Targeting Promoter Regions of *Streptococcus pyogenes* Outbreak in Distrito Federal for Biotechnological Uses


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**Introduction:** Bacteria outbreaks have worried the World Health Organization in the past few years. Recently cases have been described in Northern Europe, and in NIH Hospital in USA. Brasília faced a *Streptococcus pyogenes* outbreak that led some patients to obit. **Material and Methods:** To study the bugs that caused the outbreak we sequenced four isolated strains from obit cases, and one reference genome from a regular throat infection. After sequencing the samples we annotated the predicted genes and provided an overview of the bug metabolism. **Results and Discussion:** Using a comparative genomic approach we compared the outbreak isolates with the regular infection isolate. According to KEGG Orthology (KO), Pfam and Conserved Domains Database (CDD) assignments, we observed 191 functions that are exclusive from outbreak isolates. Not all the predicted genes could be annotated using the KEGG Orthology database, and then we also grouped the genes using the OrthoMCL software. Analyzing the OrthoMCL clusters we observed the presence of 233 groups represented only by genes from the outbreak isolates. Throught literature and BLAST searches we identified, among these functions, potential virulance factors and others mechanisms of infection that could play a role in the obit cases. Then we could analyze the synteny of these genes and focus on those that are next to each other, suggesting one unique promoter sequence that is responsible for the whole control of this region. **Conclusion:** Further studies will analyze these regions to detect possible targets for drug experiments.

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Keywords: *Streptococcus pyogenes*, bacteria outbreak, comparative genomics analysis, functional annotation.