**TITLE**: IN SILICO ANALYSIS OF EPITOPES IN MICROORGANISMS CAUSING UNCOMPLICATED URINARY TRACT INFECTIONS

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**ABSTRACT**:
Urinary tract infections (UTI) are one of the most common bacterial infections in the world. The main cause of UTIs in fertile women is *Escherichia coli*, and together with S*taphylococcus saprophyticus* is responsible for 90% of these cases. Antigen secreted by pathogenic microorganisms represent major targets for the development of diagnostic testing, treatment and immunotherapy. In previous studies, we identified 7 antigenic proteins secreted by *S. saprophyticus*, 5 of which were identified by immunoprecipitation method, and 3 by 2D-SDS-PAGE. Transglycosylase IsaA was identified by both techniques. The others proteins that have been identify are bifunctional autolysin, L-lactato dehydrogenase, alkyl hydroperoxide reductase, rhodanese-related sulfurtransferase, enolase, and a putative secretory antigen. In order to develop a rapid test for the detection of pathogens causing uncomplicated urinary tract infections, we search for homologous sequence of epitopes in eight bacteria that cause this type of infection. For this, after the acquisition of the protein sequences by using UniProt database, we used NCBI protein BLAST in order to identify homologous protein sequences in the selected organisms (*S. saprophyticus*, *E. coli*, *Klebsiela pneumoniae*, *Enterococcus faecalis*, *Streptococcus agalactiae*, *Proteus mirabilis*, *Pseudomonas aeruginosa* e *Staphylococcus aureus*). After complete sequence analysis, we selected 2 proteins that showed homologous sequences in all organisms, the bifunctional autolysin (Q49WH3) and a putative secreted antigen (Q49ZL8). Two more secretory antigen of *S. saprophyticus* (Q49ZM2 E Q49VK7) that have been identified previously by our group, were including in the next analysis. The next step was to find epitopes sequences from the four proteins identified in our studies by the ABCpred epitope prediction software, and then align the protein sequences by CLUSTALX 2.1 in order to find homologous sequence of epitopes in all analyzed microorganisms. After this analysis, 4 sequences of epitopes that presented higher homology were selected for further analysis in order to identify epitopes with potential to be used for UTI rapid diagnostic.

**Keywords**: antigenic proteins, urinary tract infection, epitopes, bioinformatics, diagnostic

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