



Data in Brief

Metagenomic exploration of the bacterial community structure at Paradip Port, Odisha, India



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ABSTRACT

This is a pioneering report on the metagenomic exploration of the bacterial diversity from a busy sea port in Paradip, Odisha, India. In our study, high-throughput sequencing of community 16S rRNA gene amplicon was performed using 454 GS Junior platform. Metagenome contain 34,121 sequences with 16,677,333 bp and 56.3% G + C content. Metagenome sequences data are now available at NCBI under the Sequence Read Archive (SRA) database with accession no. SRX897055. Community metagenome sequence revealed the presence of 11,705 species belonging to 40 different phyla. Bacteroidetes (23%), Firmicutes (19%), Proteobacteria (17%), Spirochaetes (10%), Nitrospirae (8%), Actinobacteria (7%) and Acidobacteria (3%) are the predominant bacterial phyla in this port soil. Analysis of metagenomic sequences unfolded the interesting distribution of several phyla which pointed to the significant anthropogenic intervention influencing the bacterial community character of this port.

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Specifications

Organism/cell line/tissue	Paradip Port soil sediment metagenome
Sex	Not applicable
Sequencer or array type	454 GS junior platform
Data format	Sff file
Experimental factors	Environmental sample
Experimental features	16S rRNA pyrosequencing and bacterial community structure diversity analysis using MG-RAST portal
Consent	Not applicable
Sample source location	Soil sediment from Paradip Port, Odisha, India

1. Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/sra/SRX897055>.

Microbial ecology deals with the dynamic relationship between microorganisms and their biotic and abiotic environments, predominantly comprising the analysis of abundance, composition and

activity of microbial communities. This discipline is currently undergoing a paradigm shift, driven by the development and application of genomics, transcriptomics and proteomics technologies, including metagenomic tools [1]. High-throughput pyrosequencing of PCR amplicons has emerged as a valuable technique to access the huge and diverse gene pool of unculturable bacteria which led to a 'gold rush' in the last decade [2]. Therefore, recently metagenomic approach has been implemented for divulging the microbial diversity worldwide.

Paradip Port (20° 3' N; 86° 55' E) is situated at Bay of Bengal, in Odisha at the east coast of India. It is an important port and a gateway of national and international coastal trades. Significant quantity of materials exported through Paradip Port includes iron ore, manganese ore, coal, chrome ore whereas the imported materials include coking coal, petroleum, sulphuric acid etc. For coastal fishing and deep sea fishing more than 600 small fishing trawlers and about seventy large fishing trawlers are engaged through Paradip Port day in and day out. Various activities in port and harbor affect the environment specially the coastal and estuarine water, soil, sediment and air quality. In consequence polluted coastal air and sediment further affect crop, marine plants, marine animals and their habitat, finally influencing the microbiota of the ecosystem [3].

Recent developments in molecular microbial ecology have provided means to identify microbial community in different ecosystems without the need to culture the microorganisms through metagenomic approaches. Next-generation sequencing technology is being successfully

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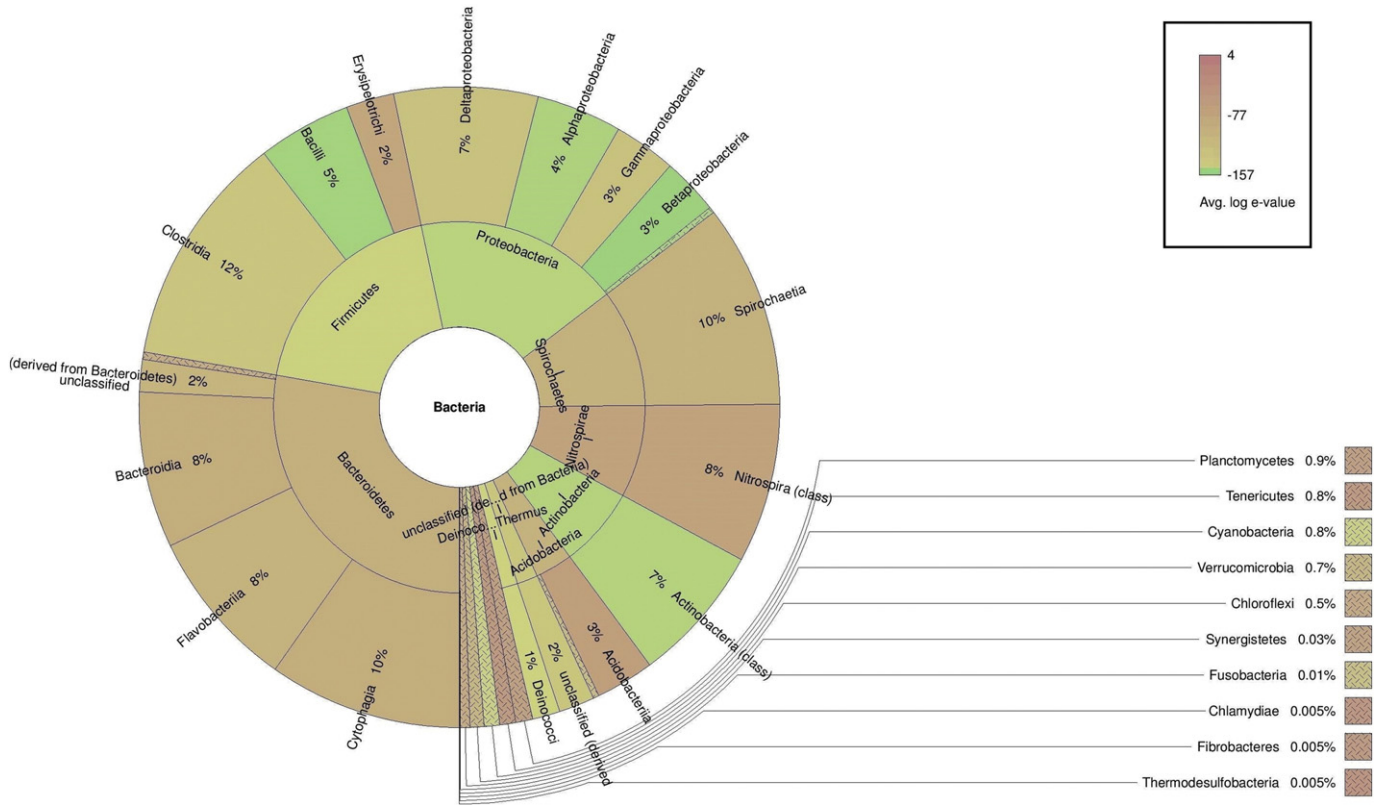


Fig. 1. Bacterial community structure of Paradip Port sediment metagenome.

applied to study bacterial diversity in different ecosystem, which has been marked as a strong pillar for the development of microbial biotechnology [4].

We investigated the prokaryotic community structure in the soil sediment of the Paradip Port by metagenomic approach (Fig. 1). Soil sediment Samples were collected in triplicate from surface sediments of the Paradip Port (20° 15' 26" N; 86° 39' 44" E).

Total metagenomic DNA was extracted by the soil DNA isolation kit (MoBio Laboratories, Carlsbad, CA). To analyze bacterial diversity, amplification of the V1–V3 region of the 16S rRNA gene was performed according to Pramanik et al. 2015 [5]. High-throughput sequencing was performed by the Pyrosequencing on a Roche 454 GS-Junior sequencing platform according to the manufacturer's protocol (454 Life Sciences, USA). Sequences were processed and analyzed with MG-RAST on-line server [6]. Bacterial species present in metagenome sequences was explored by Genome Peek online tool [7].

Soil metagenome contained 47.8 Mb data consisting of 34,121 sequences with a G + C content of 56.3%. A total of 40 phyla were detected and the dominant phyla were Bacteroidetes (23%) followed by Firmicutes (19%), Proteobacteria (17%), Spirochaetes (10%), Nitrospirae (8%), Actinobacteria (7%) and Acidobacteria (3%). Dominating bacterial species *Paludibacter propionigenes* was found in our metagenomic sample which belongs to phyla Bacteroidetes (Fig. 2).

This study is a de novo reporting of bacterial communities applying high-throughput pyrosequencing methods in Paradip Port soil. The phyla Bacteroidetes and Firmicutes are potential indicators of anthropogenic intervention in the soil sediment. The excessive abundance of these phyla supports the huge anthropogenic pressure in the Paradip Port and also indicates altered eco-dynamics due to cargo handling induced pollution.

2. Nucleotide sequence accession number

Metagenome sequence data from this study were submitted to the NCBI Sequence Read Archive (SRA) under accession numbers: SRR1825760 (Paradip Port).

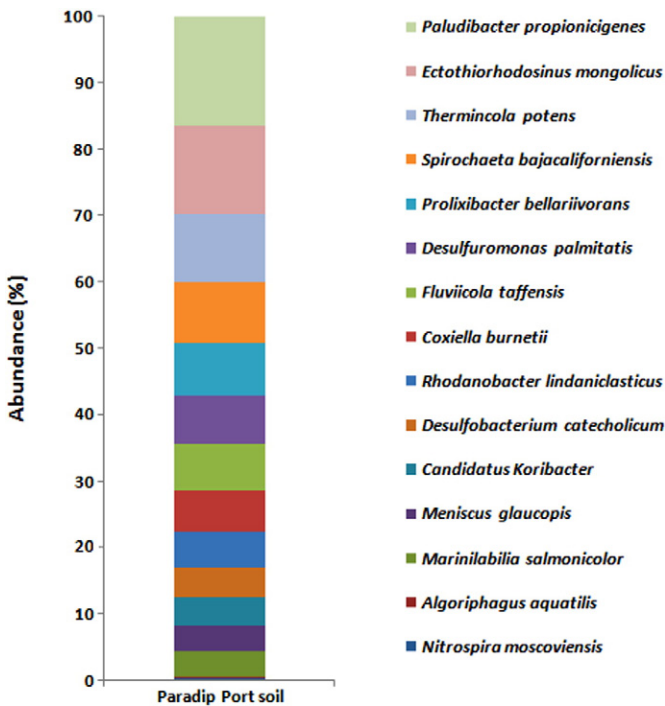


Fig. 2. Abundance comparison among the major bacterial species found in Paradip Port sediment metagenome.

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