

The Australian Group on Antimicrobial Resistance

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***Staphylococcus aureus* Programme 2004 (SAP 2004)
Community Survey
MRSA Epidemiology and Typing Report**

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**Epidemiology and Typing Report of Methicillin Resistant
Staphylococcus aureus (MRSA) Isolates from the Australian Group on
Antimicrobial Resistance (AGAR) 2004
Staphylococcus aureus Surveillance Programme (SAP 2004)**

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1.0 Overview

- The proportion of infections due to Community MRSA (cMRSA) strains as a proportion of all *S aureus* increased from 4.7% in 2000 to 7.3% in 2004.
- cMRSA strains accounted for >10% of all clinical outpatient isolates of *S aureus* in the NT/Qld and WA regions.
- The proportion of cMRSA strains in the Tas/Vic region remained lower than in other regions and did not increase substantially.
- ST1-MRSA-IV (WA-1 MRSA) was still the most common cMRSA strain. It was isolated throughout the country but still represented the lower proportion of *S aureus* in the eastern states. 7.8% of strains from this clone were PVL positive.
- ST93-MRSA-IV (Queensland MRSA) was the second most common cMRSA strain and has increased by 39% since the 2002 survey. It predominated in the NT/Qld and ACT/NSW regions and was found in all regions surveyed except Tas/Vic. 96.6% of strains from this clone were PVL positive.
- ST30-MRSA-IV (WSPP MRSA or Oceania MRSA) was the third most common cMRSA strain and remained prominent in the NT/Qld and ACT/NSW regions. Apart from these regions only one other isolate came from WA. 96.1% of strains from this clone were PVL positive
- ST129-MRSA-IV (WA-2 MRSA) was largely limited to WA however four isolates were found in the Tas/Vic region in 2004.
- Overall 46.4% of cMRSA were PVL positive.
- Epidemic MRSA (EMRSA) or health care associated strains ST239-MRSA-III and ST22-MRSA-IV also known as Aus-2/Aus-3 EMRSA and UK EMRSA-15 respectively, were commonly isolated in outpatient settings with a prevalence (7.5%) roughly equivalent to the community strains. ST22-MRSA-IV appears to be increasing gradually in the eastern states.

2.0 Summary

From the AGAR SAP 2004, 395 MRSA were forwarded to the Gram-positive Bacteria Typing and Research Unit for epidemiological typing.

2.1 Epidemic MRSA (EMRSA) (Healthcare Associated)

201 (50.9%) MRSA were classified as Epidemic MRSA (EMRSA) or healthcare associated MRSA. These strains were classified into three international clones:

- ST239-MRSA-III (previously known as Aus-2/3 EMRSA, UK EMRSA-1, Portuguese/Brazilian clone or the Vienna clone).
- ST22-MRSA-IV (previously known as UK EMRSA-15 or the German Barnim strain).
- ST36-MRSA-II (previously known as UK EMRSA-16).

In this survey ST239-MRSA-III, a multiresistant EMRSA, was the predominant MRSA isolated (n = 137). 34.7% of MRSA and 68.2% of EMRSA were identified as ST239-MRSA-III. Although ranging from 17.7% to 74.2% of MRSA in the central and eastern regions of Australia, ST239-MRSA-III was not isolated in WA.

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 the ACT/NSW region and Aus-3 EMRSA in 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 (24). This clone has now become established throughout Australia. Overall 15.7% of MRSA and 30.8% of EMRSA were identified as ST22-MRSA-IV. Rates varied from 7.3% in the NT/Qld region to 21.4% in the ACT/NSW region.

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

2.2 Community MRSA (cMRSA)

194 (49.1%) MRSA were classified as community MRSA. Epidemiological typing has shown these strains have emerged from diverse genetic backgrounds. The eleven MLST clones identified were grouped into 9 clonal complexes or as singletons. All have acquired SCC*mec* type IV, a community SCC*mec* type.

- Clonal Complex 1
ST1-MRSA-IV (WA MRSA-1)
- Clonal Complex 5
ST5-MRSA-IV (WA MRSA-3)
- Clonal Complex 8
ST8-MRSA-IV (WA MRSA -5 and -12)
- Clonal Complex 9
ST584-MRSA-IV (WA MRSA-13)
- Clonal Complex 45
ST45-MRSA-IV (WA MRSA-23)
- Clonal Complex 59
ST59-MRSA-IV (WA MRSA-15)
- Clonal Complex 30
ST30-MRSA-IV (WSPP MRSA)
- Clonal Complex 80
ST583-MRSA-IV (WA MRSA-17)
- Clonal Complex 298
ST129-MRSA-IV (WA MRSA-2)
- Singletons
ST93-MRSA-IV (Queensland MRSA)
ST75-MRSA-IV (WA MRSA-8)

93.3% (n=181) of cMRSA were classified into five major community clones:

- ST1-MRSA-IV (n = 64)
Isolated throughout Australia ranging from 3.2% in the Tas/Vic region to 45.1% of MRSA in WA. 7.8% (n=5) of strains were PVL positive.

- ST93-MRSA-IV (n = 58)
Isolated in most regions of Australia ranging from 3.9% in WA to 29.4% of MRSA in the NT/Qld region (not isolated in the Tas/Vic region). 96.6% (n=56) of strains were PVL positive.
- ST30-MRSA-IV (n = 26)
Isolated in most regions of Australia ranging from 2% in WA to 17.6% of MRSA in the NT/Qld region (not isolated in the SA and Tas/Vic regions). 96.1% (n=25) of strains were PVL positive.
- ST129-MRSA-IV (n = 19)
Isolated in most regions of Australia ranging from 1.5% in the NT/Qld region to 25.5% of MRSA in WA (not isolated in ACT/NSW region). All strains were PVL negative.
- ST5-MRSA-IV (n = 14)
Isolated throughout Australia ranging from 1.2% in the ACT/NSW region to 9.8% of MRSA in SA. All strains were PVL negative

In addition to the three mentioned PVL positive clones (ST1-MRSA-IV, ST93-MRSA-IV and ST30-MRSA-IV), PVL positive strains were also detected in the following cMRSA clones:

ST8-MRSA-IV (WA MRSA-12)

ST583-MRSA-IV (WA MRSA-17)

Overall 46.2% of cMRSA isolated were PVL positive.

60.3% (n=117) of cMRSA were resistant to the beta lactam antibiotics only. 77 strains (39.7%) were resistant to at least one non beta lactam antibiotic including:

29.4% (n=57) resistant to one non beta lactam antibiotic

8.8% (n=17) resistant to two non beta lactam antibiotics

1.5% (n=3) resistant to three non beta lactam antibiotics

The emergence of PVL positive and multiresistant cMRSA in Australia is a public health concern which may require the modification of guidelines for the treatment and control of community-acquired infection due to *Staphylococcus aureus*.

3.0 Commencement Date

1st November 2004

4.0 Isolates

Approximately 100 consecutive isolates of *Staphylococcus aureus* from 100 different patients at each site were tested by 27 laboratories located across Australia (total number of isolates = 2,652). Isolates were collected from outpatients only and excluded dialysis and day surgery patients.

5.0 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 (1)

Royal Hobart Hospital

Northern Territory (1)

Royal Darwin Hospital

Victoria (5)

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

Queensland (3)

Princess Alexandra Hospital
Royal Brisbane Hospital
Sullivan Nicolaides Pathology

Western Australia (4)

Fremantle Hospital
PathCentre
Royal Perth Hospital
Saint John of God Pathology

6.0 Methicillin Susceptibility Testing

Breakpoint agar dilution (CLSI) (1)

- Mueller Hinton agar (BBL Mueller Hinton II, Cat No. 11438, Acumedia, Cat No. 7101) supplemented with 2% (w/v) NaCl and oxacillin 2mg/L.
- Plates incubated at 35°C for 24 hours.

7.0 Epidemiological Typing

Performed by the Gram-positive Bacteria Typing and Research Unit

- Department of Microbiology and Infectious Diseases, Royal Perth Hospital, Perth Western Australia.
- Molecular Genetics Research Unit, School of Biomedical Sciences, Curtin University of Technology, Bentley, Western Australia.

7.1 MRSA Nomenclature

The Gram-positive Bacteria Typing and Research Unit employs the international MRSA nomenclature system described by *Enright et al.* (2). 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 which is determined multiplex PCR. 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 UK EMRSA-15).

7.2 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 (<http://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.

7.3 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 *SCCmecs* differ depending on variations in the 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 IVpaediatric 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.

8.0 Panton-Valentine Leucocidin (PVL) Toxin

cMRSA have been shown to acquire several virulence genes including the determinants for PVL (3). 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 (4). However, in Australia, it has been reported that cMRSA infrequently carry the genes encoding PVL (5). 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 (6). ST93-MRSA-IV was first identified as a cause of community-acquired infection in the Caucasian population in Ipswich, Queensland in 2000 (7). Both clones are now frequently isolated in several regions of Australia especially on the east coast (8).

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 (7,12,13). This suggests that the PVL determinants are being transferred and raises the prospect that more cMRSA in Australia may become PVL positive in the future.

9.0 Methods

9.1 Epidemiological Typing Methods

9.1.1 Antibigram

Breakpoint Agar Dilution (CLSI) (1)

oxacillin (2mg/L) tetracycline (4mg/L), erythromycin (0.5mg/L), trimethoprim (8mg/L), gentamicin (4mg/L), ciprofloxacin (1mg/L), rifampicin (1mg/L), fusidic acid (1mg/L), mupirocin (1mg/L)

Resistance was defined as growth on the concentration tested; a fine haze was ignored for tetracycline and trimethoprim.

9.1.2 Resistogram

Disk Diffusion (14, 15)

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

9.1.3 Urease

Christensen's Urea slop incubated for 24hrs at 37°C (16).

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

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

9.1.5 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 (5).

9.1.6 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).

9.1.7 Multi Locus Sequence Typing (MLST)

MLST was performed on selected isolates as specified by *Enright et al.* (2). 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.

9.1.8 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 (20, 21, 22)

9.2 Identification of EMRSA Clones

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

Antibiogram
Resistogram
CHEF

9.2.2 ST22-MRSA-IV (UK EMRSA-15)

Antibiogram
Urea Slope
Coagulase PCR/RFLP

9.2.3 ST36-MRSA-II (UK EMRSA-16)

Antibiogram
Urea Slope
Coagulase PCR/RFLP
CHEF

9.3 Identification of cMRSA Clones

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

Antibiogram
Coagulase PCR/RFLP
CHEF

9.3.2 ST93-MRSA-IV (Queensland MRSA)

Antibiogram
Coagulase PCR/RFLP
CHEF

9.3.3 “WA MRSA”

ST1-MRSA-IV (WA-1)
ST129-MRSA-IV (WA-2)
ST5-MRSA-IV (WA-3)
ST8-MRSA-IV (WA-5)
ST75-MRSA-IV (WA-8)

Antibiogram
Coagulase PCR/RFLP
CHEF

ST8-MRSA-IV (WA-12)
ST584 MRSA-IV (WA-13)
ST59-MRSA-IV (WA-15)
ST583-MRSA-IV (WA-17)
ST45-MRSA-V (WA-23)

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

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

The presence of the PVL determinants was detected by PCR using previously published primers (23). The PVL PCR products of all new clones were confirmed by sequencing.

10.0 Results

In SAP 2004, 395 (14.9%) of *Staphylococcus aureus* were classified as MRSA.

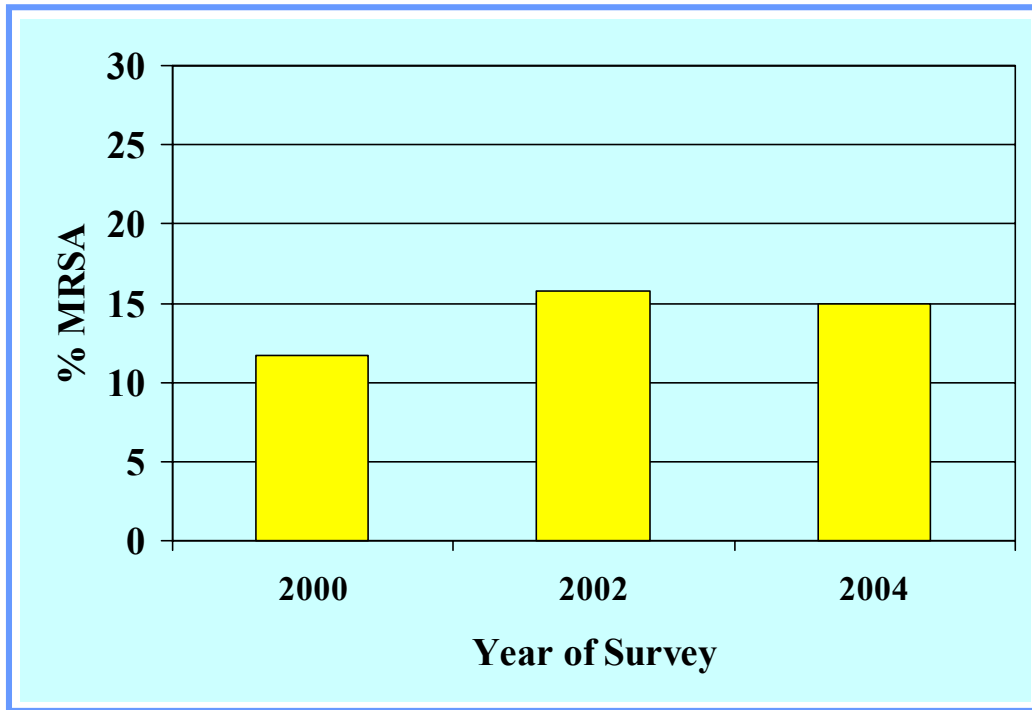
10.1 Typing Tests Performed: SAP 2004

Test	n
Antibiogram	395
Coagulase Gene PCR-RFLP Assay	295
Resistogram	136
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	376
Urease Reaction	64
Multi Locus Sequencing Typing (MLST)	13
SCC mec PCR	13
Panton-Valentine leucocidin PCR	194

10.2 AGAR Community MRSA SAPs 2000 – 2004

10.2.1 AGAR Community MRSA SAPs 2000 – 2004: %MRSA

SAP	Laboratories (n)	<i>S aureus</i> (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

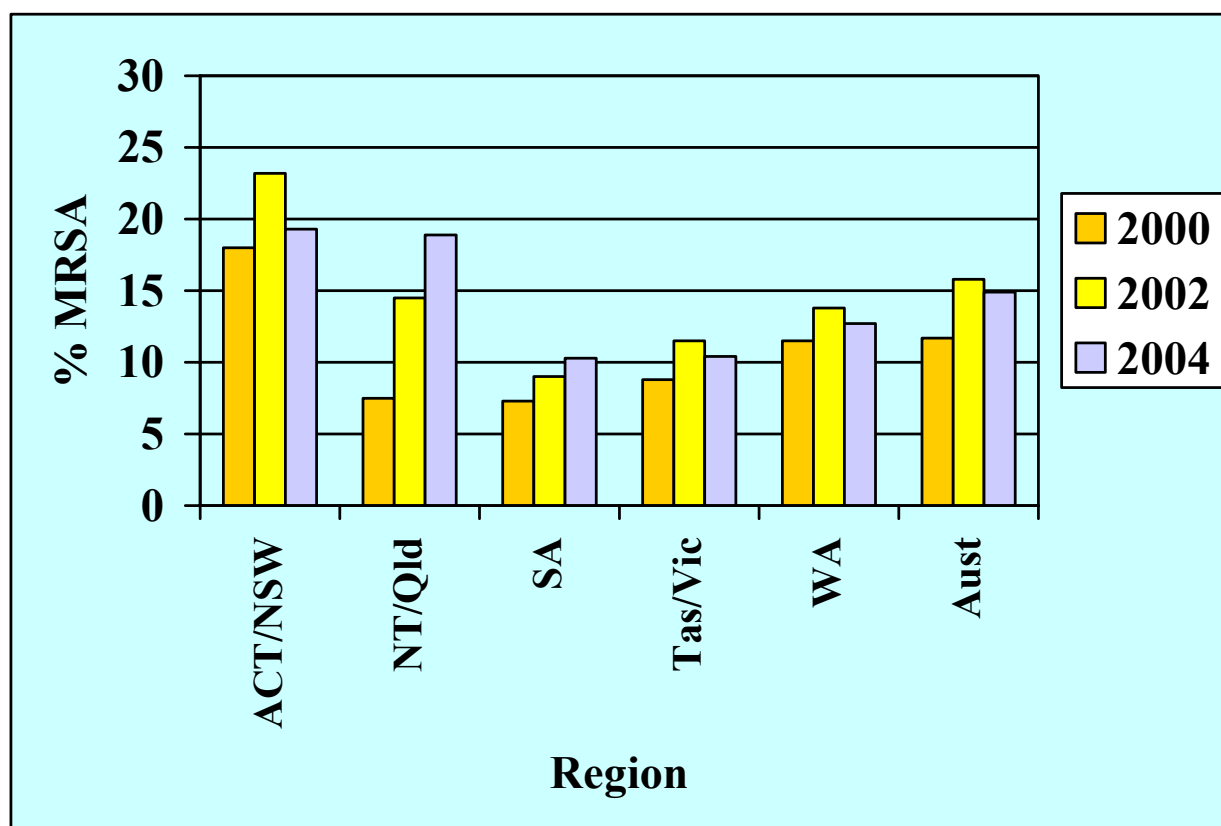


Percentage of *Staphylococcus aureus* identified as MRSA: Community SAPs 2000 - 2004

10.2.2 AGAR Community MRSA SAP 2000 – 2004: Regional Distribution of MRSA

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

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



Regional Distribution of MRSA: Community SAPs 2000 - 2004

10.3 SAP 2004

10.3.1 SAP 2004: Regional Distribution of EMRSA and cMRSA

Region	EMRSA (%)	cMRSA (%)	Total MRSA
ACT/NSW	111 (64.2)	62 (35.8)	173
NT/Qld	17 (25.0)	51 (75.0)	68
SA	15 (36.6)	26 (63.4)	41
Tas/Vic	51 (82.3)	11 (17.7)	62
WA	7 (13.7)	44 (86.3)	51
TOTAL	201 (50.9)	194 (49.1)	395

Percentage figures relate to the total number of MRSA isolates

10.3.2 AGAR Community MRSA SAP 2000 – 2004: Regional Distribution of EMRSA and cMRSA

Region	2000 (n = 257) ^a		2002 (n = 364) ^b		2004 (n = 395)	
	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)
NT/Qld	7 (25.9)	20 (74.1)	24 (44.4)	30 (55.6)	17 (25.0)	51 (75.0)
SA	13 (52.0)	12 (48.0)	11 (31.4)	24 (68.6)	15 (36.6)	26 (63.4)
Tas/Vic	30 (83.3)	6 (16.7)	35 (77.8)	10 (22.2)	51 (82.3)	11 (17.7)
WA	4 (9.1)	40 (90.9)	13 (23.6)	42 (76.4)	7 (13.4)	44 (86.3)
TOTAL	139 (54.1)	118 (45.9)	208 (57.3)	155 (42.7)	201 (50.9)	194 (49.1)

Percentage figures relate to the total number of MRSA isolates

^aIn SAP 2000 only 257 of the 293 MRSA were fully characterised

^bIn SAP 2002 only 363 of the 378 MRSA were fully characterised

10.3.3 AGAR Community MRSA SAP 2000 – 2004: Regional Distribution of EMRSA and cMRSA as a Proportion of *Staphylococcus aureus*

Region	2000			2002			2004		
	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)
NT/Qld	399	7 (1.8)	20 (5.0)	400	24 (6.0)	30 (7.5)	359	17 (4.7)	51 (14.2)
SA	399	13 (3.3)	12 (3.0)	400	11 (2.8)	24 (6.0)	399	15 (3.8)	26 (6.5)
Tas/Vic	500	30 (6.0)	6 (1.2)	399	35 (8.8)	10 (2.5)	599	51 (8.5)	11 (1.8)
WA	400	4 (1.0)	40 (10.0)	398	13 (3.3)	42 (10.8)	400	7 (1.8)	44 (11.0)
TOTAL	2498	139 (5.6)	118 (4.7)	2386	208 (8.7)	155 (6.5)	2,652	201 (7.6)	194 (7.3)

10.3.4 SAP 2004: EMRSA by Laboratory

Region	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	TOTAL
ACT/NSW (11)	1	3				3
	2	8		8		16
	3	5		6		11
	4	9	2	2		13
	5	14	2	5		21
	6	12		3		15
	7			2		2
	8	9	2	11		22
	9	5		3		8
NT/Qld (17)	10	4	1			5
	11	2	3			5
	12	1		1		2
SA (15)	13	1		4		5
	14	2		3	1	6
	15	1	1	1		3
	16					0
	17		4	2		6
Tas/Vic (51)	18		1			1
	19	9	11	1		21
	20		1	1		2
	21					0
	22		6			6
	23	5	13	3		21
	24			2		2
WA (7)	25			1		1
	26			3		3
	27				1	1
TOTAL		90	47	62	2	201

10.3.5. SAP 2004: cMRSA by Laboratory

Region	LAB	ST1 MRSA IV (WAI)	ST129 MRSA IV (WA2)	ST5 MRSA IV (WA3)	ST8 MRSA IV (WA5)	ST75 MRSA IV (WA8)	ST8 MRSA IV (WA12)	ST584 MRSA IV (WA13)	ST93 MRSA IV (QLD)	ST30 MRSA IV (WSPP)	ST59 MRSA IV (WA15)	ST583 MRSA IV (WA17)	ST45 MRSA IV (WA23)	TOTAL
ACT/NSW (62)	1								2					2
	2	2		1						1				4
	3								13	3				16
	4	1							2	4		1		8
	5	1		1			2		2					6
	6								6	2				8
	7	1				1			4	2				8
	8				1				3	1				5
	9	4							1					5
NT/QLD (51)	10	5		1		1			2	3				12
	11	5							13	5	1			24
	12	1		1			1	1	3	4				11
	13	1	1						2					4
SA (26)	14	3	1											4
	15	1		2										3
	16	8		1					2					11
	17	6		1					1					8
	18			1		1								2
Tas/Vic (11)	19		1											1
	20	1		1									1	3
	21							1						2
	22	1	1											2
	23												1	1
	24	10	4						2	1				17
WA (44)	25	4	3	3										10
	26	7	5								1			13
	27	2	1	1										4
TOTAL		64	19	14	1	1	4	2	58	26	2	1	2	194

10.4 EMRSA

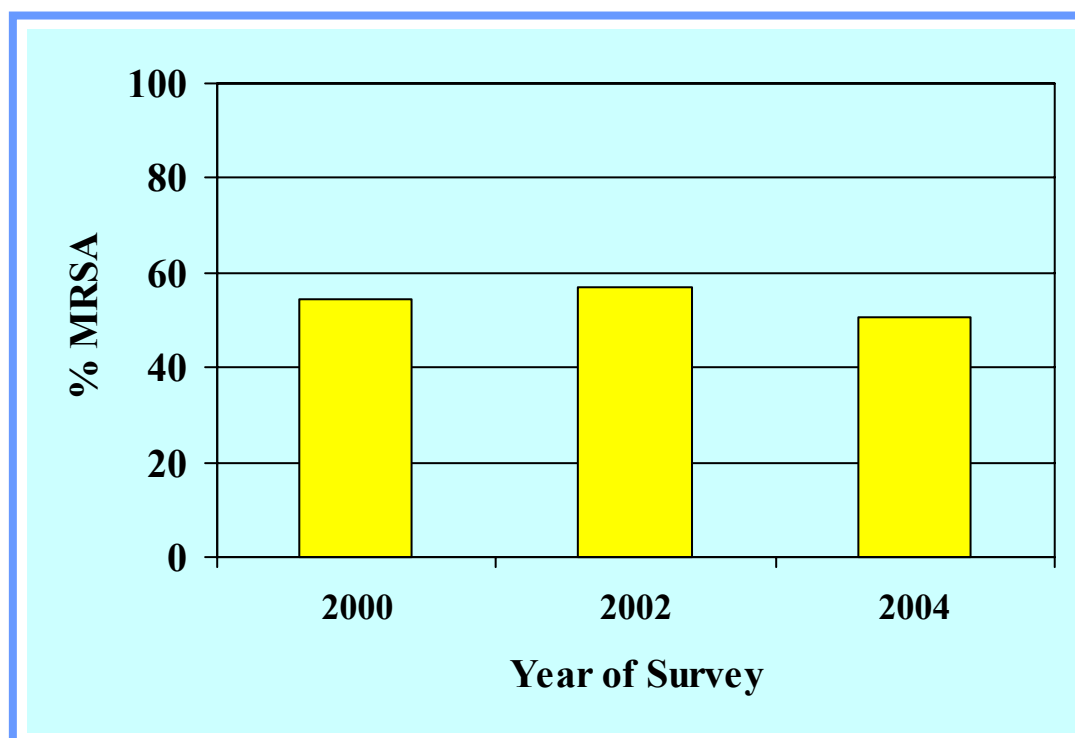
Certain strains of MRSA are known to spread easily between and within hospitals and are designated epidemic MRSA (EMRSA) or healthcare associated MRSA.

In SAP 2004 three international EMRSA clones (201 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST239-MRSA-III	Aus -2 and Aus -3 EMRSA	137(68.2)
ST22-MRSA-IV	UK EMRSA-15	62 (30.8)
ST36-MRSA-II	UK EMRSA-16	2 (1.0)
TOTAL		201

Percentage figures relate to epidemic MRSA isolates

10.4.1 AGAR Community SAPs 2000 – 2004: Percentage of MRSA Identified as EMRSA

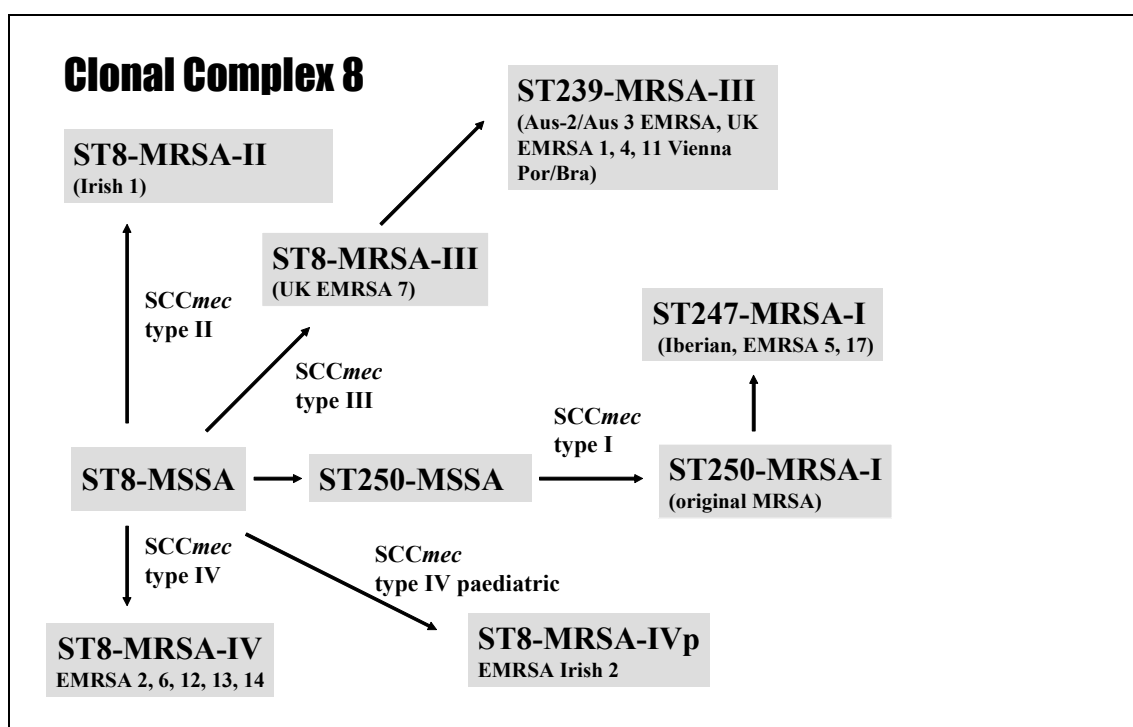


10.4.2 ST239-MRSA-III

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

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 (UK EMRSA -2, -6, -12, -13 and -14) and ST247-MRSA-I (Iberian or UK EMRSA-17). The original MRSA clone ST250-MRSA-I, and ST8-MRSA-IV_{paediatric} (Irish-2 EMRSA) are also located within this clonal complex.



10.4.2.1 Phenotypic Characteristics

Antibiogram:	Aus-2 EMRSA (n = 90)	Aus-3 EMRSA (n = 47)
Erythromycin ^R	100%	96%
Tetracycline ^R	92%	87%
Trimethoprim ^R	99%	100%
Gentamicin ^R	96%	96%
Ciprofloxacin ^R	100%	100%
Fusidic Acid ^R	1%	8%
Rifampicin ^R	6%	15%
Mupirocin ^R	3%	0%

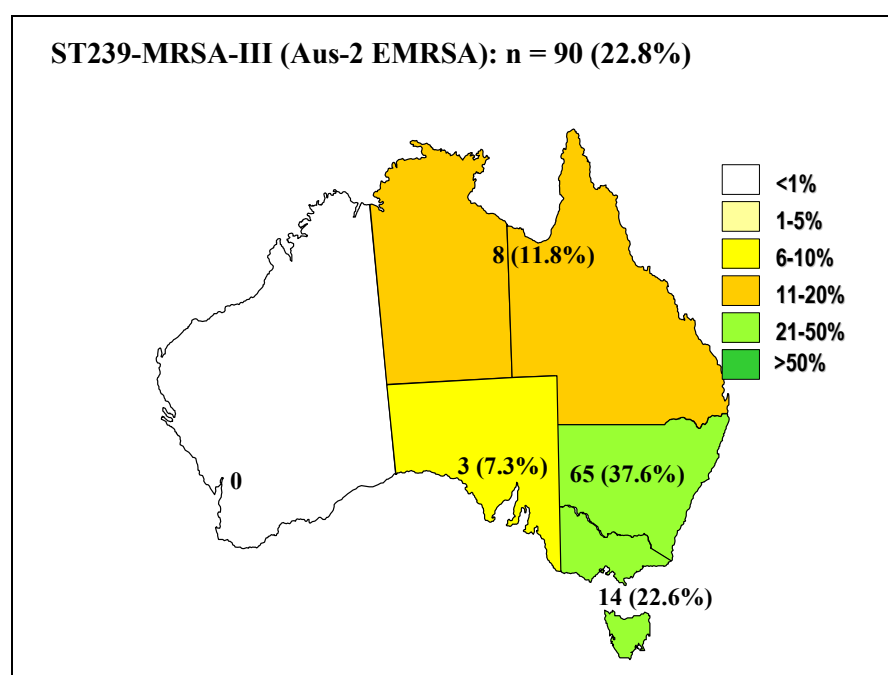
Resistogram:

Mercuric Acetate ^R	< 1%	> 99%
Mercuric Chloride ^R	< 1%	> 99%

Urease: Positive Positive

10.4.2.2 Epidemiology

10.4.2.2.1 Aus-2 EMRSA

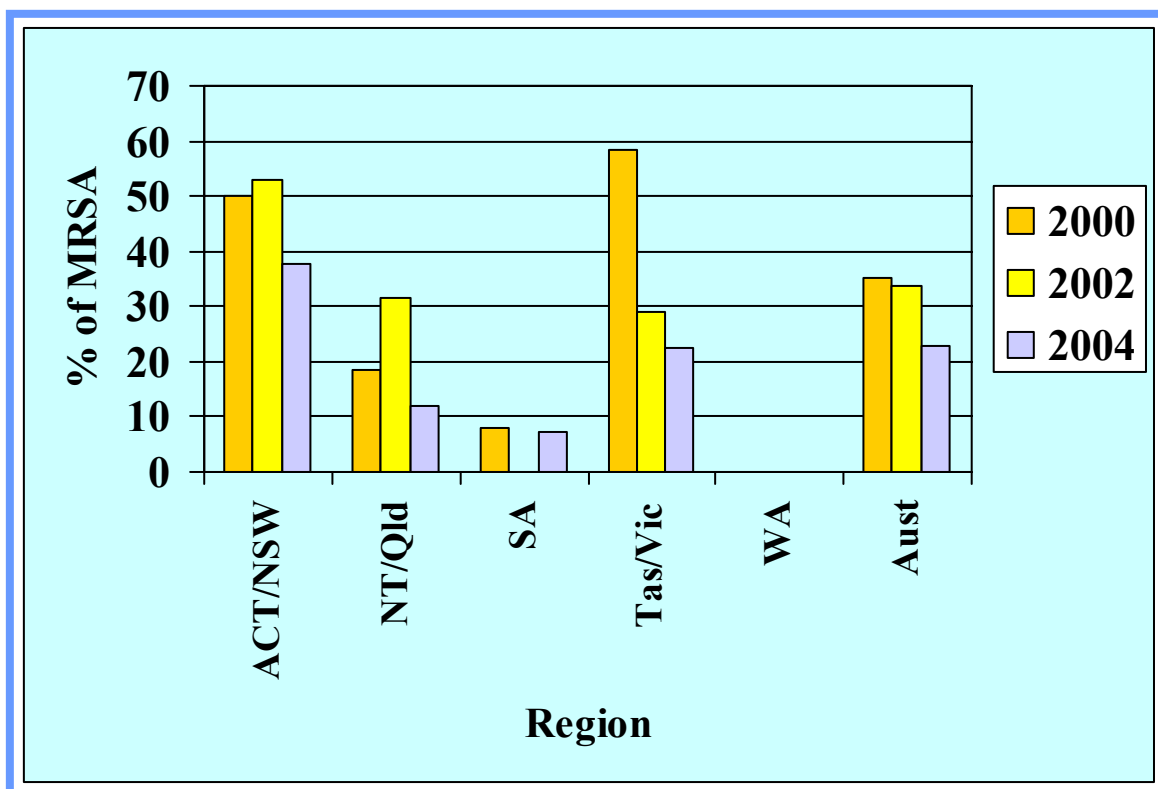


90 (22.8%) MRSA isolated in SAP 2004 were characterised as Aus-2 EMRSA which accounted for 44.8% of EMRSA. Although reported in most regions of Australia, Aus-2 EMRSA was the dominant MRSA in the ACT/NSW region. In the previous community *Staphylococcus aureus* survey, SAP 2002, 33.9% of MRSA (n=123) were characterised as Aus-2 EMRSA.

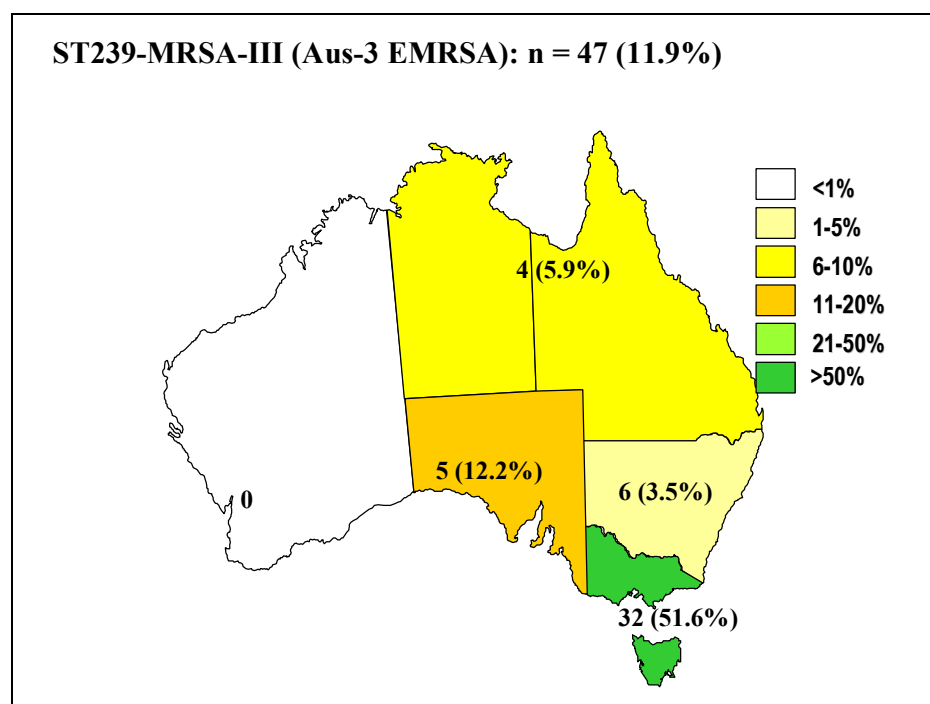
Region	SAP 2000	SAP 2002	SAP 2004
ACT/NSW	62 (49.6%)	93 (53.4%)	65 (37.6%)
NT/Qld	5 (18.5%)	17 (31.5%)	8 (11.8%)
SA	2 (8.0%)	0	3 (7.3%)
Tas/Vic	21 (58.3%)	13 (28.9%)	14 (22.6%)
WA	0	0	0
Total	90 (35.0%)	123 (33.9%)	909 (22.8%)

Percentage figures relate to total MRSA isolates

10.4.2.2 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST239-MRSA-II (Aus-2 EMRSA)



10.4.2.2.3 Aus-3 EMRSA

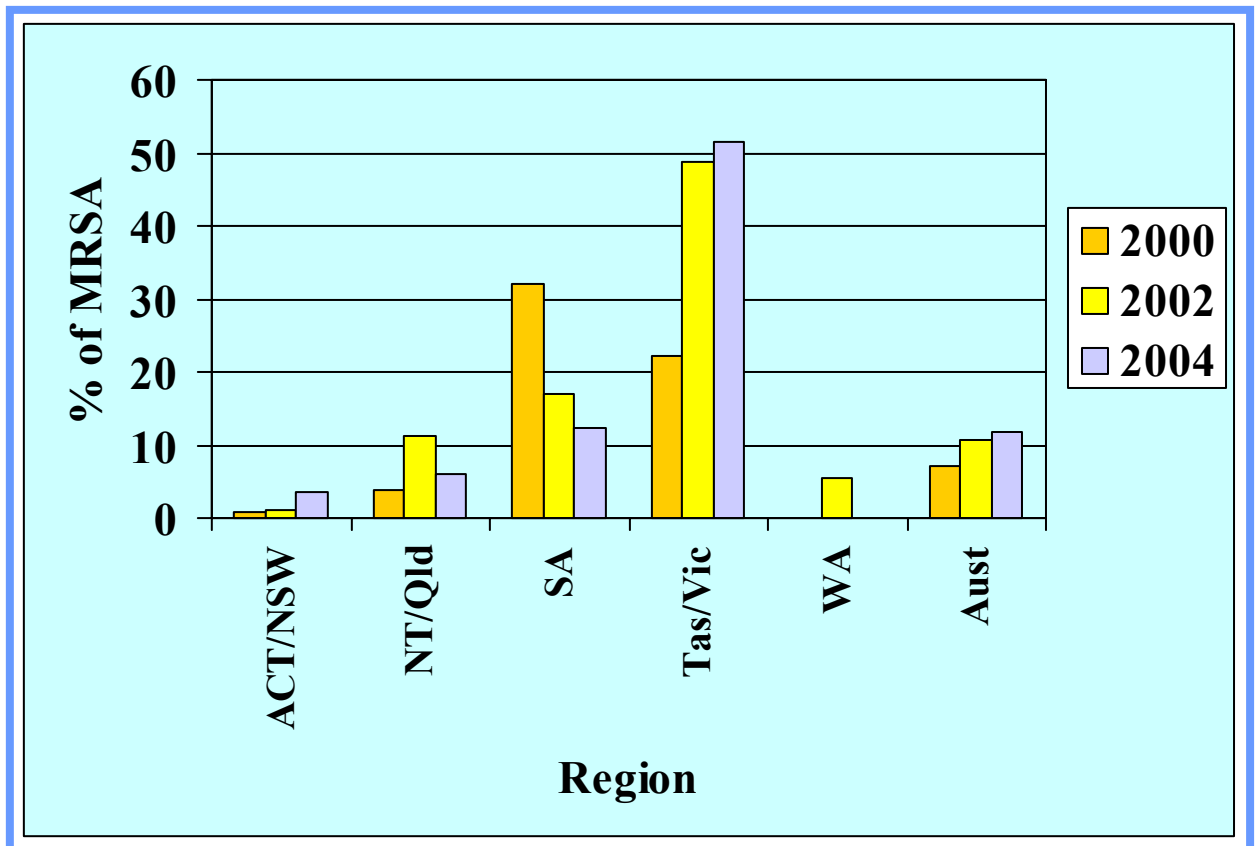


47 (11.9%) MRSA isolated in SAP 2004 were characterised as Aus-3 EMRSA which accounted for 23.4% of EMRSA. Although reported in most regions of Australia, Aus-3 EMRSA was the dominant MRSA clone isolated in the Tas/Vic region (51.6%). In the previous community *Staphylococcus aureus* Survey, SAP 2002, 10.7% of MRSA (n=39) were characterised as Aus-3 EMRSA.

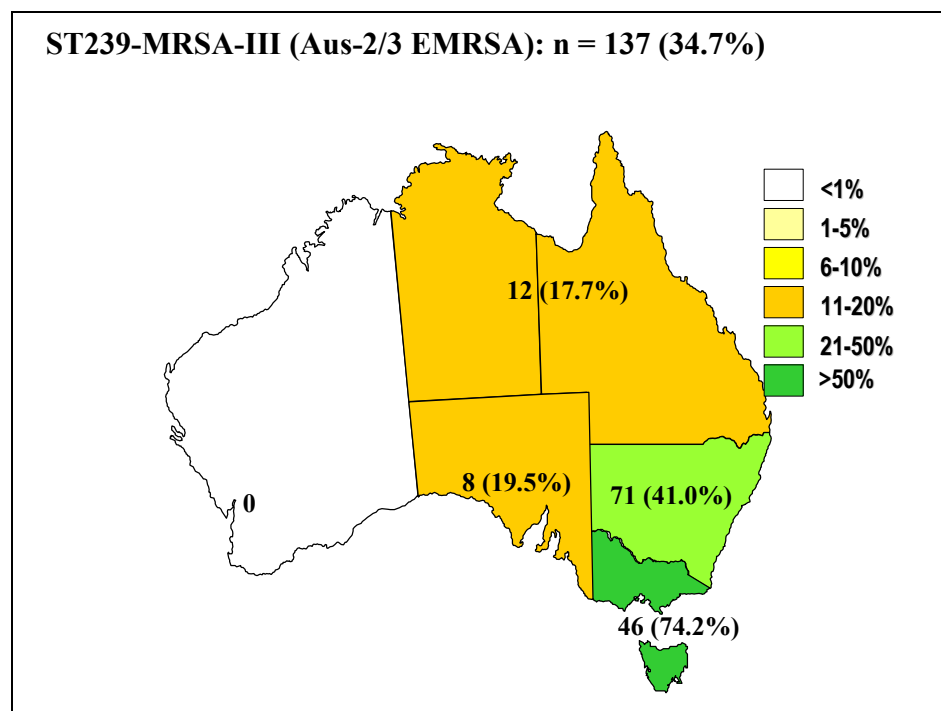
Region	SAP 2000	SAP 2002	SAP 2004
ACT/NSW	1 (0.8%)	2 (1.1%)	6 (3.5%)
NT/Qld	1 (3.7%)	6 (11.1%)	4 (5.9%)
SA	8 (32.0%)	6 (17.1%)	5 (12.2%)
Tas/Vic	8 (22.2%)	22 (48.9%)	32 (51.6%)
WA	0	3 (5.5%)	0
Total	18 (7.0%)	39 (10.7%)	47 (11.9%)

Percentage figures relate to total MRSA isolates

10.4.2.2.4 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST239-MRSA-III (Aus-3 EMRSA)



10.4.2.2.5 Aus-2 and Aus-3 EMRSA



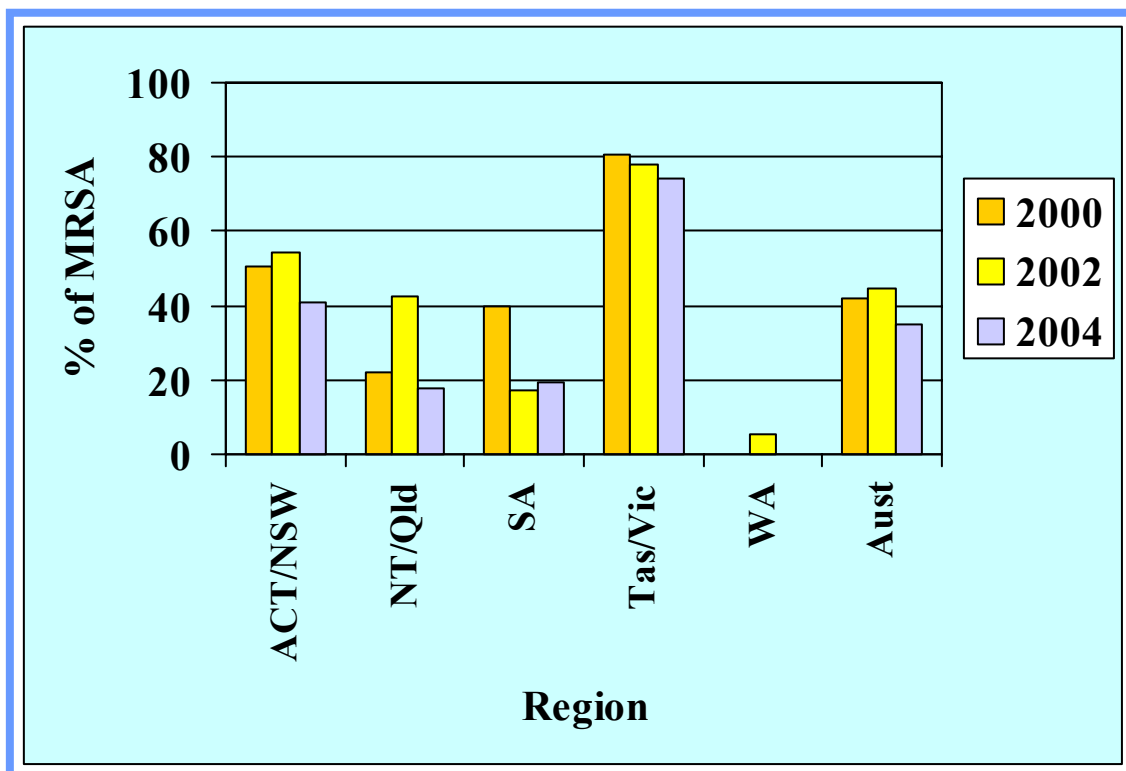
137 (34.7%) MRSA isolated in SAP 2004 were characterised as either Aus-2 or Aus-3 which accounted for 68.2% of EMRSA isolated. However this clone was not isolated on the western coast.

ST239-MRSA-III was the dominant MRSA clone in most regions of Australia including NT/Qld, NSW/ACT, Tas/Vic and SA. In the previous community *Staphylococcus aureus* Survey, SAP 2002, 44.6% of MRSA (n=162) were characterised as ST239-MRSA-III.

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

Percentage figures relate to total MRSA isolates

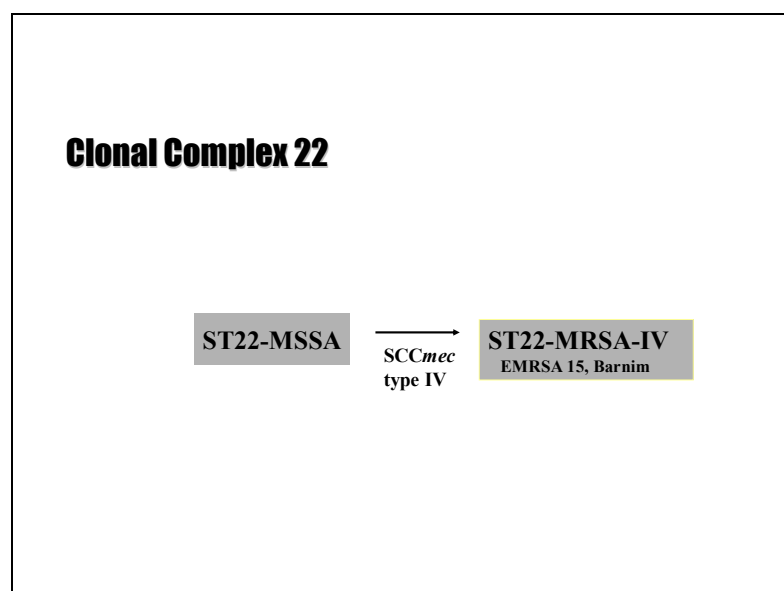
10.4.2.2.6 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST239-MRSA-III (Aus-2 and Aus-3 EMRSA)



10.4.3 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.

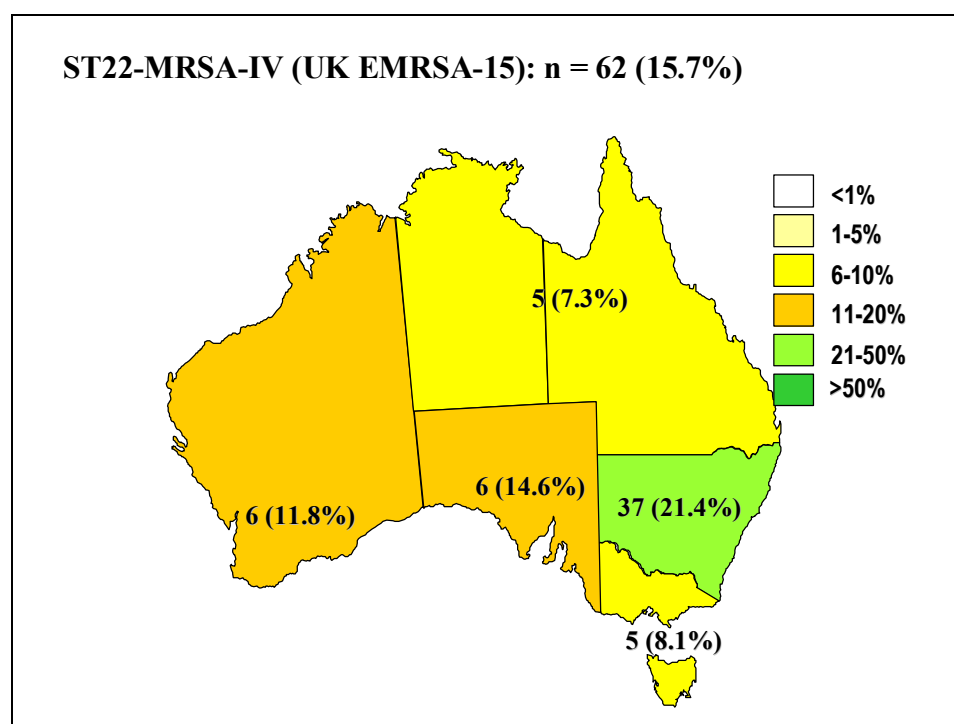
ST22 belongs to clonal complex 22. Although it is considered to be a health care associated MRSA it has acquired the type IV community *SCCmec* which lacks transposons, integrated plasmids and other antibiotic resistance genes. Clonal complex 22 has a single epidemic clone that is believed to have evolved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



10.4.3.1 Phenotypic Characteristics

Antibiogram:	Erythromycin ^R (55%) Ciprofloxacin ^R (100%) Fusidic Acid ^R (1.6%) Tetracycline ^R (1.6%) Trimethoprim ^R (3.3%) Rifampicin ^R (0%) Mupirocin ^R (0%) Gentamicin ^R (0%)
Urease:	Negative

10.4.3.2 Epidemiology



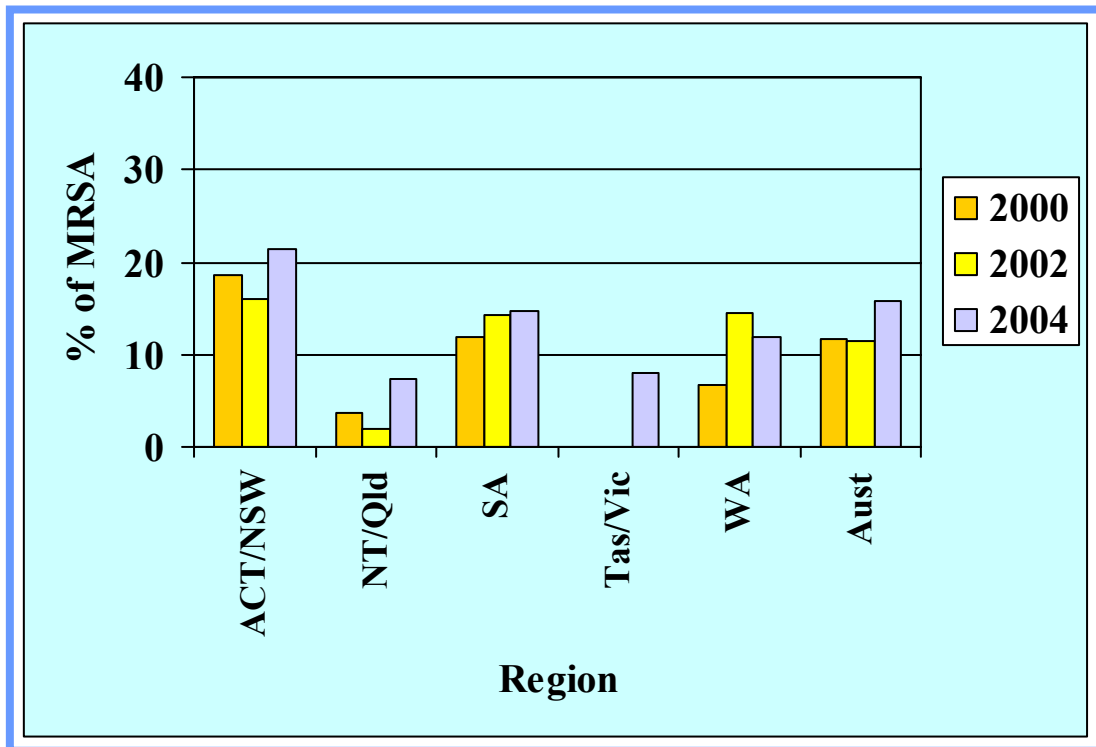
62 (15.7%) MRSA isolated in SAP 2004 were characterised as ST22-MRSA-IV which accounted for 30.8% of EMRSA isolated. Although reported in all regions of Australia this clone was predominantly isolated in the ACT/NSW region.

In the previous community *Staphylococcus aureus* Survey, SAP 2002, 11.65% (n=42) of MRSA were characterised as ST22-MRSA-IV.

Region	SAP 2000	SAP 2002	SAP 2004
ACT/NSW	23 (18.4%)	28 (16.1%)	37 (21.4%)
NT/Qld	1 (3.7%)	1 (1.9%)	5 (7.3%)
SA	3 (12.0%)	5 (14.3%)	6 (14.6%)
Tas/Vic	0	0	5 (8.1%)
WA	3 (6.8%)	8 (14.5%)	6 (11.8%)
Total	30 (11.7%)	42 (11.6%)	62 (15.7%)

Percentage figures relate to total MRSA isolates

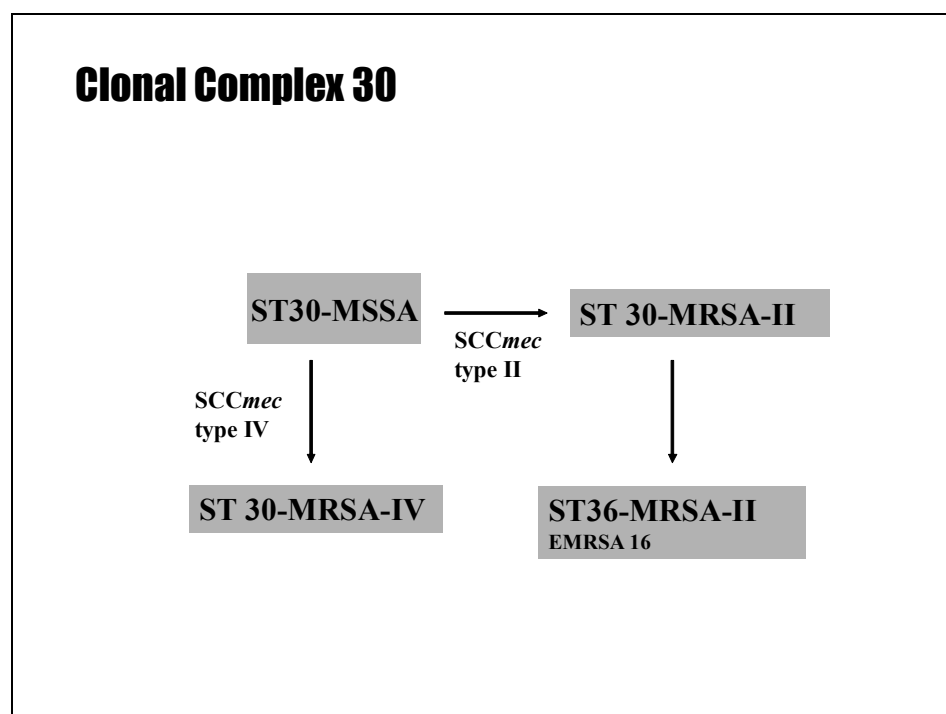
10.4.3.3 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST22-MRSA-IV



10.4.4 ST36-MRSA-II

Also known as “UK EMRSA-16”, 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. SCC*mec* type II is a health care associated SCC*mec* which carries *aadD*, the gene for tobramycin and kanamycin resistance, and *Tn554* which carries the erythromycin resistance gene *ermA*.



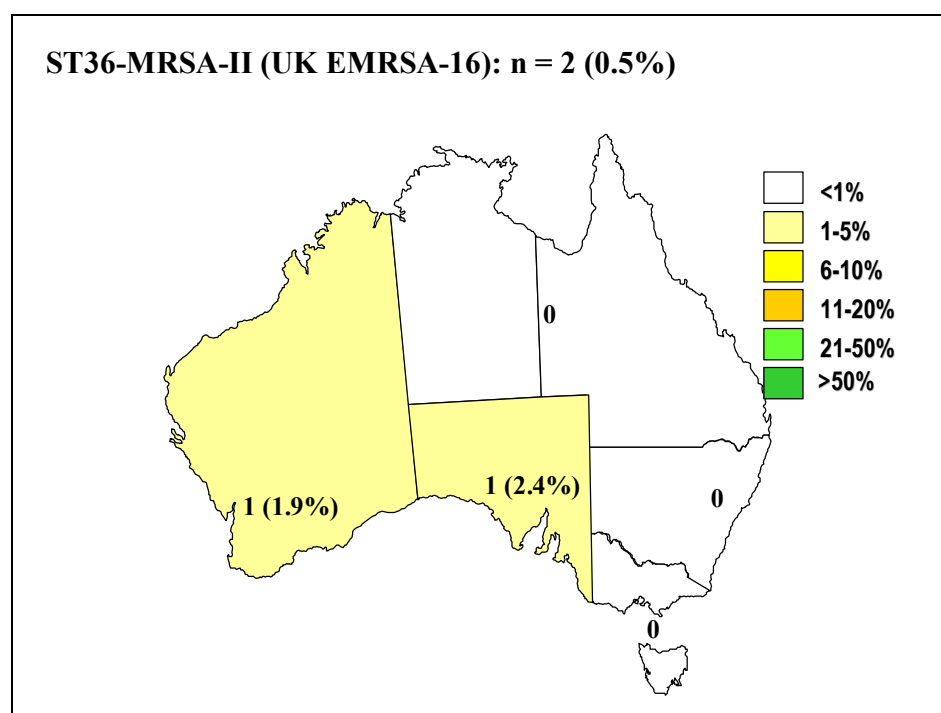
10.4.4.1 Phenotypic Characteristics

Antibiogram: Erythromycin^R
Ciprofloxacin^R
(Mupirocin^R)

Fusidic Acid^S
Tetracycline^S
Trimethoprim^S
Rifampicin^S
Gentamicin^S

Urease: Positive

10.4.4.2 Epidemiology



Two isolates of ST36-MRSA-II were reported in SAP 2004. In the previous community *Staphylococcus aureus* Survey, SAP 2002, 0.3% (n=1) of MRSA were characterised as ST36-MRSA-II.

Region	SAP 2000	SAP 2002	SAP 2004
ACT/NSW	0	0	0
NT/Qld	0	0	0
SA	0	0	1 (2.4%)
Tas/Vic	0	0	0
WA	0	1 (1.8%)	1 (1.9%)
Total	0	1 (0.3%)	2 (0.5%)

Percentage figures relate to total MRSA isolates

10.4.5 Summary of EMRSA Isolated in AGAR SAPs 2000 – 2004

Clone	Alternative Name	2000	2002	2004
ST239-MRSA-III	Aus-2, -3 EMRSA	108 (77.7%)	162 (77.9%)	137 (68.2%)
ST22-MRSA-IV	UK EMRSA-15	30 (21.6%)	42 (20.2%)	62 (30.8%)
ST36-MRSA-II	UK EMRSA-16	0	1 (0.5%)	2 (1.0%)
ST8-MRSA-II	Irish-1 EMRSA	0	3 ^b (1.4%)	0
ST8-MRSA-IVp	Irish-2 EMRSA	1 ^a (0.7%)	0	0
Total		139	208	201

Percentage figures relate to the epidemic MRSA isolates

^aIsolated in Western Australia

^bIsolated in New South Wales /Australian Capital Territory (n=2) and Western Australian (n=1)

10.5 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 (6). 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” (7). Although both strains initially caused skin infections they have now been associated with serious invasive disease and have been shown to be PVL positive.

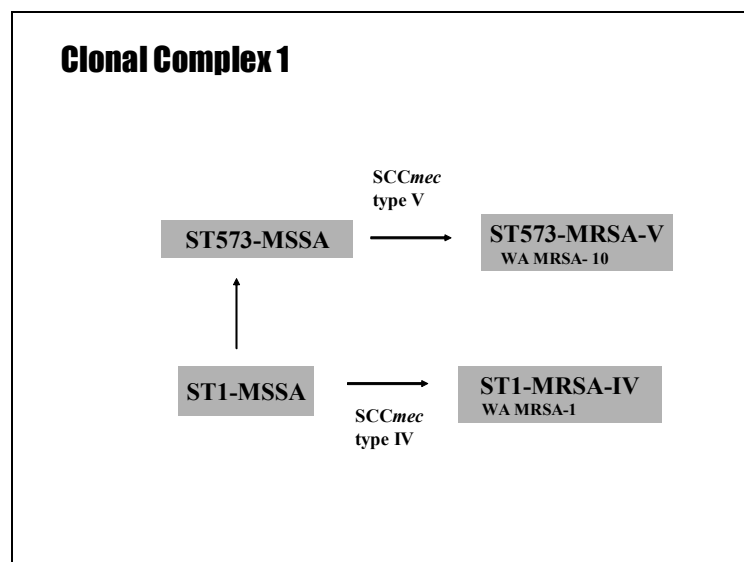
In SAP 2004 twelve community MRSA clones (eleven MLST clone types) were identified

Clone	Clonal Complex	Alternative Name	n (%)
ST1-MRSA-IV	1	WA MRSA -1	64 (33.0%)
ST93-MRSA-IV	Singleton	Queensland MRSA	58 (29.9%)
ST30-MRSA-IV	30	WSPP MRSA	26 (13.4%)
ST129-MRSA-IV	298	WA MRSA – 2	19 (9.8%)
ST5-MRSA-IV	5	WA MRSA – 3	14 (7.2%)
ST8-MRSA-IV	8	WA MRSA – 12	4 (2.1%)
ST584-MRSA-IV	9	WA MRSA – 13	2 (1.0%)
ST59-MRSA-IV	59	WA MRSA – 15	2 (1.0%)
ST45-MRSA-IV	45	WA MRSA – 23	2 (1.0%)
ST8-MRSA-IV	8	WA MRSA – 5	1 (0.5%)
ST75-MRSA-IV	Singleton	WA MRSA – 8	1 (0.5%)
ST583-MRSA-IV	80	WA MRSA – 17	1 (0.5%)
Total			194

Percentage figures relate to community MRSA isolates

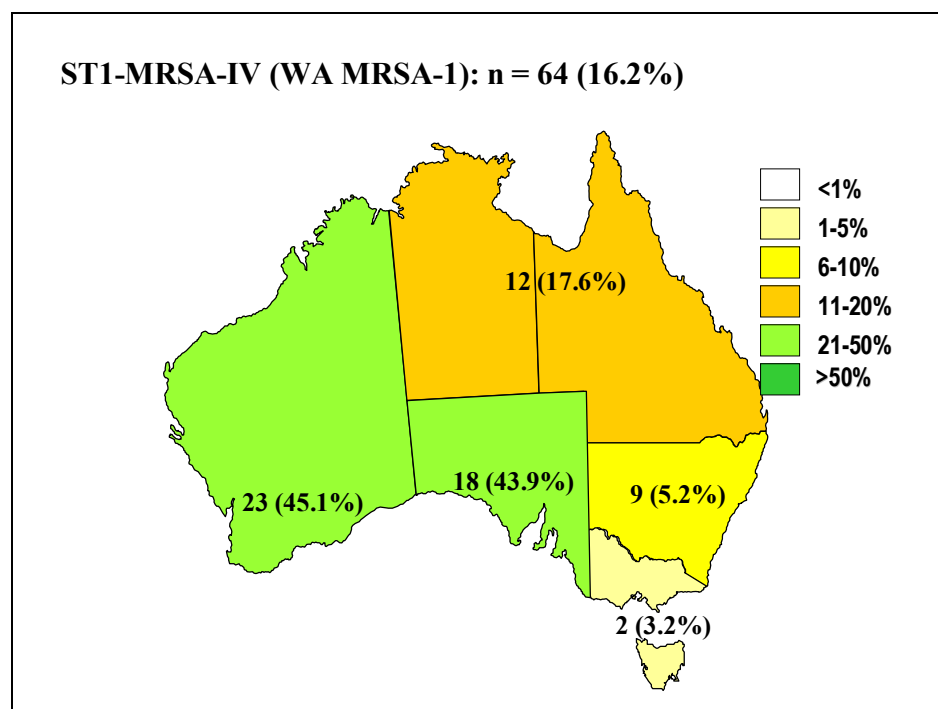
10.5.1 ST1-MRSA-IV

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.



10.5.1.1 Epidemiology

ST1-MRSA-IV is the most frequently isolated cMRSA in Australia. 64 (16.2%) MRSA isolated in SAP 2004 were characterised as ST1-MRSA-IV which accounted for 33.0% of cMRSA.



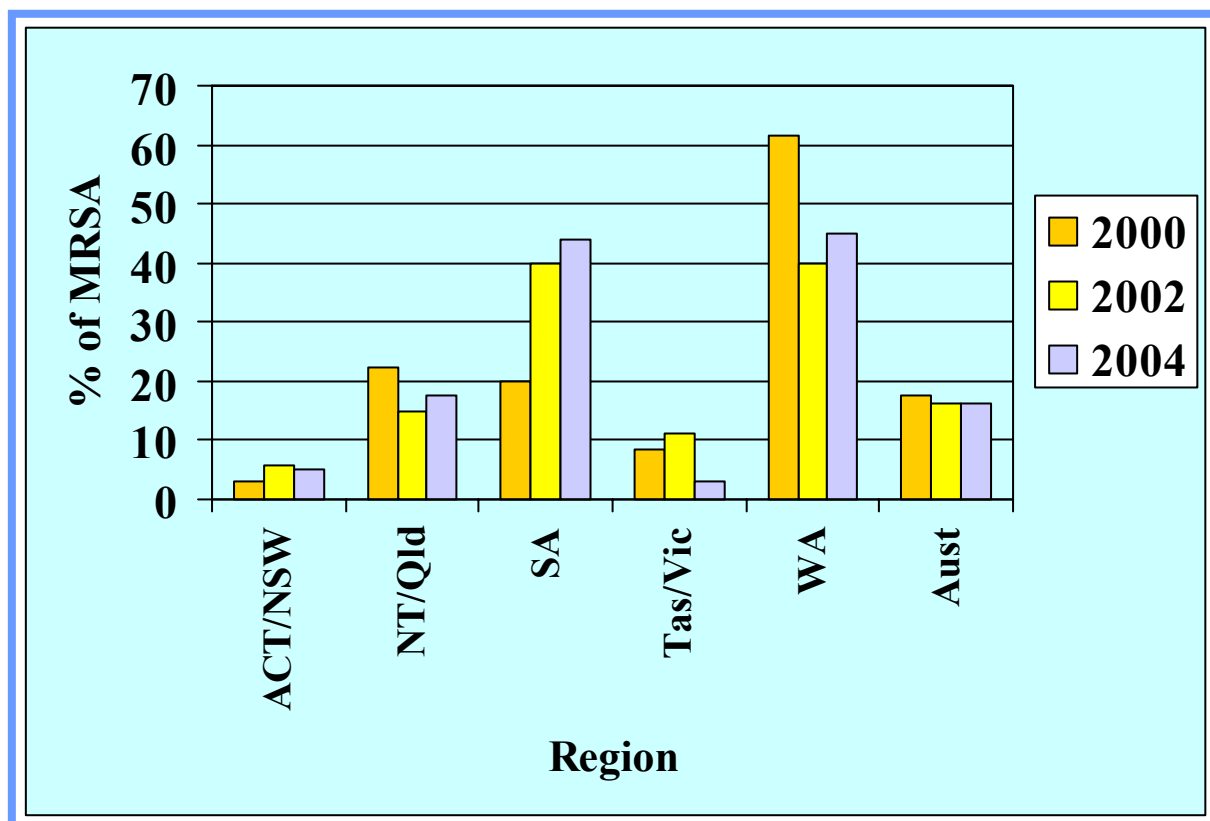
Although reported in all Australian regions this clone was predominantly isolated in the WA and SA regions (45.1% and 43.9% of MRSA respectively).

In the previous community *Staphylococcus aureus* Survey, SAP 2002, 16.3% (n=59) of MRSA were characterised as ST1-MRSA-IV.

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

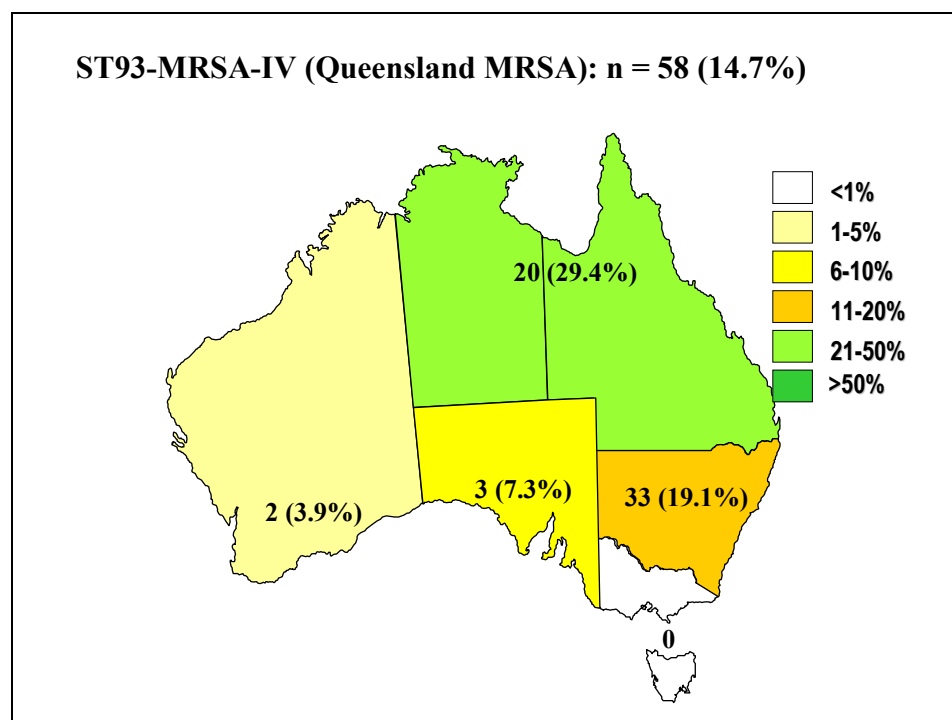
Percentage figures relate to total MRSA isolates

10.5.1.2 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST1-MRSA-IV



10.5.2 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.



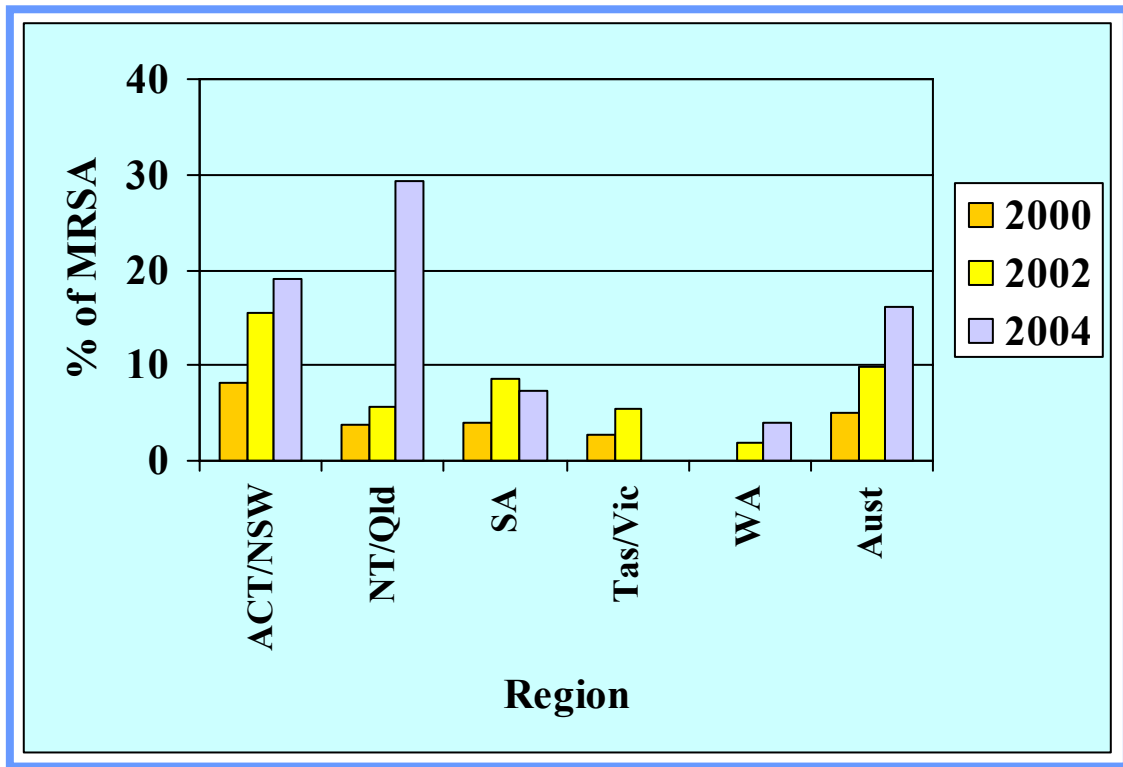
10.5.2.1 Epidemiology

58 (14.7%) MRSA isolated in SAP 2004 were characterised as ST93-MRSA-IV which accounted for 29.9% of cMRSA. ST93-MRSA-IV was isolated in most regions of Australia predominantly in the NT/Qld and ACT/NSW regions. In the previous community *Staphylococcus aureus* Survey, SAP 2002, 9.9% (n=36) of MRSA were characterised as ST93-MRSA-IV.

Region	SAP 2000	SAP 2002	SAP 2004
ACT/NSW	10 (8.0%)	27 (15.5%)	33 (19.1%)
NT/Qld	1 (3.7%)	3 (5.6%)	20 (29.4%)
SA	1 (4.0%)	3 (8.6%)	3 (7.3%)
Tas/Vic	1 (2.8%)	2 (5.4%)	0
WA	0	1 (1.8%)	2 (3.9%)
Total	13 (5.1%)	36 (9.9%)	58 (14.7%)

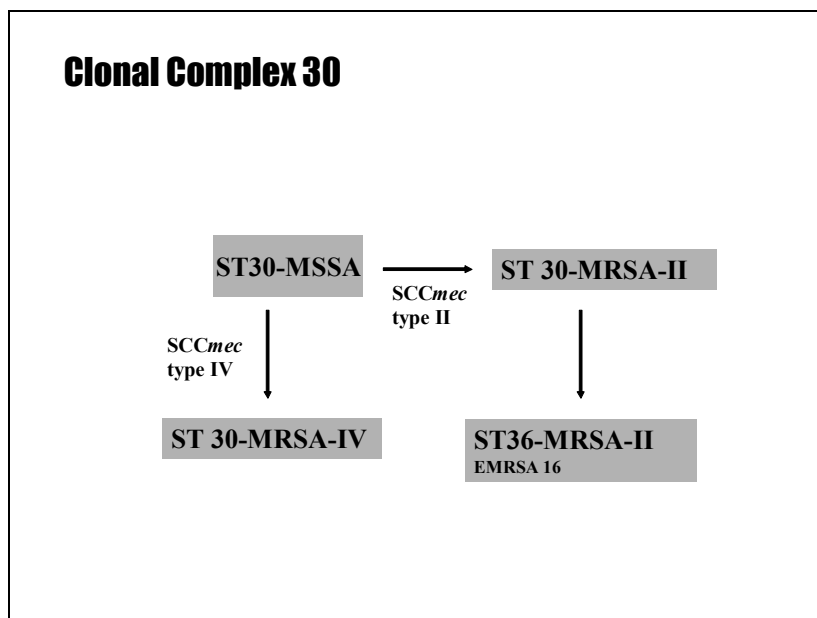
Percentage figures relate to total MRSA isolates

10.5.2.2 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST93-MRSA-IV



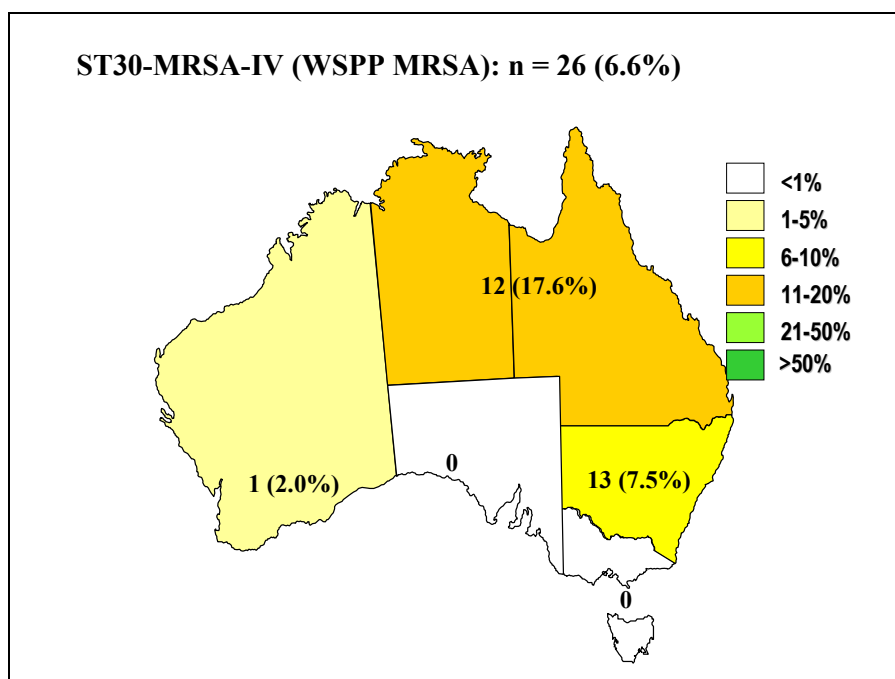
10.5.3 ST30-MRSA-IV

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.



10.5.3.1 Epidemiology

26 (6.6%) MRSA isolated in SAP 2004 were characterised as ST30-MRSA-IV accounting for 13.4% of cMRSA. Strains of ST30-MRSA-IV were isolated in several regions.

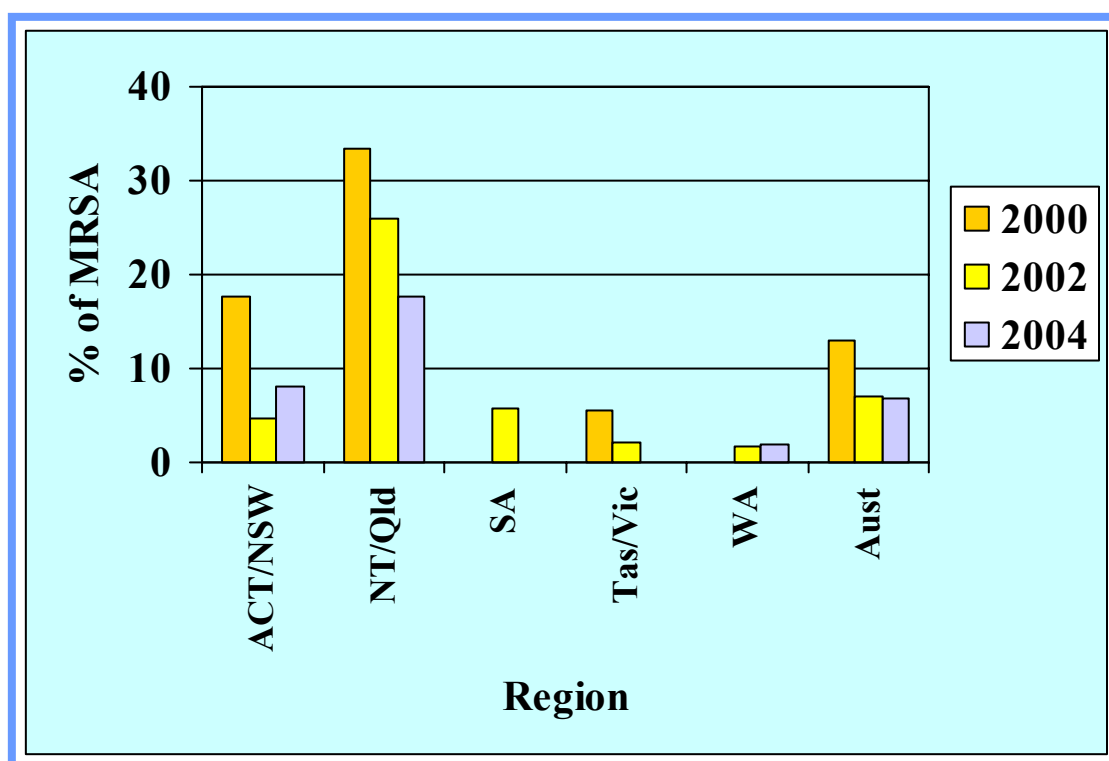


In the previous community *Staphylococcus aureus* Survey, SAP 2002, 7.2% (n=26) of MRSA were characterised as ST30-MRSA-IV.

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

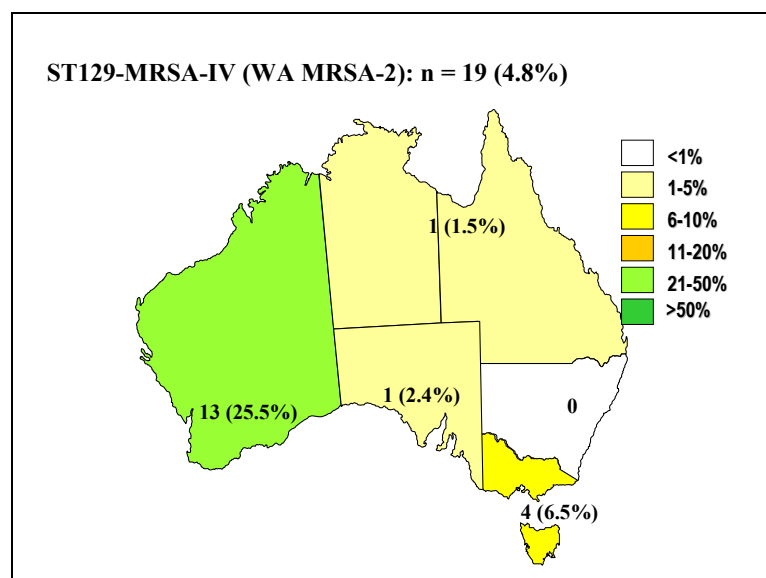
Percentage figures relate to total MRSA isolates

10.5.3.2 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST30-MRSA-IV



10.5.4 ST129-MRSA-IV

Also known as “WA MRSA-2”, ST129-MRSA-IV forms part of clonal complex 298. Within this complex several cMRSA clones have been identified including ST78, ST255 and ST257. Clonal complex 298 is a small clonal complex that includes strains from Australia, Europe and Japan.



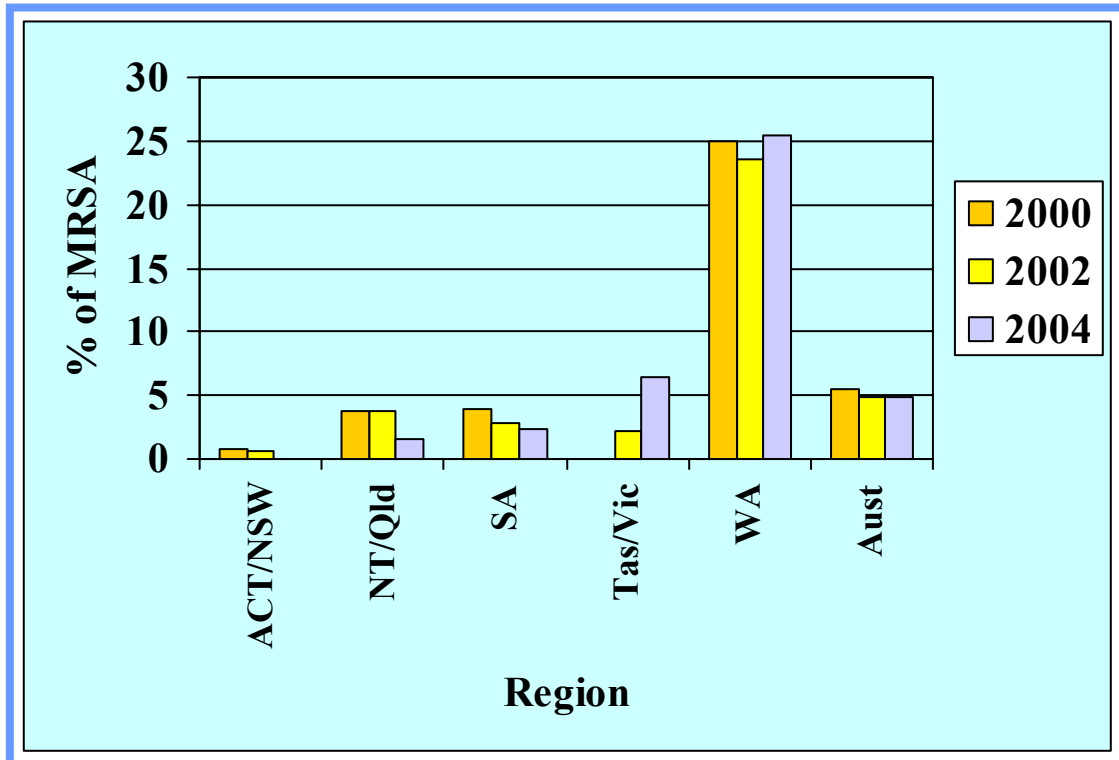
10.5.4.1 Epidemiology

19 (4.8%) MRSA isolated in SAP 2004 were characterised as ST129-MRSA-IV which accounted for 9.8% of cMRSA. ST129-MRSA-IV was predominately isolated in the WA region (25.5% of MRSA). In the previous community *Staphylococcus aureus* Survey, SAP 2002, 5.09% (n=18) of MRSA were characterised as ST129-MRSA-IV.

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

Percentage figures relate to total MRSA isolates

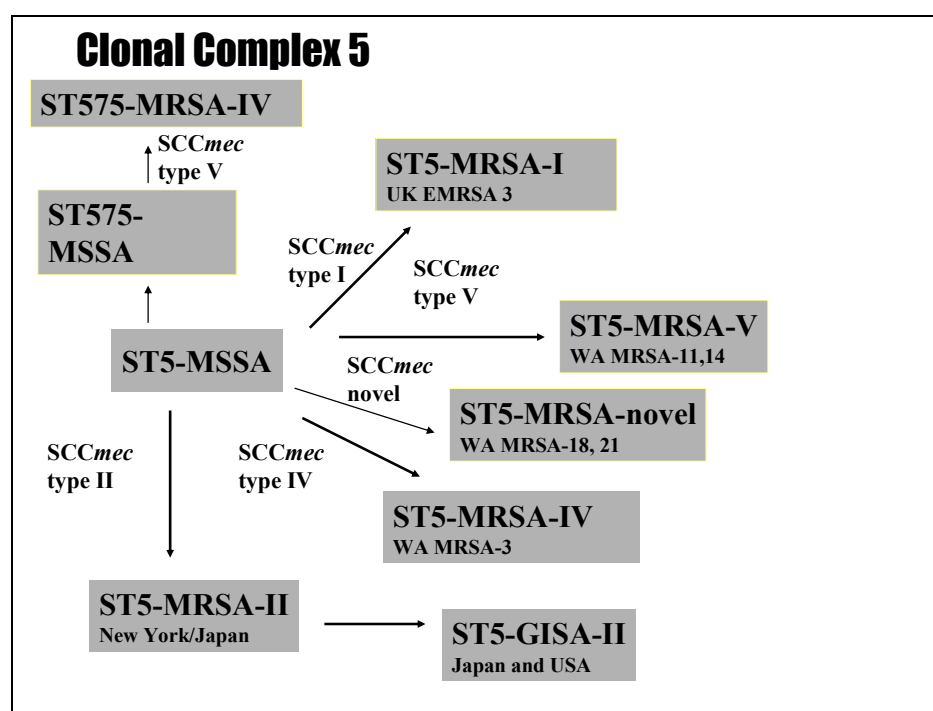
10.5.4.2 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST129-MRSA-IV



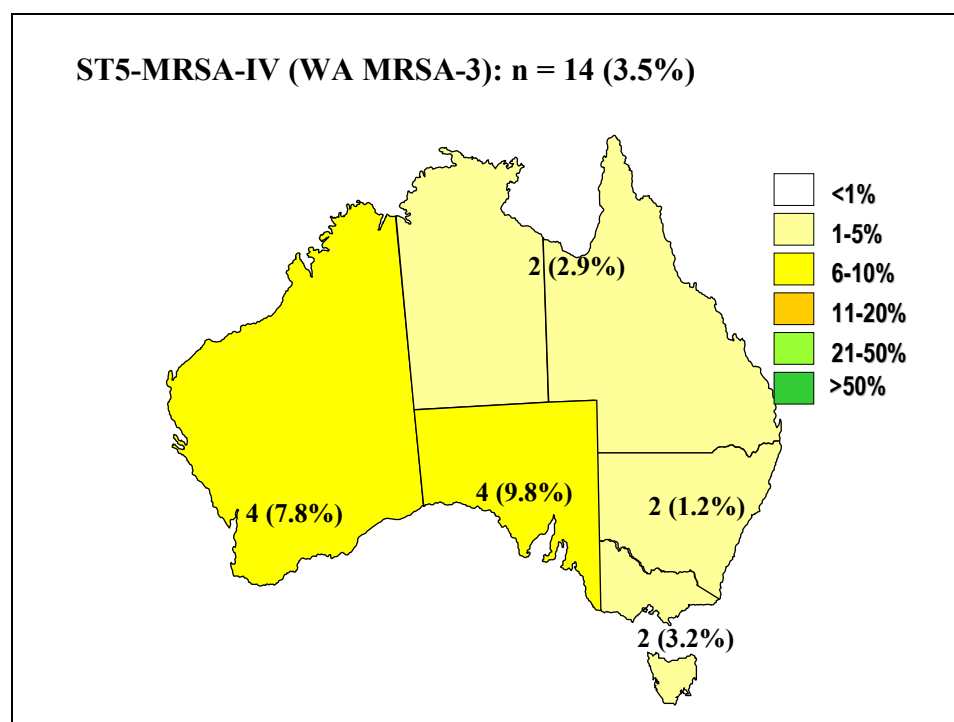
10.5.5 ST5-MRSA-IV

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

This clonal complex has a least four cMRSA clones, ST5-MRSA-IV, ST5-MRSA-V, ST5-MRSA-novel and ST575-MRSA-IV and two EMRSA clones, ST5-MRSA-II, also known as the “New York/Japan EMRSA”, and ST5MRSA-I also known as “UK EMRSA-3”. The original hVISA, ST5-GISA-II, is thought to have evolved from the New York/Japan EMRSA clone.



10.5.5.1 Epidemiology



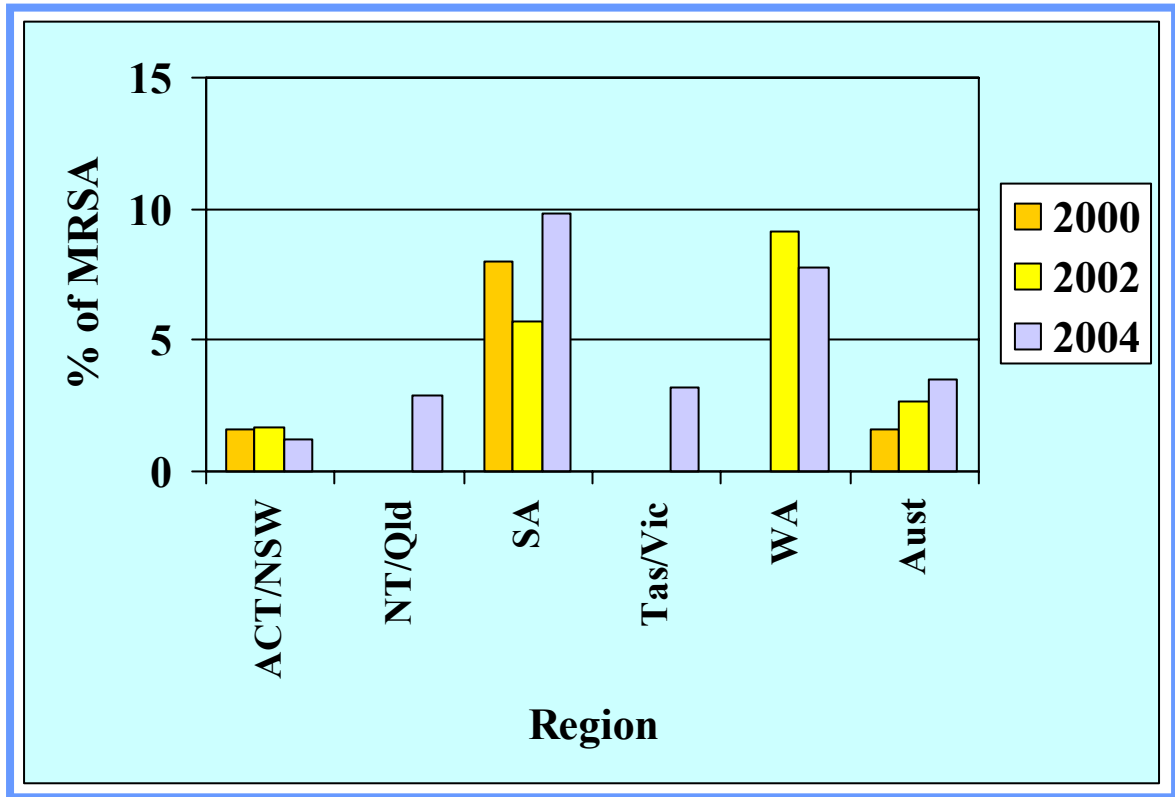
14 (3.5%) MRSA isolated in SAP 2004 were characterised as ST5-MRSA-IV which accounted for 7.2% of cMRSA. ST5-MRSA-IV was predominately isolated in the SA and WA regions (9.8% and 7.8% of MRSA respectively).

In the previous community *Staphylococcus aureus* Survey, SAP 2002, 2.8% (n=10) of MRSA were characterised as ST5-MRSA-IV.

	SAP 2000	SAP 2002	SAP 2004
ACT/NSW	2 (1.6%)	3 (1.7%)	2 (1.2%)
NT/Qld	0	0	2 (2.9%)
SA	2 (8%)	2 (5.7%)	4 (9.8%)
Tas/Vic	0	0	2 (3.2%)
WA	0	5 (9.1%)	4 (7.8%)
Total	4 (1.6%)	10 (2.8%)	14 (3.5%)

Percentage figures relate to total MRSA isolates

10.5.5.2 AGAR Community SAPs 2000 – 2004: Regional Distribution of ST5-MRSA-IV



10.5.6 Novel cMRSA

Clone	Clonal Complex	PFGE	2000 (n = 9)	2002 (n = 6)	2004 (n = 13)
ST75-MRSA-IV	5	WA MRSA-8	2 (NT/Qld)	1 (NT/Qld)	1 (NT/Qld)
ST8-MRSA-IV	8	WA MRSA-5	0	1 (ACT/NSW)	1 (ACT/NSW)
ST45-MRSA-V	45	WA MRSA-4	3 (2 WA) (1 SA)	1 (SA)	0
ST45-MRSA-IV	45	WA MRSA-23	0	0	2 (Tas/Vic)
ST583-MRSA-IV	80	WA MRSA-17	1 (ACT/NSW)	1 (Tas/Vic)	1 (ACT/NSW)
ST59-MRSA-IV	59	WA MRSA-15	0	0	2 (1 NT/Qld) (1 WA)
ST584-MRSA-IV	9	WA MRSA-13	0	0	2 (1 ACT/NSW) (1 Tas/Vic)
ST8-MRSA-IV	8	WA MRSA-12	0	0	4 (3 ACT/NSW) (1 NT/Qld)
STnovel-MRSA-IV	Singleton		1 (NT/Qld)	1 (NT/Qld)	0
ST152-MRSA-V	Singleton		0	1 (SA)	0
ST8-MRSA-V	8		2 (SA)	0	0

10.7 Panton-Valentine Leucocidin (PVL) Toxin

Clone		Positive	Negative	Total
ST1-MRSA-IV	WA MRSA -1	5	59	64
ST93-MRSA-IV	Queensland MRSA	56	2	58
ST30-MRSA-IV	WSSP MRSA	25	1	26
ST129-MRSA-IV	WA MRSA - 2	0	19	19
ST5-MRSA-IV	WA MRSA - 3	0	14	14
ST8-MRSA-IV	WA MRSA - 12	3	1	4
ST584-MRSA-IV	WA MRSA - 13	0	2	2
ST59-MRSA-IV	WA MRSA - 15	0	2	2
ST45-MRSA-IV	WA MRSA - 23	0	2	2
ST8-MRSA-IV	WA MRSA - 5	0	1	1
ST75-MRSA-IV	WA MRSA - 8	0	1	1
ST583-MRSA-IV	WA MRSA - 17	1	0	1
Total		90	104	194

10.7.1 Pantone-Valentine Leucocidin (PVL) Toxin: Regional Distribution

Region	cMRSA n	ST1 MRSA IV (WA1)	ST129 MRSA IV (WA2)	ST5 MRSA IV (WA3)	ST8 MRSA IV (WA5)	ST75 MRSA IV (WA8)	ST8 MRSA IV (WA12)	ST584 MRSA IV (WA13)	ST93 MRSA IV (QLD)	ST30 MRSA IV (WSPF)	ST59 MRSA IV (WA15)	ST583 MRSA IV (WA17)	ST45 MRSA IV (WA23)	TOTAL n (%)
ACT/NSW	62	0	0	0	0	0	3 (100)	0	31(94)	12 (92)	0	1 (100)	0	47 (76)
NT/Qld	51	2 (17)	0	0	0	0	0	0	20 (100)	12 (100)	0	0	0	34 (67)
SA	26	1 (6)	0	0	0	0	0	0	3 (100)	0	0	0	0	4 (15)
Tas/VIC	11	0	0	0	0	0	0	0	0	0	0	0	0	0
WA	44	2 (9)	0	0	0	0	0	0	2 (100)	1 (100)	0	0	0	5 (11)
Total	194	5 (8)	0	0	0	0	3 (75)	0	56 (97)	25 (96)	0	1 (100)	0	90 (46)

10.8 cMRSA Antibiogram

	ST1 MRSA IV (WA1)	ST129 MRSA IV (WA2)	ST5 MRSA IV (WA3)	ST8 MRSA IV (WA5)	ST75 MRSA IV (WA8)	ST8 MRSA IV (WA12)	ST584 MRSA IV (WA13)	ST93 MRSA IV (QLD)	ST30 MRSA IV (WSP)	ST59 MRSA IV (WA15)	ST583 MRSA IV (WA17)	ST45 MRSA IV (WA23)	TOTAL
Ox ^R	33	1	7	1	1		1	53	20	1			117
One non beta lactam antibiotic													
Ox ^R Em ^R	8	15	4			1	1	4		1			34
Ox ^R Cp ^R	3	1	2						4			1	11
Ox ^R FA ^R	10												10
Ox ^R Gm ^R			1										1
Ox ^R Tc ^R								1					1
Two non beta lactam antibiotics													
Ox ^R Em ^R FA ^R	7												7
Ox ^R Cp ^R FA ^R	1					1							2
Ox ^R Em ^R Rf ^R	1												1
Ox ^R Em ^R Cp ^R		1										1	2
Ox ^R Em ^R Mp ^R		1											1
Ox ^R Em ^R Tm ^R						1							1
Ox ^R Em ^R Tc ^R									2				2
Ox ^R Tc ^R FA ^R											1		1
Three non beta lactam antibiotics													
Ox ^R Em ^R Cp ^R FA ^R	1												1
Ox ^R Em ^R Tc ^R Tm ^R				1									1
Ox ^R Em ^R Cp ^R Tc ^R						1							1
	64	19	14	1	1	4	2	58	26	2	1	2	194

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

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