

Title: ECOGENOMICS OF ALTEROMONAS

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Abstract:

The genus *Alteromonas* are very heterogenous and have been isolated from a variety of marine environments organisms. *Alteromonas macleodii* has captured the attention for the diversity and adaptation capacity, their large intraspecies diversity results in groups well adapted to different niches. Genomic studies are important to visualize features that allow this relationship with their respective environment. In the present study, *Alteromonas macleodii* were isolated from water samples and from three different organisms of Abrolhos Bank. The water samples were obtained from open and coastal waters of South Atlantic Ocean, Parcel dos Abrolhos and Pedra de Leste coral reefs. Algal samples and Sponge samples were obtained from Parcel dos Abrolhos (*Tedania sp.*) and the coral samples were obtained from Parcel dos Abrolhos (*Mussismilia braziliensis*) and Pedra de Leste (*Favia sp.*). The isolates were identified as *A. macleodii* through sequencing of the phylogenetic markers RNAr 16S and *dnaK*. Once identified, the complete genome sequencing and assembly was performed through Illumina Miseq and A5-Miseq. This study intends to observe, through comparative genomics, the differences between the isolates in order to understand their role on the preservation of coral reefs and characterize the evolutionary rate of this species when in contact with different habitats and organisms. First the taxonomic analysis was made with results for ANI, AAI, Karlin signature and DNA-DNA hybridization *in silico*. Such analysis highlighted the hypothesis of a new species of *Alteromonas* genus, represented by the isolate from the pelagic domain of open waters and close to the lineage *Alteromonas simiduii*. In the sequence, a phylogenetic analysis of housekeeping genes was performed through MLSA trees that showed important similarities between *A. macleodii* present in areas of human impact. The gene prediction was performed with RAST and showed different metabolisms for specific hosts and a great increase in genes related to metabolism of aromatic compounds in areas of human impact. It also showed, for benthic isolates, a dominance of genes relating to the presence and regulation of flagella, chemotaxis, utilization of nutrients and resistance to heavy metals, all of them related to a better adaptation to reef environment. In the future, evolutionary rates will be analyzed through dn/ds studies and an ATLAS map will show the specific genes that influence the adaptation in the present genomes.

Keywords: *Alteromonas*, Comparative genomics, Genomes, coral reefs

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