TITLE: COMPARATIVE PROTEOMICS ANALYSIS OF *Staphylococcus saprophyticus* PATHOGENIC STRAINS

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ABSTRACT:

Staphylococcus saprophyticus is a gram positive, coagulase negative bacteria and is one of the most common etiological agent of urinary tract infections (UTI) among sexually active young females. The infection may be led by sexual intercourse. Little is known about its molecular features in *S. saprophyticus* model. However, plasticity in the proteomic profile is detected in the genus *Staphylococcus* and can be related with infection ability. In this study we aim to analyze the metabolic differences among three different pathogenic strains of *S. saprophyticus* (ATCC 15305, 7108 and 9325) using proteomics approaches. The strains were grown in BHI medium until $O.D._{600}$ of 0.4, then the total cytoplasmic proteins were extracted through maceration in the presence of liquid nitrogen. The protein extract went through tryptic digestion and analyzed by mass spectrometry NanoUPLC-MSE via Protein Lynx Global Server (PGLS). The data obtained revealed differences in the carbohydrate metabolism, amino acid metabolism and pathogen defense against host defenses. Thioredoxin was one of the differentially expressed proteins among strains, therefore estimation of reduced thiol assays were performed to detect thioredoxin activity. These analyses showed similar levels of reduced thiol for ATCC15305 and 9325 strains, in contrast 7108 strain showed considerably low levels of reduced thiol levels when compared to the other analyzed strains. Further analyses are required to clarify whether this characteristic influences the pathogenicity of the 7108 strain or it has alternative strategies to combat reactive oxygen species. Urease is one of the most studied staphylococci virulence factors, therefore urease activity assays were also performed. ATCC15305 and 9325 strains showed reduced urease activity, meanwhile 7108 had high activity levels, corroborating the proteomic data obtained. Also, further experimental infection in mice and *ex vivo* assay using macrophages can clarify if changes in metabolic profile can cause differences in the infection ability. Considering the gathered data, these staphylococci strains show high metabolic plasticity which can reflects on its ability to survive and cause host infection.

Keywords: Proteomics, thiredoxin, urease, pathogenicity.

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