-II Phenotypic Characteristics

Antibiogram:	(Erythromycin ^R) (Fusidic Acid ^R)	(Ciprofloxacin ^R)
	Mupirocin ^S Tetracycline ^S Trimethoprim ^S	Gentamicin ^S Rifampicin ^S
Urease:	Positive	

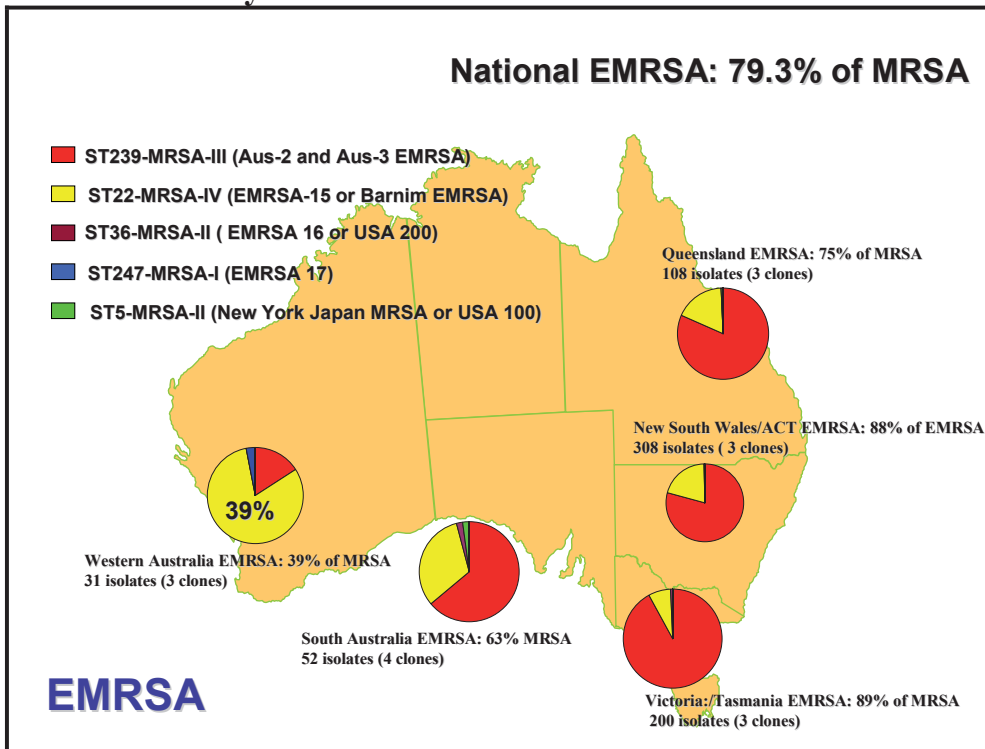
9.5.5.2 ST5-MRSA-II Epidemiology



Percentage figures in parenthesis relate to total MRSA isolates

Two isolates of ST5-MRSA-II were reported in SAP 2005: single isolates in SA and Qld.

9.5.6 Summary of EMRSA Characterised



Percentage figures in parenthesis relate to total MRSA isolates

9.6 cMRSA

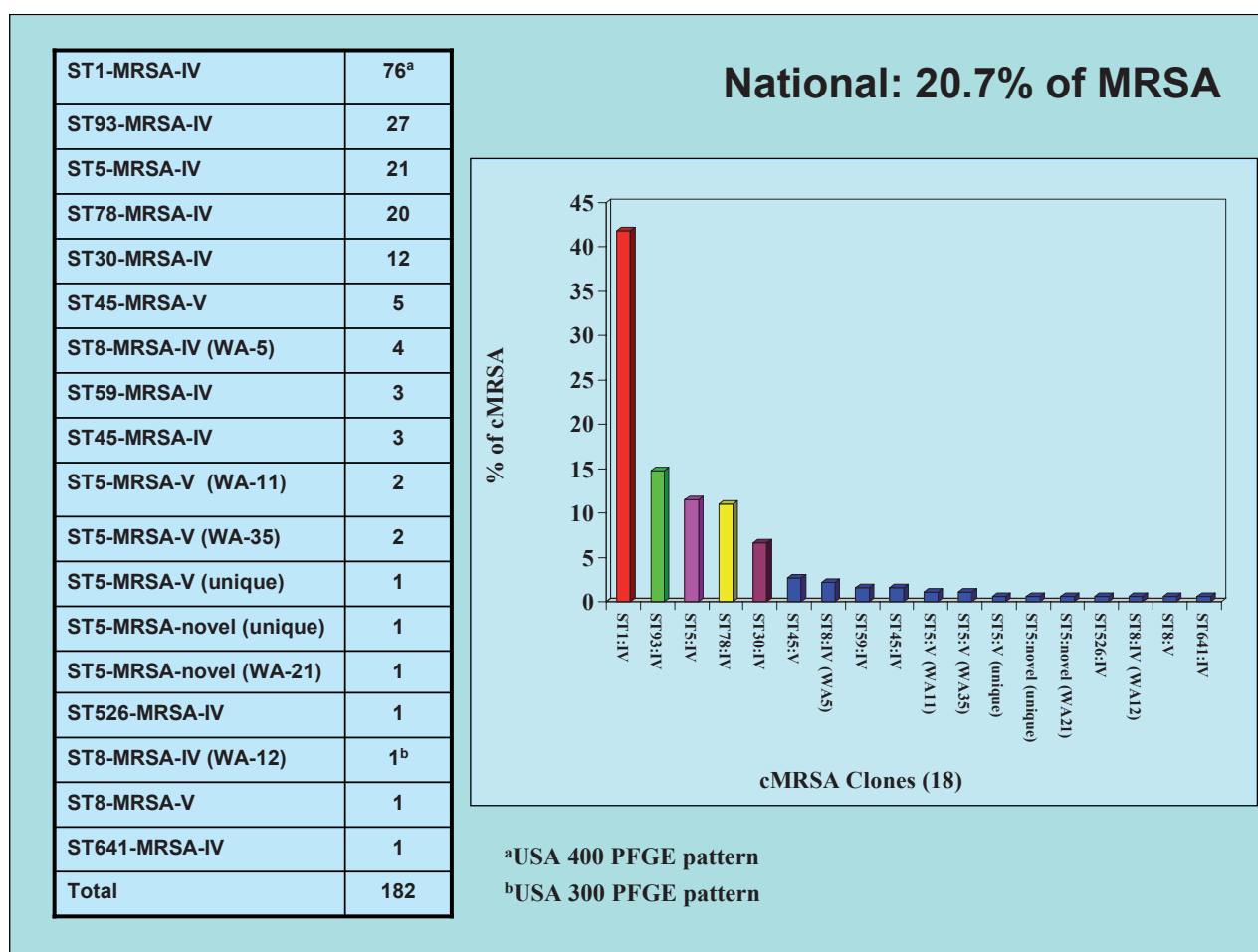
cMRSA was first reported in Australia in the early 1980s in aboriginal communities living in the Kimberley region of Western Australia (WA). Known collectively as “WA MRSA” they were subsequently isolated in other remote communities in WA, South Australia and Northern Territory. These strains are usually 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 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 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.

In SAP 2005 eighteen community MRSA clones (fifteen MLST/SCC*mec* clone types) were identified.

Clone	Clonal Complex	Alternative Name	n (%)
ST1-MRSA-IV	1	WA MRSA -1	76 (41.8)
ST93-MRSA-IV	Singleton	Queensland MRSA	27 (14.8)
ST5-MRSA-IV	5	WA MRSA – 3	21 (11.5)
ST78-MRSA-IV	78	WA MRSA – 2	20 (11.0)
ST30-MRSA-IV	30	WSPP MRSA	12 (6.6)
ST45-MRSA-V	45	WA MRSA – 4	5 (2.7)
ST8-MRSA-IV	8	WA MRSA – 5	4 (2.2)
ST59-MRSA-IV	59	WA MRSA – 15	3 (1.6)
ST45-MRSA-IV	45	WA MRSA – 23	3 (1.6)
ST5-MRSA-V	5	WA MRSA-11	2 (1.1)
ST5-MRSA-V	5	WA MRSA-35	2 (1.1)
ST5-MRSA-V	5		1 (0.6)
ST5-MRSA-novel	5		1 (0.6)

Clone	Clonal Complex	Alternative Name	n (%)
ST5-MRSA-novel	5	WA MRSA-21	1 (0.6)
ST526-MRSA-IV	5	WA MRSA-39	1 (0.6)
ST641-MRSA-IV	5		1 (0.6)
ST8-MRSA-IV	8	WA MRSA-12	1 (0.6)
ST8-MRSA-V	8		1 (0.6)
Total			182

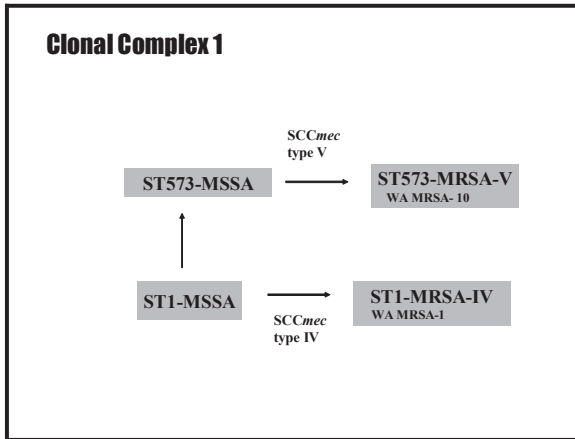
Percentage figures in parenthesis relate to community MRSA isolates



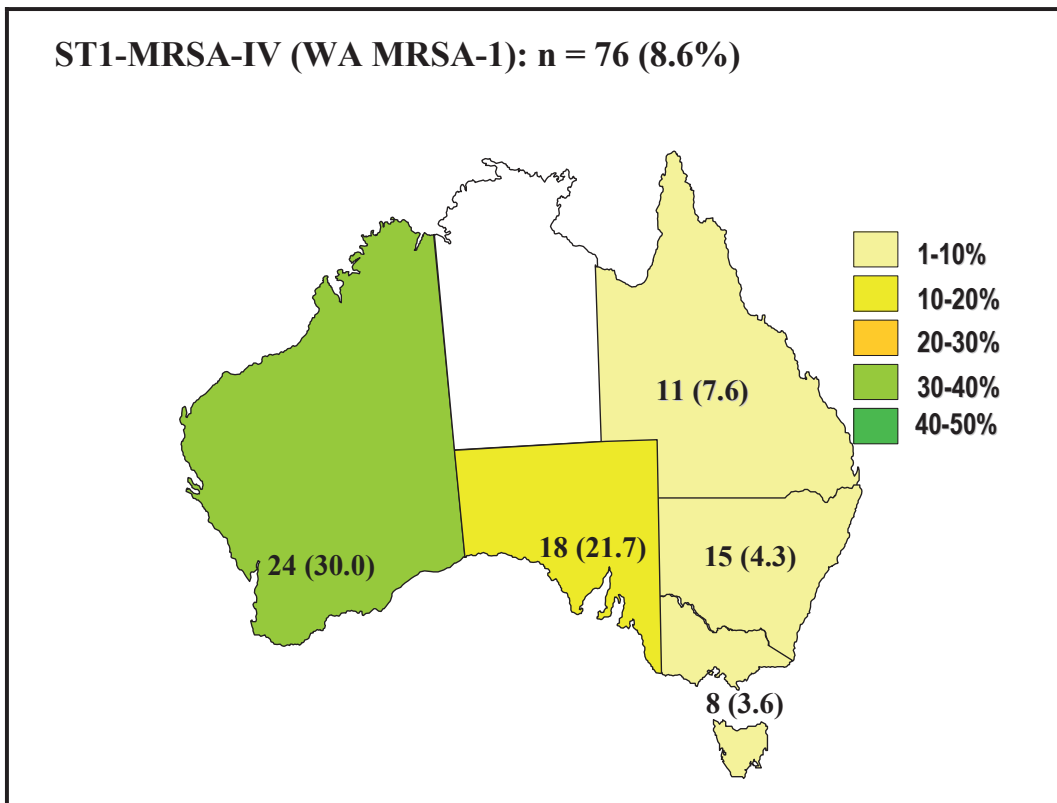
Percentage figures relate to community MRSA isolates

9.6 ST1-MRSA-IV

Also known as “WA MRSA-1”, ST1-MRSA-IV forms part of clonal complex 1. Within this complex two cMRSA clones have been identified having acquired *SCCmec* IV or V. ST1-MRSA-IV has been reported in several European countries and in the USA. The CHEF pattern of WA MRSA-1 cannot be differentiated from USA400, which is also ST1-MRSA-IV. However unlike USA400, WA MRSA-1 is generally PVL negative.



9.6.1.1. ST1-MRSA-IV Epidemiology



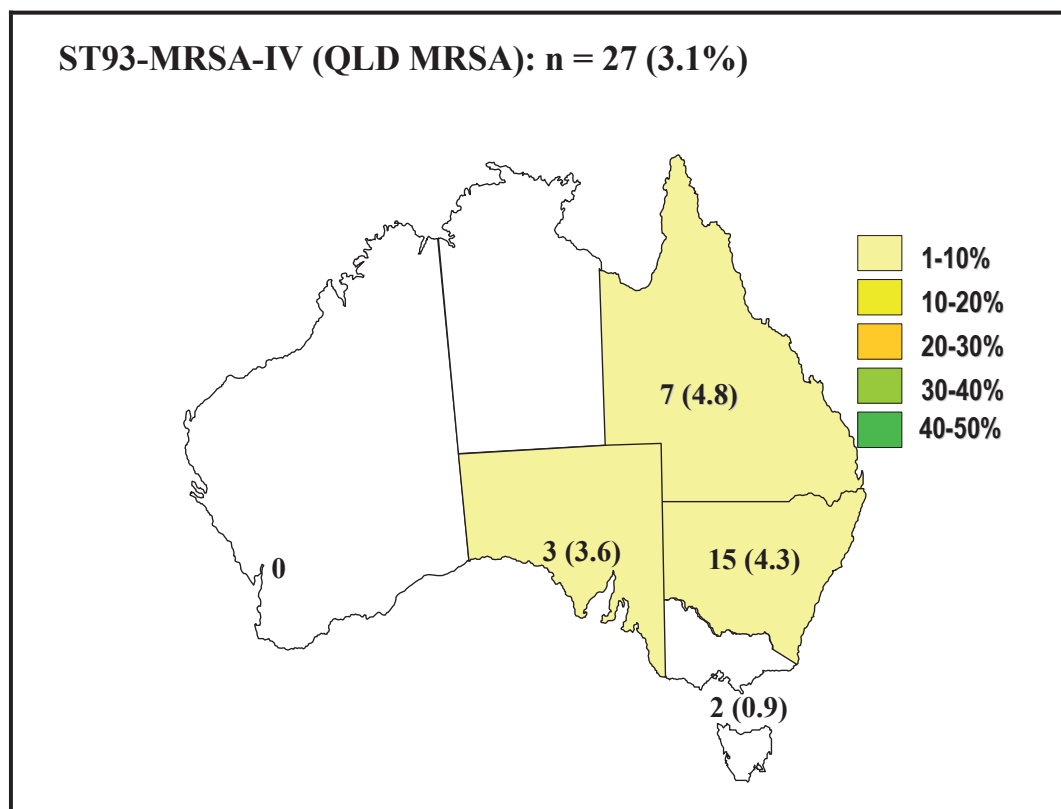
Percentage figures in parenthesis relate to total MRSA isolates

ST1-MRSA-IV is the most frequently isolated cMRSA in Australia. 76 (8.6%) MRSA isolated in SAP 2005 were characterised as ST1-MRSA-IV which accounted for 41.8% of cMRSA.

Although reported in all Australian regions this clone was predominantly isolated in WA and SA (30.0% and 21.7% of MRSA respectively).

9.6.2 ST93-MRSA-IV

Also known as the “Queensland MRSA” clone, ST93-MRSA-is a singleton (ie does not form part of a clonal complex) and was first reported in Queensland (7). ST93-MRSA-IV is PVL positive producing, a toxin that has been associated with virulence and cMRSA isolated outside Australia.



Percentage figures in parenthesis relate to total MRSA isolates

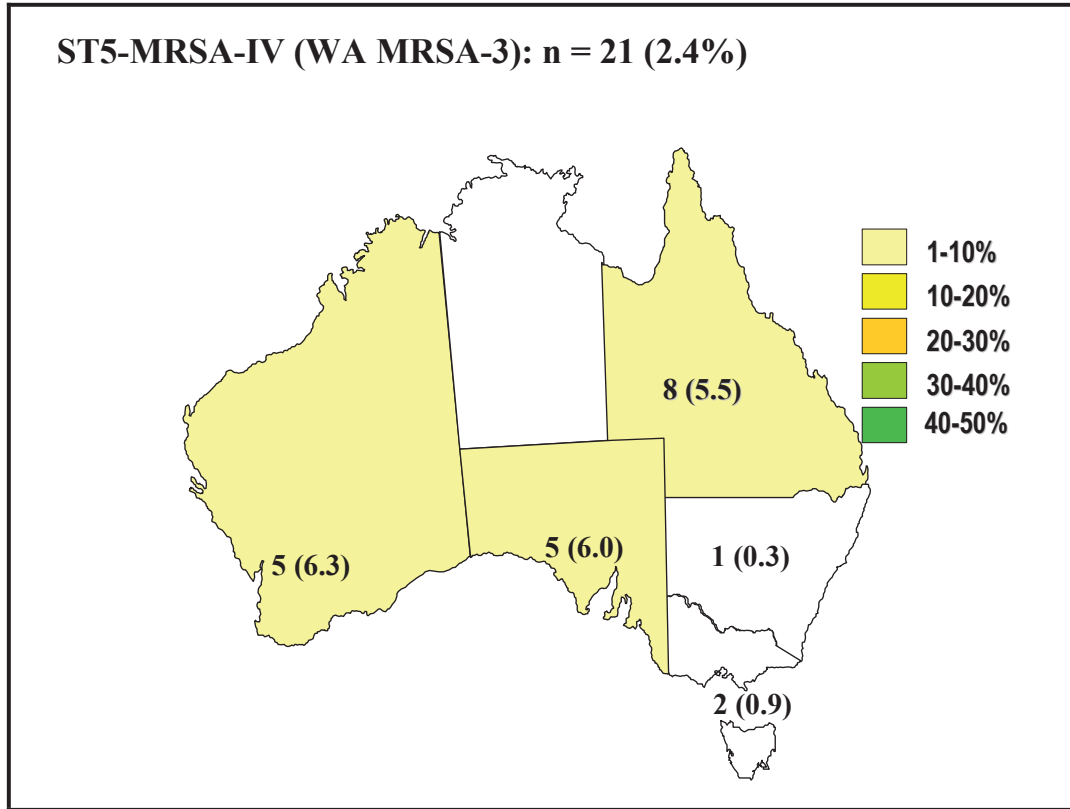
9.6.2.1 ST93-MRSA-IV Epidemiology

27 (3.1%) MRSA isolated in SAP 2005 were characterised as ST93-MRSA-IV which accounted for 14.8% of cMRSA. ST93-MRSA-IV was isolated in most areas of Australia.

9.6.3 ST5-MRSA-IV

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

9.6.3.1 ST5-MRSA-IV Epidemiology

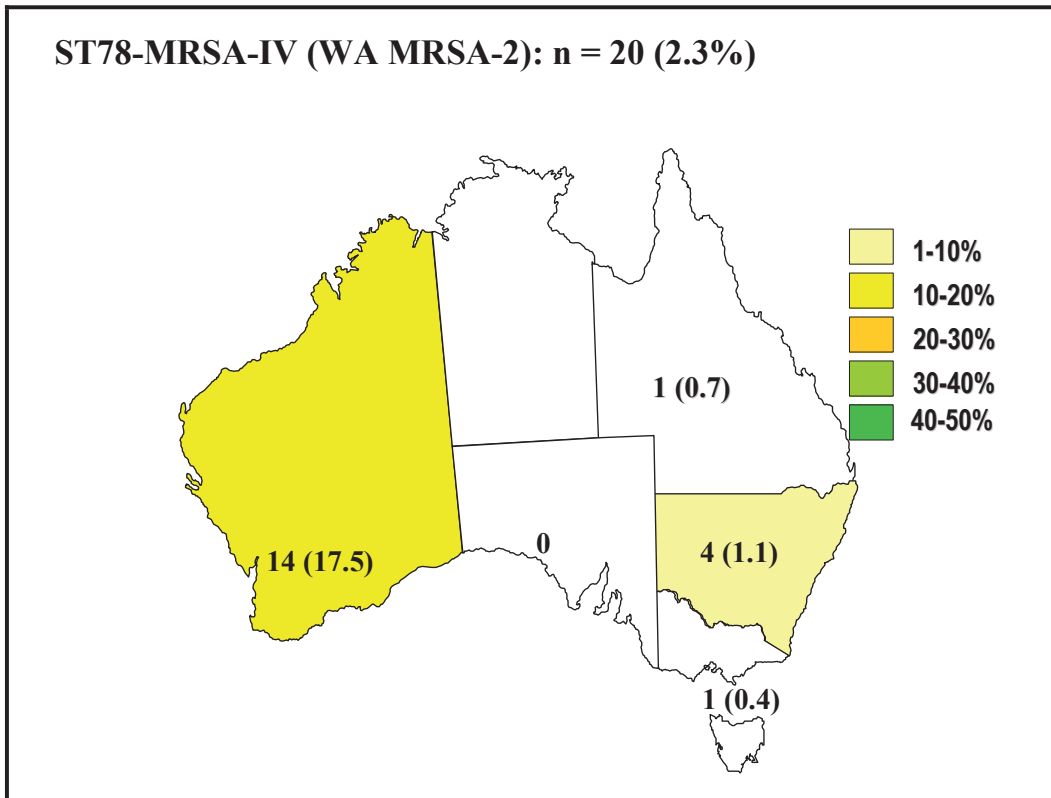


21 (2.4%) MRSA isolated in SAP 2005 were characterised as ST5-MRSA-IV which accounted for 11.5% of cMRSA. ST5-MRSA-IV was predominately isolated in the WA, SA and Qld (6.3%, 6.0% and 5.5% of MRSA respectively).

9.6.4 ST78-MRSA-IV

Also known as “WA MRSA-2”, ST78-MRSA-IV forms part of clonal complex 78. Within this complex several cMRSA clones have been identified including ST128, ST255 and ST257. Clonal complex 78 is a small clonal complex that includes strains from Australia, Europe and Japan.

9.6.4.1 ST78-MRSA-IV Epidemiology



Percentage figures in parenthesis relate to total MRSA isolates

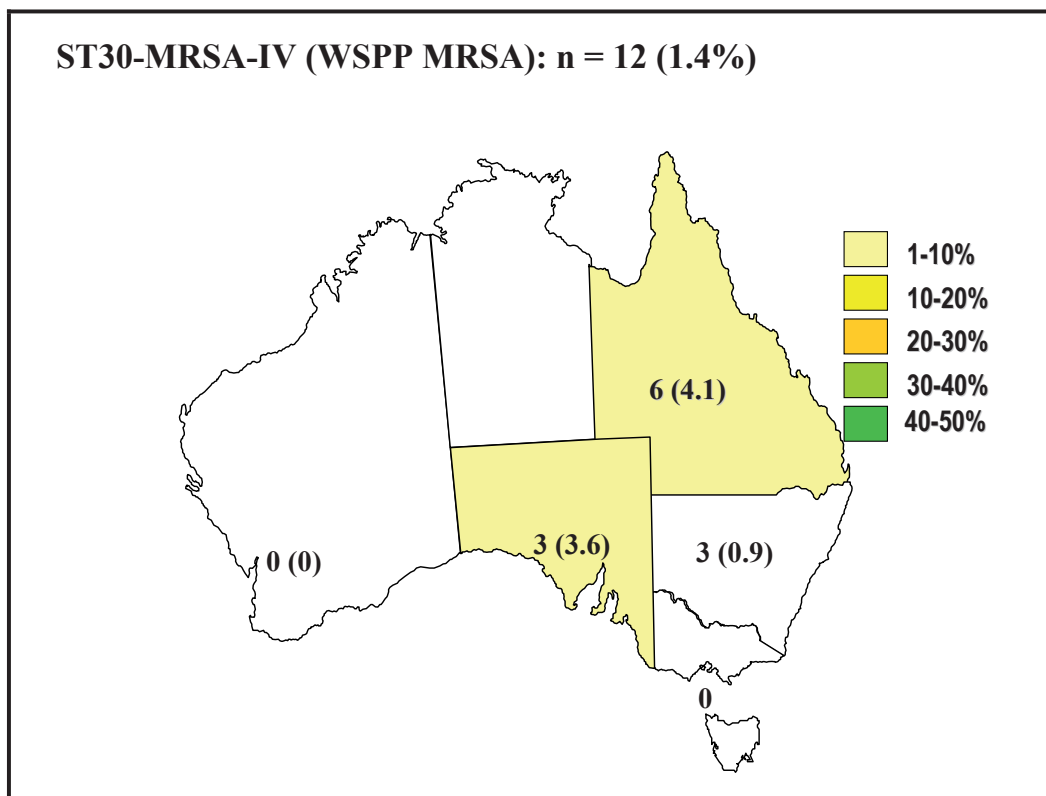
20 (2.3%) MRSA isolated in SAP 2005 were characterised as ST78-MRSA-IV which accounted for 11.0% of cMRSA. ST78-MRSA-IV was predominately isolated in WA (17.5% of MRSA).

9.6.5 ST30-MRSA-IV

Also known as “WSPP MRSA”, ST30-MRSA-IV forms part of clonal complex 30 which includes ST36-MRSA-II (UK EMRSA-16). ST30-MRSA-IV was originally described in Polynesians living in New Zealand and the Pacific islands and is PVL toxin positive.

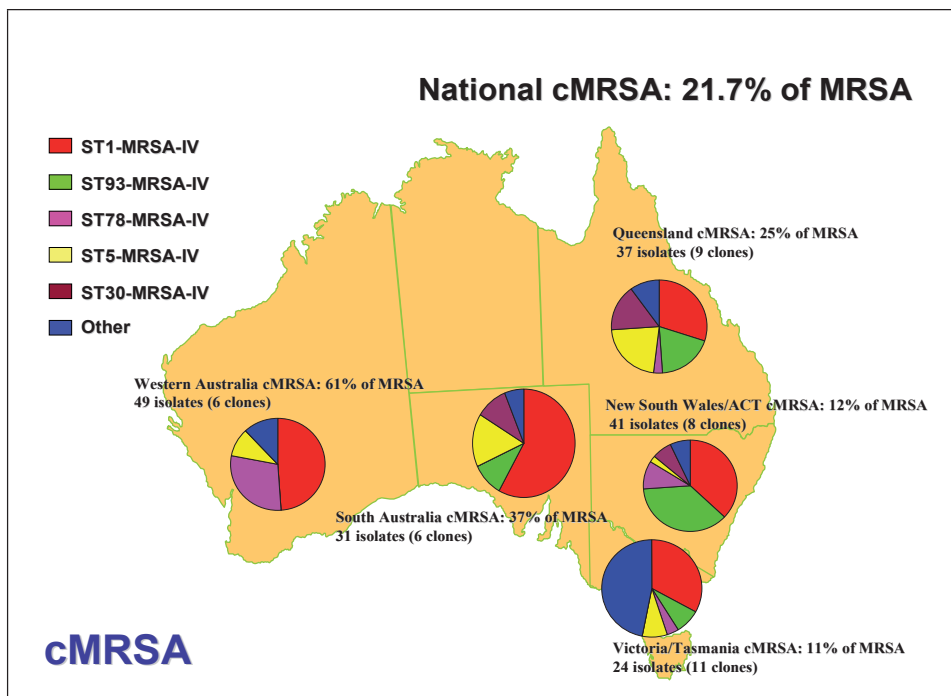
9.6.5.1 ST30-MRSA-IV Epidemiology

12 (1.4%) MRSA isolated in SAP 2005 were characterised as ST30-MRSA-IV accounting for 6.6% of cMRSA. Strains of ST30-MRSA-IV were isolated in SA, Qld and NSW/ACT.



Percentage figures in parenthesis relate to total MRSA isolates

9.6.6 Summary of cMRSA Characterised



9.7 Panton-Valentine Leucocidin (PVL) Toxin

Clone	Positive	Negative	Total
ST1-MRSA-IV	3	73	76
ST93-MRSA-IV	26	1	27
ST5-MRSA-IV	0	21	21
ST78-MRSA-IV	0	20	20
ST30-MRSA-IV	11	1	12
ST45-MRSA-V	0	5	5
ST8-MRSA-IV	0	4	4
ST59-MRSA-IV	0	3	3
ST45-MRSA-IV	0	3	3
ST5-MRSA-V	0	2	2
ST5-MRSA-V	0	2	2
ST8-MRSA-IV ^a	1	0	1
ST8-MRSA-V	0	1	1
ST641-MRSA-IV	0	1	1
ST5-MRSA-novel	0	1	1
ST5-MRSA-V	0	1	1
ST5-MRSA-novel	0	1	1
ST526-MRSA-IV	0	1	1
Total	41 (22.5)	141 (77.5)	182

^aWA MRSA-12 (USA300)

9.7.1 Panton-Valentine Leucocidin (PVL) Toxin: Regional Distribution

Region	cMRSA n	ST1 IV	ST93 IV	ST5 IV	ST78 IV	ST30 IV	ST45 V	ST8 IV	59 IV	45 IV	5 V	5 V	5 V	8 V	641 IV	5 novel	526 IV	TOTAL n (%)
ACT/NSW	41	2	14			3												19 (46.3)
Qld	37	1	7			6		1										15 (40.5)
SA	31		3			2												5 (16.1)
Tas/Vic	24		2															2 (8.3)
WA	49																	0
Total	182	3	26	0	0	11	0	1	0	0	0	0	0	0	0	0	0	41 (22.5)

^aWA MRSA-12 (USA300)

9.8 cMRSA Antibiogram

	ST1 IV	ST93 IV	ST5 IV	ST78 IV	ST30 IV	ST45 V	ST8 IV	59 IV	45 IV	5 V	5 V	8 IV ^a	8 V	641 IV	5 novel	5 V	5 novel	526 IV	TOTAL
Ox ^R	36	27	14	1	12	4		1					1	1			1		98
One non beta lactam antibiotic																			
Ox ^R Em ^R	10		6	18				1				1			1				37
Ox ^R Cp ^R	3					1	1		1				1						8
Ox ^R FA ^R	13																		13
Ox ^R Gm ^R							1			2									3
Two non beta lactam antibiotics																			
Ox ^R Em ^R FA ^R	5							1											6
Ox ^R Cp ^R FA ^R	1																		1
Ox ^R FA ^R Rf ^R	1																		1
Ox ^R Em ^R Cp ^R							2	1											3
Ox ^R Em ^R Mp ^R				1															1
Ox ^R Em ^R Gn ^R	1																		1
Ox ^R Em ^R Tc ^R	1																		1
Ox ^R Tc ^R FA ^R																		1	1
Three non beta lactam antibiotics																			
Ox ^R Em ^R Cp ^R FA ^R	2																		2
Ox ^R Em ^R Tc ^R FA ^R	1																		1
Ox ^R Em ^R Cp ^R Tc ^R									1										1
Ox ^R Gn ^R Mp ^R FA ^R	1																		1
Ox ^R Em ^R Mp ^R FA ^R	1																		1
Four non beta lactam antibiotics																			
Ox ^R Gn ^R Em ^R Cp ^R			1								1								2
Mp ^R																			
	76	27	21	20	12	5	4	3	3	2	2	1	1	1	1	1	1	1	182

Ox = oxacillin, Em = erythromycin, Cp = ciprofloxacin, FA = fusidic acid, Gm = gentamicin, Tc = tetracycline, Rf = rifampicin, Mp = mupirocin, Tm = trimethoprim
^aWA MRSA-12 (USA300)

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