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Impact of skin antiseptics on the prevalence of antibiotic-antiseptic cross-resistance genes in Staphylococcaceae

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Introduction

- 2 billion intravascular devices (IVDs) are sold in the world annually (300 million in the USA - 25 million in France) (1). Occurrence of infectious complications mainly by Staphylococcus aureus (17.3%) and Pseudomonas aeruginosa (4.9%) (2). Recommendation of the French Society of Hospital Hygiene: use of an antiseptic solution prior to catheter insertion, with broad-spectrum biocidal activity (bacteria, viruses, fungi, etc.) (ie. CHXOH : Chlorhexidine or PVI OH : Polyvidone iodine, both with OH : Alcohol; DAK : Sodium Hypochlorite in the youngest)(3). However, the association between antiseptic exposure and antibiotic resistance remains debated, despite the identification of potential cross-resistance genes (4).

Objective

To evaluate in Staphylococcus spp. isolated from colonized/infected IVDs the presence of antibiotic-antiseptic cross-resistance genes according to the antiseptic molecules used.

Methods

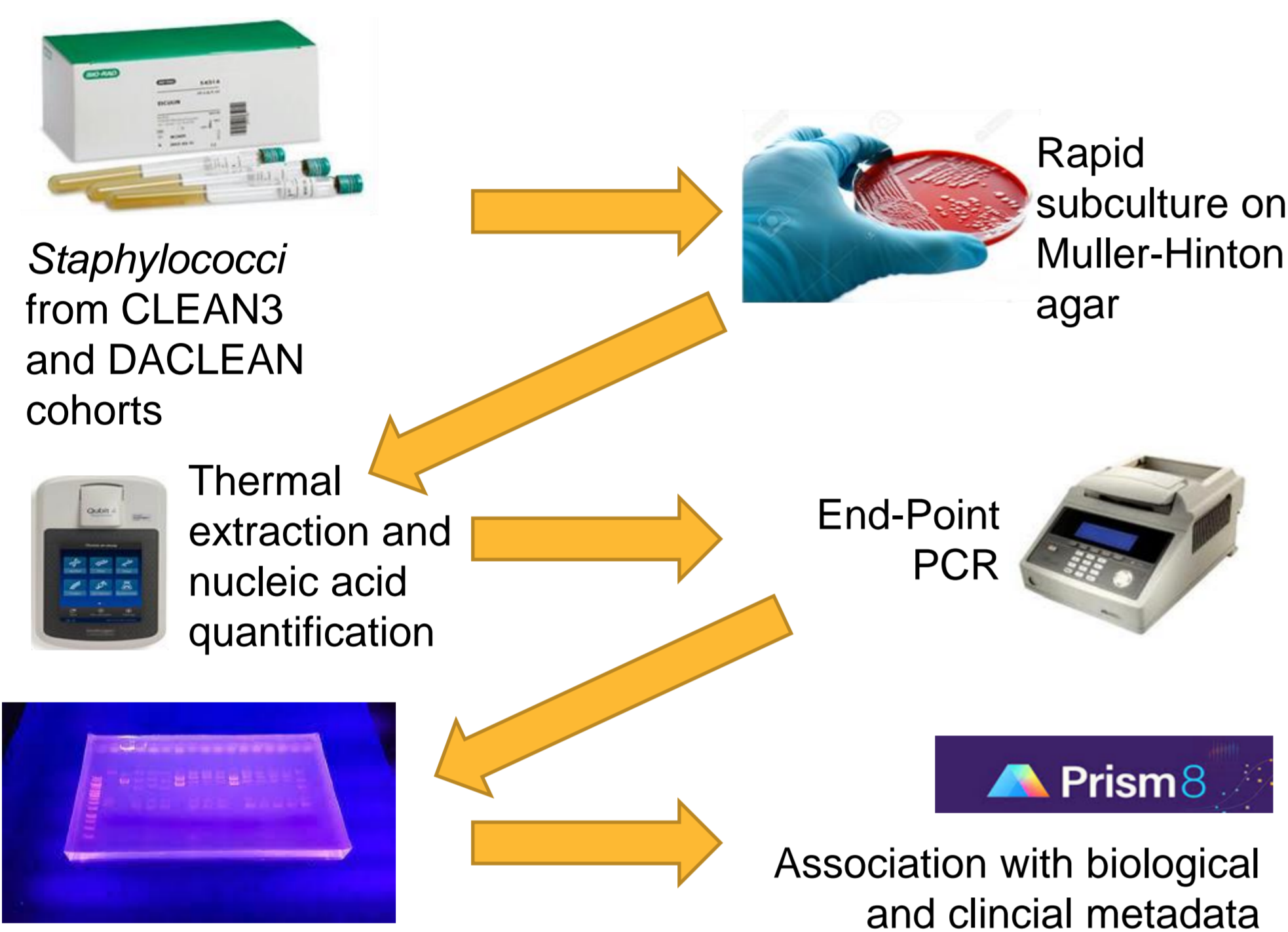


Figure 1. Analysis protocol. The strains studied (n=154) were derived from the CLEAN3 and DACLEAN clinical studies (5,6). Staphylococci were grown on blood agar before being extracted by heat shock (95°C 5 min). Extracts were assayed/diluted (100 ng per reaction) before amplification and separation of PCR products on agarose gel before statistical analysis according to the antiseptic used.

Table 1. Multiplexed PCR protocol. Amplifications were enabled by the primers published by Conceicao in two separate PCRs (7). Checks on agarose gels have been performed at the same time.

Discussion

Antibiotic resistance is different between clinical strains isolated after exposure to antiseptic molecules

In contrast to phenotypic antibiotic resistance, the results suggest that CHX selects fewer strains with cross-resistance genes than other antiseptics.

Conclusion

Larger studies are needed to evaluate the impact of antiseptic procedure on other strains of clinical interest, both Gram-positive and Gram-negative, such as Enterobacterales and Pseudomonales.

References

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Results

Table 2. Distribution of the analyzed strains according to the antiseptic procedure. Table with columns for antiseptics (PVI OH, CHXOH, DAKALL, DAK, DAKOH) and rows for various bacterial species and their percentages.

Table 2. Distribution of the analyzed strains according to the antiseptic procedure.

Table 4. Antiseptic-antibiotic cross-resistance genes vary according to the antiseptic used. Heatmap showing p-values for associations between antiseptics and resistance genes.

Table 4. Antiseptic-antibiotic cross-resistance genes vary according to the antiseptic used. Bacteria selected by the CHG antiseptic protocol are significantly less frequent carriers of resistance genes (p<0.05) compared to other antiseptics.

Table 6. Association of resistance genes with colonization of intra-vascular devices. Table with columns for gene name and number of bacteria, and rows for different genes.

Table 6. Association of resistance genes with colonization of intra-vascular devices. A trend is found between low bacterial concentration and sepA or the association qacA/B+sepA (p<0.1).

Table 8. Association of different resistance genes with antibiotic resistance phenotypes. Table with columns for antibiotic class and resistance phenotype, and rows for various genes.

Table 8. Association of different resistance genes with antibiotic resistance phenotypes. Resistance to beta-lactams, quinolones, aminoglycosides and rifampicin varies with the genes found (p<0.05) with the exception of norA and mepA (p>0.05)

Table 3. Comparison of cross-resistance gene prevalence according to the antiseptics used. Table with columns for genes and antiseptics, and rows for various genes.

Table 3. Comparison of cross-resistance gene prevalence according to the antiseptics used. Strains isolated after selection by CHG have fewer cross-resistance genes. (p<0,05).

Table 5. Association of the different resistance genes with each other. Table with columns for genes and p-values, and rows for various gene associations.

Table 5. Association of the different resistance genes with each other. sepA is statistically associated with qacA/B, smr and mepA (p<0.05). norA tends to be associated with lmrS (p<0.1).

Table 7. Difference in prevalence of cross-resistance genes according to Staphylococceae species. Table with columns for species and p-values, and rows for various gene combinations.

Table 7. Difference in prevalence of cross-resistance genes according to Staphylococceae species. lmrS, mepA and the qacA/B+sepA combination are significantly more frequent in S. aureus (p<0.05).

Table 9. Antibiotic resistance of strains isolated after antiseptics differs depending on the molecule used. Table with columns for antiseptics and antibiotic classes, and rows for various genes.

Table 9. Antibiotic resistance of strains isolated after antiseptics differs depending on the molecule used. The use of CHX is more frequently associated with resistance to beta-lactams, quinolones, aminoglycosides and rifampicin, than other antiseptic molecules (p<0.05).