

**Título: Identification and characterization of uropathogenic *Staphylococcus saprophyticus***

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**Resumo:**

*Staphylococcus saprophyticus* is an important pathogen responsible for community urinary tract infections in young sexually active women. Adherence to uroepithelial cells is one of the major virulence factors in *S. saprophyticus* and some surface proteins were characterized: a protein associated to the surface of *S. saprophyticus* (Ssp); an autolysin (Aas); an uro-adherence factor (UafA); a collagen binding protein (Sdrl) and a surface protein F of *S. saprophyticus* (SssF). Furthermore, urease and D-serine deaminase activities are important virulence factors for pathogenicity in this species. Therefore, the presented study aimed to standardize the use of a pair of primers to identify strains of *S. saprophyticus*, analyze the antimicrobial susceptibility profile and detect the virulence factors already mentioned. The strains used in this study were obtained from different sources, including clinical strains, strains isolated from coastal waters and food-borne strains. We correctly identified all the 142 strains as *S. saprophyticus* by PCR assays with species-specific primers designed in our laboratory. We further analyzed 98 strains of *Staphylococcus* spp. to evaluate the sensitivity and specificity of this molecular identification technique. Identification of the strains was confirmed by MALDI-TOF MS. The susceptibility profile of 44 clinical strains of *S. saprophyticus* was analyzed by the disk-diffusion method. The results revealed a high sensitivity rate for the 12 antimicrobials tested. However, resistance to erythromycin (n=19), penicillin (n=3), ampicillin (n=5), tetracycline (n=1), cefoxitin (n=1) were detected. For the strain that showed resistance to cefoxitin, the presence of the *mecA* gene was detected by PCR. The typing of SCC*mec* for this sample identified gene segments compatible with the SCC*mec* type IIIB. The evaluation of the distribution of virulence genes was performed by PCR. We found, in every tested strain, the presence of genes encoding the surface proteins Ssp, Aas, UafA, SssF and the DsdA and UreC enzymes. In contrast, the gene encoding Sdrl surface protein was not detected in any of the strains of *S. saprophyticus*. The results allowed establishing a molecular method for identifying *S. saprophyticus*. Furthermore, the analysis of the susceptibility profile and distribution of virulence genes provides a better understanding of the characteristics of strains of *S. saprophyticus*.

**Palavras-chaves:** Molecular identification, *Staphylococcus saprophyticus*, Surface proteins, Susceptibility profile, Virulence factors.

**Agência Fomento:** CNPq, CAPES, FAPERJ