Lacunae of Microbial Study along the Bhavnagar Coast

Hardik G. Gosai[1*], Pradeep Mankodi[2]

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Abstract

Soil microorganisms account for a significant amount of Earth's biodiversity and play an important role in biogeochemical cycles (BGC) and ecosystem function. Understanding the tremendous diversity of the soil environment's complex, microbial population is a challenge. Soil bacteria play an important role in organic matter decomposition, mineral nutrient release, and nutrient cycle. Microorganisms and their microbial activity are also important markers of soil health and can be used as bioindicators to measure pollution levels. Soil microbial diversity has been the subject of extensive research. Human influence is felt along the Bhavnagar coast of Gujarat, India, a region characterized by anthropogenic activity such as coastal industries and a ship-breaking yard, sand extraction, tourism, and ferry service. This review focuses on microbiological investigations undertaken along the Bhavnagar coast, that used reliable identification techniques such as 16S rRNA gene sequencing, the Biolog^{TM} microtitre plate methodology, extensive biochemical assays, and other methodologies. The microbial communities of the Bhavnagar coast have received relatively limited attention thus far, necessitating further research in unexplored areas.

Keywords: 16s rRNA sequencing, Bhavnagar coast, Gulf of Khambhat, Microbial diversity, Soil microorganism.

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Introduction

The anthropogenic inputs affect the presence of microorganisms present in the soil. Considering the enormous scale of the microbial population and the wide diversity of species found in this natural habitat, studying soil is a difficult task for microbiologists (Richter and Markewitz, 1995). Soil is a common substrate found across the world's terrestrial ecosystem. It is a complex mixture of flora, fauna, microbiological life forms, and finely divided mineral elements. Microorganisms not only provide critical ecological tasks in this complex ecosystem, but they also make up a significant amount of the soil's compositional framework (Stotzky and Pramer, 1972). Soil, often known as the Earth's biologically active layer, is an organized mixture of organic materials and mineral elements. The interaction of different elements, such as species, climate circumstances, geological processes, and atmospheric chemistry, influences its development. Soil is a filtration medium that governs the characteristics and availability of Earth's water resources. It is home to colonies of microorganisms that actively participate in the decomposition of organic materials and the recycling of vital chemical elements within the biosphere. Soil plays an important ecological role as the primary processing unit of the Earth's complex biosphere (Sánchez, 1994).

Soil is the Earth's greatest carbon reservoir, having approximately two times the amount of carbon found in the atmosphere and two to three times the carbon content found in all living organisms (Arias *et al.*, 2005). Soils are a multidimensional system made up of plants and microorganisms that stay within a heterogeneous solid matrix with dynamic fluctuations in chemical and physical properties at the molecular and cellular levels. Understanding soil transformations requires a thorough understanding of both chemical and biological techniques due to the reciprocal interactions between microorganisms and the soil environment. Soil microorganisms have a significant impact on the global dynamics of organic matter, participating in the recycling of organic waste materials through mineralization processes, yielding carbon dioxide (CO_2), water (H_2O), nitrogen (N_2), phosphorus (P), sulphur (S), and other essential nutrients (Bossio *et al.*, 1998). Soil is made up of mineral particles with variable sizes, shapes, and chemical properties, as well as a complex interplay of soil biota and organic molecules in various stages of decomposition. The forming of clay-organic matter complexes and the stability of clay, sand, and silt particles aided by aggregate formation are the essential structural features of the soil matrix. The size spectrum of soil matrix components ranges from 2mm aggregates to fractions of a mm containing microorganisms and colloidal particles. Prokaryotes, the most common living forms, are widely spread throughout the soil environment and can contribute significantly to the overall biomass of the soil ecosystem (Hassink *et al.*, 1993).

Role of Microorganism

Soil, recognized for its incredible ecological diversity, is home to a diverse community of soil microorganisms that includes fungi, viruses, archaea, protozoa, and bacteria. Collectively, these interacting microbial populations contribute to the complicated ecosystem functioning inside the soil environment (Kuzyakov and Blagodatskaya, 2015). Soil microbial diversity has many characteristics, including species variety, genetic

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[1]Department of Environmental Studies, Faculty of Science, The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat, India

[2]Division of Marine and Fresh Water, Department of Zoology, Faculty of Science, The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat, India

***Corresponding author:** Hardik G. Gosai, Department of Environmental Studies, Faculty of Science, The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat, India, Email: hardik.g.g-envphd@msubaroda.ac.in

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diversity, and ecosystem biodiversity. These factors all contribute to the complex and diversified microbial makeup of the soil ecosystem (Solbrig, 1991). Species richness, species evenness, and species dispersion are three key components of species diversity. The total number of unique species within a given ecological community is referred to as species richness. The relative abundance of different species in respect to one another is referred to as species evenness, and it reflects the equal distribution of individuals across species. Finally, species dispersion describes the spatial arrangement and distribution patterns of individuals within a community, revealing information about the spatial dynamics of species within their habitat. These components work together to provide an extensive overview of species variety in a given ecosystem (Øvreås, 2000). Microbial hotspots in soil are hotspots with higher microbial diversity than individual scattered microbial cells in mineral soil. Increased substrate availability stimulates microbial proliferation and the formation of a community structure unique to hotspot groups (Marschner *et al.*, 2012). Soil microbes play a critical role in controlling the biogeochemical cycles of macronutrients, micronutrients, and vital components required for plant and animal growth and development. These bacteria actively participate in nutrient transformation, mobilization, and recycling activities within the soil ecosystem, exerting significant influence over the availability and cycling of critical elements required for biological productivity (Jansson & Hofmockel, 2020). The most ecologically significant events are microbially mediated biogeochemical reactions that occur inside soils. Notably, a single gram of soil has a huge abundance of microbial cells, with counts ranging from 10^{-7} to 10^{-12}, highlighting the enormous microbial population density prevalent in this environment (Watt *et al.*, 2006).

Soil microbes play an important role in organic matter decomposition, mineral nutrient release regulation, and the cycling of key nutrients such as carbon, nitrogen, and phosphorus. They also contribute to soil aggregation processes. These microbes have a significant impact on the soil ecosystem's nutrient content, chemical-physical characteristics, fertility, and total primary productivity (Rutigliano *et al.*, 2004). Microbial growth is driven by anabolic mechanisms that convert new organic materials and nutrients into biomass rather than catabolic processes like mineralization or respiration. This metabolic shift towards biomass synthesis supports microbial population growth and development in the soil environment (Hemkemeyer *et al.*, 2021). Soil

Table 1: Microbial studies conducted along the Bhavnagar coast

Location	*Type*	*Microorganism Name*	*Identification method*	*Reference*
Bhavnagar	Bacteria	*Natrinema thermotolerant*	16S rRNA gene sequencing	Dave and Desai (2006)
Bhavnagar (Marine salter)	Bacteria	*Bacillus megaterium, Bacillus licheniformis*	16S rRNA gene sequencing	Parmar *et al.* (2021)
Alang coast	Bacteria	*Nocardiopsis* sp. Al-H10-1 (KF384482)	16S rRNA gene sequencing	Thumar and Trivedi (2021)
Ghogha	Bacteria	*Nocardiopsis* sp. GhM-HA-6	16S rRNA gene sequencing	Trivedi and Thumar (2021)
Newport & Nari	Bacteria	*Haloarcula* sp., *Halorubrum* sp., *Halobaculum* sp., *Halorubrum saccharovorum*, *Halorubrum saccharovorum*, *Halorubrum sistributum*, *Halogeometricum* sp., *Haloterrigena turkmenica*, *Haloterrigena turkmenica*, *Haloterrigena turkmenica*, *Haloterrigena turkmenica*	Biochemical characterization	Dave and Soni (2013)
Ship Scrapping Industry (Alang)	Bacteria	*Streptomyces variabilis* (strain RD-5), *Streptomyces variabilis* (strain HBUM173496), *Streptomyces variabilis* (strain 173634), *Streptomyces variabilis* (strain 173500), *Streptomyces* sp. RD4, *Streptomyces radiopugnans* (strain HBUM174024), *Streptomyces radiopugnans* (strain HBUM174024), *Streptomyces nanhaiensis* (strain JA 24), *Streptomyces atacamensis* (strain C60)	16S rRNA gene sequencing	Dholakiya *et al.* (2017)
Alang-Sosiya shipbreaking yard (ASSBY)	Bacteria	Gammaproteobacteria, Betaproteobacteria, Epsilonproteobacteria.	16S rRNA gene sequencing	Patel *et al.* (2014)
Ghogha coast	Bacteria	*Bacillius megaterium* (strain JK4h)	16s rDNA analysis, Biochemical characterization	Dhangdhariya *et al.* (2015)
Alang-Sosiya shipbreaking yard (ASSBY)	Bacteria	Proteobacteria (Arcobacter), Betaproteobacteria, Gammaproteobacteria, Acidobacteria, Actinobacteria, Cyanobacteria, and Bacteroidetes	16S rRNA gene sequencing	Patel *et al.* (2015)
Bhavnagar	Bacteria	*Bacillus pumilus*	16S rRNA gene sequencing	Nayak *et al.* (2020a)
Bhavnagar coast	Bacteria	*Haloarcula* sp. AB19	Biochemical characterization and Molecular phylogeny	Soni *et al.* (2012)

Bhavnagar coast	Bacteria	*Streptomyces* sp., *Sphingobium yanoikuyae*, *Pseudomonas aeruginosa*, *Pseudomonas* sp., *Pseudomonas aeruginosa*, *Sphingomonas* sp., *Pseudomonas stuzeri*, *Nocardia carnca*, *Sphingomonas paucimobilis*, *Mycobacterium aurum*, *Pseudomonas putida*, *Sphingomonas* sp., *Mycobacterium vanbaalenii*, *Mycobacterium* sp.,	Micro Log software (Biolog^{TM} Microtitre plate)	Rajpara *et al.* (2015)
Alang coast	Bacteria	*Pontibacter korlensis, Kocurea tirfenensis, Actinotalea, Sinorhizobium* sp., *Cellulosimicrobium funkei, Helcobacillus massiliensis, Dyadobacter fermentas*	16S rRNA gene sequencing and Biochemical test	Upadhyay *et al.* (2016)
Bhavnagar coast	Bacteria	*Planococcus maitriensis*	16S rRNA gene sequencing	Suresh Kumar *et al.* (2007)
Alang-Sosiya Ship Breaking and Recycling Yard (ASSBY)	Bacteria	*Bacillus circulans, Bacillus oceanisediminis, Lelliottia amnigena*	16S rDNA sequencing	Sachaniya *et al.* (2021)
Alang, Rammantra Mandir Sewer, Rammantra Mandir Sewer, CSIR-CSMCRI, Nava Bandar, Hathab	Bacteria	*Enterobacter ludwigii* HS1-SO, *Enterobacter mori* HS6-SOB, *Citrobacter freundii* HS7-SOB, *Enterobacter* sp. HF1-SOB, *Aerococcus* sp. HF2- SOB, *Enterobacter* soli HF3-SOB, *Klebsiella pneumoniae* HF4-SOB, *Pantoea* sp. IPS1- SOB, *Priestia fexa* IPF3- SOB, *Klebsiella* sp. IPF4- SOB, *Pseudomonas balearica* AS13-SOB, *Olivibacter* sp. PINK-SOB, *Arcobacter butzleri* RNW22-SOB, *Aeromonas caviae* 411C-SOB, *Pseudomonas stutzeri* B6-SOB, *Dietzia* sp. C2-SOB, *Gordonia hongkongensis* C7-SO, *Cytobacillus frmus* C8-SOB, *Peribacillus acanthi* C9-SOB, *Microbacterium* sp. C10-SOB, *Bacillus* sp.	16S rRNA gene sequencing	Shinde *et al.* (2022)
Bhavnagar coast	Fungus	*Aspergillus sydowii*	28S rDNA-based molecular technique	Vala (2015)
Bhavnagar	Bacteria	*Bacillus licheniformis* LRK1	Biolog® approach	Nayak *et al.* (2020b)
Bhavnagar coast	Bacteria	*Achromobacter xylosoxidans*	16S rDNA sequencing, BIOLOG^{TM} GN Microtitre plates, biochemical test	Ghevariya *et al.* (2011)
Bhavnagar	Bacteria	Proteobacteria, Bacteroidetes, Chloroflexi, Firmicutes, Actinobacteria, Acidobacteria, Planctomycetes	16S rRNA gene sequencing	Keshri *et al.* (2013)
Bhavnagar	Bacteria	*Achromobacter xylosoxidans*, *Pseudomonas* sp., *phingomonas* sp.	16S rDNA sequencing and BIOLOG^{TM} GN Microtitre plates	Dave *et al.* (2015)
Alang-Sosiya ship-breaking yard	Fungus	*Cochliobolus lunatus* strain CHR4D	16S rRNA gene sequencing	Bhatt *et al.* (2014)
Bhavnagar	Bacteria	*Jeotgalibacillus* (*Jeotgalibacillus salarius* ASL-1^{T})	16S rRNA gene sequence	Srinivas *et al.* (2016)
Alang-Sosiya ship-breaking yard	Bacteria	*Pseudomonas* sp. strain SA3	16S rRNA gene sequence	Tirkey *et al.* (2021)
New port	Bacteria	*Delftia tsuruhatensis* SJ01,	16S rRNA gene sequence	Singh *et al.* (2017)
Alang	Bacteria	*Bacillus cereus*	16S rRNA gene sequence	Shah *et al.* (2010)
Nari Salt pan	Bacteria	*Thiorhodococcus fuscus*	16S rRNA gene sequence	Prathyash Ushus *et al.* (2017)
Alang coast	Bacteria	*Stenotrophomonas* sp., *Pseudomonas stutzeri*, *Cellulomonas* sp.	MicroLog bacterial identification system	Nanjani *et al.* (2020)
Alang-Sosiya ship-breaking yard	Bacteria	*Achromobacter* sp. BAB239, *Pseudomonas* sp. DV-AL2, *Enterobacter* sp. BAB240, *Pseudomonas* sp. BAB241	16S rRNA gene sequence	Patel *et al.* (2012)
Alang	Bacteria	*Halomonas* sp.	16S rRNA gene sequence	Jain *et al.* (2016)
Ghogha coast	Fungus	*Aspergillus* sp.	18s rDNA amplicon	Gohil and Yadav (2021)
Gopnath	Bacteria	*Bacillaceae, Staphylococcaceae, Promicromonosporaceae*	16S rRNA gene sequence	Subrahmanyam *et al.* (2012)

microorganisms play two functions in the processes of soil organic carbon mineralization and carbon input stabilization into organic forms. The equilibrium between these two opposing processes is required for the net exchange of carbon dioxide (CO_2) and methane (CH_4) in the atmosphere. The fraction of carbon substrate incorporated into microbial biomass relative to the amount respired as carbon dioxide (CO_2) is characterized as the microbial carbon consumption efficiency (Bond-Lamberty *et al.*, 2018).

Bhavnagar Coast

Gujarat's coastline in India is divided into three sections: the Gulf of Khambhat, the Gulf of Kutch, and coastal Saurashtra. The Bhavnagar shoreline is located in Gujarat, India, on the western side of the Gulf of Khambhat. This coastal stretch is distinguished by the presence of various small-scale enterprises and is notably home to the world's largest ship-breaking yard, located around 50km from the city. The Bhavnagar coastline features a muddy shore at Ghogha, a combination of sandy and muddy regions between Kuda and Mithivirdi, and a rocky shoreline with muddy patches towards Gopnath (Gosai & Mankodi, 2023).

Microorganisms Reported Along The Bhavnagar Coast

Marine ecosystems cover the biggest areas of land on the planet and are home to an astonishing diversity of microbial life. Despite their importance, marine microbial populations are relatively unknown, offering excellent opportunities for future scientific research (Rathore *et al.*, 2022). Table 1 Includes microorganisms identified along the Bhavnagar coast of Gujarat using a suitable microbial identification method, such as 16S rRNA gene sequencing, biochemical testing, Biolog microtitre plate, or other authentic identification method.

CONCLUSION

The Bhavnagar shoreline has significant anthropogenic influences on its coastal zones, particularly from industrial operations in the surrounding area. Despite the presence of several studies undertaken by multiple researchers, this region has a scarcity of comprehensive investigations focusing on soil microorganisms. Furthermore, little attention has been paid to investigating microbial populations in meta-haline sites in the Bhavnagar districts. Initial reports, however, indicate the presence of microflora encompassing Proteobacteria (including Epsilonproteobacteria, Betaproteobacteria, and Gammaproteobacteria), *Bacillus* sp., *Pseudomonas* sp., *Sphingomonas* sp., *Halomonas* sp., Bacteroidetes, Chloroflexi, Firmicutes, Actinobacteria, and Acidobacteria. Given the potential usefulness of microflora in addressing polluted settings, a thorough examination of the role and application of microflora in this context is required.

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AUTHOR'S CONTRIBUTION

Hardik Giri Gosai: Data curation, Writing – original draft, review, and editing.

Pradeep Mankodi: Conceptualization, Supervision, Validation, Writing – review and editing.

CONFLICT OF INTEREST

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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