



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



Arnab Pramanik<sup>a</sup>, Pijush Basak<sup>a</sup>, Satabdi Banerjee<sup>a</sup>, Sanghamitra Sengupta<sup>a,\*</sup>,  
Dhrubajyoti Chattopadhyay<sup>b,\*</sup>, Maitree Bhattacharyya<sup>a,\*</sup>

<sup>a</sup> Department of Biochemistry, University of Calcutta, 35, Ballygunge Circular Road, Kolkata 700 019, West Bengal, India

<sup>b</sup> Amity University, Major Arterial Road, Action Area II, Kadampukur Village, Rajarhat, Newtown, Kolkata, West Bengal 700156, India

### ARTICLE INFO

#### Article history:

Received 19 November 2015

Accepted 15 December 2015

Available online 17 December 2015

#### Keywords:

Pyrosequencing

Bacteria

Diversity

Paradip Port

Metagenomics

### 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.

© 2015 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

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

\* Corresponding authors.

E-mail addresses: [sanghamitrasg@yahoo.com](mailto:sanghamitrasg@yahoo.com) (S. Sengupta), [djcbcg@caluniv.ac.in](mailto:djcbcg@caluniv.ac.in) (D. Chattopadhyay), [bmaitree@gmail.com](mailto:bmaitree@gmail.com) (M. Bhattacharyya).



## Acknowledgments

This work was financially supported by the NCSCM (National Centre for Sustainable Coastal Management-grant no. 21/RCO/CR/CMR/2013) under the Ministry of Environment and Forests, Government of India. The authors express their sincere thanks to Mr. Niladri Shekher Majumdar, Roche Diagnostics, for his technical support in pyrosequencing work. We are grateful to ICZM project, World Bank for providing the 454 GS Junior pyrosequencer facility to this work and Mr. Tapas Paul, Environment Specialist, for his continuous encouragement.

## References

- [1] S.W. Roh, G.C.J. Abell, K.H. Kim, Y.D. Nam, J.W. Bae, Comparing microarrays and nextgeneration sequencing technologies for microbial ecology research. *Trends Biotechnol.* 28 (2010) 291–299.
- [2] R. Sharma, R. Ranjan, R.K. Kapardar, A. Grover, Unculturable bacterial diversity: an untapped resource. *Curr. Sci.* 89 (2005) 72–77.
- [3] P.R. Dixit, B.B. Kar, P. Chattopadhyay, C.R. Panda, Seasonal and spatial distribution of the hydro-chemical properties of Mahanadi estuary and influence near the Mahanadi and Paradip coastal environment, East coast of India. *Bull. Environ. Pharmacol. Life Sci.* 2 (2013) 13–20.
- [4] S.D. Mandal, Z.H.T. Lalremsanga, N.S. Kumar, Bacterial diversity of Murlen National Park located in Indo–Burman biodiversity hotspot region: a metagenomic approach. *Genomics Data* 5 (2015) 25–26.
- [5] A. Pramanik, P. Basak, S. Banerjee, S. Sengupta, D. Chattopadhyay, M. Bhattacharyya, Pyrosequencing based profiling of the bacterial community in the chilika lake, the largest lagoon of India. *Genomics Data* 4 (2015) 112–114.
- [6] F. Meyer, D. Paarmann, M. D'Souza, R. Olson, E.M. Glass, M. Kubal, T. Paczian, A. Rodriguez, R. Stevens, A. Wilke, J. Wilkening, R.A. Edwards, The metagenomics RAST server – a public resource for the automatic phylogenetic and functional analysis of metagenomes. *BMC Bioinformatics* 9 (2008) 1–8.
- [7] K. McNair, R.A. Edwards, GenomePeek-an online tool for prokaryotic genome and metagenome analysis. *Peer J.* 3 (2015), e1025, <http://dx.doi.org/10.7717/peerj.1025>.