Antiseptic tolerance is common among bloodstream staphylococci and E. faecalis isolates at TCH. Among CoNS, the presence of AT genes is strongly correlated with nosocomial acquisition of infection, consistent with previous studies in S. aureus” Sommer et al (2019).

Abstract:
OBJECTIVE: The smr and qacA/B genes in Staphylococcus aureus confer tolerance to antiseptics and are associated with nosocomial acquisition of infection and underlying medical conditions. Such antiseptic tolerance (AT) genes have also been reported in coagulase-negative staphylococci (CoNS) and enterococci, however, few data are available regarding their prevalence. We sought to describe the frequency of AT genes among bloodstream isolates of S. aureus, CoNS and enterococci at Texas Children’s Hospital (TCH).

METHODS: Banked CoNS, S. aureus and enterococci isolated from blood cultures collected between October 1, 2016, and October 1, 2017, were obtained from the TCH clinical microbiology laboratory. All isolates underwent polymerase chain reaction (PCR) assay for the qacA/B and smr genes. Medical records were reviewed for all cases.

RESULTS: In total, 103 CoNS, 19 Enterococcus spp, and 119 S. aureus isolates were included in the study, and 80.6% of the CoNS possessed at least 1 AT gene compared to 37% of S. aureus and 43.8% of E. faecalis isolates (P < .001). Among CoNS bloodstream isolates, the presence of either AT gene was strongly associated with nosocomial infection (P < .001). The AT genes in S. aureus were associated with nosocomial infection (P = .025) as well as the diagnosis of central-line-associated bloodstream infection (CLABSI; P = .04) and recent hospitalizations (P < .001). We found no correlation with genotypic AT in E. faecalis and any clinical variable we examined.

CONCLUSIONS: Antiseptic tolerance is common among bloodstream staphylococci and E. faecalis isolates at TCH. Among CoNS, the presence of AT genes is strongly correlated with nosocomial acquisition of infection, consistent with previous studies in S. aureus. These data suggest that the healthcare environment contributes to AT among staphylococci.

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