

Review and phylogenetic analysis of *qac* genes that reduce susceptibility to quaternary ammonium compounds in *Staphylococcus* species - DTU Orbit (08/11/2017)

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The *qac* genes of *Staphylococcus* species encode multidrug efflux pumps: membrane proteins that export toxic molecules and thus increase tolerance to a variety of compounds such as disinfecting agents, including quaternary ammonium compounds (for which they are named), intercalating dyes and some antibiotics. In *Staphylococcus* species, six different plasmid-encoded *Qac* efflux pumps have been described, and they belong to two major protein families. *QacA* and *QacB* are members of the Major Facilitator Superfamily, while *QacC*, *QacG*, *QacH*, and *QacJ* all belong to the Small Multidrug Resistance (SMR) family. Not all SMR proteins are called *Qac* and the reverse is also true, which has caused confusion in the literature and in gene annotations. The discovery of *qac* genes and their presence in various staphylococcal populations is briefly reviewed. A sequence comparison revealed that some of the PCR primers described in the literature for *qac* detection may miss particular *qac* genes due to lack of DNA conservation. Despite their resemblance in substrate specificity, the *Qac* proteins belonging to the two protein families have little in common. *QacA* and *QacB* are highly conserved in *Staphylococcus* species, while *qacA* was also detected in *Enterococcus faecalis*, suggesting that these plasmid-born genes have spread across bacterial genera. Nevertheless, these *qacA* and *qacB* genes are quite dissimilar to their closest homologues in other organisms. In contrast, SMR-type *Qac* proteins display considerable sequence variation, despite their short length, even within the *Staphylococcus* genus. Phylogenetic analysis of these genes identified similarity to a large number of other SMR members, found in staphylococci as well as in other genera. A number of phylogenetic trees of SMR *Qac* proteins are presented here, starting with genes present in *S. aureus* and *S. epidermidis*, and extending this to related genes found in other species of this genus, and finally to genes found in other genera.

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