Comparative genomics of Acinetobacter baumannii strains

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Abstract

Acinetobacter baumannii is an important opportunistic pathogen causing meningitis, bacteremia, pneumonia, erysipelas and genitourinary tract infections. In recent years, this etiologic agent has acquired multiple mechanisms of resistance to a diverse range of antimicrobials. Its ability to survive in different environments combined with its resistance to drugs makes it extremely difficult to treat patients suffering from infections associated with this pathogen. In this context, this research aims to elucidate in silico analysis from the genome of different strains of A. baumannii to elucidate some mechanisms of resistance related to multiple drug efflux pumps, as well as, to search for genomic resistance islands among 122 A. baumannii strains. By means of the in silico comparison of fifteen different strains of A. baumannii, it was possible to observe a phylogenetic approximation of the A. baumannii individuals, with the presence of few polymorphic points in the conserved 16S rRNA gene, as well as the presence and metabolic analysis of 14 proteins related to efflux pumps in each of the selected strains, all of which were evaluated after automatic annotation and manual curation, where the results maintained the functionality of the proteins with reliability. In conclusion, there is great phylogenetic proximity between the A. baumannii strains studied. However, regarding comparative genomics and sequence annotation, there are differences between the products generated automatically and manually, showing possible points of polymorphism. In addition, the search for metabolic islands revealed the presence of resistance islands that may elucidate the prolonged survival of this bacterial species.