



## Complex bacterial communities in the deep-sea sediments of the Bay of Bengal and volcanic Barren Island in the Andaman Sea



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### ABSTRACT

Deep-sea environments are gaining global attention as potential sources of useful microorganisms, thereby warranting a better understanding of the diversity and genomic potential of the microbes present. To this end, here we provide the first insights into the composition of the bacterial communities in deep-sea sediment samples from the southwestern Bay of Bengal and the geographically distinct volcanic Barren Island in the Andaman Sea. High-throughput 16S rRNA gene sequencing of the sediments revealed the presence of >44,000 operational taxonomic units (OTUs) in each of the samples, suggesting high bacterial diversity. Actinobacteria was the most dominant phylum, representing >20% of the taxonomically assignable OTUs, followed by Firmicutes, Proteobacteria, and Chloroflexi. Numerous bacteria that are potentially involved in the sulfur cycle were observed in the Barren Island sediment sample, while bacteria with clinical and industrial potential were observed in the samples from the southwestern Bay of Bengal. Correlation analysis of the biotic and abiotic parameters showed that the differences in bacterial richness and community composition between the sampling sites were mainly dependent on sediment texture. Using a predictive functional metagenomic approach, this study also discusses the genetic variations that may provide an adaptive advantage to sediment bacterial communities for survival in these extreme deep-sea environments. The results from this study should aid future studies focused on bioprospecting and geochemical cycling in the deep sea.

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### 1. Introduction

The deep sea is gaining global attention as one of the most important microbial-driven ecosystems. It is broadly characterized by the presence of high hydrostatic pressures (up to 1100 atm), low temperatures (~2 °C), the absence of light, and general oligotrophy (Bell, 2012; Jørgensen and Boetius, 2007). Therefore, it is considered an extreme environment with remarkably diverse microbial consortia (Thaler et al., 2012; Jørgensen et al., 2013; Sogin et al., 2006). As a strategy for adaptive survival, microbes in the deep sea have evolved special biochemical mechanisms to tolerate the aforementioned abiotic stresses. These microbes play crucial roles in the ecological and biogeochemical cycles, and in addition to bioactive molecules, can be mined for novel enzymes (Parkes et al., 1994; De Vitis et al., 2015).

In natural microbial communities, the culturable bacteria constitute a minor portion of the total bacteria, and their census is rarely a representation of the true diversity (Ben-Dov et al., 2009). Therefore,

culture-independent molecular techniques are a powerful tool to explore the true genetic diversity, community composition, and relative abundance. Next-generation sequencing (NGS) is a novel technique that offers the necessary sequencing depth that cannot be otherwise achieved with other typical culture-independent methods, such as genetic fingerprinting and clone libraries (Novais and Thorstenson, 2011). This technique has successfully been used to decipher the bacterial diversity in the deep parts of different oceans, such as the Pacific (Jing et al., 2013), Atlantic (Schauer et al., 2010), and Arctic (Galand et al., 2009; Nguyen and Landfald, 2015). However, the microbiomes of the deep-sea environments surrounding the Indian sub-continent, specifically, the northeastern part of the Indian Ocean, have not yet been explored.

The present study aimed to investigate the structure of the bacterial communities in deep-sea sediment samples from the Bay of Bengal (the largest bay in the world) and the Andaman Sea. We hypothesized that the site-associated microbial diversity would depend on sea-sediment composition and anthropogenic impact. To address these questions, three sampling sites were investigated, one off the coast of Chennai and one off the coast of Cuddalore in the southwestern Bay of Bengal,

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which are approximately 28 and 16 NM, respectively, from the Indian mainland, and one site in the Andaman Sea close to the volcanic Barren Island (the only active volcano in south Asia; Fig. 1). The human populations in Chennai and Cuddalore coastal areas are 8.6 and 2.6 million, respectively (<http://www.census2011.co.in>), and the difference in the population size may have a differential impact on the deep-sea sediment microbial community owing to marine pollution. The sample collected off the Barren Island (1.7 NM from the coast) was chosen because this site is geographically distinct, uninhabited, and the sediment is presumed to possess different physicochemical properties because of volcanic activity. To the best of our knowledge, this is the first detailed investigation of the bacterial diversity in a deep-sea environment around the Indian sub-continent using NGS. The taxonomic analysis, comparison of 16S rRNA gene amplicon libraries, and relationship with abiotic factors will shed light on the bacterial diversity and distribution and the influence of environmental factors on the bacterial community. It will also provide information on the distribution of taxa known to produce valuable bioactive compounds, like the genera

*Streptomyces* and *Micromonospora*, which will aid in the design of future bioprospecting studies of the deep sea.

## 2. Materials and methods

### 2.1. Sample collection and sediment characteristics

The deep-sea sediment samples were collected from three locations, one off the coast of Barren Island in the Andaman Sea (NIOT.BAR.001; 12°19.440'N lat. And 93°51.450'E long.), one off the coast of Chennai (NIOT.CHE.001; 13°14.192'N lat. And 80°49.061'E long.), and one off the coast of Cuddalore (NIOT.CUD.001; 11°45.681'N lat. And 80°03.718'E long.) in the Bay of Bengal during the months of February (cruise No. 003/12 ORV Sagar Manjusha) and May 2012 (cruise No. 011/12 ORV Sagar Manjusha), respectively (Fig. 1). Other geographical details and sample characteristics are shown in Table 1. Samples were collected with a gravity corer on board a research vessel and were mostly undisturbed and compact. The average lengths of the sediment cores

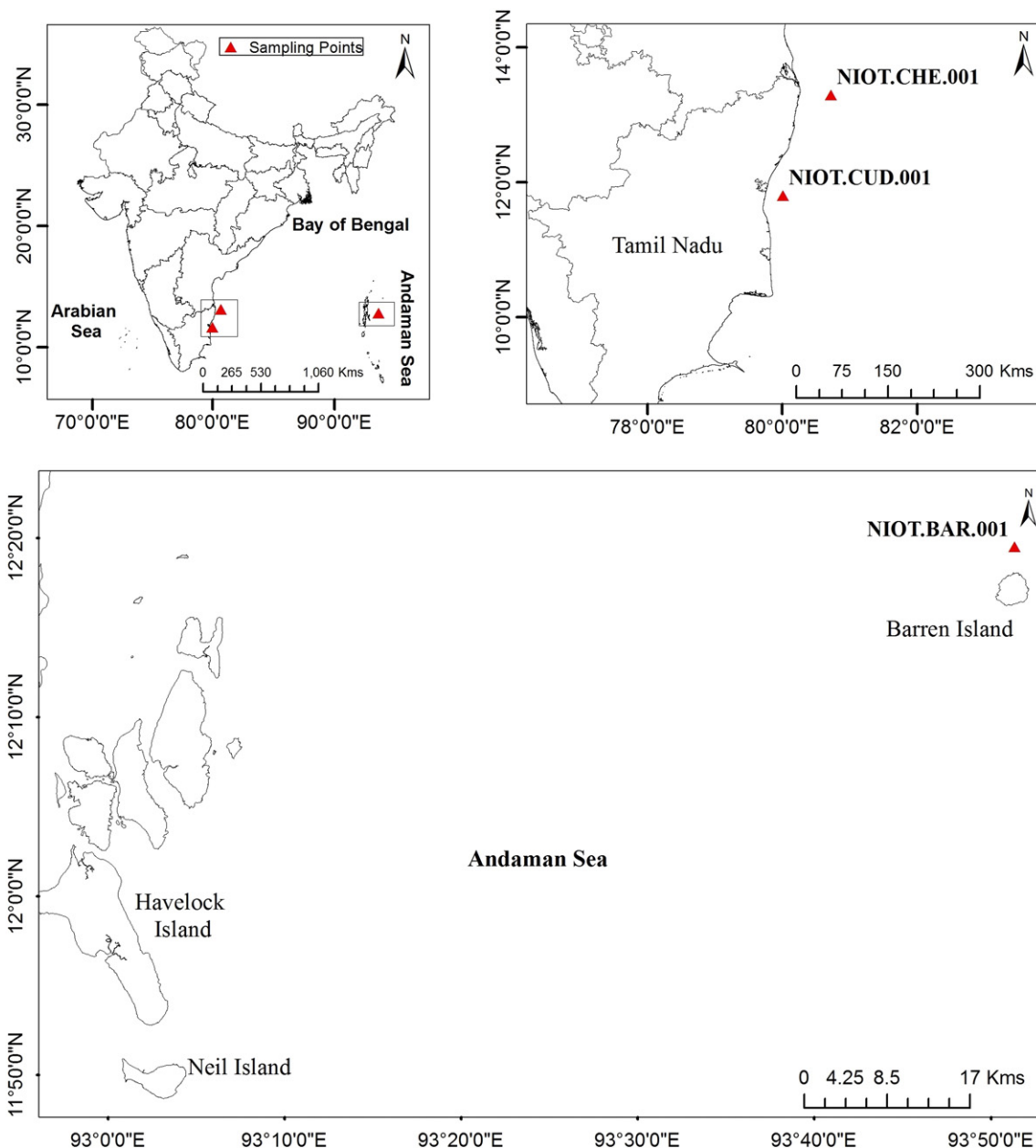


Fig. 1. Map displaying the location of the three deep-sea sediment sampling sites in the Bay of Bengal (NIOT.CHE.001 and NIOT.CUD.001) and the Andaman Sea (NIOT.BAR.001).

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