P47 Mining bioactive molecules from extreme environments using sequence-based metagenomics

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The unique features of extreme habitats, particularly the high temperature and salinity, make them promising reservoirs for the bioprospection and discovery of novel and interesting bioactive molecules. In fact, the microorganisms inhabiting this type of environments have adopted survival strategies to thrive under hostile conditions, synthesizing several biochemical compounds valuable for many biotechnological applications. Culture-independent techniques, namely metagenomics, have emerged as powerful tools to access and explore the genetic and metabolic diversity of the microbial communities present in extreme and complex ecosystems. Two different metagenomic approaches can be applied, namely, sequence- and function-based metagenomics. The sequence-based studies allow finding new gene sequences that reveal similarities with the annotated genomes available in the databases.

In this study, thermophilic composting samples were collected from two Portuguese composting units (Terra Fértil and Lipor), which handle different types of wastes. The metagenomic DNA was extracted from the composting samples and sequenced through shotgun sequencing. A novel multi-step bioinformatic pipeline was developed to characterize the taxonomic and functional profiles of the metagenomes using both reads and metagenome-assembled genomes (MAGs) as input. Their microbiome was dominated by Bacteria, where the classes Gammaproteobacteria, Alphaproteobacteria and Balneolia stood out for their higher abundance. These data confirm the richness of the composting habitats in bacterial strains known to survive and play an important role in harsh conditions, namely extreme saline environments. Furthermore, the combined analysis of functional annotation against KEGG and COG databases revealed a clear dominance of the contigs associated with the metabolism of carbohydrates, energy, amino acids and xenobiotics biodegradation and metabolism. This work represents the first comparative study on the taxonomic and functional profiles of Portuguese composting samples.

Keywords: *Metagenomics, extreme environments, bioactive molecules*