**The Prevalence of Antiseptic Tolerance Genes Among Gram-Positive Bloodstream Pathogens in Children**

Lauren M. Sommer, MS, Jennifer Krauss, PhD, Kristina G. Hultén, PhD, James Dunn, PhD, Sheldon L. Kaplan, MD and J. Chase McNeil, MD

Department of Pediatrics, Section of Infectious Diseases, and Department of Pathology, Baylor College of Medicine and Texas Children’s Hospital, Houston, Texas

**ABSTRACT**

The prevalence of antimicrobial resistance and the use of antiseptics in hospital settings have both increased dramatically in recent years. As a result, there is an urgent need to understand the complex interplay of factors that determine resistance. The presence of resistance-conferring genes on the chromosomes of Gram-positive pathogens is of particular concern due to their potential to confer susceptibility to multiple classes of antibiotics. This study aimed to assess the prevalence of antiseptic tolerance genes in bloodstream isolates from children with bloodstream infection (BSI). The study included 241 consecutive episodes of BSI from 302 children. The prevalence of qacA/B and smr genes was assessed using qPCR and was compared with susceptibility testing. The prevalence of qacA/B was 35% and 66% for qacA/B-Positive, smr-Negative and qacA/B-Positive, smr-Positive isolates, respectively. The prevalence of smr was 63% and 95% for qacA/B-Positive, smr-Negative and qacA/B-Positive, smr-Positive isolates, respectively. The prevalence of qacA/B and smr genes was significantly higher in gram-positive organisms associated with treatment failure and nosocomial infection. The presence of qacA/B and smr genes was associated with a higher MIC of CHG in qacA/B-Positive, smr-Positive isolates. These findings highlight the potential role of antiseptic tolerance genes in the emergence of resistance in bloodstream isolates from children and the need for additional efforts to mitigate their impact.

**RESULTS**

- *Antimicrobial tolerance genes were detected in 60.5% of CoNS. 57% of S. aureus and 48% of E. faecalis (Figure 3).*
- Both qacA/B and smr genes were associated with nosocomial acquisition of infection in CoNS (Table 2 and Table 3).

**Figure 3. Distribution of Antimicrobial Tolerance Genes Across Species**

**Table 2. Comparison of CoNS With and Without qacA/B**

**RESULTS**

- Numerous differences exist between antimicrobial tolerant and susceptible S. aureus (Table 4).
- Antimicrobial tolerant S. aureus were associated with more treatment failures.
- There was no association between antimicrobial tolerance and E. faecalis or any other examined variable.

**Table 4. Comparison of Antimicrobial Tolerance Genes and S. aureus**

**CONCLUSIONS**

- Antimicrobial tolerance genes are common among bloodstream staphylococci and E. faecalis.
- The presence of antimicrobial tolerance genes in S. aureus was strongly associated with nosocomial acquisition of infection in BSI. CoNS and E. faecalis are a focus for the hospital environment in selecting for those pathogens.
- The presence of qacA/B tolerance genes in CoNS is associated with subtle elevations in CHG MIC.

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