



Unraveling the microbial and functional diversity of Coamo thermal spring in Puerto Rico using metagenomic library generation and shotgun sequencing



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ABSTRACT

In Puerto Rico, the microbial diversity of the thermal spring (ThS) in Coamo has never been studied using metagenomics. The focus of our research was to generate a metagenomic library from the ThS of Coamo, Puerto Rico and explore the microbial and functional diversity. The metagenomic library from the ThS waters was generated using direct DNA isolation. High molecular weight (40 kbp) DNA was end-repaired, electro eluted and ligated into a fosmid vector (pCCFOS1); then transduced into *Escherichia coli* EPI300-T1_R using T1 bacteriophages. The library consisted of approximately 6000 clones, 90% containing metagenomic DNA. Next-Generation-Sequencing technology (Illumina MiSeq) was used to process the ThS metagenome. After removing the cloning vector, 122,026 sequences with 33.10 Mbps size and 64% of G + C content were annotated and analyzed using the MG-RAST online server. Bacteria showed to be the most abundant domain (95.84%) followed by unidentified sequences (2.28%), viruses (1.67%), eukaryotes (0.15%), and archaea (0.01%). The most abundant phyla were *Proteobacteria* (95.03%), followed by unidentified (2.28%), unclassified from viruses (1.74%), *Firmicutes* (0.20%) and *Actinobacteria* (0.18%). The most abundant species were *Escherichia coli*, *Polaromonas naphthalenivorans*, *Albidiferax ferrireducens* and *Acidovorax* sp. Subsystem functional analysis showed that 20% of genes belong to transposable elements, 10% to clustering-based subsystems, and 8% to the production of cofactors. Functional analysis using NOG annotation showed that 82.79% of proteins are poorly characterized indicating the possibility of novel microbial functions and with potential biomedical and biotechnological applications. Metagenomic data was deposited into the NCBI database under the accession number SAMN06131862.

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Specifications	
Organism/cell line/tissue	Metagenomic library of thermal spring waters in Coamo, Puerto Rico
Sex	Not applicable
Sequencer or array type	Illumina MiSeq
Data format	Raw data: or FASTQ file
Experimental factors	Environmental sample
Experimental features	Metagenomic library and shotgun sequencing performed from water obtained from Coamo thermal spring in Coamo, Puerto Rico
Consent	Not applicable
Sample source location	Water sample, thermal spring, Coamo, Puerto Rico (18°02' 16.6"N 66°22'27.6"W)

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Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/biosample/6131862>.

1. Introduction

Different oligotrophic water environments, such as oceans, rivers and thermal springs from hot vents have been the focus of metagenomics, specifically because of the microbial diversity contribution to the ecosystem's stability and its life maintaining. High temperature aquatic ecosystems such as thermal springs, harbor unique thermophilic and hyperthermophilic microorganisms [3,4,13]. Classic microbiology has studied environmental microorganisms using culture-dependent approaches. Emerging sciences have led to research evidencing that approximately 0.1%–1.0% of the microbial community can be cultivable. Metagenomics is a culture-independent approach based on the isolation of environmental genomic material to provide a comprehensive taxonomic and functional evaluation of all the collected microorganisms [8]. One of the advantages of performing metagenomic

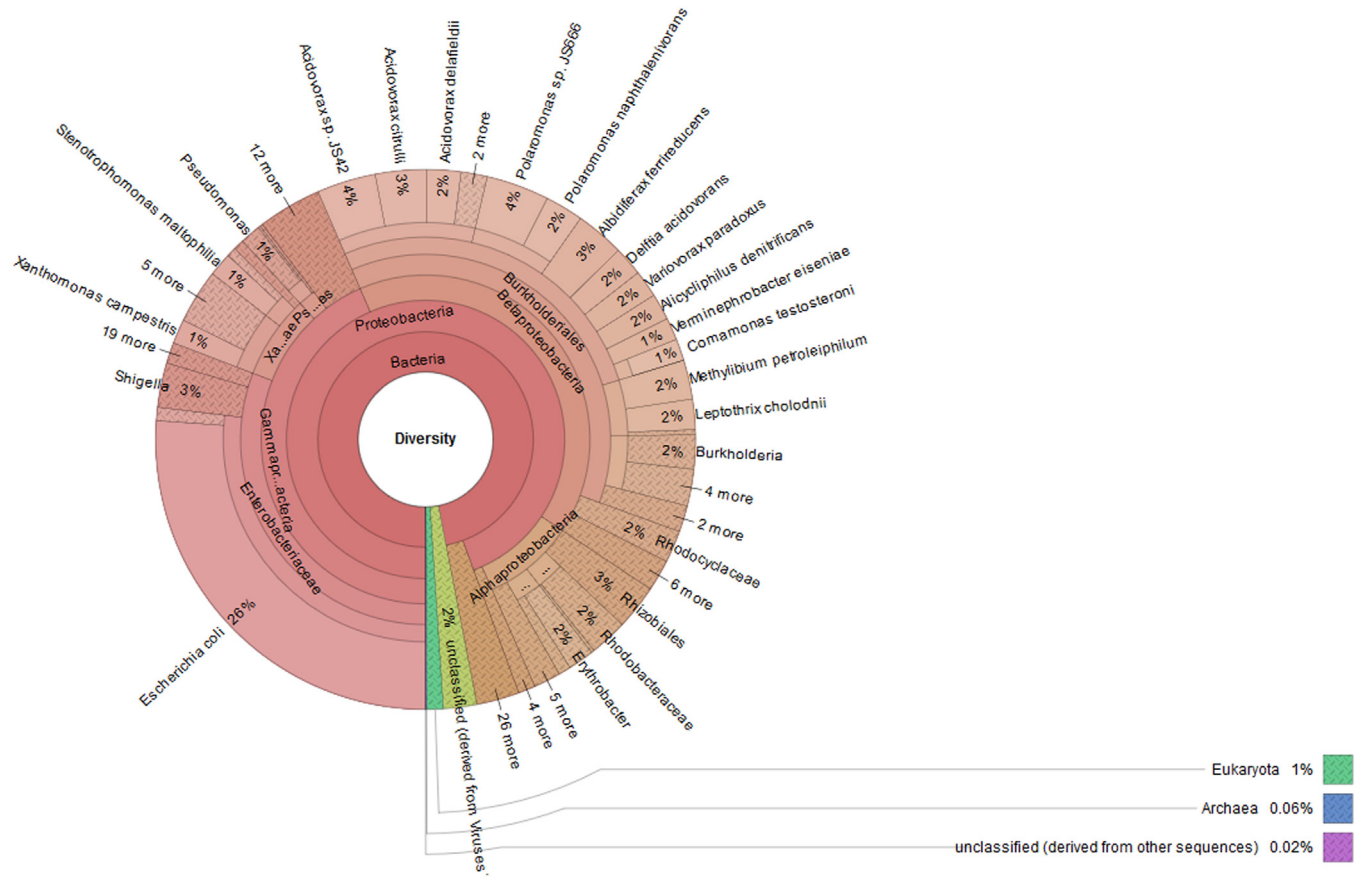


Fig. 1. Community structure of Coamo thermal spring metagenome.

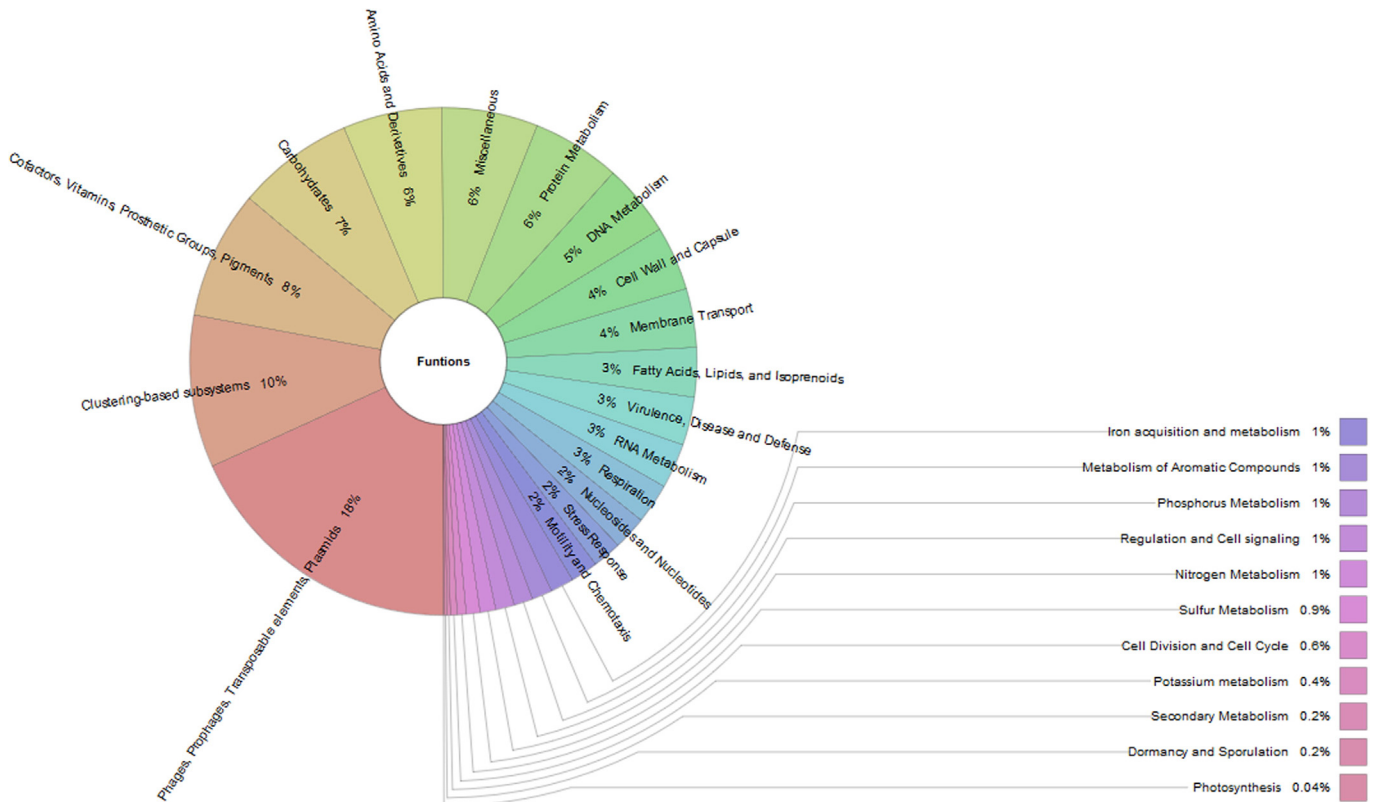


Fig. 2. Functional structure of Coamo thermal spring metagenome using subsystem annotation.

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