



## Data in Brief

# Cataloguing the bacterial diversity of the Sundarbans mangrove, India in the light of metagenomics



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## ABSTRACT

In this present study we report the profile of bacterial community at variable depth of soil sediment in the world's largest tropical mangrove sediments of Sundarbans, India using 16S rRNA gene amplicon sequencing. Metagenome of three samples consisted of 61301 sequences with 32.0 Mbp and 55.6% G + C content. Metagenome data of this study are available at NCBI under the Biosample data base accession no. SRX883521. The taxonomic analysis of 2746 species belonged to 33 different phyla revealing the dominance of Proteobacteria, Firmicutes, Chloroflexi, Bacteroidetes, Acidobacteria, Nitrospirae and Actinobacteria respectively. Remarkably less than 5.0% sequences belong to a poorly characterized group. Our pyrosequencing data report unfolds the bacterial community profile at different depth of soil sediment indicating the changing community pattern, in the light of specific chronology.

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Specifications	
Organism	Sundarbans sediment soil metagenome
Sex	Not applicable
Sequencer or array type	454 GS junior platform
Data format Raw data:	Sff file
Experimental factors	Environmental sample
Experimental features	16S rRNA pyrosequencing
analysis using	Silva-NGS online server
Consent	Not applicable
Sample source location	Mangrove soil sediment, Sundarbans, India

## Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/sra/SRX883521>.

Metagenomics collaborating with Next Generation Sequencing Technology has paved a way to unlock massive uncultured microbial communities prevailing in the environment. This recent advancement in the scientific world has not only helped to overcome the barriers of culture dependent techniques but also has the potential of providing

the widest, unbiased view of the microbial diversity related to both taxonomy and potential functioning [1] in a single snapshot with high resolution, thereby, contributing immensely to the global increase in microbial diversity study employing samples from different ecosystem. It has also unlocked the massive biotechnological potential possessed by the varying microbial communities [1].

Sundarbans mangrove ecosystem lies in the delta of Ganga, Brahmaputra and Meghna river, shared between Bangladesh (~60%) and India (~40%) [2] providing a unique ecological dynamics for diverse microbial community that plays an important role to sustain productivity, conservation, remediation, and the overall sustainability of this ecosystem [3]. As for instance, in one of the surveys at Sundarbans, pseudomonas was identified as a key player in petroleum degradation, since contamination by oil spill is the major crisis faced by this ecosystem [4]. High rainfall, periodic variations in tidal inundation and humidity, simultaneously with extremely variable environmental factors such as sea-induced salinity leading to anaerobic conditions, light, temperature, nutrient availability [5,6] along with anthropogenic interventions [7] makes Sundarbans a tremendously diverse environment for microorganisms to thrive and strongly influence the microbial community profile in the sediments, that are not only intimately related to biogeochemical cycling but are also involved in bioremediation and production of substances such as enzymes of biotechnological interest [1]. The aim of our study was directed towards study of bacterial community structure at different sediment depths collected from two sampling stations of Sundarbans mangrove forest, i.e., Bonnie Camp (9 m and 5 m depth) and Dhanchi (5 m depth), using parallel 16S rRNA gene tag sequencing.

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Soil was collected after recession when the land was exposed, in triplicate from a depth of 5 m and 9 m from Bonnie Camp (21° 49' 53.581" N, 88° 36' 44.860" E) and from a depth of 5 m from Dhanchi (21° 42' 06.41" N, 88° 25' 54.682" E) in a sealed sterile container. Metagenomic DNA was extracted from soil subsamples using Mo-Bio DNA Power Soil kit (MoBio Laboratories, Carlsbad, CA). To analyze bacterial diversity, the V1–V3 regions of bacterial 16S rRNA gene were amplified by PCR. Pyrosequencing was performed for 200 cycles on a Roche 454 GS-Junior sequencing instrument according to the manufacturer's protocol (454 Life Sciences, USA). The output was 61,363 sequences with size 30,875,597 bp and 56 G + C%. All sequence reads were processed by the NGS analysis pipeline of the SILVA rRNA gene database project (SILVA ngs 1.2) [8].

Higher species richness was observed at Dhanchi 5 m depth (total number of sequences 20,953 with 11.1 Mbp data and G + C content

56.5%), with total 31 different bacterial phyla, followed by 25 and 24 different bacterial phyla at Bonnie Camp 9 m (total number of sequences 15,282 with 7.8 Mbp data and G + C content 55.8%) and 5 m (total number of sequences 25,066 with 13.1 Mbp data and G + C content 54.5%) depth respectively. In both the stations, Proteobacteria and Firmicutes formed the most abundant bacterial phyla, with percentages varying at different depths. This is in accordance to previous metagenomic studies done at Sundarbans ecosystem, which reported Proteobacteria as the dominating phyla in the soil sediments [9,10]. From the experimental data 67% and 19% Proteobacteria was found at Bonnie Camp at 9 m and 5 m depth respectively and 36% at Dhanchi at 5 m depth. Firmicutes formed 76% and 5% of the total bacterial population at a depth of 5 m and 9 m of Station A respectively and 27% of the major population at a depth of 5 m Station B. The third abundant bacterial phyla were Chloroflexi (11%) at Dhanchi (5 m depth) with decreasing percentage

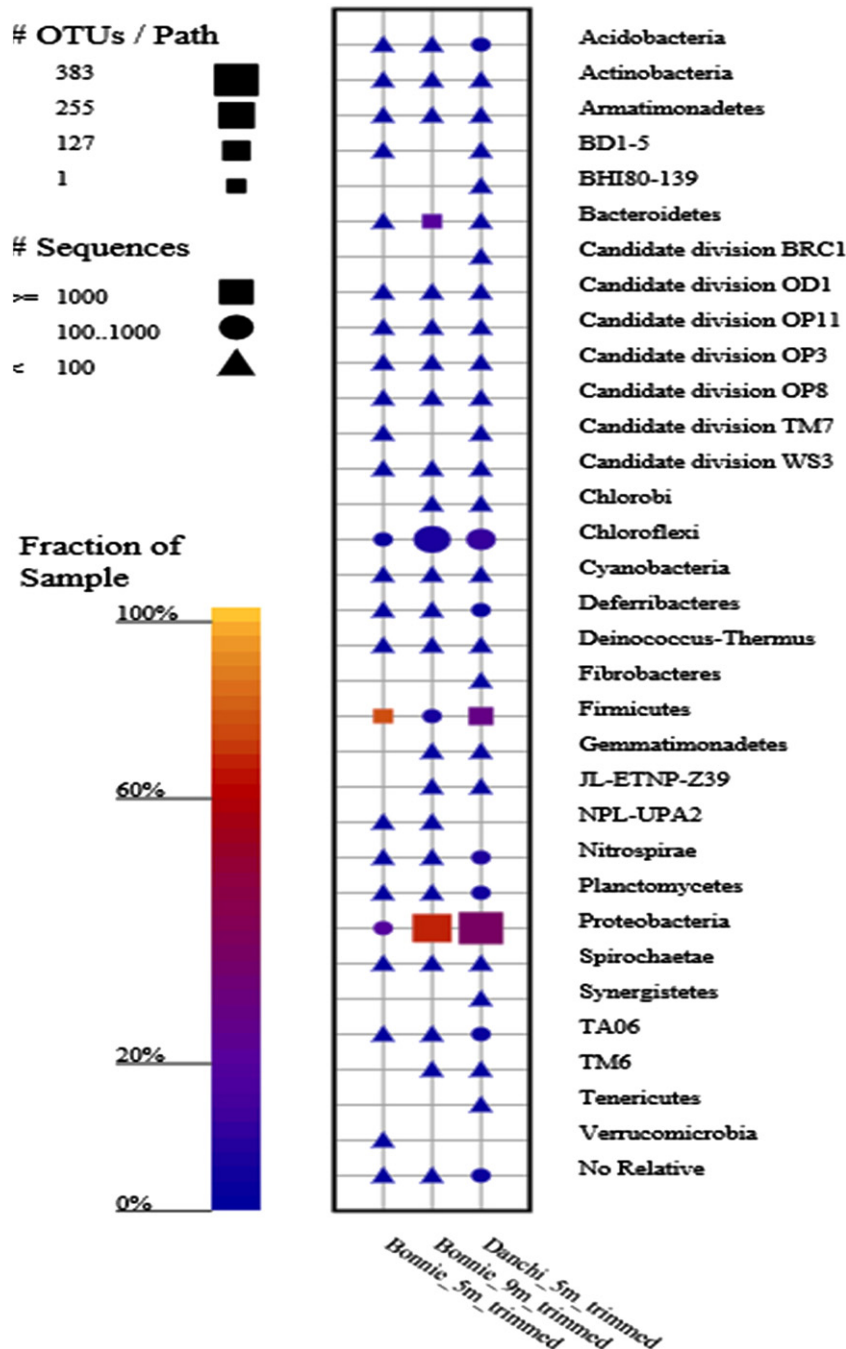


Fig. 1. Bacterial community structure of soil sediment samples collected from different depth of Sundarbans Mangrove.

(6% and 3%) at Bonnie Camp (9 m and 5 m depth respectively). Bacteroidetes forms the third most major phyla at Bonnie Camp at 9 m depth with negligible abundance at Bonnie Camp at 5 m and Dhanchi at 5 m depth. Nitrospirae and Acidobacteria were found in greater abundance (7% and 2% respectively) at Dhanchi (5 m depth) while insignificant abundance were detected at Bonnie Camp 5 m and 9 m depth (Fig. 1).

16S rRNA pyrosequencing analysis performed on the world's largest mangrove ecosystem, Sundarbans sediment revealed the presence of diverse bacterial population. Abundance distribution of different phyla in such productive environment plays an important role towards bacterial behavior. Furthermore genome based study will explore new dimension for the discovery of natural products in the future from Sundarbans ecosystems and genomic sequences will exhibit potential route for synthetic biology approaches and metabolic research.

#### Nucleotide sequence accession numbers

All sequence data from this study were submitted to the NCBI Sequence Read Archive (SRA) under accession numbers SRR1810820 (Bonnie camp\_9m), SRR1810821 (Bonnie camp\_5m), SRR1810822 (Dhanchi\_5m).

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