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Occurrence and variability of *norA* and other main multidrug efflux pump determinants across the *Staphylococcus* genus

03. Bacterial susceptibility & resistance

3a. Resistance surveillance & epidemiology: MRSA, VRE & other Gram-positives

Likely attendance

Onsite

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Background

Multidrug efflux pumps (MDR EPs) play a major role in the emergence of antimicrobial resistance (AMR). NorA is one of the main native MDR EPs of *Staphylococcus aureus*, contributing to reduced susceptibility towards fluoroquinolones and biocides[1,2]. In *S. aureus*, its gene occurs in several allelic variants[3], but less is known about the occurrence of *norA* and other MDR EPs across the *Staphylococcus* genus. In this work, we analyze the presence of *norA* across staphylococci and identify other main MDR EP determinants in four additional pathogenic staphylococcal species.

Methods

The *norA* nucleotide sequences from 61 *Staphylococcus* species were retrieved from public databases and aligned. The corresponding predicted polypeptide sequences were also aligned and the impact of possible residue substitutions on NorA activity was analyzed. Other MDR EP genes were searched in public databases for *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus lugdunensis* and *Staphylococcus hominis*. Additionally, sequences homologues to *S. aureus norB/C*, *sdrM*, *lmrS*, *mepA* and *mdeA* were screened by BLAST search in the complete genome of representative strains of each species.

Results

The *norA* phylogenetic tree follows the evolutionary relations of the *Staphylococcus* genus highlighting the presence of *norA* in the early branching of the genus. Comparative analyses suggest a conservation of NorA function in staphylococci. Over 30 putative MDR EP genes were identified for *S. epidermidis*, *S. haemolyticus* and *S. lugdunensis*. Homologues of *S. aureus norB/C* and *sdrM* were identified in both *S. epidermidis* and *S. hominis*, while *mepA* and *mdeA* were only detected in *S. hominis* and *lmrS* in *S. epidermidis*.

Conclusions

Our results suggest an overall conservation of NorA function across staphylococci, indicating that *norA* is part of the staphylococcal core genome. The identification of main MDR EP determinants in other staphylococcal species of clinical relevance opens new avenues for the study of their impact on AMR.

Keyword 1

Antimicrobial resistance (AMR)

Keyword 2

Genomics and metagenomics

Keyword 3

Efflux

References, word count: 30 words

1. Ubukata et al., *Antimicrob. Agents Chemother.* 1989; 33:1535-1539 2. Neyfakh et al., *Antimicrob. Agents Chemother.* 1993; 37:128-129 3. Costa et al., *Front Genet.* 2019; 9:710

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Conflicts of interest

Do you have any conflicts of interest to declare?

No

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