Prevalence of antiseptic resistance genes qacA/B and specific sequence types of methicillin-resistant Staphylococcus aureus in the era of hand hygiene

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Sir,

In an attempt to control the spread of methicillin-resistant Staphylococcus aureus (MRSA) and other multiresistant organisms in hospitalized patients, hand hygiene campaigns have promoted the widespread use of alcohol-based hand solutions containing antiseptic agents such as chlorhexidine and quaternary ammonium compounds. The use of these products, however, has led to increased resistance to these antiseptic agents in MRSA strains.1–5 qacA/B are plasmid-borne resistance genes coding for multidrug efflux pumps that confer high-level resistance to chlorhexidine, quaternary ammonium compounds and other antiseptic compounds commonly used in hand hygiene solutions.5 They are associated with higher MICs and tolerance of these antiseptic agents.1,4,5 qacA/B genes have been found in healthcare-associated MRSA (HA-MRSA) isolates from around the world.2–8 In addition, the prevalence of qacA/B genes has been associated with particular sequence types (STs) of HA-MRSA.1,3,4,6 To our knowledge, the prevalence of MRSA strains harbouring these genes has not been researched in Australia. In this study, we characterize the prevalence of qacA/B genes in HA-MRSA isolates in our institution spanning 10 years, from 2000 to 2009. We determined whether the national hand hygiene campaign implemented in 2006 had any impact on the prevalence of these genes and, in addition, if any relationship exists between the different STs of HA-MRSA and qacA/B gene prevalence.

All (total 151) clinically significant unique HA-MRSA isolates from the period 2000–09 from Nepean Hospital, a 490 bed tertiary referral hospital in Sydney, were used in this study. The presence of qacA/B gene in these isolates was evaluated by real-time PCR using the following primers: qacA/B forward primer 5'-CTATGGAATAGGATATGGTGT and reverse primer 5'-CCACTACAGTTCTACGCTACAT.7 The HA-MRSA isolates were categorized into STs using their antibiograms and correlations with pre-existing typing performed on HA-MRSA isolates in our institution by the Australian Group on Antimicrobial Resistance.9 Quantities of hand hygiene solutions used by the hospital were obtained via the pharmacy database.

A sustained >6-fold increase in antiseptic-containing alcohol-based hand solution use occurred as a result of the hand hygiene campaign (‘Clean hands saves lives’) implemented in 2006 [amounts of 0.5% chlorhexidine gluconate and quaternary ammonium compounds used (average litres per year) were 968 and 150 L before the hand hygiene campaign (2004–06) and 3967 and 2958 L after the hand hygiene campaign (2007–09), respectively).

The yearly prevalence of qacA/B genes in HA-MRSA isolates from 2000 to 2009 ranged from 65.0% to 94.7% (mean 78.6%). This is higher than that previously found in the UK (8%–26%),3,6 Europe (63%)2 and Asia (33%–61%),3,4 but comparable to that found in a recent study in Geneva (79%).8

The HA-MRSA isolates in this study comprise two STs: ST239 MRSA-III Aus-2 EMRSA and ST22 MRSA-IV EMRSA-15. The ST239 type was the predominant strain throughout the study period (mean yearly prevalence of ST239 from 2000 to 2009 was 84.3%, range 75%–100%).

Comparing the prevalence of the qacA/B genes before (2000–06) and after (2007–09) the hand hygiene campaign, we did not find an increase in the prevalence of these genes despite the marked increase in antiseptic hand solutions after 2006 [mean yearly prevalence of qacA/B-positive MRSA isolates between 2000 and 2006 and between 2007 and 2009 was 78.6% and 73.5%, respectively (P=0.53; x²=0.39, df=1)]. Similarly, there was no change in the incidence of MRSA ST239 [mean yearly prevalence of MRSA ST239 between 2000 and 2006 and between 2007 and 2009 was 85.6% and 78.6%, respectively (P=0.37; x²=0.81, df=1)].

Interestingly, we found a significant association between qacA/B gene positivity and MRSA type ST239 [94.5% of qacA/B-positive isolates were ST239 and 88.9% of ST239 isolates were qacA/B positive (OR=29.09, CI=8.93–94.82)]. This relationship between qacA/B and MRSA ST239 has been suggested in previous studies in the UK and Taiwan;1,4,6 however, the prevalence...
of this MRSA strain, as well as qacA/B genes, was much lower in these studies.

MRSA ST239 is found in significantly high numbers in Eastern Australia,\(^9\) and is associated with a broad spectrum of antimicrobial resistance and epidemic potential. The qacA/B genes are thought to be located on multiresistance plasmids, such as pSK1, and co-transmitted with plasmid-mediated antimicrobial resistance genes;\(^10\) hence their association with this multiresistant strain of MRSA is logical.

The high prevalence of this ST239 strain could be due to selective pressure from the use of antiseptic products and/or the widespread use of antimicrobial agents. Our findings suggest the latter, given the absence of a corresponding rise in qacA/B genes with increased antiseptic hand solution use; however, the baseline use of antiseptic agents within the hospital could also explain the high prevalence of qacA/B genes even prior to the hand hygiene campaign.

In either case, the high prevalence of qacA/B-carrying MRSA strains is concerning and carries potential implications for antimicrobial treatment, infection control and also MRSA decolonization regimes that are becoming increasingly popular. Clinical studies evaluating the impact of these resistance genes on hand hygiene treatments are currently lacking. However, a recent study showed that colonization with chlorhexidine-resistant strains of MRSA was associated with an increased risk of persistent MRSA carriage after decolonization therapy.\(^8\) In addition, chlorhexidine decolonization protocols have been shown to select for MRSA ST239 strains, all of which carried qacA/B genes.\(^1\) In regions where the prevalence of MRSA ST239 already exists at high levels, the potential for decolonization treatment failure with these agents exists and warrants further attention.

In conclusion, a high prevalence of qacA/B genes was found in HA-MRSA isolates in this study. These genes correlated closely with the MRSA strain ST239. These findings highlight the need for further evaluation into the clinical implications of these genes in this era of increasing antiseptic use in hand hygiene and decolonization strategies.

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### Transparency declarations

None to declare.

### References


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**Characterization of a multidrug-resistant Acinetobacter baumannii strain carrying the bla\textsubscript{NDM-1} and bla\textsubscript{OXA-23} carbapenemase genes from the Czech Republic**

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