



## Evaluation of resistance islands in the analyzed *Staphylococcus saprophyticus* strains

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### ABSTRACT

*Staphylococcus saprophyticus* is a uropathogenic bacterium of the urinary tract (UTIs), which mainly affects young and sexually active women. In addition, it may be related to other less common complications such as acute pyelonephritis, epididymitis and prostatitis. Thus, there is a clinical concern regarding the existence of antibiotic-resistant strains in *S. saprophyticus* making it difficult to treat infections. This abstract presents bioinformatics procedures for the evaluation of antibiotic resistance islands in *S. saprophyticus* strains. In the research, the genes present in the sixteen strains of *S. saprophyticus* from their complete genomes are analyzed. The data were obtained through the public database National Center for Biotechnology Information (NCBI). Subsequently, the creation of the phylogenetic tree was performed by the MEGAX program, using the Maximum Parsimony method with 1000 bootstrap replicates, from the *rpoB* gene having that the multiple alignment was performed by the BioEdit program, through the ClustalW program, and as an outgroup, the genome of the *Escherichia coli* str. K-12 substrain MG1655 was used. For the analysis of resistance islands, the Gipsy program and the *S. saprophyticus* strain UTI-045 were used. As a result of the analysis of the resistance islands, five possible genomic islands and four possible resistance islands were identified. The investigation of the genes present in these islands may help to understand the mechanisms of antibiotic resistance exerted by this pathogen.