Metagenomic data of vertical distribution and abundance of bacterial diversity in the hypersaline sediments of Mad Boon-mangrove ecosystem, Bay of Bengal

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### Value of the data

- Comparison between the microbial community from different types of hypersaline sediments and this data to identify the core community is possible.
- This data is useful for comparison of saline and freshwater bacteria communities.
- Data could aid restoration of the bacterial community near the coastal regions for the agricultural process.
- The raw sequence data would allow other researchers to do their analyses with different bioinformatics tools.

### 1. Data

The 16S rRNA amplicon Pyrosequencing (TEFAP, Tag-encoded amplicons Pyrosequencing) produce 5890, 13959 and 10006 sequences. After quality checks (i.e. < 250 bps lengths were removed) a total of 3919, 7298 and 7399 reads were obtained. The raw sequence can be accessed from NCBI SRA using the accession numbers SRR627695, SRR630101 and SRR631012. The phylum *Proteobacteria* was found to dominate all the three hypersaline layers followed by *Acidobacteria*, *Chloroflexi*, *Bacteroidetes* and other phyla (Fig. 1). The difference in the bacterial communities was seen even in class (Fig. 2), order (Fig. 3), family and genus level (Supplementary Data Table 1 and Supplementary Data Table 2 respectively), Diversity richness Shannon and cho1 index (Table 1).
Fig. 1. The abundance of bacterial community at the Phylum level.

Fig. 2. The abundance of bacterial community at the Class level.
2. Experimental design, material and methods

2.1. Sample collection

The study was conducted in Mad Boon (Pichavaram), South India, Bay of Bengal in a natural area, located at Latitude 11°25’01” N; Longitude 79°47’06.39” E in September 2012. The sample was collected in a single location using 10.5 cm wide and 40 cm height corer. The top 0–30 cm sediments were sampled and transferred to the lab using sterilized polyethylene bags. The sediments were separated into three bases on the salinity top 1–5 cm HS1 (110 PSU), middle 6–15 cm (85 PSU) and bottom 16–30 cm (67 PSU). Physico-chemical properties of sediments were analysed in soil testing lab, Chidambaram, Tamil Nadu (Table 2) followed by the procedure in [1].

2.2. DNA extraction

Brieﬂy, 1 g of sediments were taken from each layer and the DNA extraction was done by using FASTDNA SPIN Kit for soil (Qiagen, Valencia, CA, USA). DNA extraction was conducted in triplicate. The

Fig. 3. The abundance of bacteria community at the Order level.
2.3. Sequencing

The quality and concentration of eDNA were estimated. Next, the corresponding eDNA were pooled together. 100 ng of eDNA from each layer, 16S rRNA specific V5-V9 primers [3] 939F (5’ TTGACGGGGGCCGCCAC3’) and 1492R (5’ TACCTTGTTACGACTT3’) primer were used to amplify the fragments using the titanium reagents, Hot Star Taq Plus master mix Kit (Qiagen, Valencia, CA). TEFAP procedures and sequencing were carried out at the Research and Testing Laboratory (RTL), Lubbock, TX, USA using Genome Sequencer FLX System (Roche, Nutley, N.J., USA) based on RTL protocols.

2.4. Data analysis

The TEFAP generated sff files (Three) were submitted to NCBI’s Bio project, BioSample, and SRA. The sequences were quality trimmed according to the procedure in [4], and the sff files were

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**Table 1**

Hypersaline bacterial diversity, richness derived from multiple diversity estimators for individual sediment samples 3%, OTUs, Shannon and Chao1 index of the samples.

| Vertical Location Sample ID | Sequence library size | Number of OTUs | Shannon (H') | Chao 1 richness | ACE |
|-----------------------------|-----------------------|----------------|--------------|----------------|-----|
| HS1                         | 3919                  | 1164           | 6.48703      | 1,436.81       | 1436.81 |
| HS2                         | 7026                  | 1645           | 6.72401      | 1,950.66       | 1886.87 |
| HS3                         | 7377                  | 1547           | 6.64978      | 1,843.67       | 1547 |

**Table 2**

Abiotic parameters of hypersaline soil.

| Physico chemical characters | Sample  |
|-----------------------------|---------|
| Temperature (°C)            | 30 ± 1.2 |
| pH                          | 7.6 ± 0.3 |
| Salinity (PSU)              | 117 ± 2.672 |
| Macronutrients (mg/g)       |         |
| Total N                     | 6.2 ± 1.50 |
| P                           | 1.92 ± 0.062 |
| K                           | 9.0 ± 1.98 |
| NH₄                         | 5.76 ± 3.9 |
| SO₄                         | 6.59 ± 1.67 |
| Total organic C             | 30.0 ± 7.23 |
| Micronutrients and heavy metals (µg/g) |         |
| Al                          | 135.4 ± 2.03 |
| B                           | 0.631 ± 0.066 |
| Cd                          | 0.041 ± 0.004 |
| Co                          | 11.59 ± 0.325 |
| Cr                          | 1.979 ± 0.023 |
| Cu                          | 0.335 ± 0.002 |
| Fe                          | 129.7 ± 5.06 |
| Mg                          | 43.13 ± 3.23 |
| Mn                          | 1.81 ± 0.072 |
| Ni                          | 184.4 ± 9.54 |
| Pb                          | 0.309 ± 0.008 |
| Zn                          | 9.756 ± 2.4 |

quality and concentration of extracted eDNA were estimated using 1% agarose gel and Nanodrop ND-2000 (Thermo Scientific) [2].
converted into FASTA and QUAL file formats using Mothur v.1.12.0 [5]. Then the sequence was trimmed, aligned, filtered, and the chimeras were removed using Mothur commands. Then, the sequences were classified against Silva Database [6]. The sequence data generated in this study can be downloaded from NCBI SRA.

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.12.028.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.12.028.

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