Data in Brief

Rhizospheric metagenome of the terrestrial mangrove fern *Acrostichum* from Indian Sunderbans

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**ABSTRACT**

This study reports the analyses of the rhizospheric microbiome of the terrestrial mangrove fern *Acrostichum aureum* Linn. from the Indian Sunderbans. Samples were collected using standard protocols and 16S rRNA gene V3–V4 region amplicon sequencing was performed to identify the microbial communities prevalent in the rhizosphere. A total of 1,931,252 quality checked reads were assembled into 204,818 contigs and were analysed using QIIME to reveal the abundance of Proteobacteria, Acidobacteria and Planctomycetes. The data is available at the NCBI - Sequence Read Archive with accession number: SRX2660456. This is the first report of the rhizospheric microbiome belonging to a fern species.

**Specifications**

| Organism/cell line/ tissue | Rhizospheric metagenome of *Acrostichum aureum* |
|---------------------------|-----------------------------------------------|
| Sex                       | Hermaphrodite                                  |
| Sequencer or array type   | Illumina MiSeq                                 |
| Data format               | Raw reads                                      |
| Experimental factors      | Regular habitat in Sunderban Region           |
| Experimental features     | Analyses of Rhizospheric soil sample          |
| Consent                   | Not applicable                                 |
| Sample source location    | Rangabalia, Sunderban [22.16°N 88.80°E]        |

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/sra/SRX2660456[accn].

2. Introduction

It has been more than 100 years since the characterisation of the rhizosphere as a region where various important life processes occur. In contrast with non-rooted mass soil, the soil compartment specifically around plant roots, which defines the rhizosphere, is significantly populated by microorganisms [1]. The rhizosphere is a zone of active interchange between plants and soil bacteria. Large quantities of organic carbon are released by plant roots resulting in an enrichment of the microbial populace and their associated functions [2–4]. Plants influence the function of the rhizosphere microbiome and recruit function specific microbes by regulating processes such as quorum sensing, various mechanisms involving antibiotic production, biofilm formation, conjugation, motility, symbiosis, and virulence [5]. Ferns are found in and around the riverine mangrove forests of India. Fern flora of the Sunderbans region was once very abundant and extensive. However, due to environmental and unauthorised anthropogenic influences, it is under serious threat. Further recent reports suggest that a few species such as *Acrostichum* with its unique terrestrial habitat have migrated from their original habitat in the northern side of the Sunderbans to the southern side where the anthropogenic pressure is much less. *Acrostichum aureum* Linn. belongs to the family Pteridaceae and is an erect terrestrial fern with a tail of 1–1.5 m; the stipes are woody, which arise from a strong woody rhizome and are generally glabrous; fronds uni-pinnate; with 8–14 alternate pinnae, the upper pinnae are...
ruddy-brown in colour and are soriferous. Sori are densely aggregated generally along the undersurface and are non-indusiate. Sori are generally formed during June to October. In India, this species occurs in a disjunct manner in Sunderbans and Mahanadi estuarine forests along the east coast, in some parts of Kerala and in the Andaman and Nicobar islands. This work attempts to analyse the rhizospheric abundance of microorganisms around *Acrostichum aureum* Linn. as a measure for estimating the optimum microbial content for proper sustenance of the fern taxon [6,7]. This is one of the first studies which reports a fern rhizospheric assemblage of microorganisms.

3. Experimental design, materials and methods

3.1. Rhizospheric soil collection and metagenomic sequencing

The 16S rRNA gene consists of nine hypervariable regions interspersed between conserved regions, which has been widely used to study and characterize the bacterial community of an environmental sample. In the present study, microbial community structure was identified by targeting V3–V4 region, as these regions are highly variable to distinguish bacterial subtypes.

3.1.1. Sample preparation

Genomic DNA was isolated from a rhizosphere sample using an in-house standardized protocol. DNA quality was assessed by Nanodrop and on agarose gel, quantified using QUBIT. The library preparation was carried out using Illumina standardized V3-V4 regions of the 16S rRNA library protocol. The enriched library was quantified and validated using qPCR and Agilent Bioanalyzer (DNA 1000 chip). The library generated containing V3-V4 amplicons was sequenced on Illumina MiSeq using 300 × 2 PE chemistry.

3.1.2. Bioinformatic analysis

The quality control of raw reads was carried out using FASTQC toolkit (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). The quality processed paired end reads were clustered into OTU's (Operational Taxonomic Units) by using QIIME software (qiime.org) to identify the microbial community. These OTU's were further used for taxonomic assignment (Greengenes database), phylogenetic and diversity analysis. During initial bioinformatics analysis, processed reads were assembled into contigs by QIIME (Quantitative Insights Into Microbial Eclogy) [8]. The contigs were categorised into 10,987 OTU clusters (Table 1).

A large number of microbial communities were identified from the study. Proteobacteria was observed as the most abundant phylum followed by Acidobacteria and Planctomycetes [Fig. 1]. Further analysis at species level revealed *Heliobacterium modesticaldum*, a gram positive nitrogen fixing phototrophic bacterium, to be the most abundant species followed by *Pseudoflavonifractor capillosus* and *Caldanaerobacter subterraneus* [Fig. 2]. The comparative analyses from the data reveals similar microbial community structure as reported in previous metagenomic assemblies from the Sunderbans with the exception in the abundance of *Heliobacterium* species. Basak et al. [9] reported the soil metagenome from three different locations of the Indian Sunderbans, where they have identified the abundance of bacteroides and acidobacteria, whereas in our study we observed the highest abundance of proteobacteria followed by Acidobacteria. This is perhaps due to the variation caused by the rhizospheric environment.

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