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Molecular study of resistance of Staphylococcus aureus to antiseptic quaternary ammonium compounds

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Objectives: This study determined the prevalence of qac and smr genes in clinical Staphylococcus aureus isolates from hospital-acquired infections and their susceptibility to quaternary ammonium compounds (QACs) and antibiotics, and correlated the presence of antiseptic resistance genes with antibiotic resistance.

Methods: Susceptibility of 150 non-duplicate clinical S. aureus isolates to antimicrobials and benzalkonium chloride (BAC) was determined by disk diffusion and MIC method, respectively. Resistant strains were analysed by multiplex PCR for the presence of qac and smr genes.

Results: Reduced susceptibility to BAC was detected in 30% of isolates (MIC cut-off >8mg/L). QAC resistance genes were detected in 13 isolates with reduced BAC susceptibility. The most frequently detected genes were qacA/B (10 isolates; 22.2%), followed by qacJ (10; 22.2%), smr (8; 17.8%), qacG (8; 17.8%) and qacH (3; 6.7%). There was a strong positive correlation between presence of QAC resistance genes and higher BAC MIC associated with qacA/B, qacJ and smr genes. There was a statistically significant prevalence of antiseptic resistance genes among isolates resistant to cefoxitin, ciprofloxacin, clindamycin, oxacillin, tetracycline and erythromycin.

Conclusion: This study highlights the prevalence of qac and smr genes in clinical S. aureus isolates with resistance to QACs. There was an association between the presence of antiseptic resistance genes and resistance to different antibiotics, which may be attributed to the presence of both groups of genes on the same plasmid or to selection of resistant strains. More studies are needed on the clinical relevance of the presence of genes controlling resistance to antiseptics.

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