Methicillin-resistant *Staphylococcus aureus* in the Australian community: an evolving epidemic

Graeme R Nimmo, Geoffrey W Coombs, Julie C Pearson, Francis G O'Brien, Keryn J Christiansen, John D Turnidge, Iain B Gosbell, Peter Collignon and Mary-Louise McLaws, on behalf of the Australian Group for Antimicrobial Resistance (AGAR)

ABSTRACT

Objective: To describe antimicrobial resistance and molecular epidemiology of methicillin-resistant *Staphylococcus aureus* (MRSA) isolated in community settings in Australia.

Design and setting: Survey of *S. aureus* isolates collected prospectively Australia-wide between July 2004 and February 2005; results were compared with those of similar surveys conducted in 2000 and 2002.

Main outcome measures: Up to 100 consecutive, unique clinical isolates of *S. aureus* from outpatient settings were collected at each of 22 teaching hospital and five private laboratories from cities in all Australian states and territories. They were characterised by antimicrobial susceptibilities (by agar dilution methods), coagulase gene typing, pulsed-field gel electrophoresis, multilocus sequence typing, SCC*mec* typing and polymerase chain reaction tests for Panton–Valentine leukocidin (PVL) gene.

Results: 2652 *S. aureus* isolates were collected, of which 395 (14.9%) were MRSA. The number of community-associated MRSA (CA-MRSA) isolates rose from 4.7% (118/2498) of *S. aureus* isolates in 2000 to 7.3% (194/2652) in 2004 ($P = 0.001$). Of the three major CA-MRSA strains, WA-1 constituted 45/257 (18%) of MRSA in 2000 and 64/395 (16%) in 2004 ($P = 0.89$), while the Queensland (QLD) strain increased from 13/257 (5%) to 58/395 (15%) ($P = 0.0004$), and the south-west Pacific (SWP) strain decreased from 33/257 (13%) to 26/395 (7%) ($P = 0.01$). PVL genes were detected in 90/195 (46%) of CA-MRSA strains, including 5/64 (8%) of WA-1, 56/58 (97%) of QLD, and 25/26 (96%) of SWP strains. Among health care-associated MRSA strains, all AUS-2 and AUS-3 isolates were multidrug-resistant, and UK EMRSA-15 isolates were resistant to ciprofloxacin and erythromycin (50%) or to ciprofloxacin alone (44%). Almost all (98%) of CA-MRSA strains were non-multiresistant.

Conclusions: Community-onset MRSA continues to spread throughout Australia. The hypervirulence determinant PVL is often found in two of the most common CA-MRSA strains. The rapid changes in prevalence emphasise the importance of ongoing surveillance.

MJA 2006; 184: 384–388

For editorial comment, see page 374. See also pages 404 and 420

The emergence of new hypervirulent strains of methicillin-resistant *Staphylococcus aureus* (MRSA) causing moderate to severe community-acquired infections is now a worldwide phenomenon. Epidemics have been reported in Canada,[1] the United States,[2] and Europe.[3] These reports have a number of findings in common including: lack of association with risk factors for health care-associated acquisition of MRSA; lack of resistance to non-β-lactam antibiotics; frequent association with indigenous populations; and association with subcutaneous abscess formation and necrotising pneumonia. The latter clinical conditions have been shown to correlate strongly with possession of the genes for Panton–Valentine leukocidin (PVL), an extracellular toxin that destroys leucocytes and causes tissue necrosis.[3,4]

In Australia, non-multiresistant MRSA associated with community infection (CA-MRSA) was first observed in Western Australia in the early 1990s, initially in Indigenous people in remote communities, and became known as WA-MRSA.[5] Subsequently, other strains of CA-MRSA appeared in WA. Infection caused by CA-MRSA was first noted in the eastern states in the mid-1990s.[6] Studies in Queensland[7] and New South Wales[8] initially reported a strong association between community-acquired infection with non-multiresistant MRSA and Polynesian background. The "south-west Pacific" (SWP) strain of CA-MRSA causing these infections was indistinguishable from that reported previously in Auckland, New Zealand,[7,8] and was initially characterised by the western Samoan phage typing pattern. A second strain, the "QLD" strain, was first identified in Queensland in 2000, causing community-acquired infection in people of European background.[9]

Both the SWP and QLD strains, but not the WA strains, usually carry PVL genes and are associated with abscess formation, bacteraemia and necrotising pneumonia.[3,10,11] However, PVL genes are carried on prophages, which are capable of generating bacteriophages (viruses that infect baceria) and consequently have the potential to spread to other strains of *S. aureus*.[12]

The epidemiology of community-onset MRSA can be confusing. Because of the differences in virulence, spectrum of infection and antibiotic sensitivity patterns, it is important to distinguish between infections caused by MRSA strains circulating in the community and not found in hospitals, and infections with onset in the community caused by health care-associated strains (HA-MRSA). The spread of the latter into the community is well documented, although these strains do not spread readily from person to person in the community.[13] The distinction between these two types of acquisition is based on the patient's risk factors for health care acquisition, such as recent hospitalisation, surgery, antibiotic medication, chronic medical conditions, long-term care and health care occupational status.[14] It is also possible to discriminate between these epidemiologically distinct strains by a variety of molecular typing methods.

The Australian Group for Antimicrobial Resistance (AGAR) previously established that the predominant MRSA strains circulating in the community are WA-1, SWP and QLD, which are now widely dispersed geographically.[15] This report describes changes in prevalence and geographic range of community-associated strains and the extent of PVL gene carriage in community-associated strains.

1 Number of isolates of health care-associated and community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) and percentage of all *S. aureus* isolates in participating Australian cities in 2000, 2002 and 2004

	Staphylococcus aureus isolates			Health care-associated isolates (HA-MRSA)				Community-associated isolates (CA-MRSA)			
City	2000	2002	2004	2000	2002	2004	*P*	2000	2002	2004	*P*
Perth	400	398	400	4 (1%)	13 (3%)	7 (2%)	0.45	40 (10%)	42 (11%)	44 (11%)	0.65
Darwin	99	100	59	1 (1%)	11 (11%)	5 (9%)	0.03	5 (5%)	10 (10%)	12 (20%)	0.003
Brisbane	300	300	300	6 (2%)	13 (4%)	12 (4%)	0.16	15 (5%)	20 (7%)	39 (13%)	< 0.001
Sydney	700	689	699	85 (12%)	120 (17%)	100 (14%)	0.25	36 (5%)	46 (7%)	55 (8%)	0.04
Newcastle	na	na	96	na	na	8 (8%)	—	na	na	5 (5%)	—
Canberra	100	100	100	0	5 (5%)	3 (3%)	0.09	4 (4%)	3 (3%)	2 (2%)	0.41
Adelaide	399	400	399	13 (3%)	11 (3%)	15 (4%)	0.69	12 (3%)	24 (6%)	26 (7%)	0.03
Hobart	100	100	99	0	1 (1%)	1 (1%)	0.38	2 (2%)	5 (5%)	2 (2%)	0.38
Melbourne	400	299	500	30 (8%)	34 (11%)	50 (10%)	0.23	4 (1%)	5 (2%)	9 (2%)	0.99
Total	2498	2386	2652	139 (5.6%)	208 (8.7%)	201 (7.6%)	0.006	118 (4.7%)	155 (6.5%)	194 (7.3%)	0.001

na = not available (no survey conducted). ◆

METHODS

Survey method

Isolates were collected from patients attending primary care clinics, outpatient clinics, emergency departments or other outpatient settings, or residing in long-term residential facilities. Twenty-two teaching hospital laboratories and five private pathology laboratories in nine Australian cities participated in the study. Up to 100 consecutive clinical isolates of *S. aureus* were collected at each laboratory between 1 July 2004 and 8 February 2005. Isolates from infection control screening specimens were excluded, as were duplicate clinical isolates, as determined by antimicrobial susceptibility phenotype.

The results were compared with two previous similar surveys which used the same isolate inclusion criteria and involved the same laboratories, except that two fewer teaching hospital laboratories participated (one in Newcastle and one in Melbourne).[15]

Isolate characteristics

S. aureus was identified by standard methods, as described elsewhere.[15] Susceptibility testing was performed by agar dilution according to Clinical Laboratory Standards Institute methodology, using a single breakpoint concentration of antimicrobial.[16] Antimicrobials were incorporated into agar plates at the following concentrations: penicillin G, 0.125 mg/L; oxacillin, 2 mg/L; vancomycin, 2 mg/L; teicoplanin, 2 mg/L; rifampicin, 1 mg/L; fusidic acid, 1 mg/L; gentamicin, 4 mg/L; chloramphenicol, 8 mg/L; erythromycin, 0.5 mg/L; clindamycin, 0.5 mg/L; tetracycline, 4 mg/L; trimethoprim, 8 mg/L; ciprofloxacin, 1 g/L; and mupirocin, 1 mg/L. An antibiotic-free control plate and five control organisms were included in each batch.[15] Resistogram typing was performed by disk diffusion against a panel of six chemicals and dyes, as previously described.[15]

Coagulase gene restriction fragment length polymorphism typing was performed as described elsewhere.[15] Pulsed-field gel electrophoresis (PFGE) of chromosomal DNA was performed using the CHEF DR III System (Bio-Rad Laboratories, Sydney, NSW) and interpreted as described elsewhere.[15] Representative isolates were characterised by multilocus sequence typing (MLST) and staphylococcal chromosomal cassette *mec* (SCC*mec*) typing (where *mec* is the mobile genetic element responsible for methicillin resistance, classifiable into five major types), with results interpreted as described previously.[15]

Strains are reported with their common names (eg, WA-1) followed by the sequence type (ST), methicillin resistance phenotype, and SCC*mec* type (I to V) (eg, ST1-MRSA-IV). Strains are classified into two groups on the basis of previously published evidence: those implicated in health care-associated infection (HA-MRSA); and those implicated in community-associated infection (CA-MRSA).[15]

CA-MRSA isolates were assayed for the presence of PVL genes using polymerase chain reaction (PCR) primers for a 1554-bp region from *lukS-PV* and *lukF-PV* as follows: forward, 5′ GGCCTTTCCAATACAATATTGG 3′; and reverse, 5′ CCCAATCAACTTCATAAATTG 3′.[17]

Statistical analysis

We determined the proportions of *S. aureus* isolates which were considered CA-MRSA and HA-MRSA in each surveillance period and in each city, and also the proportions of the six major HA-MRSA and CA-MRSA strain types among all HA-MRSA and CA-MRSA isolates, respectively. Differences in proportions were tested over the survey periods using the χ^2 test for trend, where data were available for all three survey periods, or a test for the difference between two proportions, where data were available for only two survey periods. Differences were tested between cities and within cities over the survey periods. All tests for significance were two-sided with α set at the 5% level and were performed using Epi Info version 6.0.4 (Centers for Disease Control and Prevention, Atlanta, Ga, USA).

The survey did not require ethical approval as all *S. aureus* isolates were from routine diagnostic specimens referred to the participating laboratories; information pertaining to isolates was de-identified; and there was no change to the routine processing or reporting practices in the participating laboratories.

RESULTS

In the 2004 survey, we assessed 2652 isolates of *S. aureus*, compared with 2486 in the 2000 survey, and 2488 in 2002. In 2004, 14.9% of isolates (395/2652) were resistant to oxacillin (and therefore methicillin), compared with 10.3% in 2000 (257/2498), and 15.2% in 2002 (363/2386).

The proportion of *S. aureus* isolates which were HA-MRSA and CA-MRSA differed significantly between the three surveys ($P = 0.006$ and $P = 0.001$, respectively; Box 1). However, when analysed by city, HA-MRSA proportions differed significantly between surveys only in Darwin ($P = 0.03$).

2 Number of isolates of the most common community-associated and health care-associated MRSA strains and percentage of all MRSA isolates in participating Australian cities in 2000, 2002 and 2004

A: Community-associated MRSA (CA-MRSA) strains*

	WA-1 (ST1)				QLD (ST93)				SWP (ST30)			
City	2000	2002	2004	*P*	2000	2002	2004	*P*	2000	2002	2004	*P*
Perth	27 (61%)	22 (40%)	23 (45%)	0.13	0	1 (2%)	2 (4%)	0.95	0	1 (2%)	1 (2%)	0.95
Darwin	3 (50%)	2 (10%)	5 (29%)	0.79	0	0	2 (12%)	—	0	5 (24%)	3 (18%)	0.95
Brisbane	3 (14%)	6 (18%)	7 (14%)	0.84	1 (5%)	3 (9%)	18 (35%)	0.001	9 (43%)	9 (27%)	9 (18%)	0.03
Sydney	4 (3%)	10 (6%)	5 (3%)	0.89	9 (7%)	26 (16%)	30 (19%)	0.02	20 (17%)	6 (4%)	13 (8%)	0.03
Newcastle	na	na	4 (31%)	—	na	na	1 (8%)	—	na	na	0	—
Canberra	0	0	0	—	1 (25%)	1 (13%)	2 (40%)	0.56	2 (50%)	2 (25%)	0	0.83
Adelaide	5 (20%)	14 (40%)	18 (44%)	0.06	1 (4%)	3 (9%)	3 (7%)	0.66	0	2 (6%)	0	—
Hobart	2(100%)	3 (50%)	0	0.90	0	2 (33%)	0	—	0	0	0	—
Melbourne	1 (3%)	2 (5%)	2 (3%)	0.98	1 (3%)	0	0	—	2 (6%)	1 (3%)	0	0.90
National	45 (18%)	59 (16%)	64 (16%)	0.89	13 (5%)	36 (10%)	58 (15%)	< 0.001	33 (13%)	26 (7%)	26 (7%)	0.01

* Strain common name and sequence type. na = not available (no survey conducted).

B: Health care-associated MRSA (HA-MRSA) strains*

	AUS-2 (ST239)				AUS-3 (ST239)				UK EMRSA-15 (ST22)			
City	2000	2002	2004	*P*	2000	2002	2004	*P*	2000	2002	2004	*P*
Perth	0	0	0	—	0	3 (6%)	0	—	3 (7%)	8 (15%)	6 (12%)	0.48
Darwin	0	8 (38%)	4 (24%)	0.34	1 (17%)	3 (14%)	1 (6%)	0.39	0	0	0	—
Brisbane	5 (24%)	9 (24%)	4 (8%)	0.04	0	3 (9%)	3 (6%)	0.90	1 (5%)	1 (3%)	5 (10%)	0.32
Sydney	61 (50%)	88 (53%)	57 (37%)	0.02	1 (0.8%)	2 (1%)	6 (4%)	0.05	23 (19%)	28 (17%)	37 (24%)	0.27
Newcastle	na	na	5 (39%)	—	na	na	0	—	na	na	3 (23%)	—
Canberra	0	5 (63%)	3 (60%)	0.62	0	0	0	—	0	0	0	—
Adelaide	2 (8%)	0	3 (7%)	0.71	8 (32%)	6 (17%)	5 (12%)	0.06	3 (12%)	5 (14%)	6 (15%)	0.48
Hobart	0	1 (17%)	0	—	0	0	1 (33%)	—	0	0	0	—
Melbourne	22 (65%)	12 (31%)	14 (24%)	< 0.001	8 (24%)	22 (56%)	31 (53%)	0.02	0	0	5 (9%)	—
National	90 (35%)	123 (34%)	89 (23%)	< 0.001	18 (7%)	47 (12%)	24 (6%)	0.46	30 (12%)	42 (12%)	62 (16%)	0.17

* Strain common name and sequence type. na = not available (no survey conducted). ◆

Significant increases in CA-MRSA occurred over the same period in four cities: Darwin (5% to 20%, $P = 0.003$), Brisbane (5% to 13%, $P < 0.0001$), Sydney (5% to 8%, $P = 0.04$), and Adelaide (3% to 7%, $P = 0.03$). The total proportion of CA-MRSA also increased significantly, from 4.7% in 2000 to 7.3% by 2004 ($P = 0.001$). In 2004, CA-MRSA strains accounted for over 10% of all clinical outpatient isolates of *S. aureus* in Darwin, Brisbane and Perth. The proportion of CA-MRSA strains in Melbourne and Hobart remained lower than in other states and did not increase significantly.

Community-associated strains

Three major strains of CA-MRSA predominated in all three surveys, with WA-1 (ST1-MRSA-IV) consistently the most common CA-MRSA strain (Box 2A). This strain is isolated throughout the country, but represents a lower proportion of MRSA in the eastern states than in the west. The proportion of isolates that were strain WA-1 did not change significantly over the three survey periods ($P = 0.89$).

The QLD strain (ST93-MRSA-IV) is now the second most common CA-MRSA strain and has increased significantly since 2000 ($P = 0.0004$), with a 1.5-fold increase as a proportion of MRSA, and a fourfold increase as a proportion of *S. aureus* by 2004. In 2004, this strain predominated in Brisbane (35%) and Sydney (19%), and was found in all other participating cities, except Melbourne and Hobart.

The SWP strain (ST30-MRSA-IV) is the third most common CA-MRSA strain. It remained prominent in Brisbane, Sydney and Darwin, but declined overall, from 13% in 2000 to 7% by 2004 ($P = 0.01$).

In 2004, nine other CA-MRSA strains were found: WA-2 (ST129-MRSA-IV), 19 isolates, predominantly in SA and WA); WA-3 (ST5-MRSA-IV), 14, predominantly in SA and WA; WA-12 (ST8-MRSA-IV), 4, in Sydney and Brisbane; WA-15 (ST59-MRSA-IV), 2, in Perth and Brisbane; WA-13 (ST584-MRSA-IV), 2, in Melbourne and Brisbane; WA-23 (ST45-MRSA-IV), 2, in Melbourne; WA-17 (ST583-MRSA-IV) and WA-5 (ST8-MRSA-IV), 1 each in Sydney; and WA-8 (ST75-MRSA-IV), 1, in Darwin. Thus 12 strains of CA-MRSA carried SCC*mec* type IV in 2004, compared with four in 2000 and five in 2002.

Health care-associated strains

Among HA-MRSA strains, the proportion of AUS-2 (subtype of ST239-MRSA-III) decreased significantly over the three surveys ($P = 0.0003$), while there was no significant trend for AUS-3 (also a subtype of ST239-MRSA-III) ($P = 0.46$) (Box 2B). None of the participating cities experienced a significant change in the other major strain, UK EMRSA-15 (ST22-MRSA-IV) over the three survey periods, nor was there a significant change overall ($P = 0.17$). Two isolates of

another UK HA-MRSA strain, EMRSA-16 (ST36-MRSA-II) were also found in the 2004 survey.

Isolate characteristics

Antibiotic resistance phenotype differed strikingly between HA-MRSA and CA-MRSA. All AUS-2 and AUS-3 (HA-MRSA) isolates were resistant to at least four non-β-lactam antimicrobials: 86% were resistant to the combination of gentamicin, erythromycin and tetracycline; and only 4% were sensitive to gentamicin. UK EMRSA-15 isolates were usually resistant to ciprofloxacin and erythromycin (50%) or ciprofloxacin alone (44%), and differed from all other MRSA isolates in being urease-negative (with the exception of one WA-1 isolate with no non-β-lactam resistance). On the other hand, 60% of CA-MRSA isolates were resistant only to β-lactams, and 29% were resistant to only one other antimicrobial, while 2% were resistant to more than three non-β-lactams, and one isolate was resistant to gentamicin.

The PVL gene was detected in 90 isolates belonging to five CA-MRSA strains. The proportion of PVL-positive isolates varied markedly between strains ($P < 0.0001$): WA-17, 1 (100%; 95% CI, 3%–100%); QLD, 56 (97%; 95% CI, 88%–100%); SWP, 25 (96%; 95% CI, 80%–100%); WA-12, 3 (75%; 95% CI, 19%–99%); and WA-1, 5 (8%; 95% CI, 3%–17%). The proportion of PVL-positive isolates also varied markedly between cities ($P < 0.0001$): Canberra, 100%; Sydney, 80%; Brisbane, 74%; Darwin, 42%; Newcastle, 17%; Adelaide, 15%; Perth, 11%; and Melbourne and Hobart, 0. Thirteen (14%) of the PVL-positive isolates were resistant to erythromycin.

DISCUSSION

The concurrent emergence and expansion of multiple PVL-positive CA-MRSA clones on different continents has been rapid and striking. This epidemic has been very well documented in Australia by AGAR: annual studies conducted exclusively in teaching hospitals from 1989 to 1999 showed that non-multiresistant MRSA, a surrogate marker for CA-MRSA, began to increase in Perth in the early 1990s and in more easterly cities in the late 1990s.[10]

The biennial studies reported here and previously have established the major strains causing community-onset MRSA infection in Australia.[15] Clearly, CA-MRSA now represents a major clinical and public health problem. The large distances between Australian cities have been no barrier to the rapid spread of the major epidemic strains, WA-1, SWP and QLD. The first two of these are pandemic strains which have appeared on multiple continents.[3,18,19] Demonstration of the presence of the relatively small SCC*mec* type IV element (one of a range of elements responsible for methicillin resistance) in increasing numbers of lineages of *S. aureus* is of great concern: this element is of a size (about 28 kilobases) to allow spread by bacteriophage transduction.

The increase in prevalence of CA-MRSA is due to two mechanisms: first, clonal expansion of successful lineages, such as the QLD strain; and second, the transmission of SCC*mec* to an increasing number of lineages of *S. aureus*. This raises the prospect of widespread acquisition of methicillin resistance in *S. aureus*, similar to the spread of penicillin resistance seen in the latter half of the 20th century, which led to penicillin resistance levels greater than 80%.[10,20] Furthermore, the ability of CA-MRSA strains to acquire resistance to other antimicrobials will almost certainly pose a longer term challenge. While only 2% of CA-MRSA isolates were resistant to more than three non-β-lactam antimicrobials in the 2004 survey, no CA-MRSA isolates had that level of resistance in the previous two surveys.

The spread of virulence genes is also a potential problem. PVL genes are carried on a prophage and so can be transmitted to receptive strains by transduction.[12] We demonstrated the presence of PVL in five CA-MRSA strains, three of which (WA-1, QLD and SWP) are major epidemic strains. PVL has been described in WA-1 only recently,[21,22] and clinical data on the association of this strain with severe infections are lacking. Nonetheless, it has recently been suggested that drugs that shut down ribosomal translation of proteins in *S. aureus*, such as clindamycin and linezolid, might decrease production of toxins such as PVL. Therefore, these drugs may be specifically indicated in the treatment of serious CA-MRSA infections.[23] This hypothesis remains to be tested in vivo.

As CA-MRSA strains are now common in many parts of Australia, it is important that doctors consider that any staphylococcal infection — acquired in the community or in hospital — may be caused by MRSA. It is important to collect appropriate microbiological specimens, such as swabs for localised infections and blood cultures for systemic infections, for culture and susceptibility testing. Delay in recognition that these infections are caused by MRSA can in turn delay definitive treatment, and this may lead to increased mortality or prolonged morbidity.[11,24] Laboratories need to expedite detection of MRSA, report sensitivity to an appropriate range of non-β-lactam antibiotics, and provide advice on suitable antimicrobials.

The choice of empirical treatment should be guided by the severity of infection, the presence of risk factors for HA-MRSA infection, and the local prevalence of CA-MRSA. Where MRSA is likely, vancomycin is suggested for cases of severe or life-threatening infection, while linezolid may be considered as a second-line agent.[25]

If infection is mild, it is still reasonable to prescribe flu(di)cloxacillin (or alternative β-lactams in cases of intolerance or allergy), given that most strains of *S. aureus* are still sensitive to β-lactams. However, should MRSA be isolated, therapy should be changed to an appropriate agent. A number of readily available oral agents can be used in mild to moderate infections. Clindamycin has been suggested, but may not always be appropriate because of the presence of inducible resistance in some CA-MRSA strains.[25] Erythromycin is the best indicator of this type of resistance in Australia, and we found that 14% of PVL-positive CA-MRSA isolates in this survey were resistant to erythromycin. The use of tetracyclines such as doxycycline is supported by a retrospective case series and case reports.[26] Trimethoprim–sulfamethoxazole was found to be equivalent to vancomycin in serious MRSA infections in injecting drug users,[27] and there is also evidence of its success in less serious community MRSA infections.[28]

Therefore, clindamycin, doxycycline or trimethoprim–sulfamethoxazole may be used for mild to moderate CA-MRSA infections, depending on susceptibility results. However, tetracyclines should not be used in children aged under 8 years, and trimethoprim–sulfamethoxazole should not be used in infants under 8 weeks. Ongoing surveillance is essential to assess progress of the epidemic of MRSA in the community in Australia and changes in susceptibility of the epidemic strains.

ACKNOWLEDGEMENTS

The Australian Group for Antimicrobial Resistance (AGAR) comprises: Joan Faoagali, Narelle George (Queensland Health Pathology Service [QHPS], Royal Brisbane Hospital, QLD); Graeme Nimmo, Jacqueline Harper, Jacqueline Schooneveldt (QHPS, Princess Alexandra Hospital, QLD); Peter

Collignon, Susan Bradbury (The Canberra Hospital, ACT); Sue Tiley (Hunter Area Pathology Service, NSW); Tom Gottlieb, Glenn Funnell (Concord Repatriation General Hospital, NSW); Clarence Fernandes (Royal North Shore Hospital, NSW); Richard Benn, Barbara Yan (Royal Prince Alfred Hospital, NSW); Iain Gosbell, Helen Ziochos, Alison Vickery (South Western Area Pathology Service, NSW); David Mitchell (Westmead Hospital, NSW); Sam Ryder, James Branley (Nepean Hospital, NSW); Denis Spelman, Clare Franklin (Alfred Hospital, VIC); Sue Garland, Gena Gonis (Royal Children's and Women's Hospitals, VIC); Mary Jo Waters, Linda Joyce (St Vincent's Hospital, VIC); Peter Ward (Austin Health, VIC); John Andrew (Gribbles Pathology, VIC); Alistair McGregor, Rob Peterson (Royal Hobart Hospital, TAS); John Turnidge, Jan Bell (Women's and Children's Hospital, SA); Irene Lim, Rachael Pratt (Institute of Medical and Veterinary Science, SA); Hendrik Pruul (Flinders Medical Centre, SA); Leigh Mulgrave (PathCentre, WA); Keryn Christiansen, Geoff Coombs (Royal Perth Hospital, WA); David McGechie, Graham Francis (Fremantle Hospital, WA); Gary Lum (Royal Darwin Hospital, NT); Miriam Paul (Douglass Hanly Moir Pathology, NSW); Jenny Robson (Sullivan Nicolaides Pathology, QLD); P C Lee (Gribbles Pathology, SA); Sue Benson (St John of God Pathology, WA).

Multi-locus sequence typing of the 2000 MRSA isolates was supported by a grant from the 20th International Conference on Chemotherapy Research Trust Fund. Sequencing of the 2002 and 2004 MRSA isolates was performed by the WA Genome Resource Centre, Department of Clinical Immunology and Biochemical Genetics, Royal Perth Hospital, WA.

COMPETING INTERESTS

The Australian Group for Antimicrobial Resistance was supported financially by Eli Lilly (Australia) (manufacturer of vancomycin) from 1987 to 2001, and is currently supported by a grant from the Australian Government Department of Health and Ageing. Neither funding body had any role in study design, data collection, analysis and interpretation, and writing or publication of this article.

AUTHOR DETAILS

Graeme R Nimmo, FRCPA, FASM, MPH, MSc, Director of Microbiology,[1] and Associate Professor of Molecular Pathology[2]
Geoffrey W Coombs, BAppSc(Med Sc), PGDipBiomedSC, Principal Scientist[3]
Julie C Pearson, BSc(Biol), Senior Scientist[3]
Francis G O'Brien, BAppSc, PhD, Research Scientist[4]
Keryn J Christiansen, FRCPA, Head of Department[3]
John D Turnidge, FRACP, FRCPA, Director of Pathology,[5] and Professor of Pathology and Paediatrics[6]
Iain B Gosbell, MD, FRACP, FRCPA, Director,[7] and Conjoint Associate Professor[8]
Peter Collignon, FRACP, FRCPA, FASM, Director of Microbiology and Infectious Diseases,[9] and Professor[10]
Mary-Louise McLaws, DPHTM, MPH, PhD, Associate Professor and Director[11]

1 Microbiology Department, Queensland Health Pathology Service, Brisbane, QLD.
2 University of Queensland, Brisbane, QLD.
3 Department of Microbiology and Infectious Diseases and Gram-Positive Bacteria Typing and Research Unit, PathWest Laboratory Medicine WA, Perth, WA.
4 Molecular Genetics Research Unit and Gram-Positive Bacteria Typing and Research Unit, School of Biomedical Sciences, Perth, WA.
5 Women's and Children's Hospital, Adelaide, SA.
6 University of Adelaide, Adelaide, SA.
7 Department of Microbiology and Infectious Diseases, South Western Area Pathology Service, Sydney, NSW.
8 School of Pathology, University of New South Wales, Sydney, NSW.
9 The Canberra Hospital, Canberra, ACT.
10 Australian National University, Canberra, ACT.
11 Hospital Infection Epidemiology and Surveillance Unit, University of New South Wales, Sydney, NSW.

Correspondence:
Graeme_Nimmo@health.qld.gov.au

REFERENCES

1 Embil J, Ramotar K, Romance L, et al. Methicillin-resistant *Staphylococcus aureus* in tertiary care institutions on the Canadian prairies 1990-1992. *Infect Control Hosp Epidemiol* 1994; 15: 646-651.
2 Naimi TS, LeDell KH, Boxrud DJ, et al. Epidemiology and clonality of community-acquired methicillin-resistant *Staphylococcus aureus* in Minnesota, 1996-1998. *Clin Infect Dis* 2001; 33: 990-996.
3 Vandenesch F, Naimi T, Enright MC, et al. Community-acquired methicillin resistant *Staphylococcus aureus* carrying Panton-Valentine Leukocidin genes: worldwide emergence. *Emerg Infect Dis* 2003; 9: 978-984.
4 Jarraud S, Mougel C, Thioulouse J, et al. Relationships between *Staphylococcus aureus* genetic background, virulence factors, *agr* groups (alleles), and human disease. *Infect Immun* 2002; 70: 631-641.
5 Udo EE, Pearman JW, Grubb WB. Genetic analysis of community isolates of methicillin-resistant *Staphylococcus aureus* in Western Australia. *J Hosp Infect* 1993; 25: 97-108.
6 Collignon P, Gosbell I, Vickery A, et al. Community-acquired meticillin-resistant [sic] *Staphylococcus aureus* in Australia. Australian Group on Antimicrobial Resistance [letter]. *Lancet* 1998; 352:145-146.
7 Nimmo GR, Schooneveldt J, O'Kane G, et al. Community acquisition of gentamicin-sensitive MRSA in south-east Queensland. *J Clin Microbiol* 2000; 38: 3926-3931.
8 Gosbell IB, Mercer JL, Neville SA, et al. Non-multiresistant and multiresistant methicillin-resistant *Staphylococcus aureus* in community-acquired infections. *Med J Aust* 2001; 174: 627-630.
9 Munckhof WJ, Schooneveldt J, Coombs GW, et al. Emergence of community-acquired methicillin-resistant *Staphylococcus aureus* (MRSA) infection in Queensland, Australia. *Int J Infect Dis* 2003; 7: 259-267.
10 Nimmo GR, Playford EG. Community-acquired MRSA bacteraemia: four additional cases including one associated with severe pneumonia [letter]. *Med J Aust* 2003; 178: 245.
11 Peleg AY, Munckhof WJ. Fatal necrotising pneumonia due to community-acquired methicillin-resistant *Staphylococcus aureus* (MRSA) [letter]. *Med J Aust* 2004; 181: 228-229.
12 Narita S, Kaneko J, Chiba J, et al. Phage conversion of Panton-Valentine leukocidin in *Staphylococcus aureus*: molecular analysis of a PVL-converting phage, phiSLT. *Gene* 2001; 268: 195-206.
13 Cookson BD. Methicillin-resistant *Staphylococcus aureus* in the community: new battlefronts, or are the battles lost? *Infect Control Hosp Epidemiol* 2000; 21: 398-403.
14 Herold BC, Immergluck LC, Maranan MC, et al. Community-acquired methicillin-resistant *Staphylococcus aureus* in children with no identified predisposing risk. *JAMA* 1998; 279: 593-598.
15 Coombs GW, Nimmo GR, Bell JM, et al. Community methicillin-resistant *Staphylococcus aureus* in Australia: genetic diversity in strains causing outpatient infections. *J Clin Microbiol* 2004; 42: 4735-4743.
16 National Commmittee for Clinical Laboratory Standards. Methods for dilution antimicrobial susceptibility tests for bacteria that grow aerobically. Approved standard. 5th ed. NCCLS Document M7-A5. Wayne, Pa, USA: NCCLS, 2000.
17 Fey PD, Saïd-Salim B, Rupp ME, et al. Comparative molecular analysis of community- or hospital-acquired methicillin-resistant *Staphylococcus aureus*. *Antimicrob Agents Chemother* 2003; 47: 196-203.
18 Ma XX, Galiana A, Pedreira W, et al. Community-acquired methicillin-resistant *Staphylococcus aureus*, Uruguay. *Emerg Infect Dis* 2005; 11: 973-976.
19 Wannet WJ, Spalburg E, Heck ME, et al. Emergence of virulent methicillin-resistant *Staphylococcus aureus* strains carrying Panton-Valentine leucocidin genes in the Netherlands. *J Clin Microbiol* 2005; 43: 3341-3345.
20 Gillespie MT, May JW, Skurray RA. Antibiotic resistance in *Staphylococcus aureus* isolated in an Australian hospital between 1946 and 1981. *J Med Microbiol* 1985; 19: 137-147.
21 Barbagiannakos T, Darbar A, Kumari P, et al. Clinical and epidemiological survey of MRSA from hospitals in South Western Sydney, New South Wales, Australia. In: 11th International Symposium on Staphylococci and Staphylococcal Infections. Charleston, SC, USA; 2004: 127.
22 Stephens A, Huygens F, Nimmo G, et al. Variable binary gene typing increases resolution of methicillin-resistant *Staphylococcus aureus* MLST clonal groups defined by SNP typing. In: 11th International Symposium on Staphylococci and Staphylococcal Infections. Charleston, SC, USA; 2004: 156.
23 Etienne J. MRSA communautaires (entre autre). Seminar of the Catholic University of Louvain, Brussels. Available at: http://www.md.ucl.ac.be/seminfect/Etienne-24-02-05/Etienne-24-02-05.pdf (accessed Dec 2005).
24 Gosbell IB, Mercer JL, Neville SA, et al. Community-acquired, non-multiresistant oxacillin-resistant *Staphylococcus aureus* (NORSA) in South Western Sydney. *Pathology* 2001; 33: 206-210.
25 Zetola N, Francis JS, Nuermberger EL, et al. Community-acquired meticillin-resistant [sic] *Staphylococcus aureus*: an emerging threat. *Lancet Infect Dis* 2005; 5: 275-286.
26 Ruhe JJ, Monson T, Bradsher RW, et al. Use of long-acting tetracyclines for methicillin-resistant *Staphylococcus aureus* infections: case series and review of the literature. *Clin Infect Dis* 2005; 40: 1429-1434.
27 Markowitz N, Quinn EL, Saravolatz LD. Trimethoprim-sulfamethoxazole compared with vancomycin for treatment of *Staphylococcus aureus* infection. *Ann Intern Med* 1992; 117: 390-398.
28 Grim SA, Rapp RP, Martin CA, et al. Trimethoprim-sulfamethoxazole as a viable treatment option for infections caused by methicillin-resistant *Staphylococcus aureus*. *Pharmacotherapy* 2005; 25: 253-264.

(Received 19 Aug 2005, accepted 4 Jan 2006) ❑