Widespread Dissemination of the Panton-Valentine Leucocidin ST93-MRSA-IV (Qld CA-MRSA) Clone in the Australian Community

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Background & Objective

Community-onset methicillin-resistant *Staphylococcus aureus* (CO-MRSA) has become a worldwide phenomenon. This global change in MRSA epidemiology has resulted in a marked increase in the prevalence of staphylococcal community onset infections ranging from mild skin and soft-tissue infections (SSTI) to severe invasive infections including necrotising fasciitis and rapidly progressive necrotising pneumonia. Although polyclonal, five major community-associated MRSA (CA-MRSA) clones have been described: ST80-MRSA-IV (Europe), ST8-MRSA-IV [USA300] and ST1-MRSA-IV [USA400] (United States of America), ST59-MRSA-V_T (Asia) and ST30-MRSA-IV (Western Pacific Region). All carry the Panton-Valentine leucocidin (PVL) genes. Australia has a unique experience with CO-MRSA caused by CA-MRSA in that the first CA-MRSA epidemic was documented earlier than in most countries. It was initially due to a PVL-negative ST8-MRSA-IV clone and subsequently due to multiple CA-MRSA clones, including some that are PVL-positive. The objective of this study is to describe the prevalence and epidemiology of the PVL-positive ST93-MRSA-IV (Queensland [Qld] CA-MRSA) clone in the Australian community.

Materials & Methods

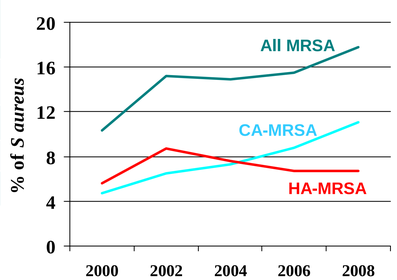
In 2008 the 5th biennial community *S aureus* surveillance programme (SAP08) was performed by the Australian Group for Antimicrobial Resistance (AGAR). Up to 100 clinically significant consecutive, non-duplicate outpatient isolates of *S aureus* were collected by 31 laboratories located throughout Australia. Of the 3,075 *S aureus* isolated 18.0% (553) were identified as MRSA. 547 of the 553 MRSA were characterised by pulsed-field gel electrophoresis (PFGE) and clonality determined by multilocus sequence typing (MLST) and staphylococcal chromosomal cassette *mec* (SCC*mec*) typing. The presence of PVL determinants was detected by PCR.

Results

	Community-Associated MRSA [number]	Healthcare-Associated MRSA [number]
Singleton	ST93-MRSA-IV (Qld CA-MRSA)* [150]	
Clonal Complex 1	ST1-MRSA-IV (WA MRSA-1) [63] ST1-MRSA-V [1]	
Clonal Complex 5	ST5-MRSA-IV (WA MRSA-3) [20] ST73-MRSA-IV (WA MRSA-65) [5] ST5-MRSA-V [2] ST5-MRSA-IV [1]	ST5-MRSA-II (USA100) [1]
Clonal Complex 8	ST8-MRSA-IV (USA300)* [10] ST8-MRSA-IV (WA MRSA-5) [1]	ST239-MRSA-III (Aus2/Aus3 EMRSA) [93]
Clonal Complex 9	ST834-MRSA-IV (WA MRSA-13 [1]	
Clonal Complex 22		ST22-MRSA-IV (EMRSA-15) [112]
Clonal Complex 30	ST30-MRSA-IV (WSPP)* [47]	ST36-MRSA-II (EMRSA-16 or USA200) [1]
Clonal Complex 45	ST45-MRSA-V (WA MRSA-84) [7] ST45-MRSA-V (WA MRSA-4) [2] ST45-MRSA-IV (WA MRSA-23) [2]	
Clonal Complex 59	ST59-MRSA-IV (WA MRSA-15) [2] ST59-MRSA-V (Taiwan CA-MRSA)* [1]	
Clonal Complex 72	ST72-MRSA-IV (WA MRSA-44) [2]	
Clonal Complex 75	ST1304-MRSA-IV (WA MRSA-72) [1]	
Clonal Complex 80	ST80-MRSA-IV (European CA-MRSA)* [2]	
Clonal Complex 88	ST78-MRSA-IV (WA MRSA-2) [18] ST88-MRSA-V [1]	
Clonal Complex 509	ST207-MRSA-V [1]	

*PVL POSITIVE STRAIN

In Australia there has been a significant increase in the percentage of community-onset *S aureus* infections caused by MRSA ranging from 11.7% in 2000 to 18.0% in 2008 (p <0.0001). This increase has been due to the emergence of CA-MRSA.



SAP08 CA-MRSA

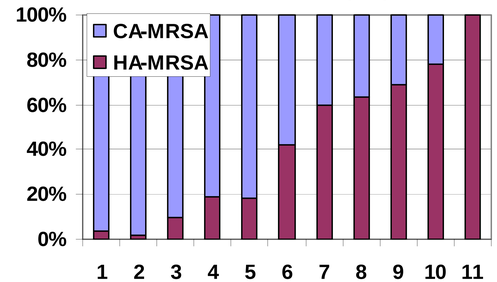
62.2% (n=340) of isolates were identified as CA-MRSA strains.
19 MLST/SCC*mec* types [15 sequence types and two SCC*mec* types {types IV and V} from 22 PFGE types were characterised.

SAP 08 HA-MRSA

37.8% (n=207) of isolates were identified as healthcare-associated MRSA [HA-MRSA] strains.
4 MLST/SCC*mec* types [4 sequence types and three SCC*mec* types {II, III and IV} from four PFGE types were characterised.

Results cont

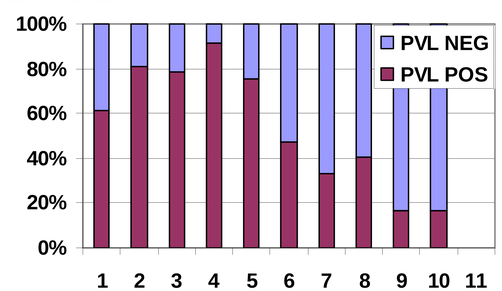
Proportion of CA-MRSA and HA-MRSA per patient decade



The proportion of MRSA identified as CA-MRSA was higher per decade in young patients, while the proportion of HA-MRSA was highest in the elderly.

The mean age of patients with infections due to CA-MRSA strains (40 years; median 35 years) was significantly lower (p<0.001) than the mean age of patients with infections due to HA-MRSA (69 years; median 74 years).

Proportion of PVL-positive & PVL-negative CA-MRSA per patient decade



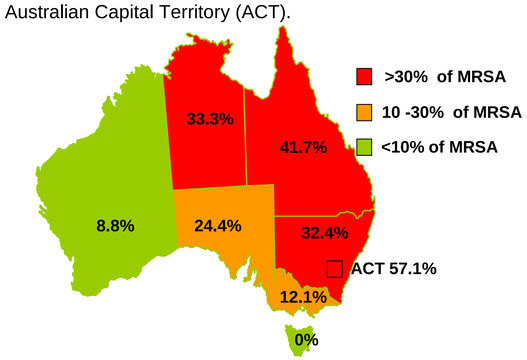
For CA-MRSA the proportion of PVL-positive CA-MRSA peaked in the 30 – 39 age group, and apart from the 70-79 age group, fell steady in the older decades.

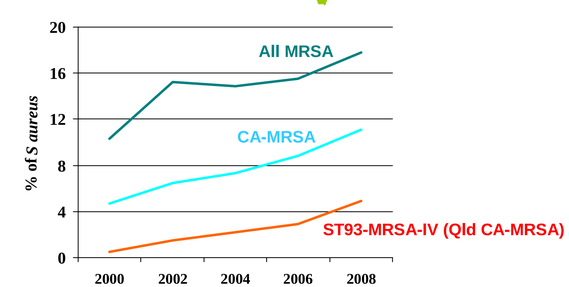
The mean age of patients with PVL-positive CA-MRSA strains (40 years; median 35 years) was significantly lower (p<0.001) than the mean age of patients with infections due PVL-negative CA-MRSA strains (69 years; median 74 years).

ST93-MRSA-IV (Qld CA-MRSA)

First identified in SSTI in patients living in Queensland in 2000, the PVL-positive ST93-MRSA-IV (Qld CA-MRSA) strain has been associated with necrotising pneumonia (including fatal cases), deep abscesses, osteomyeltis and septic arthritis. The epidemic potential of ST93-MRSA-IV (Qld CA-MRSA) has been demonstrated in rural Australia where it has caused outbreaks of boils in aboriginal communities.

In SAP08 ST93-MRSA-IV (Qld CA-MRSA) was the most frequently isolated MRSA clone in Australia accounting for 27.4% of MRSA and 44.1% of CA-MRSA. ST93-MRSA-IV (Qld CA-MRSA) was isolated in most regions ranging from 8.8% of MRSA in Western Australia to 57.1% in the Australian Capital Territory (ACT).





This predominance of ST93-MRSA-IV (Qld CA-MRSA) has resulted in a significant change in the percentage of CA-MRSA in Australia that are PVL positive and the number of SSTI in young Australians.

Conclusion

The rapid geographical expansion and epidemiology of ST93-MRSA-IV (Qld CA-MRSA) in Australia has parallels with the CA-MRSA epidemics in the USA. ST93-MRSA-IV (Qld CA-MRSA) has become the Australian equivalent of the USA300 clone.

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