

Prediction, identification and characterization of genomic islands in *Aeromonas* spp.

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Abstract

Aeromonas are pathogenic bacteria, mostly aquatic and with wide environmental distribution. These bacteria can cause infections in humans, varying in severity, for example in cases of uncomplicated acute gastroenteritis, where the disease does not pose serious health risks, and septicemia, which can be fatal. Virulence is the ability of a microorganism to cause disease in a host, and several features of the *Aeromonas* genome have been proven to be associated with virulence. Even though virulence characteristics are similar between species, there are not many studies that discuss the behavior of these genes in the *Aeromonas* genome in general. However, it is already known that one of the main mechanisms that bacteria use to share genetic material is the genomic islands (GIs). In this perspective, to understand and identify the main genes related to pathogenic potential and virulence mechanisms in *Aeromonas* strains, this study aims to characterize and compare the gene content and respective function of GIs in *Aeromonas*, as well as to analyze their GIs distribution between different species of this bacteria. For this, complete genomes of 58 *Aeromonas* were obtained from the NCBI Database. GI prediction was performed using IslandViewer4 software, which combines analyzes by comparative genomics and sequence composition; the two most used methodologies to identify these regions. To determine GI functions, we used the ARDB, CARD, NDARO (antibiotic resistance), Patric, VFDB, VICTORS (Virulence), DrugBank, TTD (drug targets) databases. Analysis of GI distribution among species was performed using the CD-HIT-2D cluster with a 70% self-score similarity. To evaluate the content of complete genomes in all *Aeromonas* studied, a phylogenetic tree was constructed using SWeeP method. The results showed that it is possible to determine the genetic diversity of these organisms and to characterize GIs according to their related functions and products using clustering and phylogeny. It was possible to identify the relationships between the origin of GIs (clinical / environmental / animal) in the total set of *Aeromonas*. Phylogenetic analysis complemented cluster analysis by showing that bacteria are misclassified, such as *Aeromonas hydrophila* YL17 and *Aeromonas hydrophila* 4AK4 strains that are not *hydrophila* species.

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