Unexpected high prevalence of qac A/B and smr genes among Staphylococcus spp isolates from individuals attending a Sexually Transmitted Infections (STI) clinic

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BACKGROUND

Quaternary ammonium compounds (QAC) and chlorhexidine (CHX) are disinfectants/antiseptics widely used in hospitals as part of the measures to prevent nosocomial infections. Plasmid-borne qac A/B and smr genes encode for multidrug efflux pumps and are associated with reduced susceptibility to QAC and CHX. The prevalence of these genes in community isolates is not well described in Canada. As part of a prevalence survey of Staphylococcus aureus (SA) carriage among people attending the STI clinic in Calgary1, we analyzed the prevalence of qac A/B and smr genes among Staphylococcus spp isolates.

METHODS

Participants: Following Ethics Board approval, written informed consent was obtained, swabs from multiple body sites (n=8) were collected from a STI clinic population over a 9 month period.

Microbiology and Molecular methods: A convenience sample of 263 Staphylococcus spp isolates out of 438 swabs from nose (84), throat (57), upper back (17), axilla (15), interdigital web spaces (IWS) (27), groin (25), perineal-perianal (32) and vaginal (6) sites were analyzed. Following broth enrichment, SA and coagulase-negative staphylococci (CNS) were isolated using standard laboratory procedures. Identification of qac A/B and smr genes was done with a novel multiplex PCR assay with 6 targets: 16s RNA (to detect Staphylococcus sp), nuc (to distinguish SA from CNS), mecA (to distinguish between methicillin-resistant [MRSA] vs methicillin-sensitive SA [MSSA]), qacA/B, smr, mupA (to identify high-level mupirocin resistance).1

Statistical analysis. Differences of prevalence among MS-CNS and MR-CNS was analyzed with x2.