



## Resistance islands investigation in complete genomes of *Brucella abortus*

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*Brucella abortus* is a gram-negative bacterium that causes bovine brucellosis characterized by spontaneous abortions in pregnant ruminants, causing significant economic losses in farming. The development of islands of resistance to antibiotics is a major concern among strains of *B. abortus*, making it difficult to treat the infection. In addition, anthropic actions regarding the improper disposal of antibiotics have influenced the formation of antibiotic-resistant strains. With the present work, we evaluated the genes present in resistance islands in complete *B. abortus* genomes with the help of bioinformatics tools. A total of twenty-three (23) complete genomes of *B. abortus* and one of *Escherichia coli* str. K-12 substr. MG165 were selected through the National Center for Biotechnology Information (NCBI), for the creation of the phylogenetic tree from the *rpoB* gene, using the MEGAX tool for multiple alignment by the CrustalW method and construction of the tree using the Maximum Parsimony method with 1000 bootstrap replicates. As an external group, the genome of the *Escherichia coli* str. K-12 substr. MG1655 available in the NCBI database under the accession number NC\_000913.3 was used. After building the phylogenetic tree, the Gipsy program was used to identify the resistance islands using two strains. One of the selected strains was the non-pathogenic *Escherichia coli* str. K-12 substr. MG1655 and the other was the pathogenic *Brucella abortus* CIIMS-NV-4. In the genomic analysis seven (7) possible genomic islands and four (4) possible resistance islands were found, showing alterations, such as G+C shift, and presence of genes encoding proteins linked to virulence factors that indicate that these islands may be associated with pathogenic characteristics.

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