

The Australian Group on Antimicrobial Resistance

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***Staphylococcus aureus* Programme 2008 (SAP 2008)
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) 2008
***Staphylococcus aureus* Surveillance Programme (SAP 2008)**

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***Staphylococcus aureus* Programme 2008 (SAP 2008)**

Community Survey

MRSA Epidemiology and Typing Report

1. Overview

Of the 553 S aureus classified as MRSA in the SAP 2008 Community Survey, molecular typing was performed on 547 (98.9%) isolates. The mean age of patients with infections due to community-associated MRSA (CA-MRSA) strains (40 years; median 35 years) was found to be significantly lower ($p < 0.0001$) than the mean age of patients with infections due to healthcare-associated MRSA (HA-MRSA) strains (69 years; median 74 years). Although the percentage of S aureus characterized as HA-MRSA in this survey (6.7%) was the same when compared to the 2006 survey, ST22-MRSA-IV (EMRSA-15) has emerged as a major HA-MRSA clone in most Australian communities surveyed, accounting for 20.5% of all community MRSA infections. Of continuing concern has been the rapid emergence of this clone in the Victorian/Tasmanian (0% in 2002 to 21.0% in 2008) and the ACT/NSW communities (18.4% in 2000 to 32.3% in 2008). CA-MRSA accounted for 62.2% of MRSA and 11.1% of all S aureus. Since 2000 there has been a 136% increase in the number of S aureus characterized as CA-MRSA. As in previous surveys, although CA-MRSA was multiclonal (22 clones) 90.6% of strains could be characterized into six clones. ST93-MRSA-IV (Queensland CA-MRSA), a Panton Valentine leucocidin (PVL)-positive clone, remains the most frequently isolated CA-MRSA clone in the Australian community accounting for 44.1% of all CA-MRSA and 27.4% of all MRSA infections. Overall 64.7% of CA-MRSA were PVL positive, a 26% increase when compared to the 2006 survey. The mean age of patients with PVL positive CA-MRSA infections (33 years; median 30 years) was significantly lower ($p < 0.0001$) than the mean age of patients with PVL negative CA-MRSA infections (53 years; median 56 years). The 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 CA-MRSA clones including ST30-MRSA-IV (WSPP MRSA), ST8-MRSA-IV (USA300) ST59-MRSA-V_T (Taiwan CA-MRSA) and ST80-MRSA-IV (European CA-MRSA). 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 2008 programme (SAP 2008) up to 100 clinically significant consecutive isolates of *S aureus* from different patients were collected by each of 31 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. Methicillin-resistant *S aureus* (MRSA) isolates were referred to the Western Australian

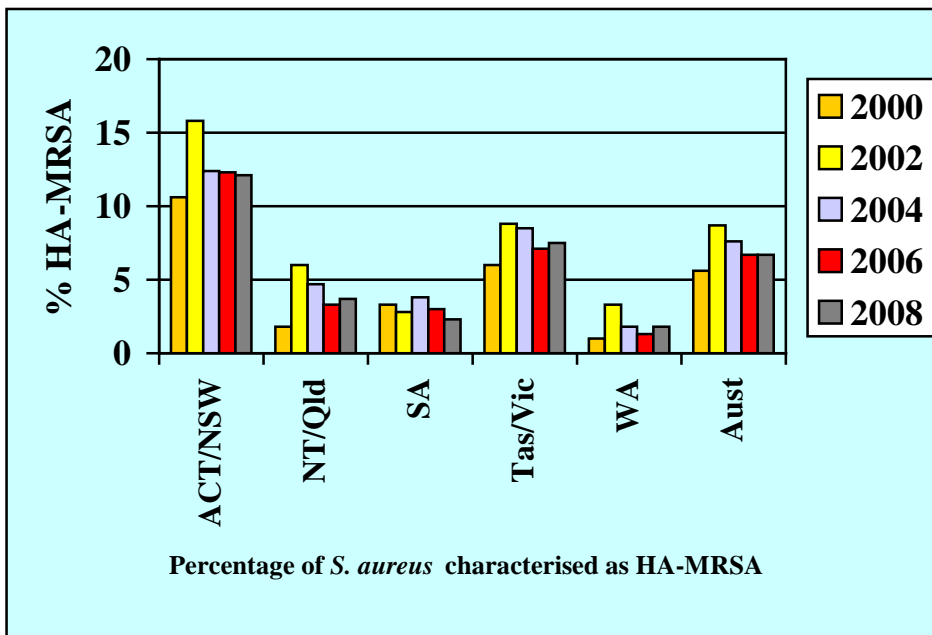
(WA) Gram-positive Bacteria Typing and Research Unit (GPBTRU) for clone characterization and Panton-Valentine leucocidin (PVL) toxin determination.

The molecular characterization of the MRSA isolates is designed to provide a “snapshot” of MRSA clones circulating in the Australian community.

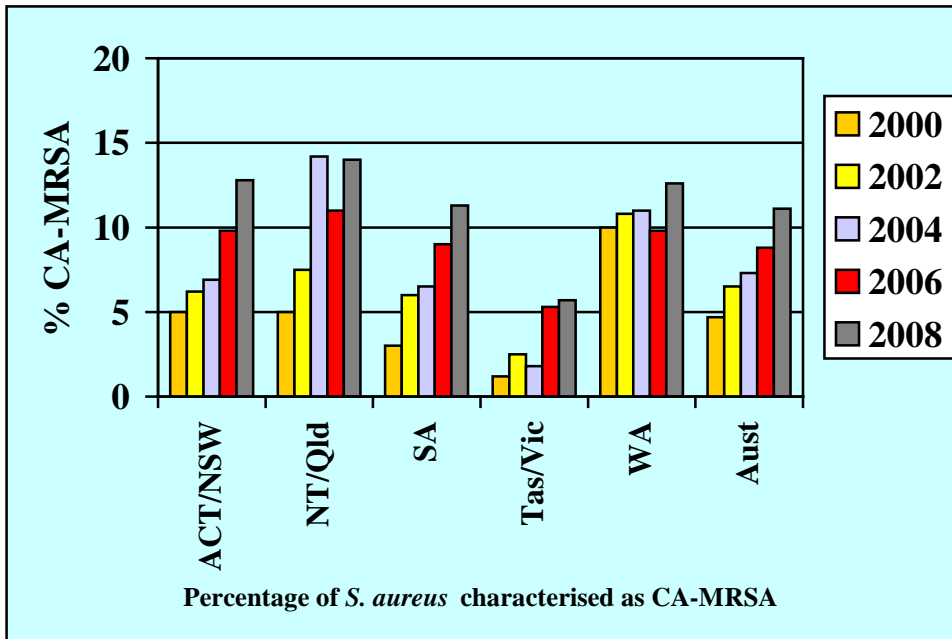
Of the 553 (18.0%) *S aureus* classified as MRSA in SAP 2008, 547 (98.9%) were referred to the WA GPBTRU. Overall 62.2% and 37.8% of MRSA were characterized as Community-associated (CA-MRSA) and Healthcare-associated (HA-MRSA) respectively. The mean age of patients with CA-MRSA infections (40 years; median 35 years) was significantly lower ($p < 0.0001$) than the mean age of patients with HA-MRSA infections (69 years; median 74 years).

Since the initial community *S aureus* surveillance study performed in 2000 there has been a significant increase ($p < 0.0001$) in the percentage of patients with MRSA infections particularly in the Tas/Vic ($p = 0.0015$), ACT/NSW ($p = 0.0015$) and NT/Qld ($p < 0.0001$) regions.

Throughout Australia the percentage of *S aureus* characterized as HA-MRSA was 6.7% ranging from 1.8% in WA to 12.1% in the ACT/NSW region.

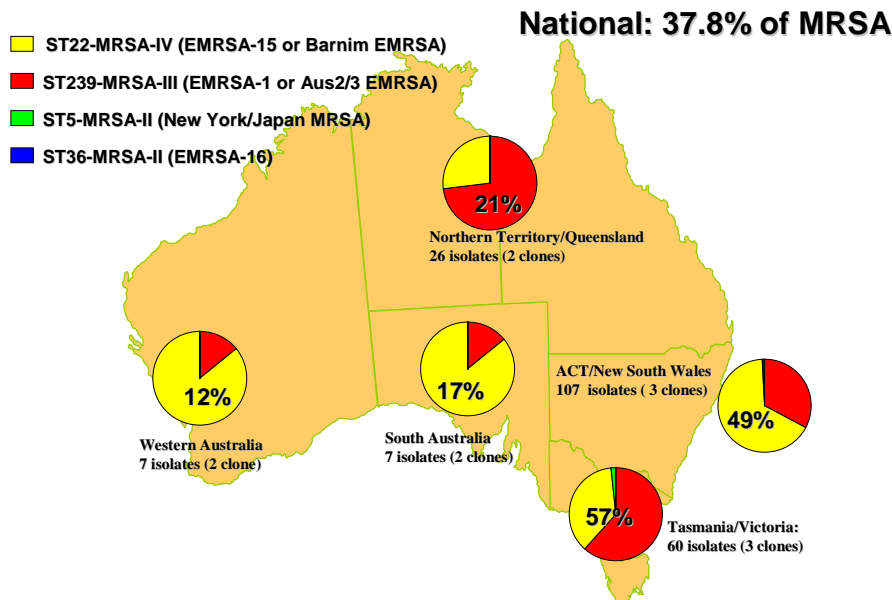


The percentage of *S aureus* characterized as CA-MRSA was 11.1% ranging from 5.7% in the Tas/Vic region to 14.0% in the NT/Qld region.



2.1. HA-MRSA

Four HA-MRSA clones were identified in the Australian community; 54.1% were ST22-MRSA-IV (EMRSA-15), 44.9% ST239-MRSA-III (Aus-2/3 EMRSA), 0.5% ST5-MRSA-II (New York/Japan MRSA) and 0.5% ST36-MRSA-II (EMRSA-16).



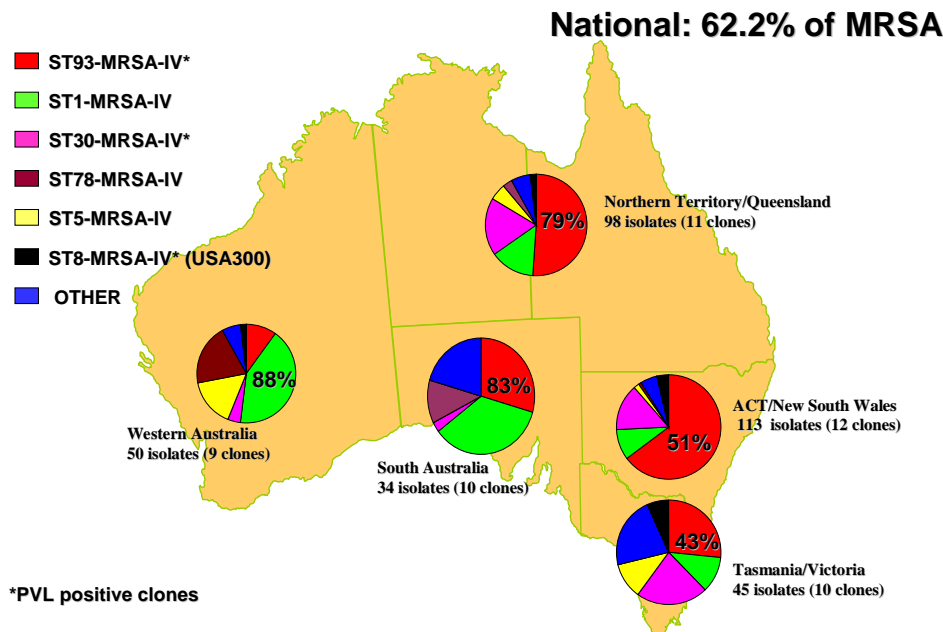
Aus2/3 EMRSA was isolated in most Australian regions, accounting for 35.2% of MRSA in the Tas/Vic region. Over the four community surveys the percentage of isolates characterized as Aus-2/3 has decreased throughout Australia. EMRSA-15, which was initially reported in Australia in 1997, accounted for 20.5% of all MRSA isolated in Australia, ranging from 5.6% in the NT/Qld region to 32.3% in the ACT/NSW region. The percentage of MRSA characterized as EMRSA-15 has increased in all Australian regions over the four surveys noticeably in the ACT/NSW and Tas/Vic regions.

2.2. CA-MRSA

Twenty two CA-MRSA clones were identified by pulsed-field gel electrophoresis (corresponding to 19 MLST/SCC_{mec} clones) of which 90.6% were made up of six clones:

- ST93-MRSA-IV [Qld CA-MRSA] (44.1%)
- ST1-MRSA-IV [WA MRSA-1] (18.5%)
- ST30-MRSA-IV [WSPP CA-MRSA] (13.8%)
- ST5-MRSA-IV [WA MRSA-3] (5.9%)
- ST78-MRSA-IV [WA MRSA-2] (5.3%)
- ST8-MRSA-IV [USA300] (2.9%)

ST93-MRSA-IV (PVL-positive Queensland clone), which was isolated in all regions, remained the predominant CA-MRSA clone isolated in Australia.

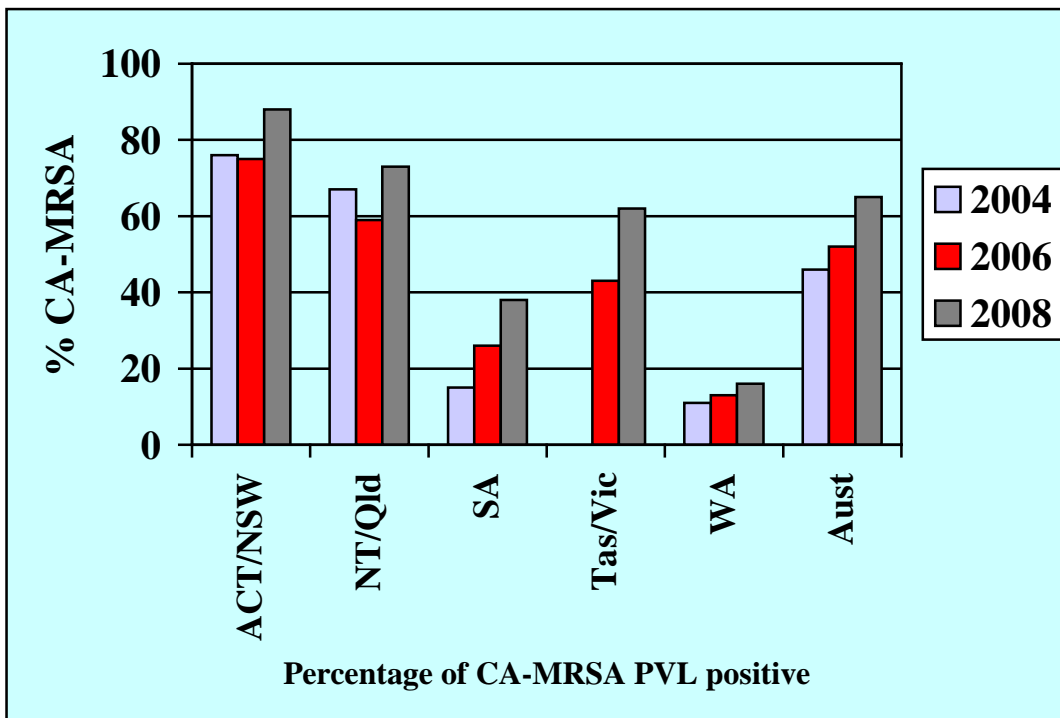


2.3. Panton-Valentine Leucocidin (PVL) Toxin

CA-MRSA

Overall 64.7% (n=220) of CA-MRSA (9 clones) were PVL positive:

- ST93-MRSA-IV (Qld CA-MRSA) – 149 isolates
- The following recognised international clones:
 - o ST30-MRSA-IV (WSPP) – 46 isolates
 - o ST8-MRSA-IV (USA300) – 10 isolates
 - o ST80-MRSA-IV (European CA-MRSA) – 2 isolates
 - o 59-MRSA-V_T (Taiwan CA-MRSA) – 1 isolates
- Nine isolates of ST1-MRSA-IV (WA MRSA-1). It is possible that these are USA400 strains however further molecular studies are required to confirm
- In addition, the following three “Australian CA-MRSA” clones also contained PVL positive isolates
 - o ST5-MRSA-IV (WA MRSA-3) – 1 isolate
 - o ST78-MRSA-IV (WA MRSA-2) – 1 isolate
 - o ST88-MRSA-V – 1 isolate



Although PVL positive CA-MRSA were also isolated throughout Australia, the percentage of CA-MRSA that were positive varied from 16% in WA to 73% and 88% in NT/Qld and ACT/NSW respectively. In the previous community survey (SAP 2006), 52% of CA-MRSA were PVL positive ranging from 13% in WA to 75% in ACT/NSW.

The mean age of patients with PVL positive CA-MRSA infections (33 years; median 30 years) was significantly lower ($p < 0.0001$) than the mean age of patients with PVL negative CA-MRSA infections (53 years; median 56 years).

HA-MRSA

A PVL-positive ST22-MRSA-IV (EMRSA-15) was identified by PCR in the ACT/NSW region. This result was confirmed by array hybridisation. The detection of PVL in a prevalent HA-MRSA 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 2008 Protocol

3.1. Commencement Date

1st July 2008

3.2. Isolates

Approximately 100 consecutive isolates of *Staphylococcus aureus* from 100 different patients at each site were tested by 31 laboratories located across Australia (total number of isolates = 3,075). Isolates were collected from outpatients' only and excluded dialysis and day surgery patients. Isolates from Nursing Homes, Long-Term Care Facilities and Hospice patients were included. Each *S aureus* isolate was from an individual patient and was judged to have come from a potentially infected site.

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
Sydney South West Pathology Service
Westmead Hospital

Northern Territory (1)
Royal Darwin Hospital

Queensland (6)
Pathology Queensland Cairns Base
Hospital
Pathology Queensland Gold Coast
Hospital
Pathology Queensland Prince Charles
Hospital
Pathology Queensland Princess
Alexandra Hospital
Pathology Queensland Central Laboratory
Sullivan Nicolaidis Pathology

South Australia (3)
SA Pathology, Flinders Medical Centre
SA Pathology, Institute of Medical
Veterinary Science
SA Pathology, 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-P579 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.
- School of Pathology and Laboratory Medicine, University of Western Australia, Crawley, 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 *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).

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](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. 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* (*SCCmec*)

The gene for methicillin resistance, *mecA*, is contained within a mobile element known as the *mec* region or staphylococcal cassette chromosome *mec* (*SCCmec*). The *SCCmecs* differ depending on variations in the *mecA* regulatory region (*mec* complex),

the type of cassette chromosome recombinases (*ccr* genes), and the resistance determinants they have acquired due to the integration of plasmids and transposons.

Eight SCC*mec* types have been identified globally. Types I, II, III and VI are associated with “health-care-associated MRSA” (HA-MRSA) while Types IV, V, VII and VIII are normally associated with “community associated MRSA” (CA-MRSA).

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

3.7. Panton-Valentine Leucocidin (PVL) Toxin

CA-MRSA clones have been shown to acquire several virulence genes including the determinants for PVL (2). PVL is a necrotizing toxin that causes leucocyte destruction and tissue necrosis and is associated with abscesses and severe pneumonia. It is present in the majority of CA-MRSA studied in Europe and USA (3). In Australia, it was initially reported that CA-MRSA infrequently carry the genes encoding PVL (4). However, two CA-MRSA 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 CA-MRSA clones have recently been identified in Australia including (8):

1. ST8-MRSA-IV (USA300)
2. ST80-MRSA-IV (European CA-MRSA)
3. ST59-MRSA-V_T (Taiwan CA-MRSA)
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 CA-MRSA 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-P579 card (BioMerieux, Durham, NC). Antimicrobials tested were benzylpenicillin, oxacillin, ceftiofloxacin, cefazolin, vancomycin, rifampicin, fusidic acid, gentamicin, erythromycin, clindamycin, tetracycline, trimethoprim/sulphamethoxazole (cotrimoxazole), ciprofloxacin, quinupristin/dalfopristin (Synercid®), teicoplanin, linezolid, nitrofurantoin, mupirocin and chloramphenicol. Penicillin susceptible strains were tested for β -lactamase production using nitrocefin. A ceftiofloxacin disc diffusion test (CLSI or CDS method) was used to confirm methicillin-resistance. The MIC of tigecycline, daptomycin and mupirocin-resistant isolates was determined by Etest® (AB Biodisk, Solna, Sweden).

Resistogram

Disk Diffusion (14,15)

mercuric chloride (HgCl₂) (0.4 μ M)
phenylmercuric acetate (PMA) (5 mM)

Urease

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

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

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

Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)

Electrophoresis of chromosomal DNA was performed as previously described (18) using the CHEF DR III System (Bio-Rad Laboratories Pty Ltd). Chromosomal patterns were examined visually, scanned with a Quantity One® and digitally analysed using FPQuest™ software (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/](http://www.mlst.net/), to assign a sequence type (ST). Using the MLST database, clones were subsequently grouped into clonal complexes.

Staphylococcal Chromosomal Cassette *mec* (SCC*mec*)

The SCC*mec* was typed by PCR using previously published primers that identified the class of *mec* complex and type of cassette chromosome recombinase (*ccr*) encoded on the element (20,21,22)

4.2. Identification of HA-MRSA Clones

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

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

ST22-MRSA-IV (EMRSA-15)

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

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

- Antibiogram
- Urea broth
- Coagulase PCR/RFLP
- CHEF

ST36-MRSA-II (UK EMRSA-16)

- Antibiogram
- Urea broth
- Coagulase PCR/RFLP
- CHEF

4.3. Identification of CA-MRSA Clones

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

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP on selected isolates

ST93-MRSA-IV (Queensland MRSA)

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP on selected isolates

ST8-MRSA-IV (USA300 MRSA)

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP on selected isolates

ST59-MRSA-V_T (Taiwan MRSA)

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP

ST80-MRSA-IV (European MRSA)

Antibiogram
Urea broth
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)
ST59-MRSA-IV (WA-15)
ST45-MRSA-IV (WA-23)
ST72-MRSA-IV (WA-44)

Antibiogram
Urea broth
CHEF
Coagulase PCR-RFLP on selected isolates

ST45-MRSA-V (WA-84)
ST834-MRSA-IV (WA-13)
ST73-MRSA-IV (WA-65)
ST1304-MRSA-IV (WA-72)
ST5-MRSA-V
ST1-MRSA-V
ST88-MRSA-V
ST5-MRSA-IV
ST207-MRSA-V

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).

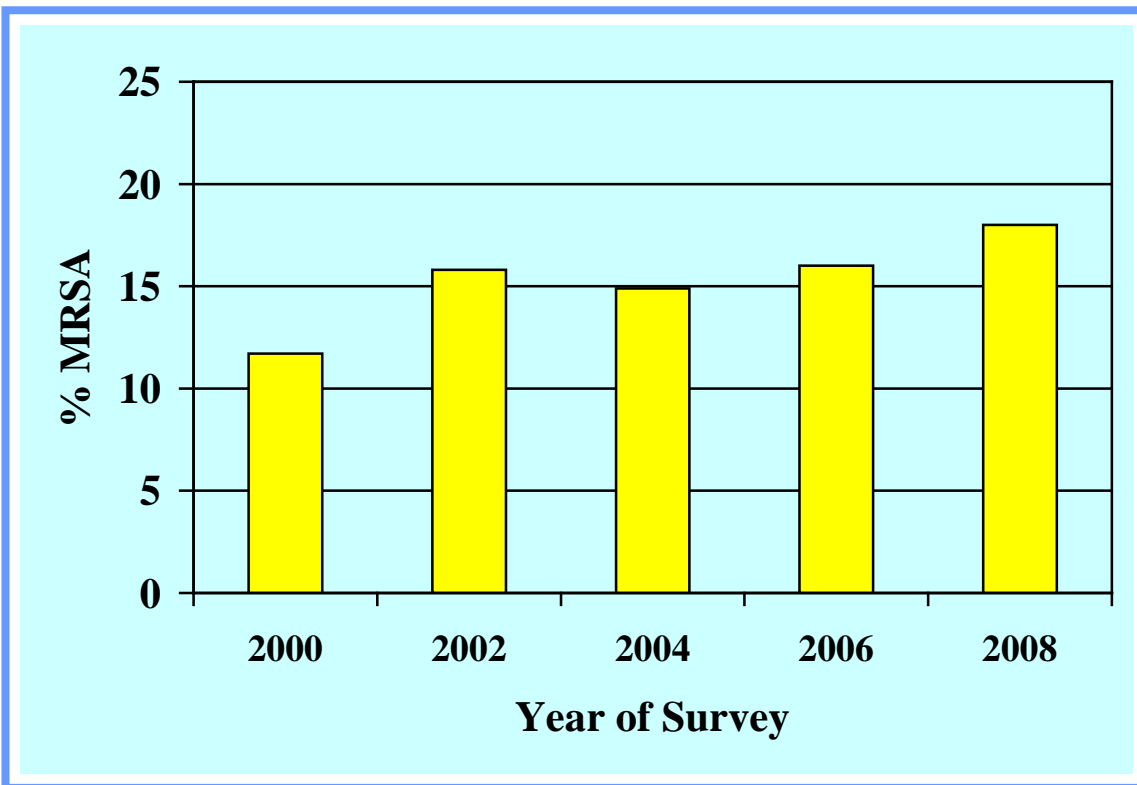
5. Results

In SAP 2008, 553 (18.0%) *Staphylococcus aureus* were classified as MRSA.

5.1. AGAR Community SAP 2000 – 2008

Percentage of *Staphylococcus aureus* Identified as 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
2006	30	2,979	476	16.0
2008	31	3,075	553	18.0

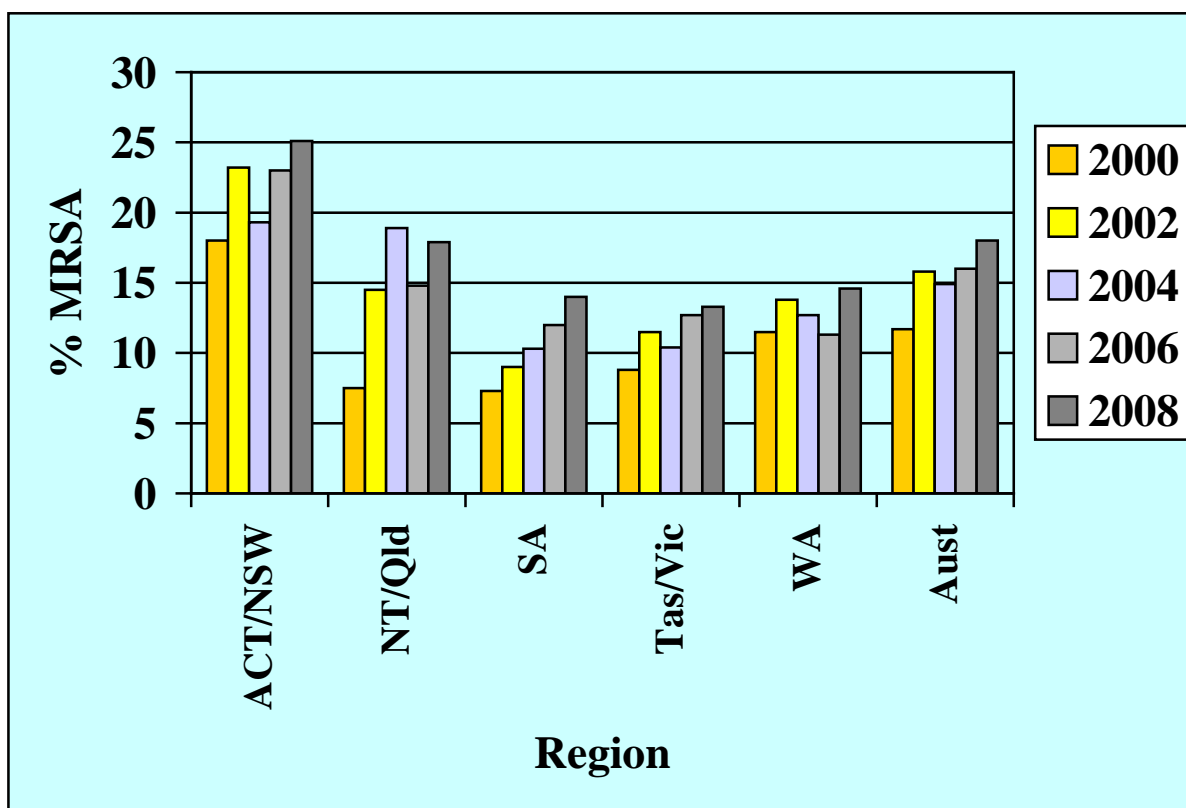


Percentage figures relate to the total number of *Staphylococcus aureus* isolates

Regional Distribution of MRSA

Region	2000	2002	2004	2006	2008
ACT/NSW	144 (18.0%)	183 (23.2%)	173 (19.3%)	206 (23.0%)	222 (25.1%)
NT/Qld	30 (7.5%)	58 (14.5%)	68 (18.9%)	89 (14.8%)	125 (17.9%)
SA	29 (7.3%)	36 (9.0%)	41 (10.3%)	36 (12.0%)	42 (14.0%)
Tas/Vic	44 (8.8%)	46 (11.5%)	62 (10.4%)	100 (12.7%)	106 (13.3%)
WA	46 (11.5%)	55 (13.8%)	51 (12.7%)	45 (11.3%)	58 (14.6%)
Total	293 (11.7%)	378 (15.8%)	395 (14.9%)	476 (16.0%)	553 (18.0%)

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 2008 Epidemiological Typing of MRSA

Of the 553 MRSA identified in SAP 2008, 547 (98.9%) were referred to the GPBTRU for epidemiological typing

Typing Tests Performed

Test	Number
Cefoxitin Susceptibility Testing	575
Coagulase Gene PCR-RFLP Assay	107
Resistogram	97
Contour-clamped Homogeneous Electric Field Electrophoresis (CHEF)	568
Urease Reaction	571
Multi Locus Sequencing Typing (MLST)	10
SCC _{mec} PCR	18
Panton-Valentine Leucocidin PCR	568

Regional Distribution of HA-MRSA and CA-MRSA

Region	HA-MRSA (%)	CA-MRSA (%)	Total MRSA
ACT/NSW	107 (48.6)	113 (51.4)	220
NT/Qld	26 (21.0)	98 (79.0)	124
SA	7 (17.1)	34 (82.9)	41
Tas/Vic	60 (57.1)	45 (42.9)	105
WA	7 (12.3)	50 (87.8)	57
TOTAL	207 (37.8)	340 (62.2)	547

Percentage figures relate to the total number of MRSA isolates

SAP 2000 – 2008: Regional Distribution of HA-MRSA and CA-MRSA

	2000 (n = 257) ^a		2002 (n = 363) ^b		2004 (n = 395)		2006 (n = 462) ^c		2008 (n=547) ^d	
Region	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)	HA-MRSA (%)	CA-MRSA (%)
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)	107 (48.6)	113 (51.4)
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)	26 (21.0)	98 (79.0)
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)	7 (17.1)	34 (82.9)
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)	60 (57.1)	45 (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)	7 (12.3)	50 (87.8)
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)	207 (37.8)	340 (62.2)

Percentage figures relate to the total number of MRSA isolates

^aIn SAP 2000, 257 of the 293 MRSA were fully characterized;

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

^cIn SAP 2006, 462 of the 476 MRSA were fully characterized

^dIn SAP 2008, 547 of the 553 MRSA were fully characterized

SAP 2000 – 2008: Regional Distribution of HA-MRSA and CA-MRSA as a Proportion of *Staphylococcus aureus*

Region	2000			2002			2004			2006		
	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)	Total	HA-MRSA (%)	CA-MRSA (%)
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)

Region	2008		
	Total	HA-MRSA (%)	CA-MRSA (%)
ACT/NSW	886	107 (12.1)	113 (12.8)
NT/Qld	698	26 (3.7)	98 (14.0)
SA	300	7 (2.3)	34 (11.3)
Tas/Vic	795	60 (7.5)	45 (5.7)
WA	396	7 (1.8)	50 (12.6)
TOTAL	3075	207 (6.7)	340 (11.1)

SAP 2008: HA-MRSA by AGAR Laboratory

LAB	ST22-MRSA-IV EMRSA-15	ST239-MRSA-III Aus-2 EMRSA	ST239-MRSA-II Aus-3 EMRSA	ST5-MRSA-II NY/Japan MRSA	ST36-MRSA-II EMRSA-16	TOTAL
ACT/NSW (107)						
1	1	1				2
2	12	8				20
3	5	4				9
4	13	5			1	19
5	7	4	1			12
6	6	8				14
7	6	1				7
8	14	3				17
9	7					7
NT/Qld (26)						
10		3	3			6
11	3	1				4
12	2	2				4
13	1					1
28		5				5
29						0
30	1	4	1			6
SA (7)						
14	6		1			7
15						0
16						0
Tas/Vic (60)						
18	1		1			2
19	5	7	8	1		21
20	1	2	2			5
21			1			1
22		2	1			3

SAP 2008: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

LAB	ST22-MRSA-IV EMRSA-15	ST239-MRSA-III Aus-2 EMRSA	ST239-MRSA-II Aus-3 EMRSA	ST5-MRSA-II NY/Japan MRSA	ST36-MRSA-II EMRSA-16	TOTAL
23	8		10			18
31	5	2	1			8
32	2					2
WA (7)						
24	3		1			4
25						0
26	2					2
27	1					1
TOTAL	112	62	31	1	1	207

SAP 2008: CA-MRSA by AGAR Laboratory

ST SCCmec	1 IV WA1	1 V	5 IV WA3	73 IV WA65	5 IV	5 V	8 IV WA5	8 IV USA 300	834 IV WA13	30 IV WSP	45 V WA4	45 V WA84	45 IV WA23	59 IV WA15	59 V Taiwan	72 IV WA44	1304 IV WA72	78 IV WA2	80 IV Eur	88 V	207 V	93 IV Qld	Total
ACT/NSW (113)																							
1													1									4	5
2	2									2												5	9
3	2		1							2												20	25
4	1				1											1		1			1	2	7
5	1		1							4				1					1			9	17
6	1							1		4												10	16
7	1							1		1												9	12
8	1							1		1												4	7
9	2							1		2												10	15
NT/Qld (98)																							
10	5		1			1																7	15
11	3	1						1		3												8	16
12	1									2						1		1				11	16
13	2							1		2												9	14
28	2									3								1				3	9

SAP 2008: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

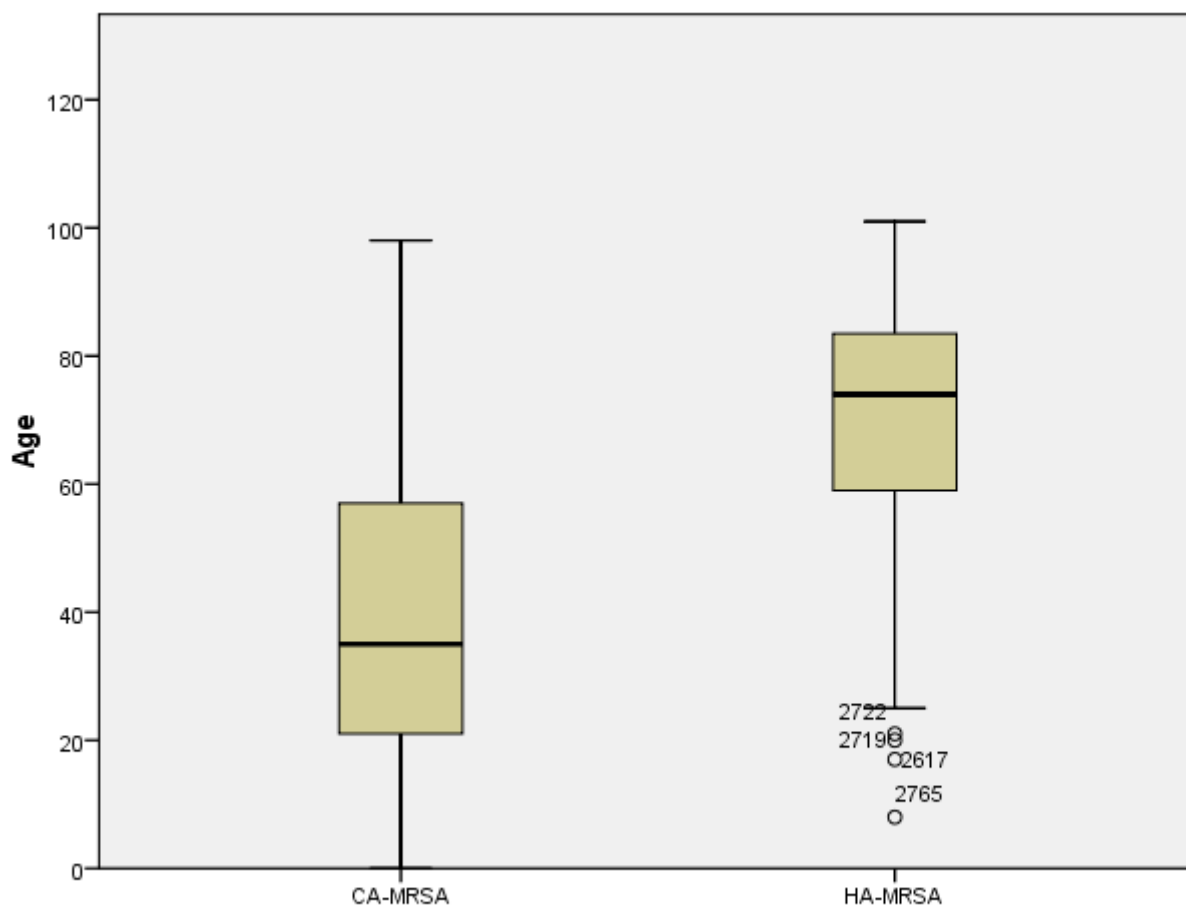
ST SCCmec	1 IV WA1	1 V	5 IV WA3	73 IV WA65	5 IV	5 V	8 IV WA5	8 IV USA 300	834 IV WA13	30 IV WSP	45 V WA4	45 V WA84	45 IV WA23	59 IV WA15	59 V Taiwan	72 IV WA44	1304 IV WA72	78 IV WA2	80 IV Eur	88 V	207 V	93 IV Qld	Total
29	1		3	2						7							1					5	19
30			1							1												7	9
SA (34)																							
14	7									1		1	1									3	14
15	1			1			1				1				1							2	9
16	4			1																		5	11
Tas/Vic (45)																							
18	1													1									2
19			1					1		3		2										3	10
20	1									1		1										5	8
21	1		3					1		1													6
22												1										1	2
23			1							1		1							1			2	6
31	2					1		1		4		1								1		1	11
32																							0
WA (50)																							
24	6		4						1	1												3	15
25	3		3																			2	12

SAP 2008: COMMUNITY MRSA EPIDEMIOLOGY AND TYPING REPORT

ST SCCmec	1 IV WA1	1 V	5 IV WA3	73 IV WA65	5 IV	5 V	8 IV WA5	8 IV USA 300	834 IV WA13	30 IV WSPP	45 V WA4	45 V WA84	45 IV WA23	59 IV WA15	59 V Taiwan	72 IV WA44	1304 IV WA72	78 IV WA2	80 IV Eur	88 V	207 V	93 IV Qld	Total
26	6		1					1										3				3	14
27	6			1						1	1												9
Total	63	1	20	5	1	2	1	10	1	47	2	7	2	2	1	2	1	18	2	1	1	150	340

Age statistics for Hospital acquisition

Boxplot of age of patients infected with CA-MRSA and HA-MRSA

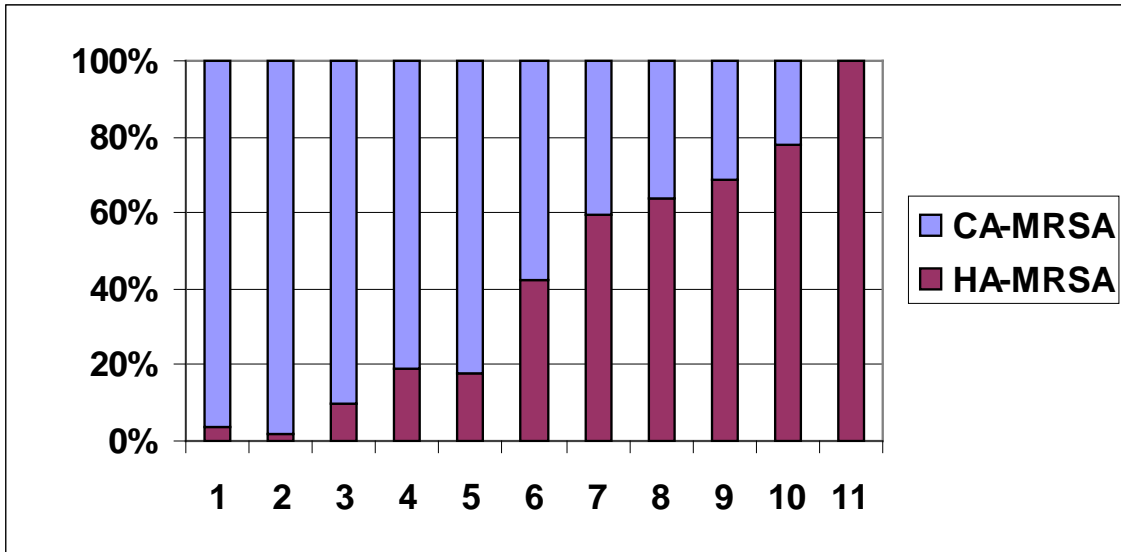


Mean, median and percentile data

Age (years)	CA-MRSA	HA-MRSA
Mean (95% CI)	40.19 (37.57 – 42.81)	69.29 (66.70 – 71.88)
Median	35.00	74.00
25 th percentile	21.00	59.00
75 th percentile	57.00	83.50

The mean age of patients with CA-MRSA is significantly lower ($P < 0.0001$) than the mean age of patients with HA-MRSA.

MRSA Acquisition (CA- or HA-MRSA) by decade of life



5.3. HA-MRSA

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

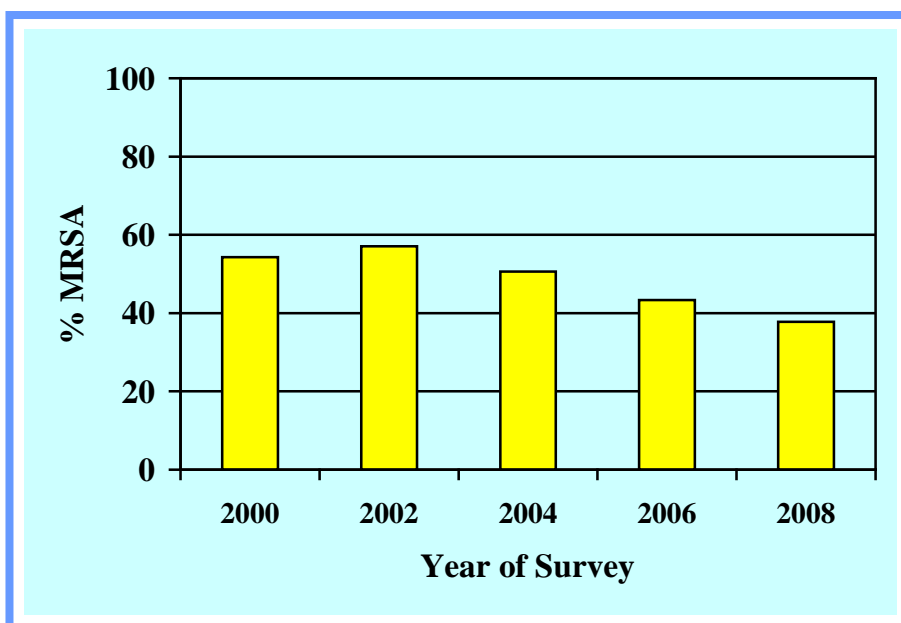
SAP 2008 HA-MRSA

In SAP 2008 four international HA-MRSA clones (207 isolates) were identified

CLONE	ALTERNATIVE NAME	n (%)
ST22-MRSA-IV	EMRSA-15	112 (54.1)
ST239-MRSA-III	Aus -2 and Aus -3 EMRSA	93 (44.9)
ST5-MRSA-II	New York/Japan MRSA	1 (0.5)
ST36-MRSA-II	EMRSA-16	1 (0.5)
TOTAL		207

Percentage figures relate to HA- MRSA isolates

SAP 2000 – 2008: Percentage of MRSA Identified as HA-MRSA



ST22-MRSA-IV

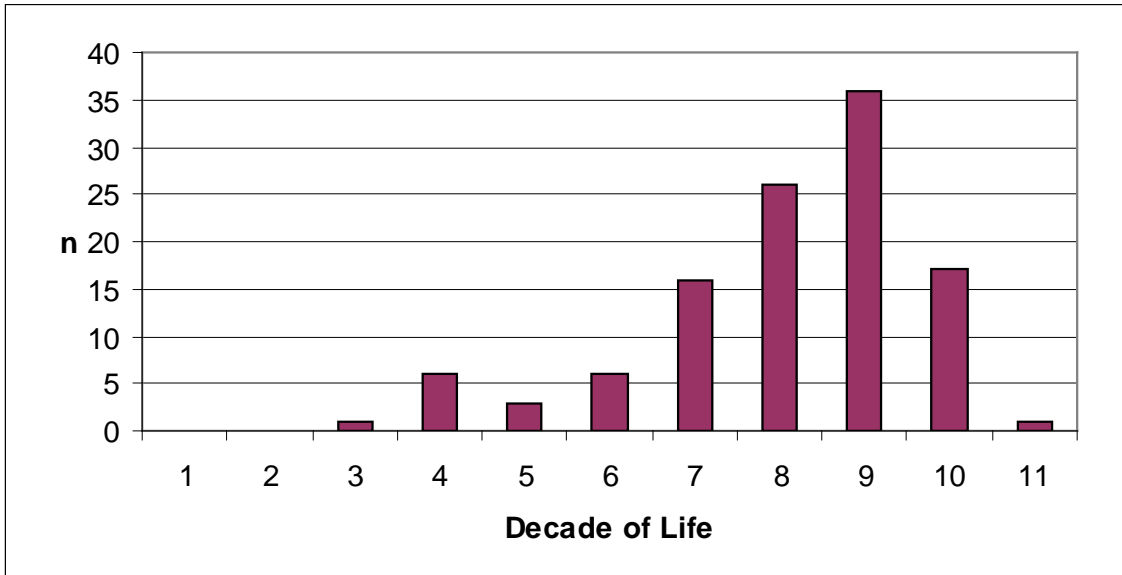
Also known as “EMRSA-15” or the “German Barnim” strain, ST22-MRSA-IV has become a major EMRSA clone in many parts of the world including Australia, United Kingdom, New Zealand, several European countries and recently Singapore. First identified in the Midlands and South-East England in the early 1990s EMRSA-15 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

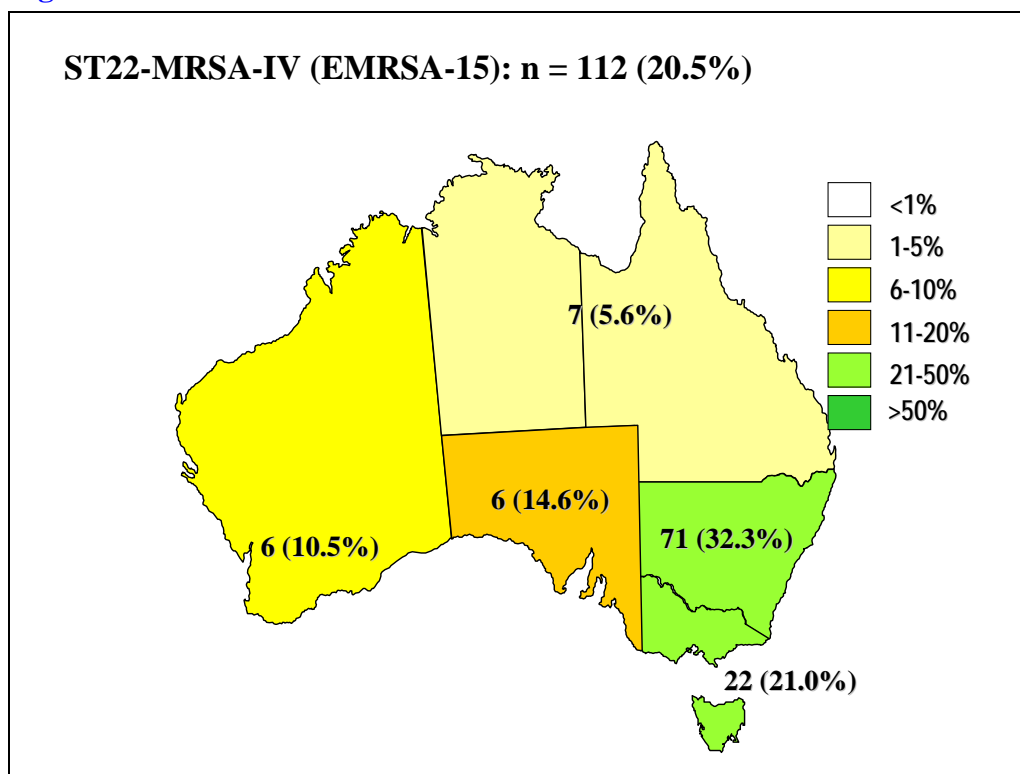
Antibiogram:	Ciprofloxacin ^R	100%
	Erythromycin ^R	63%
	Tetracycline ^R	3%
	Mupirocin ^R	<1%
	Fusidic Acid ^R	<1%
	Rifampicin ^R	0%
	Gentamicin ^R	0%
	Cotrimoxazole ^R	0%
	Mupirocin ^R	<1%
	Fusidic Acid ^R	<1%

Urease: Negative

Patients Infected with ST22-MRSA-IV by Decade of Life



Regional distribution of ST22-MRSA-IV



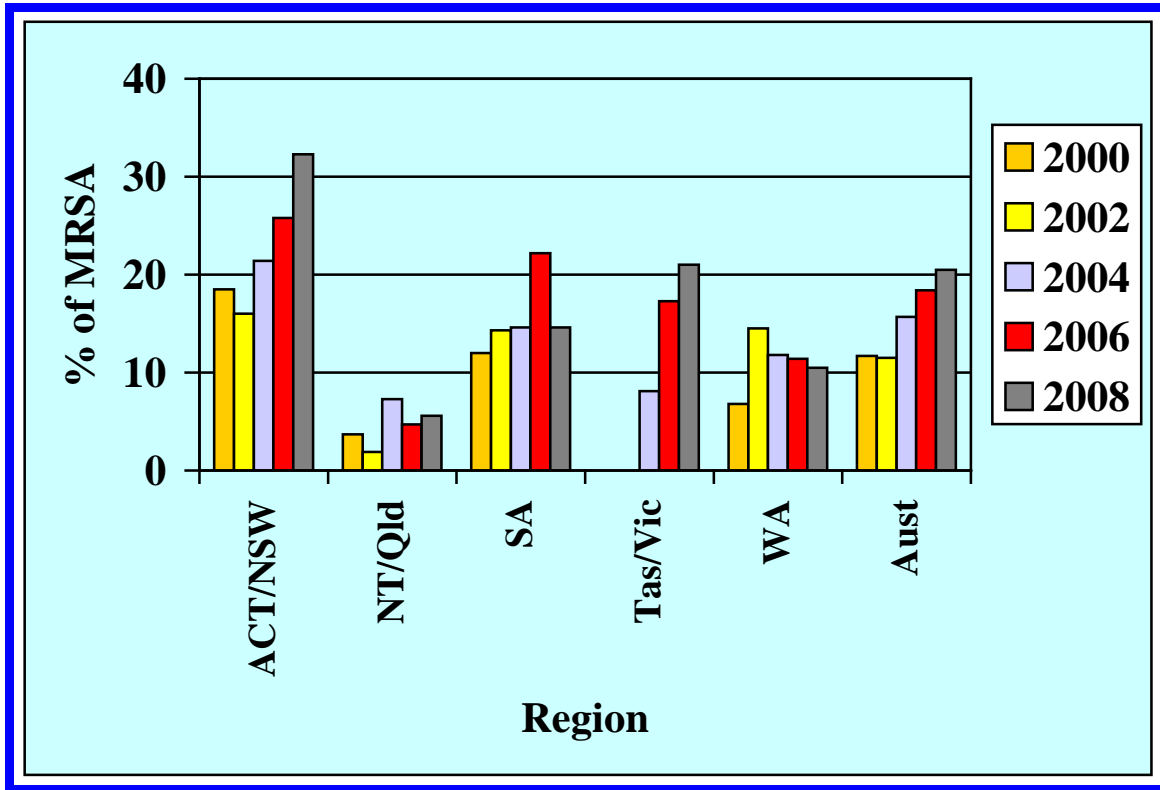
Percentage figures relate to total MRSA isolates

SAP 2000 – 2008: Regional Distribution of ST22-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	23 (18.4%)	28 (16.1%)	37 (21.4%)	51 (25.8%)	71 (32.3%)
NT/Qld	1 (3.7%)	1 (1.9%)	5 (7.3%)	4 (4.7%)	7 (5.6%)
SA	3 (12.0%)	6 (14.6%)	8 (19.5%)	8 (22.2%)	6 (14.6%)
Tas/Vic	0	0	5 (8.1%)	17 (17.3%)	22 (21.0%)
WA	3 (6.8%)	8 (14.5%)	6 (11.8%)	5 (11.4%)	6 (10.5%)
Total	30 (11.7%)	42 (11.6%)	62 (15.7%)	85 (18.4%)	112 (20.5%)

Percentage figures relate to total MRSA isolates

SAP 2000 – 2008: Regional Distribution of ST22-MRSA-IV



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 HA-MRSA clones. It is also known as “EMRSA-1”, “Portuguese/Brazilian” clone or the “Vienna” clone.

Phenotypic Characteristics

Antibiogram:

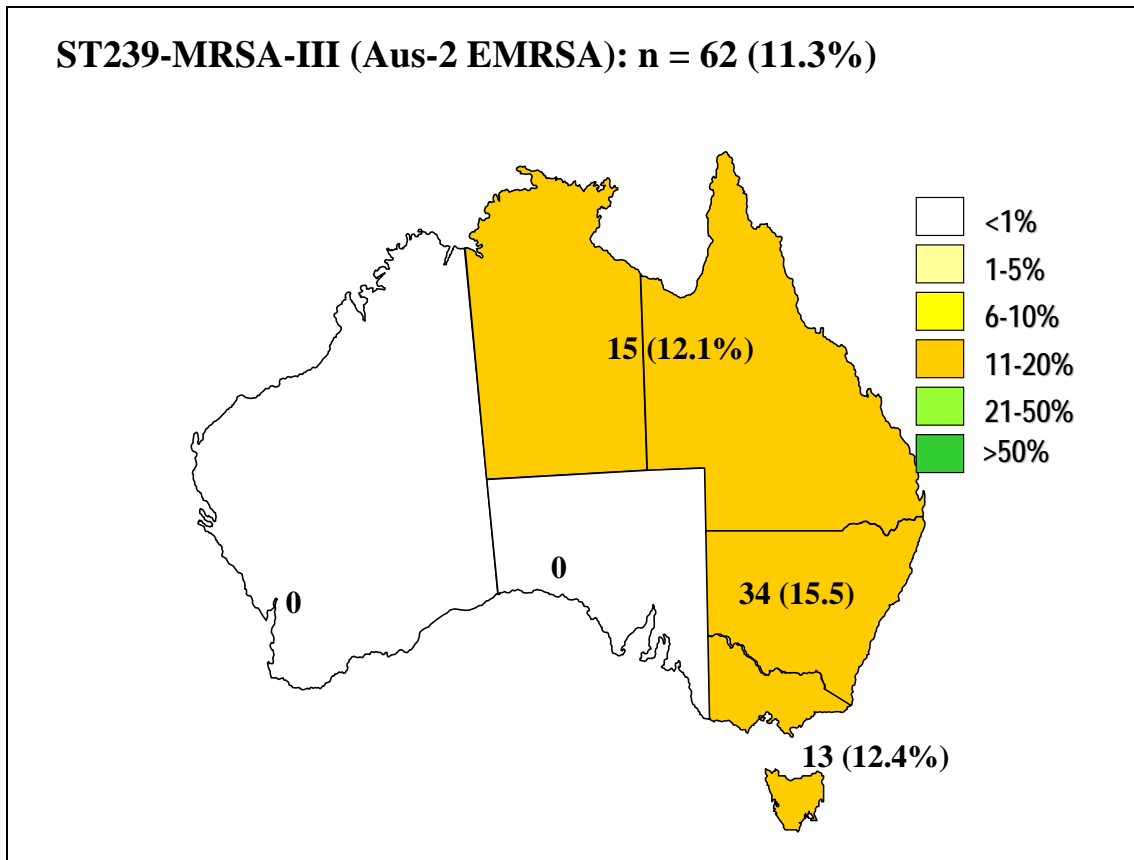
	Aus-2 EMRSA (n = 62)	Aus-3 EMRSA (n = 31)
Erythromycin^R	100	97
Tetracycline^R	98	100
Cotrimoxazole^R	98	100
Gentamicin^R	92	90
Ciprofloxacin^R	95	100
Fusidic Acid^R	2	6
Rifampicin^R	3	13
Mupirocin^R	0	3

Resistogram:

	Aus-2 EMRSA (n = 62)	Aus-3 EMRSA (n = 31)
Mercuric Acetate^R	<1%	>99%
Mercuric Chloride^R	<1%	>99%

Aus-2 EMRSA

Regional Distribution of ST239-MRSA-III (Aus-2 EMRSA)

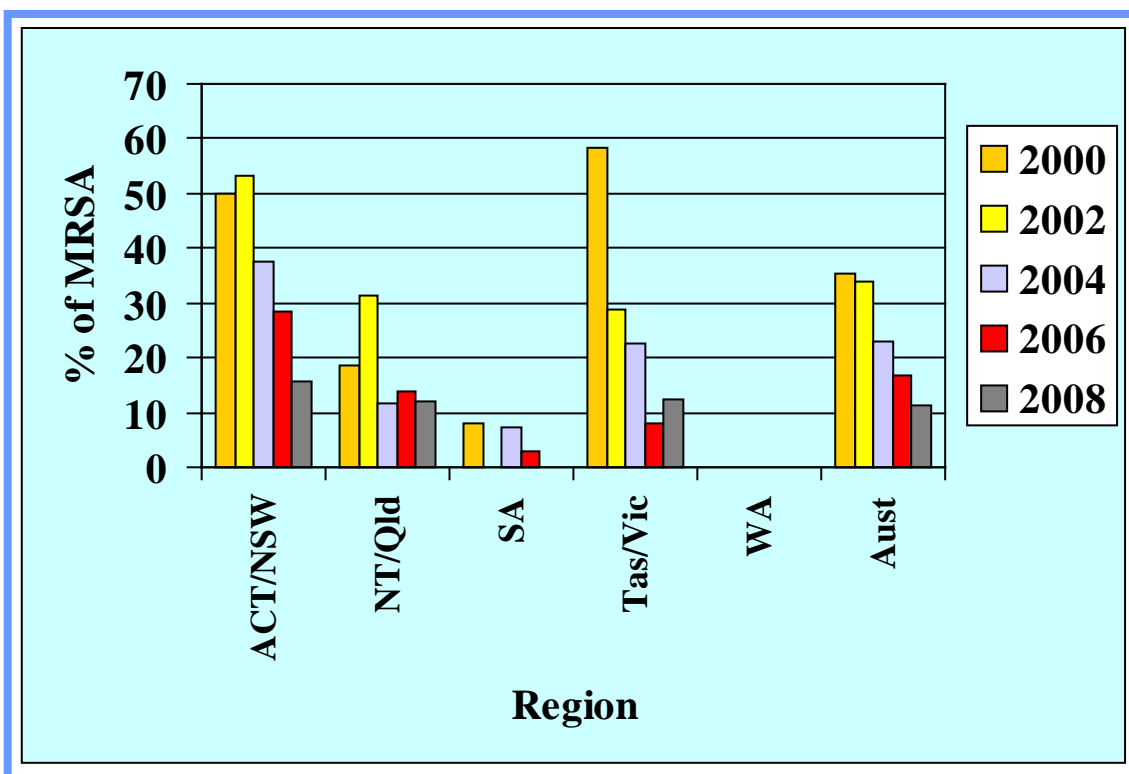


SAP 2000 – 2008: Regional Distribution of ST239-MRSA-III (Aus-2 EMRSA)

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	62 (49.6%)	93 (53.4%)	65 (37.6%)	56 (28.3%)	34 (15.5%)
NT/Qld	5 (18.5%)	17 (31.5%)	8 (11.8%)	12 (14.0%)	15 (12.1%)
SA	2 (8.0%)	0	3 (7.3%)	1 (2.8%)	0
Tas/Vic	21 (58.3%)	13 (28.9%)	14 (22.6%)	8 (8.2%)	13 (12.4%)
WA	0	0	0	0	0
Total	90 (35.0%)	123 (33.9%)	90 (22.8%)	77 (16.6%)	62 (11.3%)

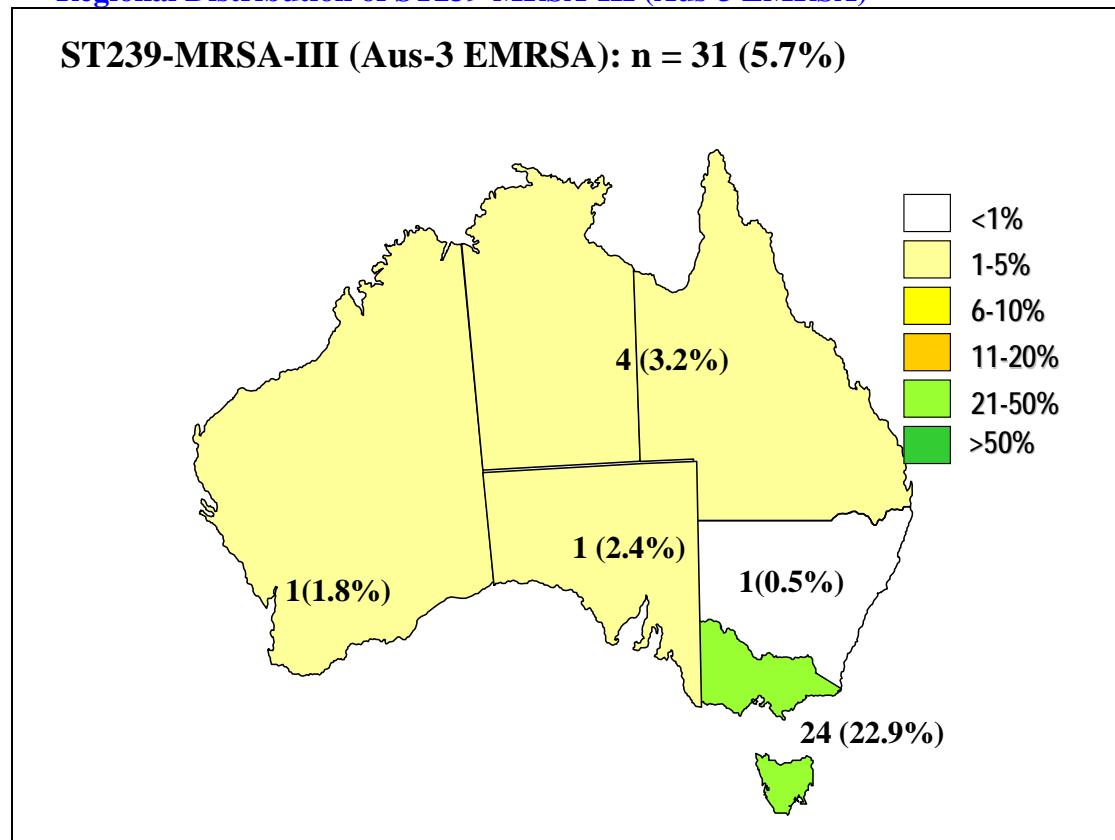
Percentage figures relate to total MRSA isolates

SAP 2000 – 2008: Regional Distribution of ST239-MRSA-III (Aus-2 EMRSA)



Aus-3 EMRSA

Regional Distribution of ST239-MRSA-III (Aus-3 EMRSA)

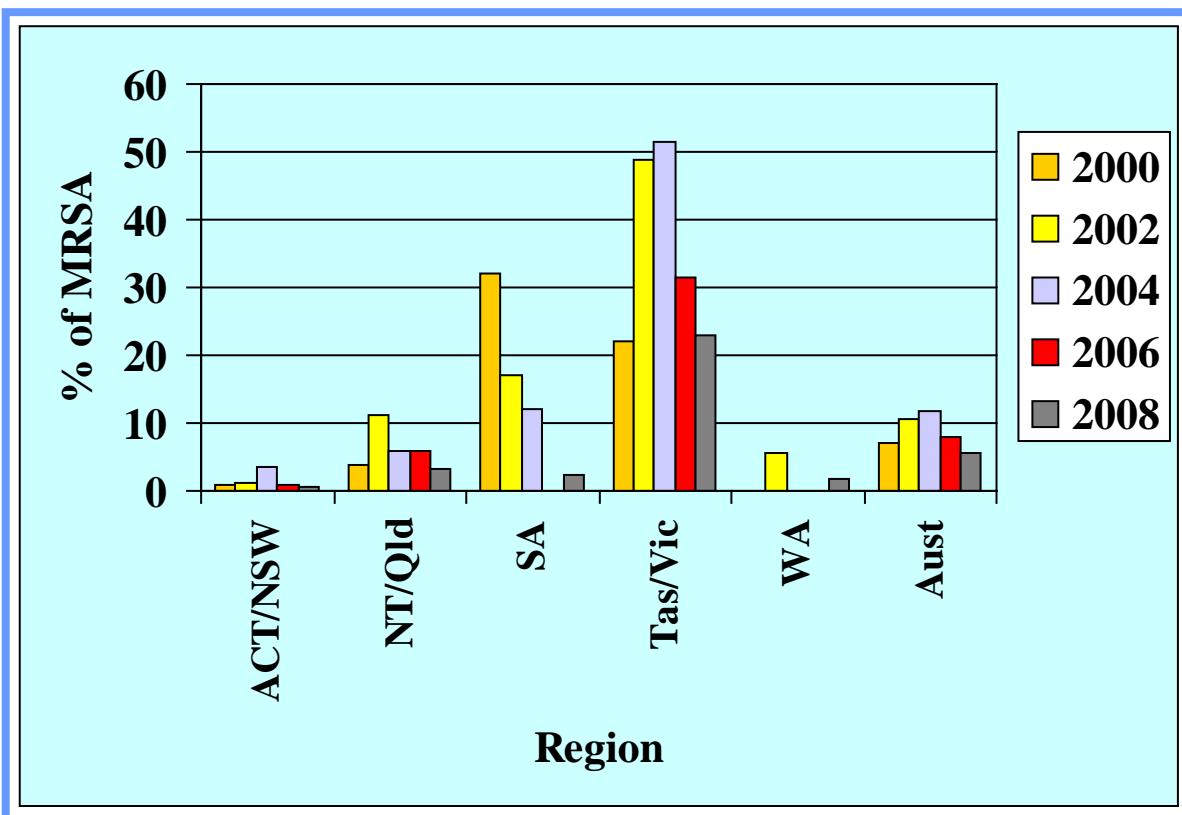


SAP 2000 – 2008: Regional Distribution of ST239-MRSA-III (Aus-3 EMRSA)

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	1 (0.8%)	2 (1.1%)	6 (3.5%)	2 (1.0%)	1 (0.5%)
NT/Qld	1 (3.7%)	6 (11.1%)	4 (5.9%)	4 (4.7%)	4 (3.2%)
SA	8 (32.0%)	6 (17.1%)	5 (12.2%)	0	1 (2.4%)
Tas/Vic	8 (22.2%)	22 (48.9%)	32 (51.6%)	31 (31.6%)	24 (22.9%)
WA	0	3 (5.5%)	0	0	1 (1.8%)
Total	18 (7.0%)	39 (10.7%)	47 (11.9%)	37 (8.0%)	31 (5.7%)

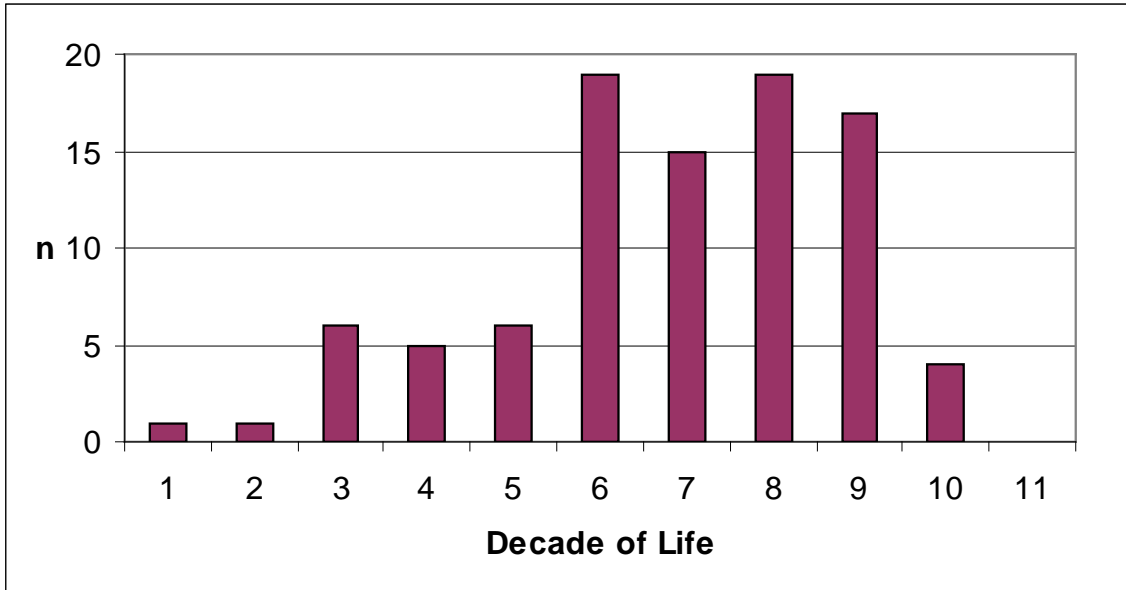
Percentage figures relate to total MRSA isolates

SAP 2000 – 2008: Regional Distribution of ST239-MRSA-III (Aus-3 EMRA)

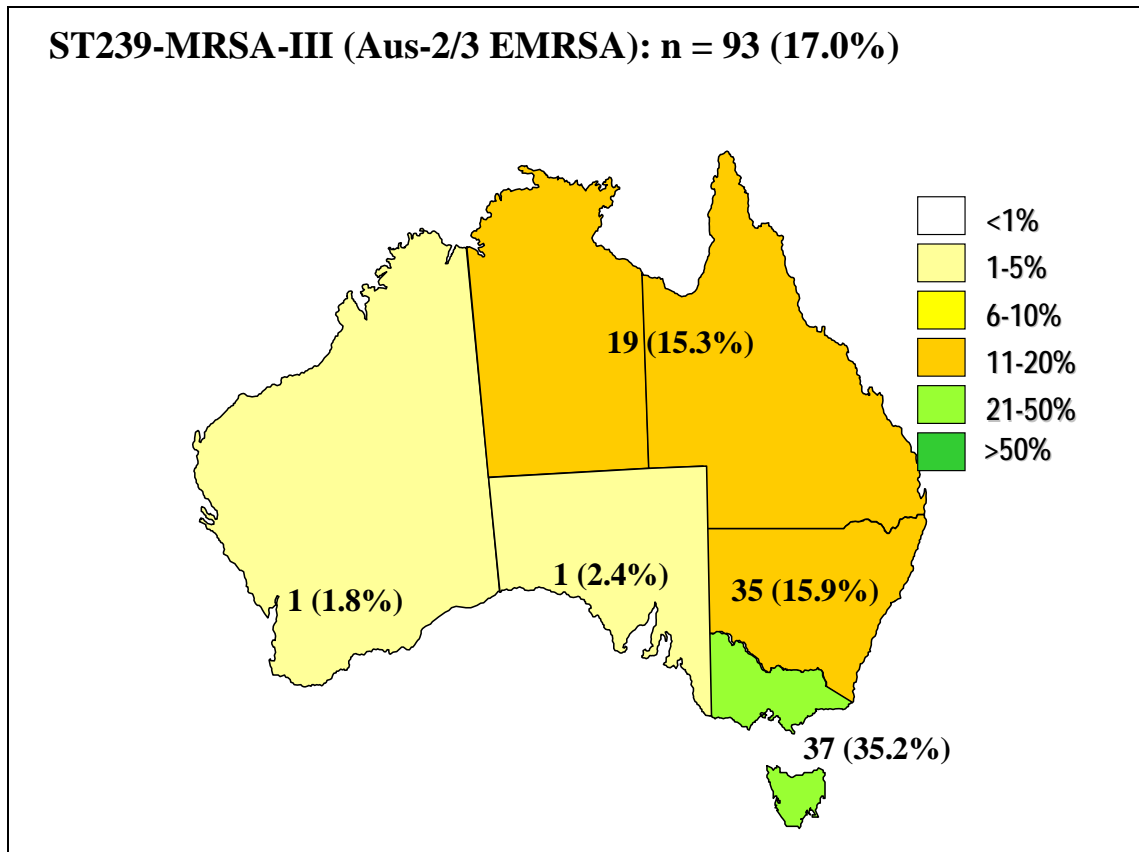


Aus-2 and Aus-3 EMRSA

Patients Infected with ST239-MRSA-III (Aus-2 and Aus-3 EMRSA) by Decade of Life



Regional Distribution of ST239-MRSA-III (Aus-2 and Aus-3 EMRSA)

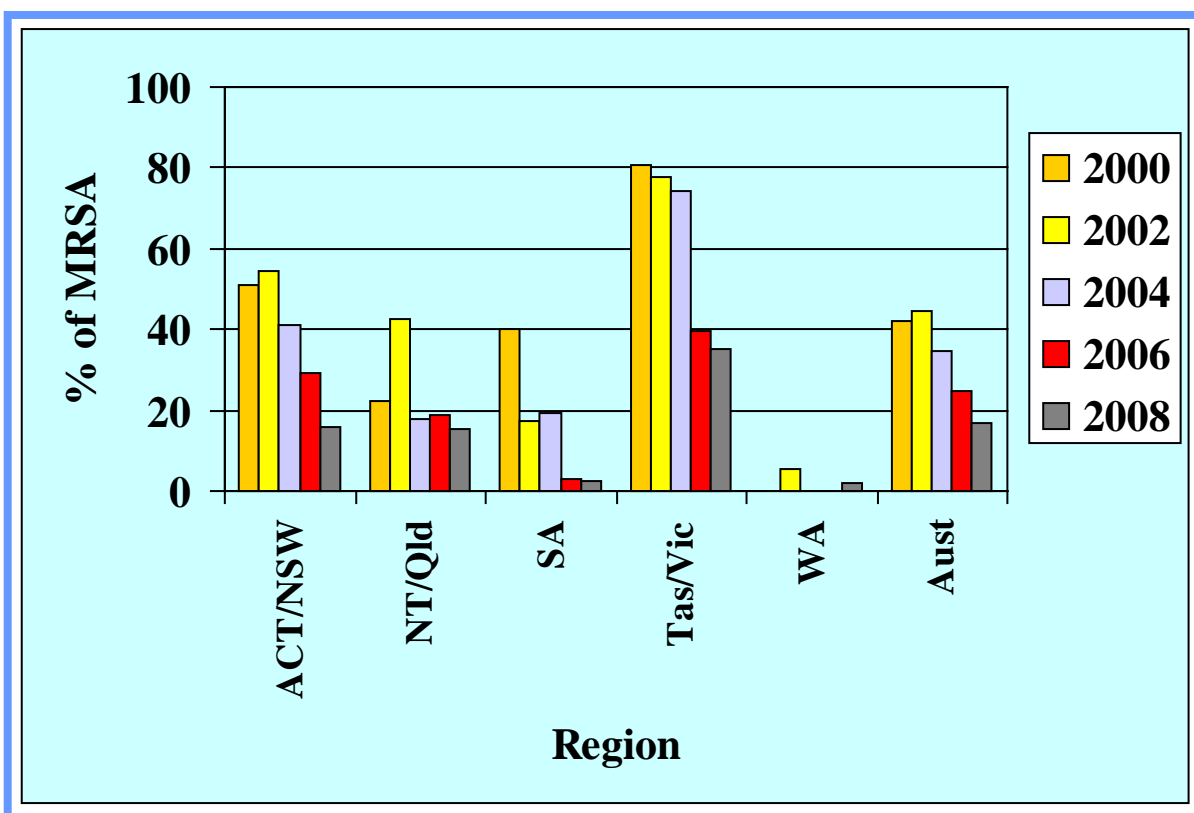


SAP 2000 – 2008: Regional Distribution of ST239-MRSA-III (Aus-2 and Aus-3 EMRSA)

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	63 (50.4%)	95 (54.6%)	71 (41.0%)	58 (29.3%)	35 (15.9%)
NT/Qld	6 (22.2%)	23 (42.6%)	12 (17.7%)	16 (18.6%)	19 (15.3%)
SA	10 (40.0%)	6 (17.1%)	8 (19.5%)	1 (2.8%)	1 (2.4%)
Tas/Vic	29 (80.6%)	35 (77.8%)	46 (74.2%)	39 (39.8%)	37 (35.2%)
WA	0	3 (5.5%)	0	0	1 (1.8%)
Total	108 (42.0%)	162 (44.6%)	137 (34.7%)	114 (24.7%)	93 (17.0%)

Percentage figures relate to total MRSA isolates

SAP 2000 – 2008: Regional Distribution of ST239-MRSA-III (Aus-2 and Aus-3 EMRSA)



ST5-MRSA-II

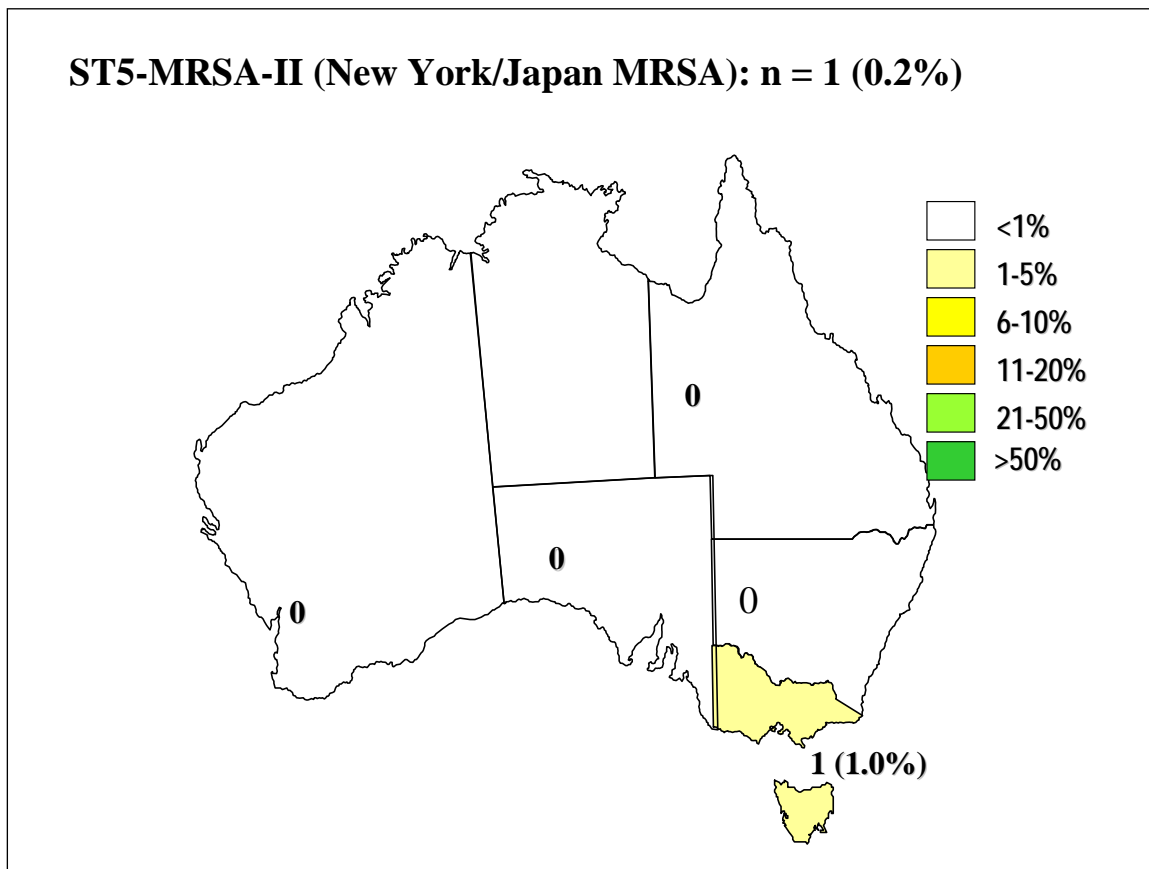
The original hVISA, ST5-GISA-II, is thought to have evolved from the New York/Japan MRSA clone.

Phenotypic Characteristics

Antibiogram: Erythromycin^R
Ciprofloxacin^R
Mupirocin^R

Urease: Positive

Epidemiology



ST36-MRSA-II

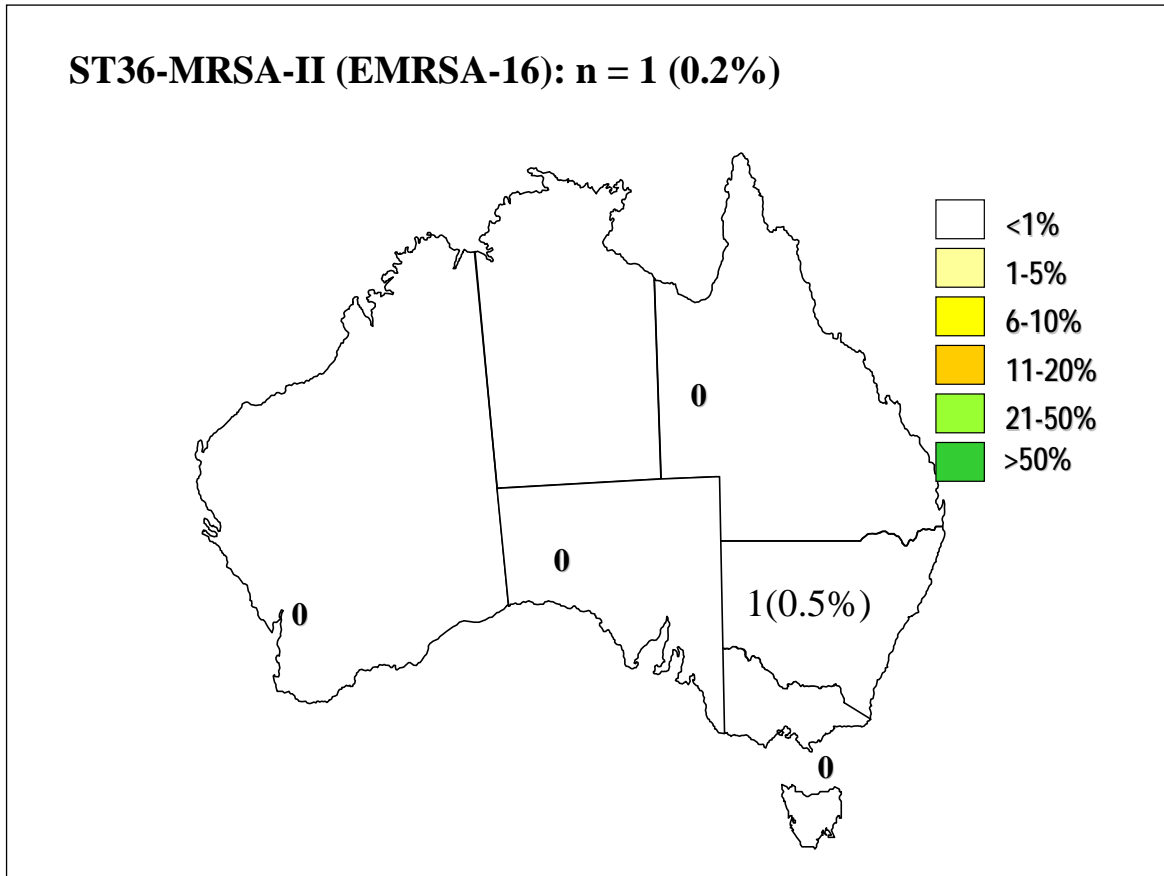
Also known as “EMRSA-16” or “USA200”, ST36-MRSA-II was first identified in a single hospital outbreak in London in 1991-2. It now accounts for almost a quarter of UK isolates sent to the Laboratory of Hospital Infection in Colindale for typing. ST36-MRSA-II has been isolated in several European countries 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.

Phenotypic Characteristics

Antibiogram: Erythromycin^R
Ciprofloxacin^R

Urease: Positive

Epidemiology



Summary of HA-MRSA Isolated in AGAR SAPs 2000 – 2008

Clone	Alternative Name	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ST22-MRSA-IV	EMRSA-15	30 (21.6%)	42 (20.2%)	62 (30.8%)	85 (42.5%)	112 (54.1%)
ST239-MRSA-III	Aus-2, -3 EMRSA	108 (77.7%)	162 (77.9%)	137 (68.2%)	114 (57.0%)	93 (44.9%)
ST5-MRSA-II	New York/Japan	0	0	0	1 ^e (0.5%)	1 ^f (0.5%)
ST36-MRSA-II	EMRSA-16	0	1 ^b (0.5%)	2 ^d (1.0%)	0	1 ^g (0.5%)
ST8-MRSA-II	Irish-1 EMRSA	0	3 ^c (1.4%)	0	0	0
ST8-MRSA-VI	Irish-2 EMRSA	1 ^a (0.7%)	0	0	0	0
Total		139	208	201	200	207

Percentage figures relate to the healthcare associated MRSA isolates

^aIsolated in WA

^bIsolated in WA

^cIsolated in ACT/NSW region (n=2) and WA (n=1)

^dIsolated in SA (n=1) and WA (n=1)

^eIsolated in ACT/NSW

^fIsolated in Vic

^gIsolated in NSW

5.4. CA-MRSA

CA-MRSA was first reported in Australia in the early 1980s in aboriginal communities living in the Kimberley region of Western Australia (WA). Known collectively as “WA MRSA” they were subsequently isolated in other remote communities in WA, South Australia and Northern Territory. These strains are usually susceptible to most non- β -lactams antibiotics. “WA MRSA” has acquired the community associated 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 2008 CA-MRSA

In SAP 2008, 22 CA-MRSA clones (19 MLST clone types) were identified:

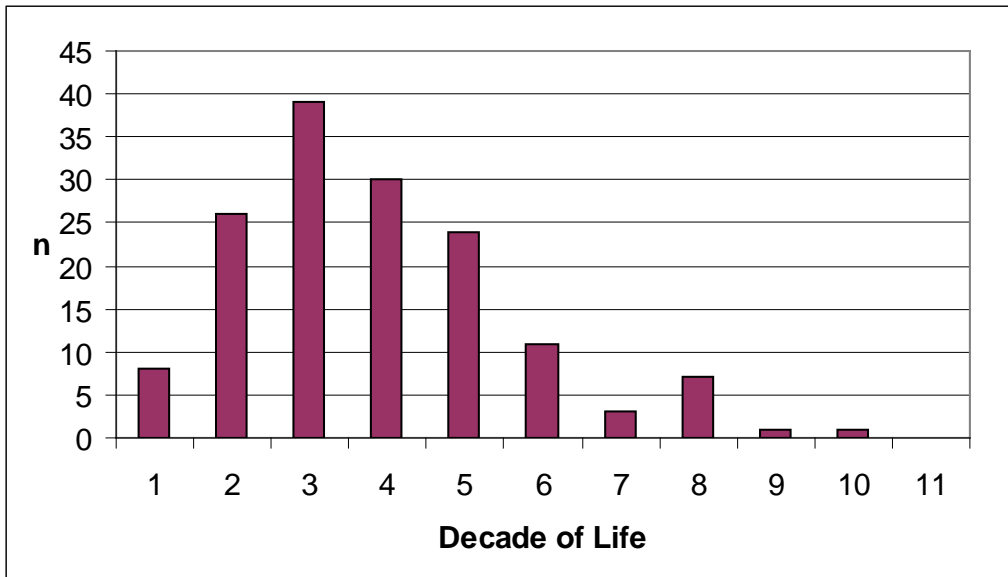
Clone	CC	Alternative Name	n (% of CA-MRSA)
ST93-MRSA-IV	Singleton	Queensland CA-MRSA	150 (44.1%)
ST1-MRSA-IV	1	WA MRSA -1	63 (18.5%)
ST30-MRSA-IV	30	WSPP MRSA	47 (13.8%)
ST5-MRSA-IV	5	WA MRSA-3	20 (5.9%)
ST78-MRSA-IV	88	WA MRSA-2	18 (5.3%)
ST8-MRSA-IV	8	USA300 MRSA	10 (2.9%)
ST45-MRSA-V	45	WA MRSA-84	7 (2.1%)
ST73-MRSA-IV	5	WA MRSA-65	5 (1.5%)
ST5-MRSA-V	5	Novel	2 (0.6%)
ST45-MRSA-V	45	WA MRSA-4	2 (0.6%)
ST45-MRSA-IV	45	WA MRSA-23	2 (0.6%)
ST59-MRSA-IV	59	WA MRSA-15	2 (0.6%)
ST80-MRSA-IV	80	European CA-MRSA	2 (0.6%)
ST72-MRSA-IV	72	WA MRSA-44	2 (0.6%)
ST1-MRSA-V	1	Novel	1 (0.3%)
ST5-MRSA-IV	5	Novel	1 (0.3%)
ST8-MRSA-IV	8	WA MRSA- 5	1 (0.3%)
ST834-MRSA-IV	9	WA MRSA-13	1 (0.3%)
ST59-MRSA-V _T	59	Taiwan CA-MRSA	1 (0.3%)
ST1304-MRSA-IV	75	WA MRSA-72	1 (0.3%)
ST88-MRSA-V	88	Novel	1 (0.3%)
ST207-MRSA-V	509	Novel	1 (0.3%)
Total			340

Major CA-MRSA Clones

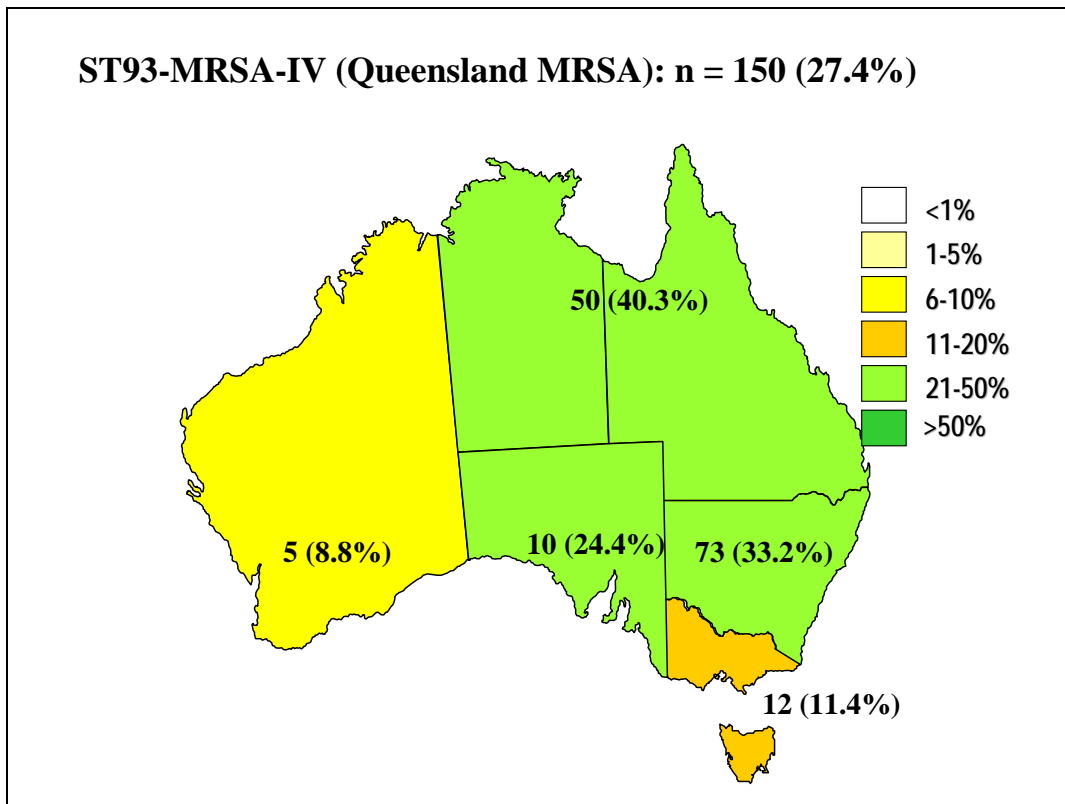
ST93-MRSA-IV

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

Patients Infected with ST93-MRSA-IV (Queensland MRSA) by Decade of Life



Regional Distribution of ST93-MRSA-IV

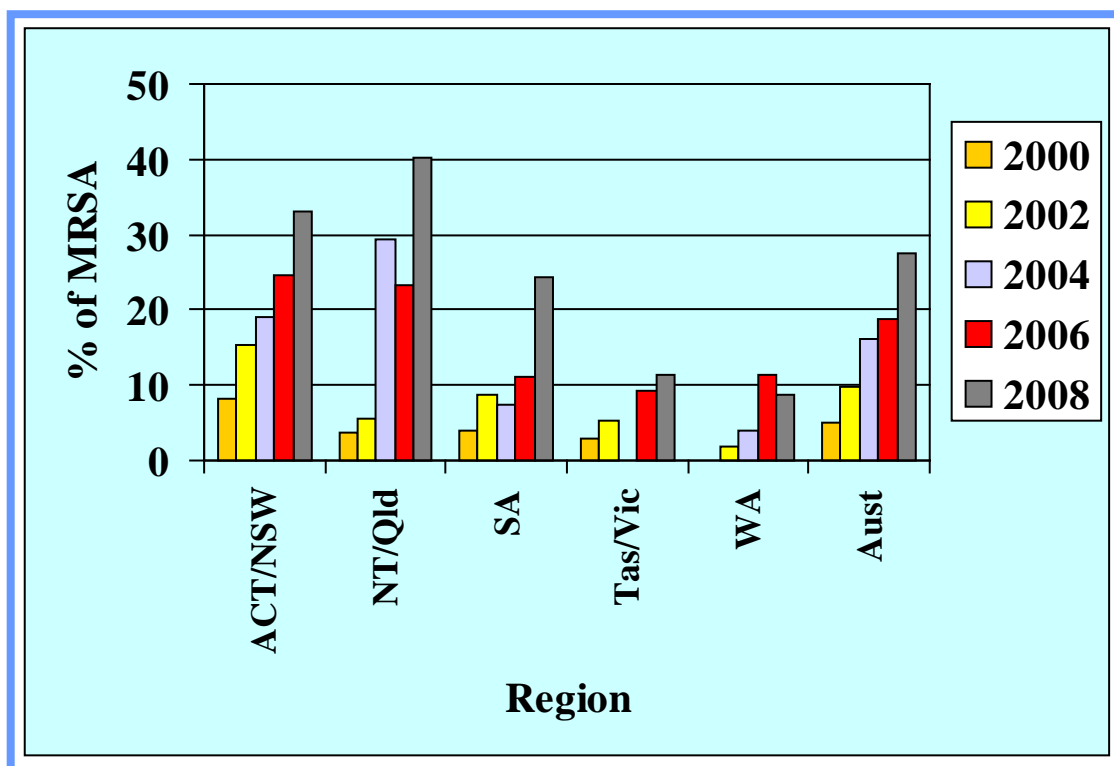


SAP 2000 to SAP 2008 Regional Distribution of ST93-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	10 (8.0%)	27 (15.5%)	33 (19.1%)	49 (24.7%)	73 (33.2%)
NT/Qld	1 (3.7%)	3 (5.6%)	20 (29.4%)	20 (23.3%)	50 (40.3%)
SA	1 (4.0%)	3 (8.6%)	3 (7.3%)	4 (11.1%)	10 (24.4%)
Tas/Vic	1 (2.8%)	2 (5.4%)	0	9 (9.2%)	12 (11.4%)
WA	0	1 (1.8%)	2 (3.9%)	5 (11.4%)	5 (8.8%)
Total	13 (5.1%)	36 (9.9%)	58 (14.7%)	87 (18.8%)	150 (27.4%)

Percentage figures relate to total MRSA isolates

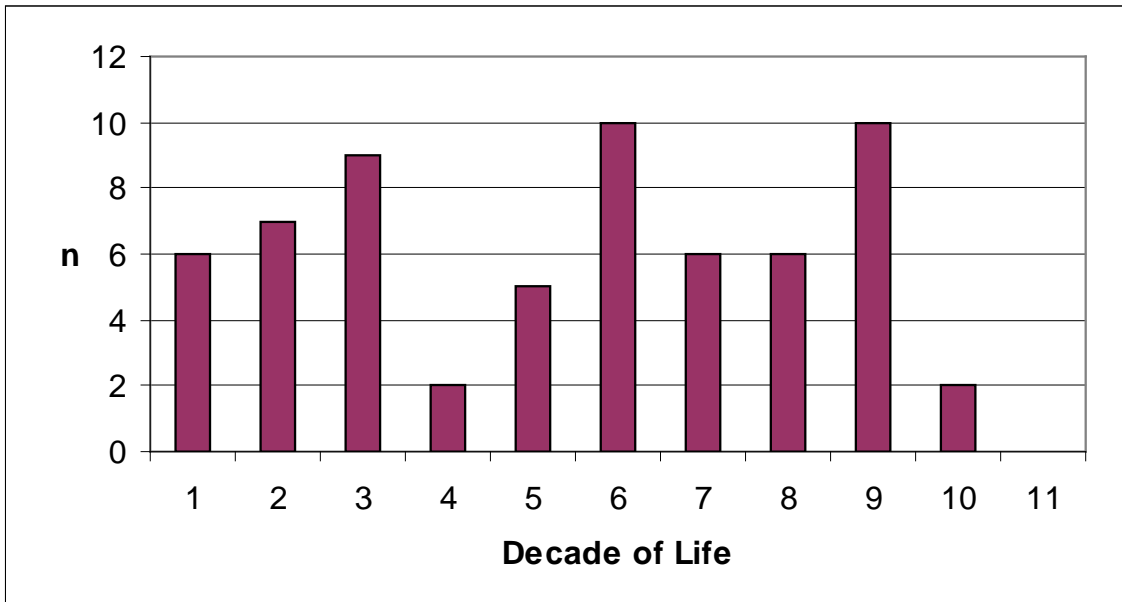
SAP 2000 to SAP 2008 Regional Distribution of ST93-MRSA-IV



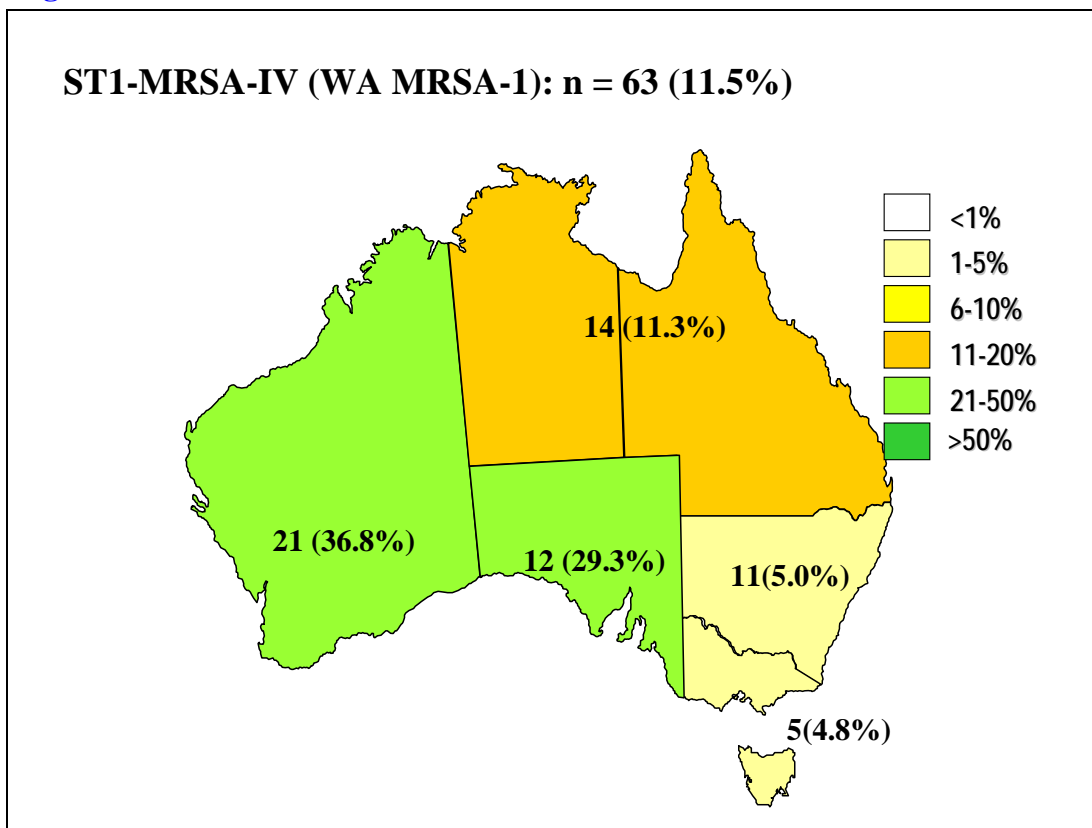
ST1-MRSA-IV

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.

Patients Infected with ST1-MRSA-IV by Decade of Life



Regional Distribution of ST1-MRSA-IV

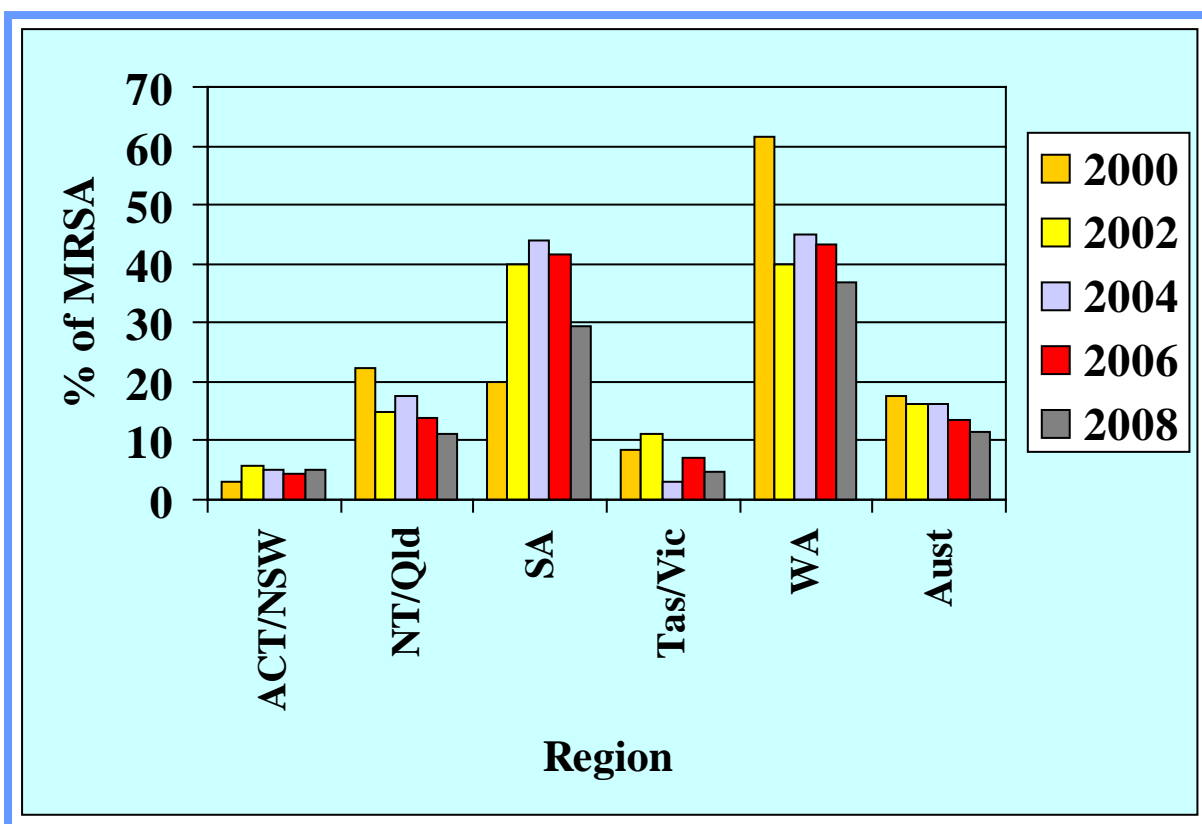


SAP 2000 to SAP 2008 Regional Distribution of ST1-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	4 (3.2%)	10 (5.7%)	9 (5.2%)	9 (4.5%)	11 (5.0%)
NT/Qld	6 (22.2%)	8 (14.8%)	12 (17.6%)	12 (14.0%)	14 (11.3%)
SA	5 (20.0%)	14 (40%)	18 (43.9%)	15 (41.7%)	12 (29.3%)
Tas/Vic	3 (8.3%)	5 (11.1%)	2 (3.2%)	7 (7.1%)	5 (4.8%)
WA	27 (61.4%)	22 (40%)	23 (45.1%)	19 (43.2%)	21 (36.8%)
Total	45 (17.5%)	59 (16.3%)	64 (16.2%)	62 (13.4%)	63 (11.5%)

Percentage figures relate to total MRSA isolates

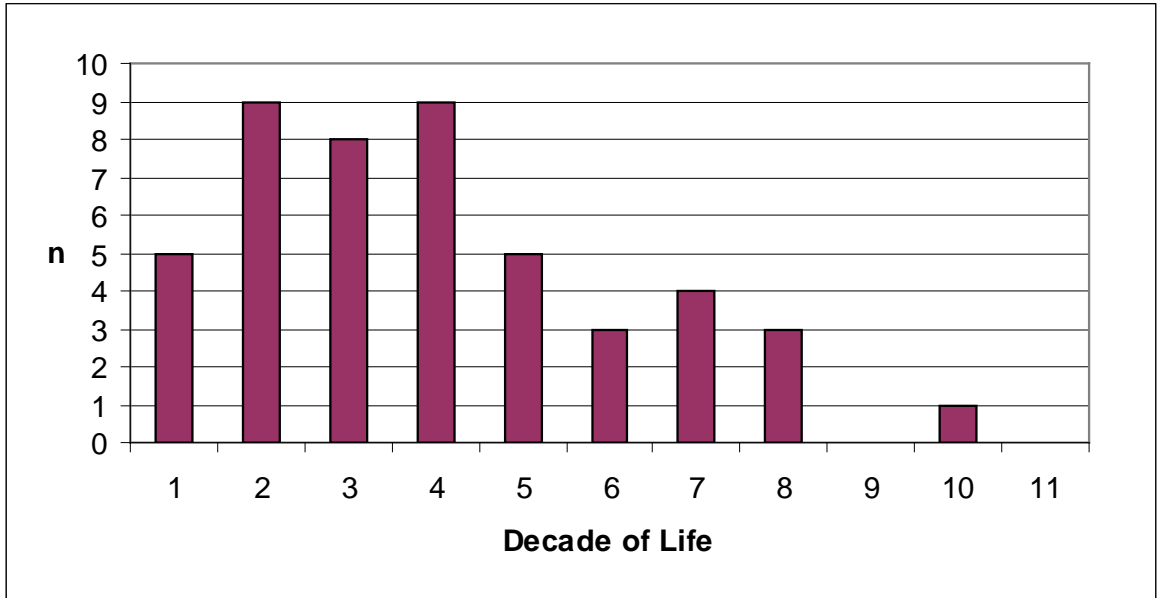
SAP 2000 to SAP 2008 Regional Distribution of ST1-MRSA-IV



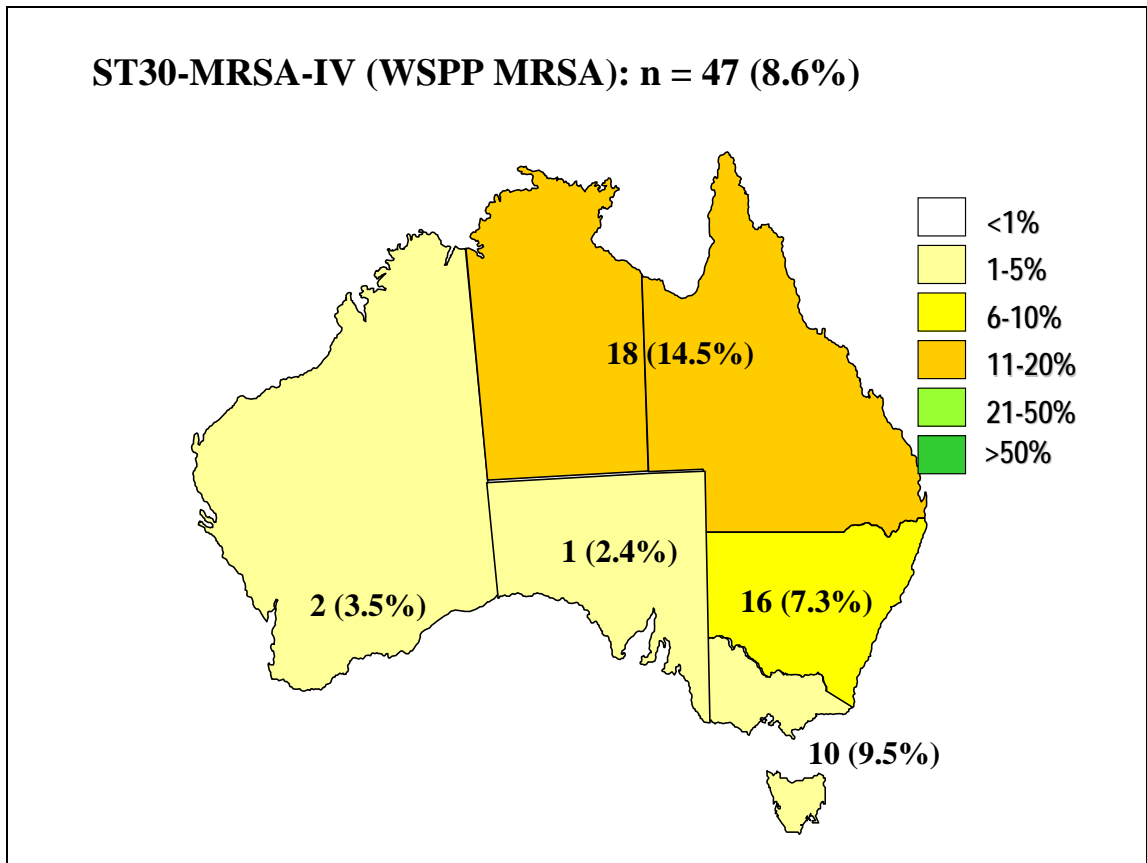
ST30-MRSA-IV

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.

Patients Infected with ST30-MRSA-IV by Decade of Life



Regional Distribution of ST30-MRSA-IV

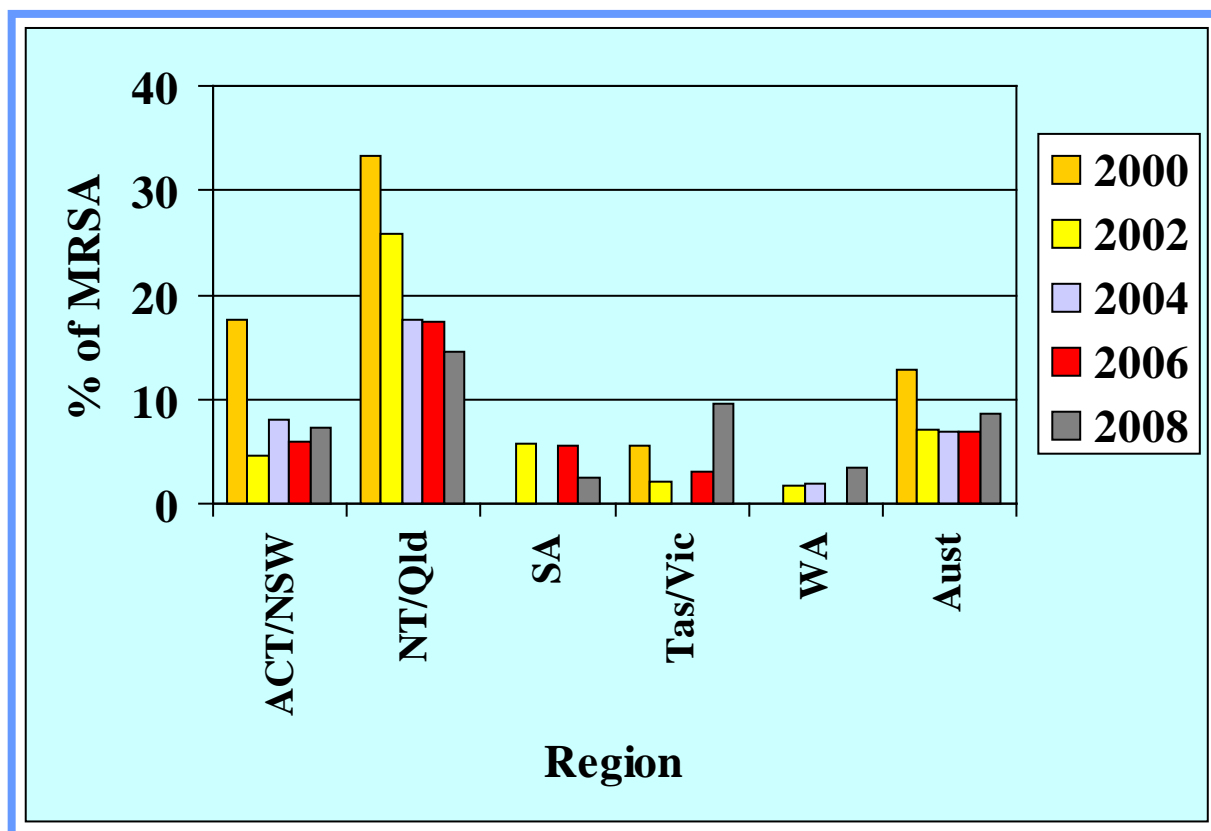


SAP 2000 to SAP 2008 Regional Distribution of ST30-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	22 (17.6%)	8 (4.6%)	13 (7.5%)	12 (6.1%)	16 (7.3%)
NT/Qld	9 (33.3%)	14 (25.9%)	12 (17.6%)	15 (17.4%)	18 (14.5%)
SA	0	2 (5.7%)	0	2 (5.6%)	1 (2.4%)
Tas/Vic	2 (5.6%)	1 (2.2%)	0	3 (3.1%)	10 (9.5%)
WA	0	1 (1.8%)	1 (2.0%)	0	2 (3.5%)
Total	33 (12.8%)	26 (7.2%)	26 (6.6%)	32 (6.9%)	47 (8.6%)

Percentage figures relate to total MRSA isolates

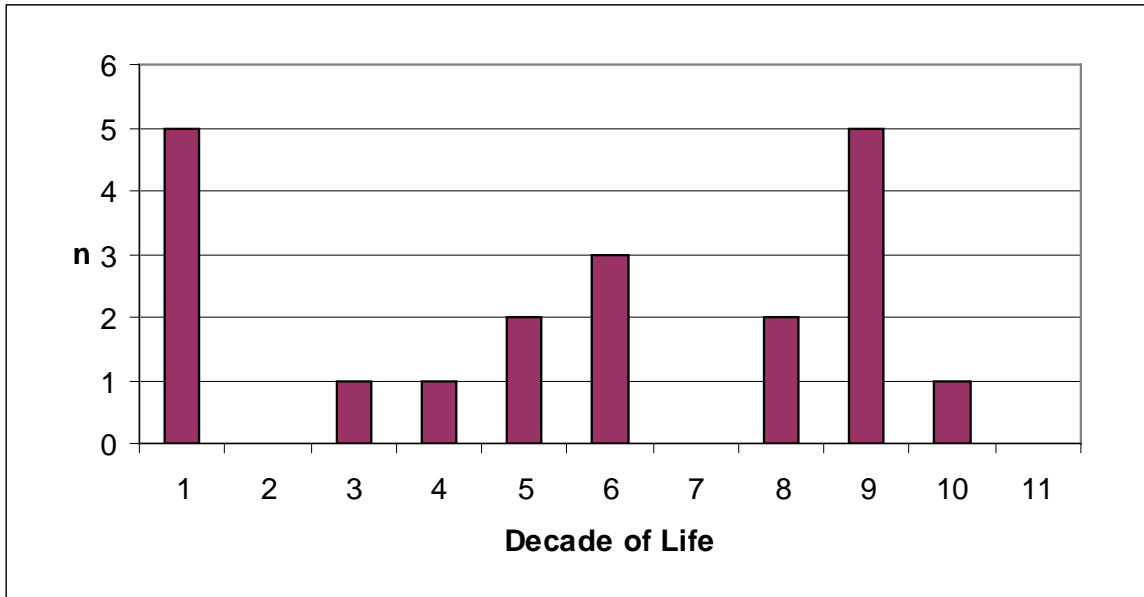
SAP 2000 to SAP 2008 Regional Distribution of ST30-MRSA-IV



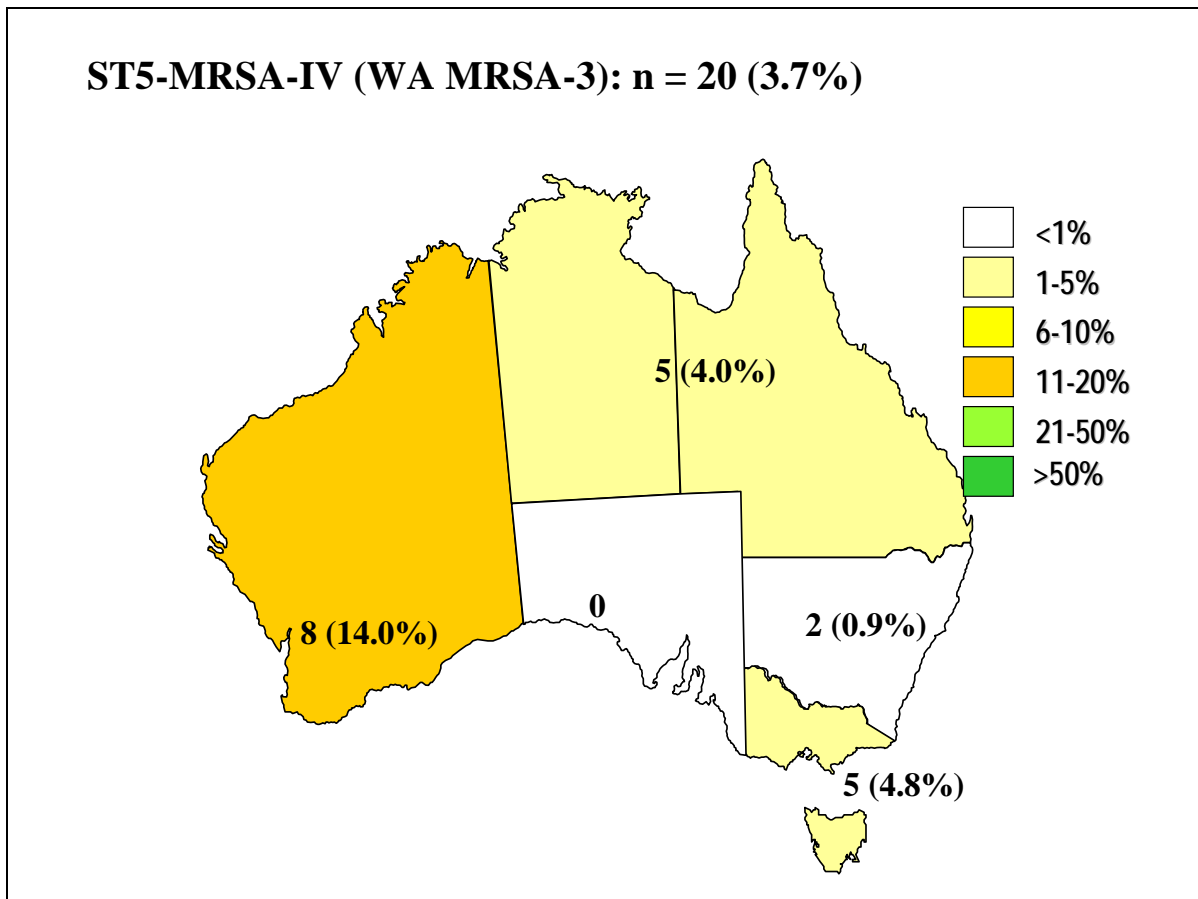
ST5-MRSA-IV

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

Patients Infected with ST5-MRSA-IV by Decade of Life



Regional Distribution of ST5-MRSA-IV

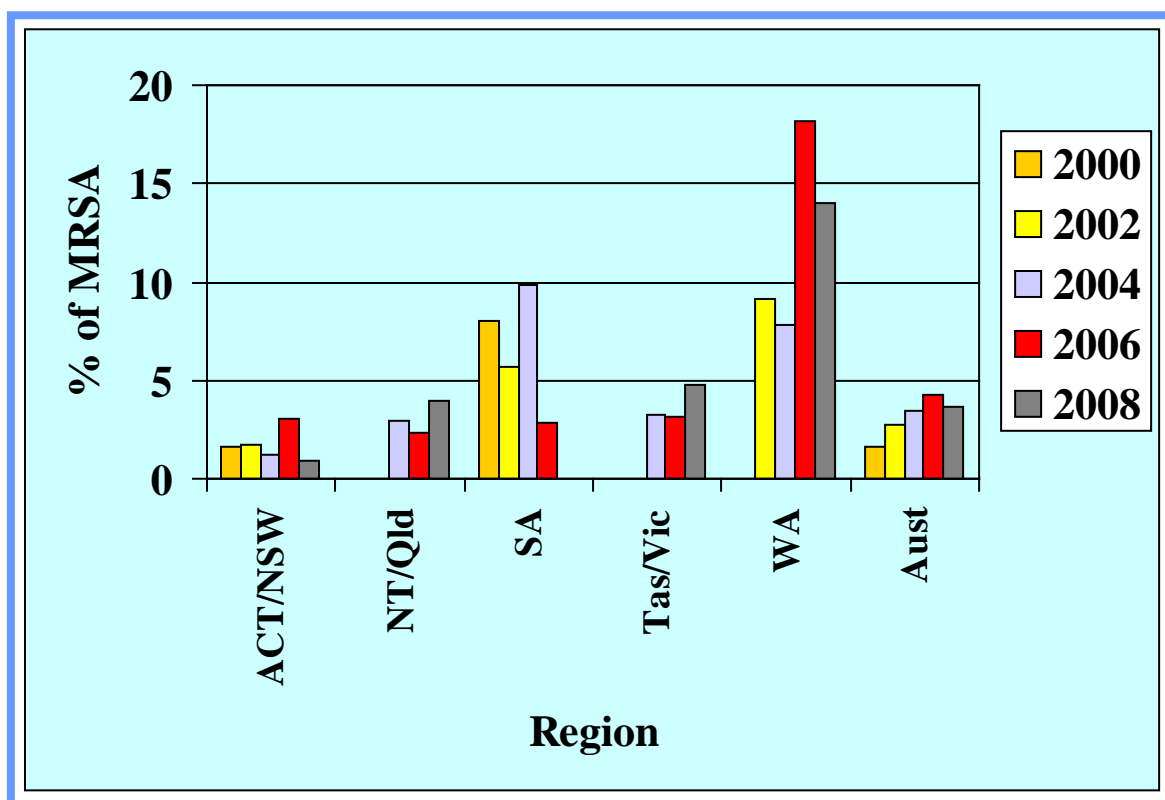


SAP 2000 to SAP 2008 Regional Distribution of ST5-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	2 (1.6%)	3 (1.7%)	2 (1.2%)	6 (3.0%)	2 (0.9%)
NT/Qld	0	0	2 (2.9%)	2 (2.3%)	5 (4.0%)
SA	2 (8%)	2 (5.7%)	4 (9.8%)	1 (2.8%)	0
Tas/Vic	0	0	2 (3.2%)	3 (3.1%)	5 (4.8%)
WA	0	5 (9.1%)	4 (7.8%)	8 (18.2%)	8 (14.0%)
Total	4 (1.6%)	10 (2.8%)	14 (3.5%)	20 (4.3%)	20 (3.7%)

Percentage figures relate to total MRSA isolates

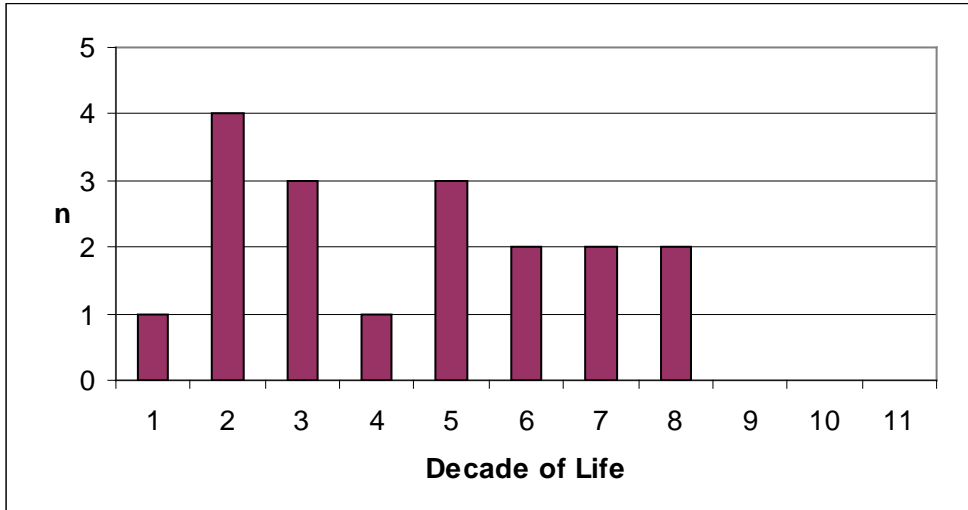
SAP 2000 to SAP 2008 Regional Distribution of ST5-MRSA-IV



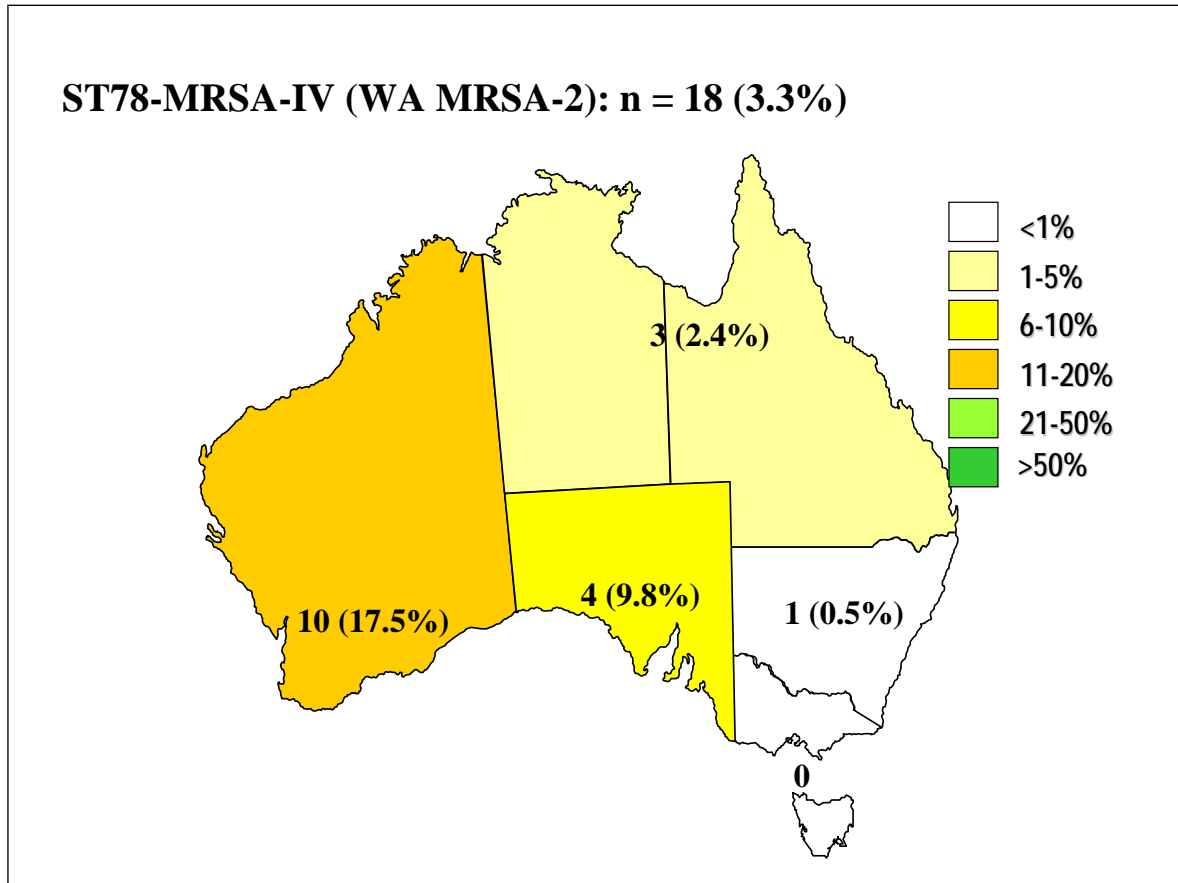
ST78-MRSA-IV

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

Patients Infected with ST78-MRSA-IV by Decade of Life



Regional Distribution of ST78-MRSA-IV

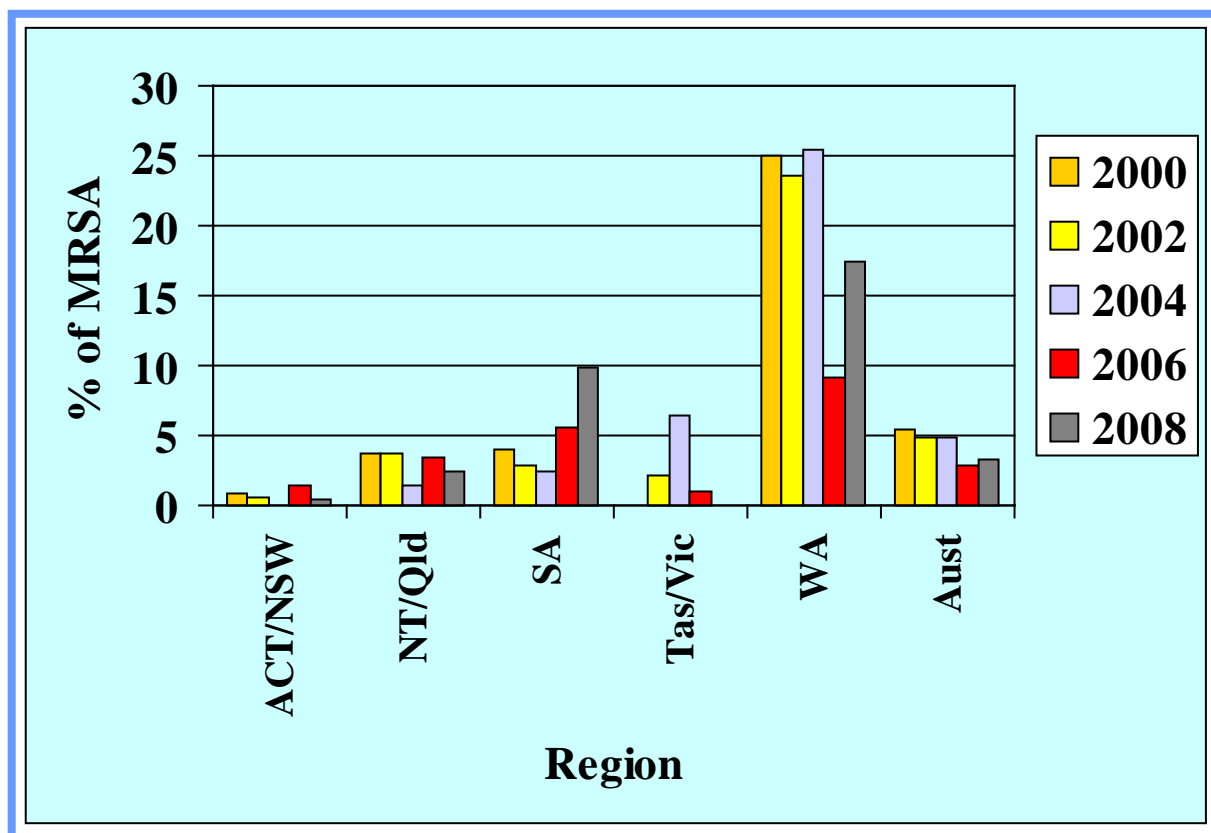


SAP 2000 to SAP 2008 Regional Distribution of ST78-MRSA-IV

Region	SAP 2000	SAP 2002	SAP 2004	SAP 2006	SAP 2008
ACT/NSW	1 (0.8%)	1 (0.6%)	0	3 (1.5%)	1 (0.5%)
NT/Qld	1 (3.7%)	2 (3.7%)	1 (1.5%)	3 (3.5%)	3 (2.4%)
SA	1 (4.0%)	1 (2.9%)	1 (2.4%)	2 (5.6%)	4 (9.8%)
Tas/Vic	0	1 (2.2%)	4 (6.5%)	1 (1.0%)	0
WA	11 (25.0%)	13 (23.6%)	13 (25.5%)	4 (9.1%)	10 (17.5%)
Total	14 (5.4%)	18 (5.0%)	19 (4.8)	13 (2.8%)	18 (3.3%)

Percentage figures relate to total MRSA isolates

SAP 2000 to SAP 2008 Regional Distribution of ST78-MRSA-IV



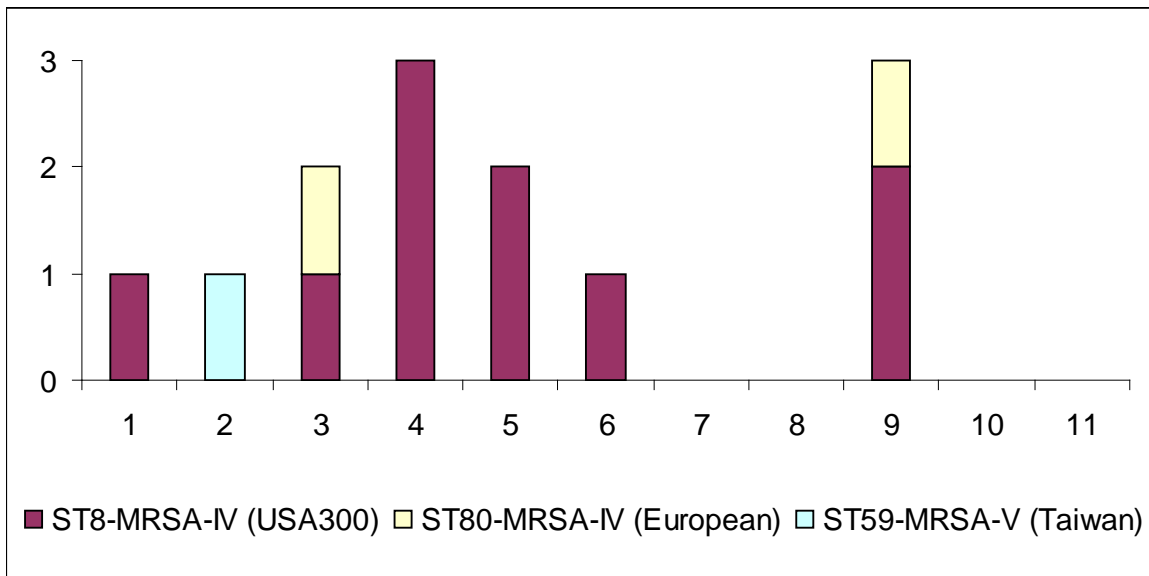
International CA-MRSA Clones

In SAP 2008, three international CA-MRSA clones were characterized. All were Panton Valentine leucocidin (PVL) positive.

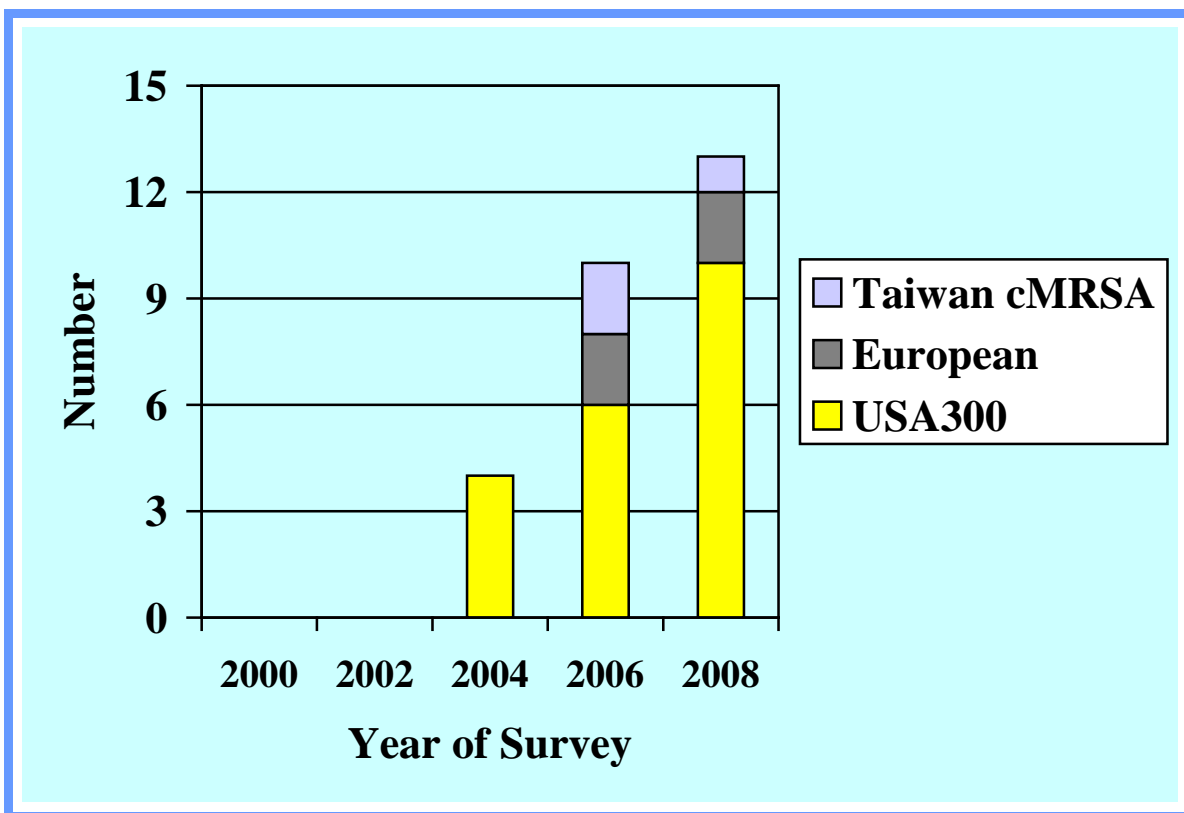
CLONE	ALTERNATIVE NAME	n (%)
ST8-MRSA-IV	USA300	10 (2.9%)
ST80-MRSA-IV	European CA-MRSA	2 (0.6%)
ST59-MRSA-V _T	Taiwan CA-MRSA	1 (0.3%)
TOTAL		13

Percentage figures relate to CA-MRSA isolates

Patients Infected with International CA-MRSA by Decade of Life



SAP 2000 – 2008: Number of MRSA Identified as International CA-MRSA

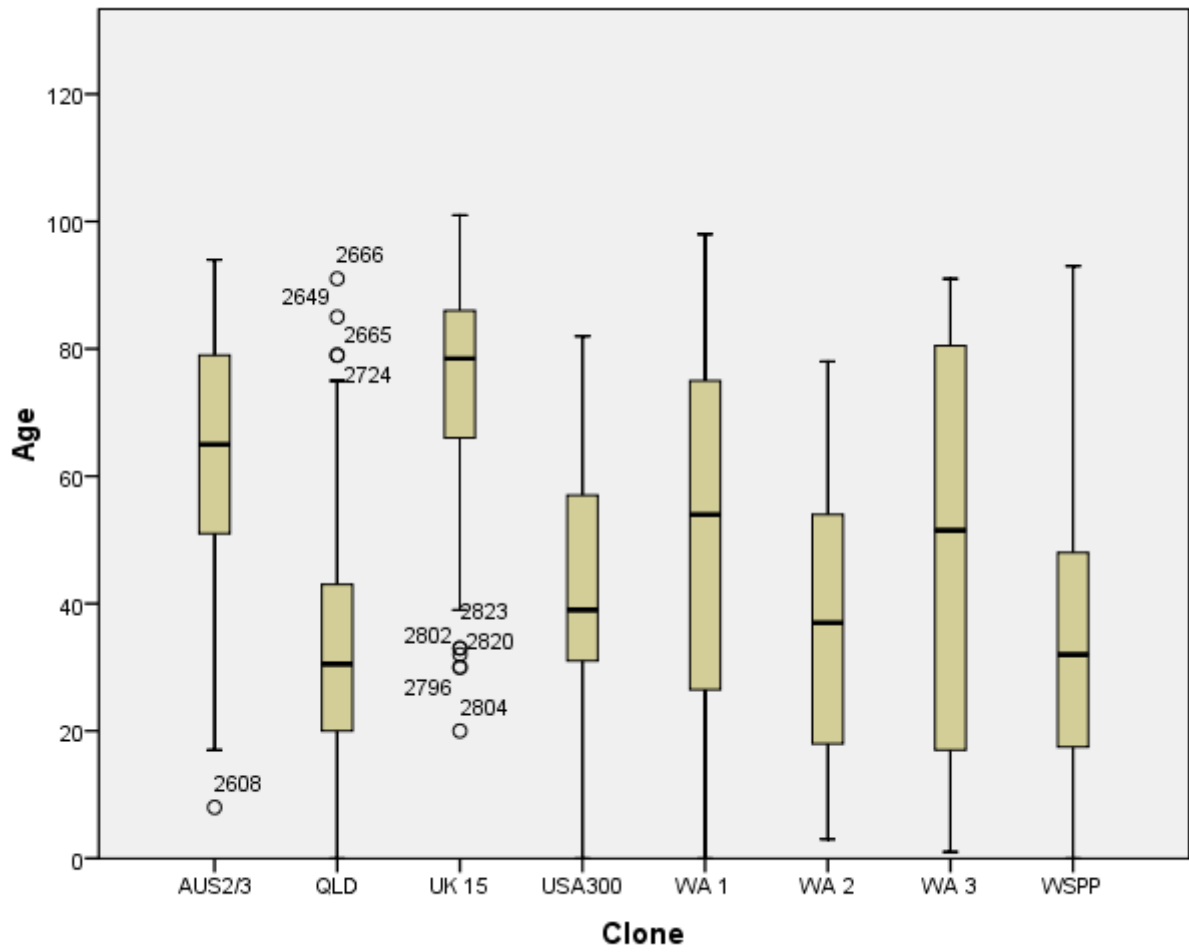


SAP 2000 – 2008: Number of MRSA Identified as International CA-MRSA

CLONE	SAP 2004			SAP 2006			SAP 2008		
	USA300	European	Taiwan	USA300	European	Taiwan	USA300	European	Taiwan
ACT/NSW	3	0	0	4	0	0	4	1	0
NT/Qld	1	0	0	2	0	0	2	0	0
SA	0	0	0	0	0	0	0	0	1
Tas/Vic	0	0	0	0	2	2	3	1	0
WA	0	0	0	0	0	0	1	0	0
Total	4	0	0	6	2	2	10	2	1

Age Statistics for Major clones (≥ 10 isolates)

Box Plot of Age of Patients Infected with a Major MRSA Clone



Mean, median and percentile data

Age (years)	ST239-MRSA-III Aus-2/3 EMRSA	ST93-MRSA-IV Queensland	ST22-MRSA-IV EMRSA-15	ST8-MRSA-IV USA300	ST1-MRSA-IV WA MRSA-1	ST78-MRSA-IV WA MRSA-2	ST5-MRSA-IV WA MRSA-3	ST30-MRSA-IV WSPP
Mean (95% CI)	62.75	32.83	74.59	43.10	49.27	38.22	48.95	34.62
95% CI of mean	58.69 – 66.81	29.93 – 35.72	71.47 – 77.71	25.12 – 61.08	42.06 – 56.48	26.71 – 49.73	33.73 – 64.17	27.94 – 41.30
Median	65.00	30.50	78.50	39.00	54.00	37.00	51.50	32.00
25 th percentile	51.00	20.00	66.00	29.25	26.00	17.50	12.00	17.00
75 th percentile	79.00	43.00	86.00	63.00	76.00	56.25	80.75	49.00

Minor CA-MRSA CLONES

Clone	Clonal Complex	CHEF	2000 (n = 9)	2002 (n = 6)	2004 (n = 13)	2006 (n=38)	2008 (n=29)
ST75-MRSA-IV	75	WA MRSA-8	2 (NT/Qld)	1 (NT/Qld)	1 (NT/Qld)	6 (NT/Qld) 1 (WA)	0
ST8-MRSA-IV	8	WA MRSA-5	0	1 (ACT/NSW)	1 (ACT/NSW)	1 (ACT/NSW) 2 (NT/Qld)	1 (SA)
ST45-MRSA-V	45	WA MRSA-4	2 (WA) 1 (SA)	1 (SA)	0	1 (ACT/NSW) 2 (SA) 2 (WA)	1 (WA) 1 (SA)
ST45-MRSA-IV	45	WA MRSA-23	0	0	2 (Tas/Vic)	9 (Tas/Vic)	1 (SA) 1 (ACT/NSW)
ST45-MRSA-V	45	WA MRSA-84	0	0	0	0	6 (Tas/Vic) 1 (SA)
ST583-MRSA-IV	80	WA MRSA-17	1 (ACT/NSW)	1 (Tas/Vic)	1 (ACT/NSW)	0	0
ST59-MRSA-IV	59	WA MRSA-15	0	0	1 (NT/Qld) 1 (WA)	1 (Tas/Vic)	1 (Tas/Vic) 1 (ACT/NSW)
ST834-MRSA-IV	9	WA MRSA-13	0	0	1 (ACT/NSW) 1 (Tas/Vic)	1 (SA)	1 (WA)
STnovel-MRSA-IV	Singleton	Novel	1 (NT/Qld)	1 (NT/Qld)	0	0	0
ST152-MRSA-V	Singleton	Novel	0	1 (SA)	0	0	0
ST8-MRSA-V	8	Novel	2 (SA)	0	0	0	0
ST1-MRSA-V	1	Novel	0	0	0	1 (NT/Qld)	0

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Clone	Clonal Complex	CHEF	2000 (n = 9)	2002 (n = 6)	2004 (n = 13)	2006 (n=38)	2008 (n=29)
ST5-MRSA-V	5	WA MRSA-35	0	0	0	1 (Tas/Vic)	0
ST5-MRSA-V	5	Novel	0	0	0	1 (Tas/Vic) 1 (ACT/NSW)	0
ST7-MRSA-V	7	Novel	0	0	0	1 (Tas/Vic)	0
ST8-MRSA-IV	8	Novel	0	0	0	1 (NT/Qld)	0
ST30slv-MRSA-IV	30	Novel	0	0	0	1 (NT/Qld)	0
ST338-MRSA-V	59	Novel	0	0	0	1 (Tas/Vic)	0
ST72-MRSA-V	72	Novel	0	0	0	1 (Tas/Vic)	0
ST20-MRSA-V	20	Novel	0	0	0	1 (NT/Qld)	0
ST12-MRSA-IV	12	WA MRSA-69	0	0	0	1 (ACT/NSW)	0
ST361-MRSA-IV	Unique	Novel	0	0	0	1 (ACT/NSW)	0
ST1-MRSA-V	1	Novel	0	0	0	0	1 (NT/Qld)
ST73-MRSA-IV	5	WA MRSA-65	0	0	0	0	1 (WA) 2 (SA) 2 (NT/Qld)
ST5-MRSA-IV	5	Novel	0	0	0	0	1 ACT/NSW)
ST5-MRSA-V	5	Novel	0	0	0	0	1 (NT/Qld) 1 (Tas/Vic)
ST72-MRSA-IV	72	WA MRSA-44	0	0	0	0	1 (ACT/NSW) 1 (NT/Qld)

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Clone	Clonal Complex	CHEF	2000 (n = 9)	2002 (n = 6)	2004 (n = 13)	2006 (n=38)	2008 (n=29)
ST1304-MRSA-IV	75	WA MRSA-72	0	0	0	0	1 (NT/Qld)
ST88-MRSA-V	88	Novel	0	0	0	0	1 (Tas/Vic)
ST207-MRSA-V	509	Novel	0	0	0	0	1(ACT/NSW)

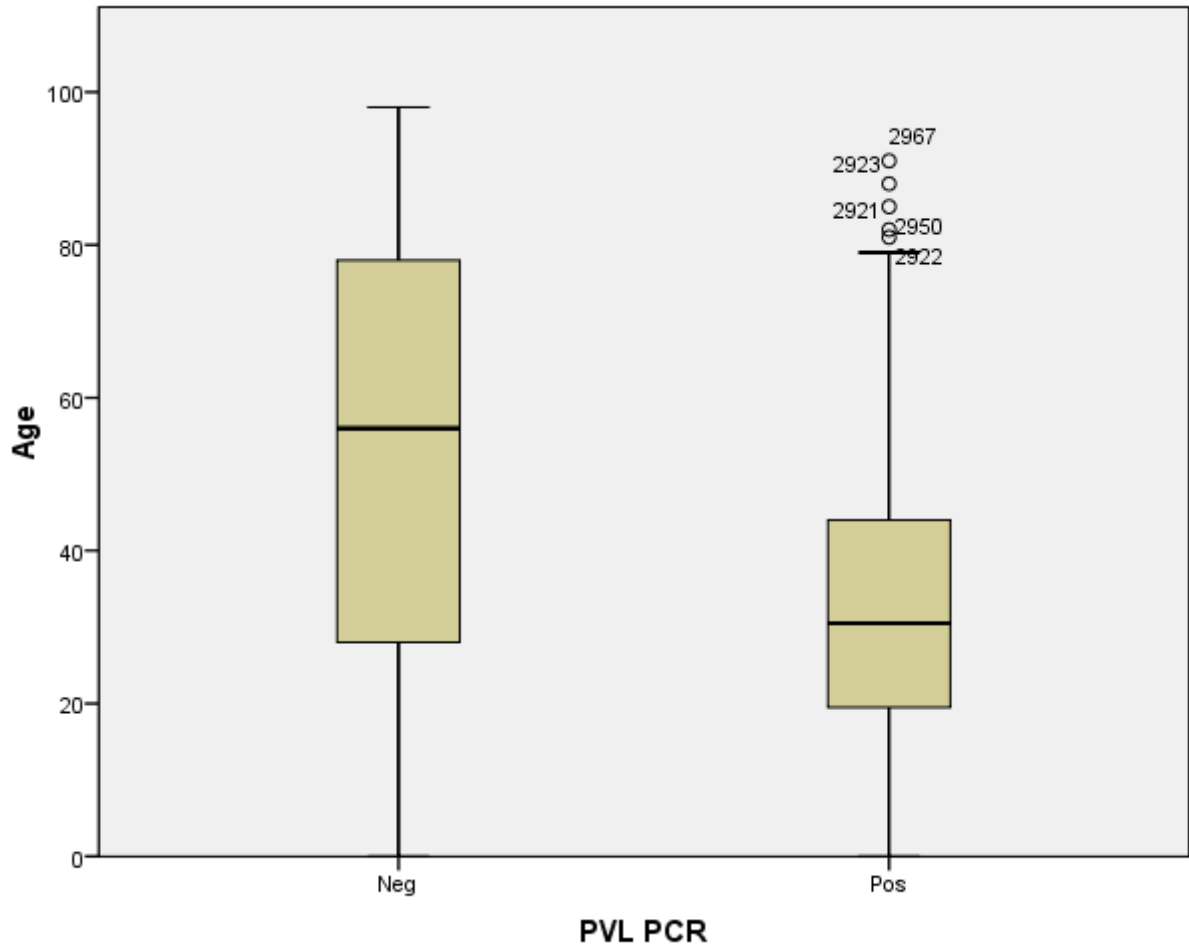
5.5. Panton-Valentine Leucocidin (PVL) Toxin

CA-MRSA

Clone	Alternative Name	Positive	Negative	Total
ST93-MRSA-IV	Queensland CA-MRSA	149	1	150
ST1-MRSA-IV	WA MRSA -1	9	54	63
ST30-MRSA-IV	WSPP MRSA	46	1	47
ST5-MRSA-IV	WA MRSA-3	1	19	20
ST78-MRSA-IV	WA MRSA-2	1	17	18
ST8-MRSA-IV	USA300 MRSA	10	0	10
ST45-MRSA-V	WA MRSA-84	0	7	7
ST73-MRSA-IV	WA MRSA-65	0	5	5
ST5-MRSA-V	Novel	0	2	2
ST45-MRSA-IV	WA MRSA-23	0	2	2
ST45-MRSA-V	WA MRSA-4	0	2	2
ST59-MRSA-IV	WA MRSA-15	0	2	2
ST80-MRSA-IV	European CA-MRSA	2	0	2
ST72-MRSA-IV	WA MRSA-44	0	2	2
ST1-MRSA-V	Novel	0	1	1
ST5-MRSA-IV	Novel	0	1	1
ST8-MRSA-IV	WA MRSA- 5	0	1	1
ST834-MRSA-IV	WA MRSA-13	0	1	1
ST59-MRSA-V _T	Taiwan CA-MRSA	1	0	1
ST1304-MRSA-IV	WA MRSA-72	0	1	1
ST88-MRSA-V	Novel	1	0	1
ST207-MRSA-V	Novel	0	1	1
Total		220 (64.7%)	120 (35.3%)	340

Age statistics for CA-MRSA by PVL status

Box Plot of Age of Patients Infected with PVL Positive and PVL Negative CA-MRSA

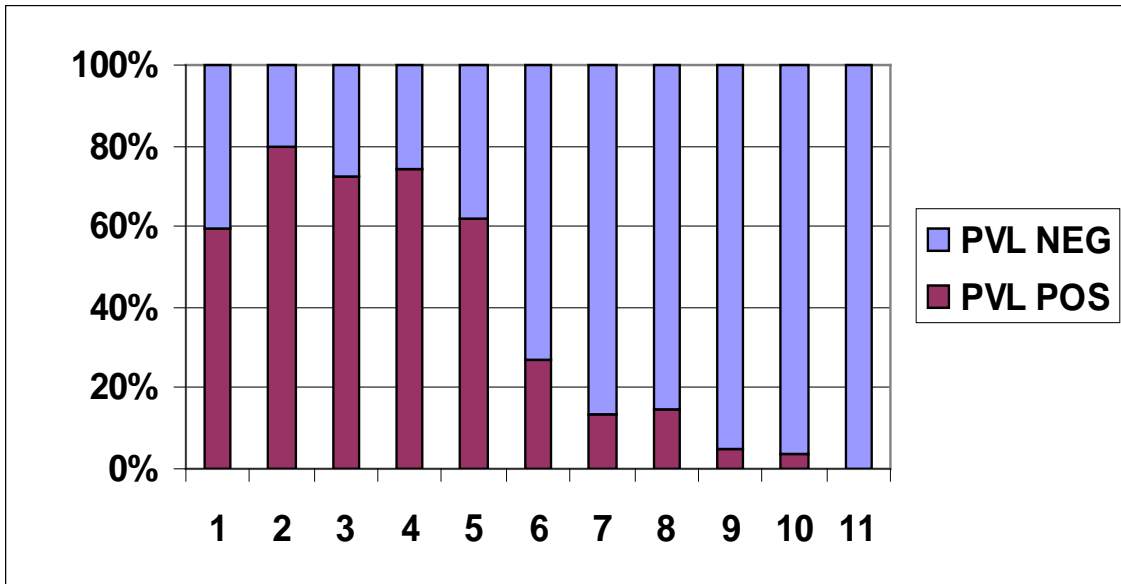


Mean, median and percentile data

Age (years)	PVL positive	PVL negative
Mean (95% CI)	33.23 (30.63 – 35.83)	52.97 (47.98 – 57.95)
Median	30.50	56.00
25 th percentile	19.75	28.00
75 th percentile	44.00	78.00

The mean age of patients with PVL-positive CA-MRSA is significantly lower ($P < 0.0001$) than the mean age of patients with PVL-negative CA-MRSA

PVL Status by Decade of Life (all MRSA)



HA- MRSA

Clone	Alternative Name	Positive	Negative	Total
ST22-MRSA-IV	EMRSA-15	1	111	112
ST239-MRSA-III	AUS-2 EMRSA	0	62	62
ST239-MRSA-III	AUS-3 EMRSA	0	31	31
ST5-MRSA-II	New York/Japan EMRSA	0	1	1
ST36-MRSA-II	EMRSA-16	0	1	1
Total		1 (0.5%)	206 (99.5%)	207

Panton-Valentine Leucocidin (PVL) Toxin: Regional Distribution

CA-MRSA

CC	1		5				8		9	30	45			59		72	75	80	88		509	S	Total
ST SCCmec	1 IV WA1	1 V	5 IV WA3	73 IV WA65	5 IV	5 V	8 IV WA5	8 IV USA 300	834 IV WA13	30 IV WSPP	45 V WA4	45 V WA84	45 IV WA23	59 IV WA15	59 V Taiwan	72 IV WA44	1304 V WA72	80 IV Eur	78 IV WA2	88 V	207 V	93 IV Qld	
ACT/NSW	5 (45%)		0					4 (100%)		16 (100%)			0	0		0		1 (100%)	1 (100%)		0	72 (99%)	99 (88%)
NT/ Qld	2 (14%)	0	0	0	0	0		2 (100%)		18 (100%)						0	0		0			50 (100%)	72 (73%)
SA	1 (8%)			0			0			1 (100%)	0	0	0		1 (100%)				0			10 (100%)	13 (38%)
Tas/Vic	1 (20%)		1 (20%)			0		3 (100%)		9 (90%)		0		0				1 (100%)		1 (100%)		12 (100%)	28 (62%)
WA	0		0	0				1 (100%)	0	2 (100%)	0								0			5 (100%)	8 (16%)
Total	9 (14%)	0	1 (5%)	0	0	0	0	10 (100%)	0	46 (98%)	0	0	0	0	1 (100%)	0	0	2 (100%)	1 (6%)	1 (100%)	0	149 (99%)	220 (65%)

HA-MRSA

A single isolate of ST22-MRSA-IV (EMRSA-15) isolated from ACT/NSW was PVL positive.

5.6. CA-MRSA Antibiogram

CC	1		5				8		9	30	45			59		72	75	80	88		509	S	Total
ST SCCmec	1 IV WA1	1 V	5 IV WA3	73 IV WA65	5 IV	5 V	8 IV WA5	8 IV USA 300	834 IV WA13	30 IV WSPP	45 V WA4	45 V WA84	45 IV WA23	59 IV WA15	59 V Taiwan	72 IV WA44	1304 V WA72	80 IV Eur	78 IV WA2	88 V	207 V	93 IV Qld	
Oxacillin only: 234 (68.8% of CA-MRSA)																							
Ox ^R	35		12	3		2				44	2					1						135	234
One non beta lactam antibiotic: 71 (20.9% of CA-MRSA)																							
Ox ^R Em ^R	7			1	1				1	2				2			1		16		1	13	45
Ox ^R Cp ^R	1		2				1	1		1		4	2										12
Ox ^R FA ^R	10	1																					11
Ox ^R Tc ^R	1																					1	2
Ox ^R Cot ^R																			1				1
Two non beta lactam antibiotic: 29 (8.5% of CA-MRSA)																							
Ox ^R Em ^R FA ^R	6																						6
Ox ^R Cp ^R FA ^R	1																						1
Ox ^R Em ^R Cp ^R			1					8				1				1			1				12
Ox ^R Em ^R Mp ^R			3																				3
Ox ^R Gm ^R Cp ^R																							1

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CC	1		5				8		9	30	45			59		72	75	80	88		509	S	Total
ST SCCmec	1 IV WA1	1 V	5 IV WA3	73 IV WA65	5 IV	5 V	8 IV WA5	8 IV USA 300	834 IV WA13	30 IV WSPP	45 V WA4	45 V WA84	45 IV WA23	59 IV WA15	59 V Taiwan	72 IV WA44	1304 V WA72	80 IV Eur	78 IV WA2	88 V	207 V	93 IV Qld	
Ox ^R Em ^R Cot ^R																						1	1
Ox ^R Gm ^R Rf ^R	1																						1
Ox ^R FA ^R Tc ^R																		1					1
Ox ^R Em ^R Tc ^R			1	1											1								3
Three non beta lactam antibiotic: 6 (1.8% of CA-MRSA)																							
Ox ^R Tc ^R Cp ^R FA ^R																		1					1
Ox ^R Em ^R FA ^R Rf ^R	1																						1
Ox ^R Em ^R Cp ^R Mp ^R								1															1
Ox ^R Em ^R Tc ^R Cp ^R												2											2
Ox ^R Gm ^R Cp ^R Cot ^R			1																				1
Total	63	1	20	5	1	2	1	10	1	47	2	7	2	2	1	2	1	2	18	1	1	180	340

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

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