Investigation of islands of pathogenicity by bioinformatics tools

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ABSTRACT

Pathogenicity islands (PAIs) are relatively large DNA segments inserted into the bacterial genome that attribute a variety of virulence characteristics to the microorganisms that possess them. They have deviations in cytosine and guanine (C+G) content different from the rest of the genome located in specific parts. In the study we analyze the genes present in the PAIs of the complete genomes of *Brucell abortus* by bioinformatics tools. The samples were obtained through the public database National Center for Biotechnology Information (NCBI), where twenty-three complete genomes of *B. abortus* were collected. After data collection, the phylogenetic tree was created by the MEGAX program, using the Maximum Parsimony method with 1000 bootstrap replicates, from the *rRNA16s* gene, and the multiple alignment was performed by the BioEdit program, through the ClustalW program. As an external group, the genome used from the *Escherichia coli* str. K-12 substr. MG1655 strain. The identification of PAIs was performed by the program Gipsy, where two strains were used, one pathogenic to *Brucella abortus CIIMS-NV-4*, and non-pathogenic *Escherichia coli str*. K-12 substr. MG1655. In the obtained analyses, four (4) possible genomic islands are found to have a high possible number of pathogenicity islands, with a total of nine (9). The lowest C+G change was 7% while the highest was 23% for PAIs. Thus, the presence of genes encoding proteins linked to virulence factors indicates that these islands are pathogenic.

Keywords: *B. abortus*, Bioinformatics, NGS, Genomic islands, Pathogenicity