Data in Brief

Metagenome sequencing of the microbial community of two Brazilian anthropogenic Amazon dark earth sites, Brazil

Leandro Nascimento Lemos a,⁎, Rosineide Cardoso de Souza b,†, Fabiana de Souza Cannavan a, André Patricio a, Victor Satler Pylro c, Rogério Eiji Hanada b, & Tsai Siu Mui a

a Laboratório de Biologia Celular e Molecular, Centro de Energia Nuclear na Agricultura CENA - Universidade de São Paulo USP, Piracicaba, Brazil
b Instituto Nacional de Pesquisas da Amazônia, Coordenação de Pesquisas de Produtos Florestais, Manaus, Brazil
c Laboratório de Microbiologia do Solo, Departamento de Ciência de Solo – ESALQ/USP, Piracicaba, Brazil

abstract

The Anthropogenic Amazon Dark Earth soil is considered one of the world's most fertile soils. These soils differ from conventional Amazon soils because of its higher organic content concentration. Here we describe the metagenome sequencing of microbial communities of two sites of Anthropogenic Amazon Dark Earth soils from Amazon Rainforest, Brazil. The raw sequence data are stored under Short Read Accession number: PRJNA344917.

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1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/bioproject/PRJNA344917.

2. Experimental design, materials and methods

2.1. Amazon dark earth (ADE) soils

Amazonian Dark Earth (ADE) or “Terra Preta” soils were likely formed between 500 and 2500 years ago by pre-Columbian populations. These soils are found in the Amazonian region distinguished by the presence of ceramic artifacts, animal bones and high amounts of charred organic materials, which are commonly referred as black carbon (BC) [2]. ADE soils are considered as model soils because their high chemical fertility (high content levels of organic C, P, Ca, Mg, Zn, and Mn) and stable organic matter [3]. Also, ADE soils are characterized by their distinct microbial communities, with a higher diversity and richness when compared to the surrounding soils [4].

2.2. Sampling, DNA extraction and sequencing

The aim of this study was to investigate the taxonomic and functional diversity of two ADE sites based on metagenomic approach. Soils were collected in the Hatahara site located in the municipality of Iranduba (03°16′49″S 60°12′34″W), in the Amazonas state, Brazil. DNA extraction from 250 mg of soil was carried out using PowerSoil DNA Isolation Kit (Mobio Laboratories, Carlsbad, CA, USA), according to the manufacturer’s protocol. DNA quality and concentration were measured by agarose gel electrophoresis and NanoDrop 1000 spectrophotometer (Thermo Scientific, Waltham, MA, USA). Soil DNA samples were used to prepare paired-end libraries (2 × 300 bp) using the MiSeq Reagent Kit v.2 (500 cycles; Illumina, San Diego, CA, USA), for further shotgun metagenomic sequencing in a MiSeq Personal Sequencing System (Illumina, San Diego, CA, USA).

2.3. Metagenomic data

A total of 3,716,966 paired-end and non-paired forward sequences (average length of 241 bp) were joined using the PEAR software [7]. Metagenomic sequences were annotated using the MG-RAST automatic annotation server [16]. Exploratory data analysis was conducted in STAMP software [5].
The most abundant phyla detected were *Proteobacteria* (40 ± 2%), *Actinobacteria* (18 ± 1%), *Firmicutes* (5 ± 0.3%) and *Acidobacteria* (4 ± 0.5%). Others phyla detected were *Plantonmycetes* (3.5 0.4%), *Chloroflexi* (2.5 ± 0.3%), *Cyanobacteria* (2.5 ± 0.1%), *Bacteroidetes* (2 ± 0.2%) and *Verrucomicrobia* (2 ± 0.2%). The *Archaea* diversity was represented by the phyla *Crenarchaeota, Euryarchaeota, Korarchaeota, Nanoarchaeota* and *Thaumarchaeota*, with approximately 1.5 ± 0.5% of total abundance. Protein annotations were grouped into functional categories and the most abundant functions were related to carbohydrates (15 ± 0.5%), clustering-based subsystems (14 ± 0.2%), aminoacids (11 ± 0.16%), Miscellaneous (7 ± 0.03%) and protein metabolism (6 ± 0.16%). The most abundant category level 3 is associated with serine-glyoxylate cycle (1.8 ± 0.5%). This cycle is associated with alternative pathways for acetate assimilation [1]. We hypothesize that these functions are related to methylotrophs and methane reducing on ADE soils, but further studies are necessary to validate this inference.

Our dataset reveals a great taxonomic and functional microbial potential to be explored by bioprospecting of new enzymes or identifying unknown microorganisms.

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