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Multiplex PCR-based detection and genotyping of Staphylococcus aureus in environmental matrices

The occurrence of environmentally transmitted *Staphylococcus aureus* is well-documented. For example, *S. aureus*-like infections have been observed in bathers in marine and fresh waters and linked to agricultural biosolids applications. Since understanding the epidemiology of *S. aureus* is important to public health, this study was conducted to develop methodology that can accurately identify *S. aureus* and classify strains to their host origin.

S. aureus was isolated from class B biosolids, human nasal swabs, and lake water samples. The isolates were confirmed as *S. aureus* using a newly-developed multiplex-PCR protocol targeting three *S. aureus*-specific genes (*nuc*, *sa0836* and *femB*). Rep-PCR was used to generate isolate fingerprints to compare *S. aureus* occurring in the environmental samples in an initial attempt to classify the isolates to their host origin. Donated *S. aureus* isolated from a known source (chicken) were also used in the fingerprinting studies.

Rep-PCR genotyping showed that isolates from biosolids clustered separately from those isolated from humans and chicken, suggesting that *S. aureus* communities in biosolids either originated from non-human/non-chicken sources, or are regionally constrained. Specifically, jackknife analysis showed that isolates from biosolids grouped with each other with 94.4% confidence and with human isolates at 5.6% confidence. Genotyping of *S. aureus* isolated from fresh water is still in progress.

Our results indicate that *S. aureus* is ubiquitous in primary and secondary environments. Furthermore, rep-PCR can effectively classify *S. aureus* isolates to a specific environment, suggesting the potential for the development of source tracking tools. The high potential for human exposure to environmentally transmitted *S. aureus* warrants future research and regular monitoring of *S. aureus* in environmental matrices.

Author: Issmat kassem
Coauthor(s): Von Sigler, Malak Esseili, Damien Terry