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Title: The Red Sea Microbiome project: Metagenomics analysis of the microbial communities in the Red Sea.

Abstract: To understand the metabolic pathway, physiological process, genomic structure, and adaptation of microbial communities in different environments in the Red Sea, regional team of scientists, from the American University in Cairo and KAUST, has initiated the ‘Red Sea Microbiome Project to establish a metagenomics database of this semi-enclosed and geologically unique tropical sea. The first metagenomic data set was established for the Atlantis II basin. This dataset is called the Atlantis II Basin Water Column (ATIIBC), which includes different convective layers of the hot brine, and the water column overlying the brine pool. Using 454 GS FLX Titanium-based metagenomic sequencing approach, we generated, and computationally analyzed a total of 2.4 gigabases of sequence from samples obtained from the ATIIBC. This magnitude of sequence coverage allowed a comprehensive metagenomic analysis, not just between the different depths of ATIIBC, but also between the ATIIBC and other environmentally distinct marine metagenomic vertical zonation studies. The extent of similarities between the ATCIIBC metagenome data set and those available publicly was performed by similarity searches against the GenBank databases including non-redundant protein sequence database (nr), nucleotide sequence database (nt), environmental protein sequence (env_nr), and environmental nucleotide sequence (env_nt). All the similarity searches were in agreement with an overall trend in matched versus non-matched sequences; in the non-surface samples a higher number of hits with no match to the current available datasets as compared with the 50 meters surface metagenome dataset. In addition, our results show differential gene content in the different ATIIBC vertical zones in agreement with the environmental characteristics of such zone. Moreover, utilizing the ATIIBC and other available sea and ocean data sets we have established gene content hierarchical clustering that have identified unique gene profile pattern characteristic of the different zones.