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Exploring bacterial diversity in seagrass meadow of *Thalassia hemprichii* and *Syringodium isoetifolium* from Tanzania's coast

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Keywords

Bacterial communities;
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PacBio;
Rhizosphere sediment;
Seagrass species

Abstract

Seagrasses are highly productive coastal ecosystems that harbor diverse bacterial communities, including both culturable and unculturable taxa. These bacteria play vital roles in ecological, biogeochemical, and biotechnological processes. In this study, a metagenomic approach using Pacific Biosciences next-generation sequencing was employed to investigate bacterial diversity associated with *Thalassia hemprichii* and *Syringodium isoetifolium* collected from the Mjimwema coast, Dar es Salaam, Tanzania. Results revealed that *T. hemprichii* supported greater bacterial species diversity (117 OTUs) compared to *S. isoetifolium* (109 OTUs). Among plant compartments, roots harbored the highest diversity, followed by rhizosphere sediment and leaves. The phylum Proteobacteria dominated across all samples (24.85–99.23%), with Gammaproteobacteria (20.58–99.11%), Vibrionales (7.86–98.91%), Vibrionaceae (7.88–98.91%), and the genus Vibrio (4.79–91.99%) as the most abundant taxa. Although this study did not establish the functional roles of the identified bacteria, it provides the first comprehensive insight into the bacterial diversity associated with *T. hemprichii* and *S. isoetifolium* in the Western Indian Ocean. The findings offer a valuable baseline for future research aimed at functional characterization of seagrass-associated microbiomes, particularly their ecological roles and potential biotechnological applications.

Introduction

Recently, numerous authors have emphasized the significant potential of marine microbes as prolific producers of bioactive substances. They have harnessed vast marine microbial resources for their potential use as drug sources and antimicrobial agents (Zhang et al. 2024; Hassan and Jin 2025). The marine environment offers the most abundant reservoir of new enzymes, genes and natural products that can be utilized in industrial applications. Specifically, microbial species inhabiting extreme conditions serve as exceptional natural reservoirs of stable and efficient enzymes. Enzymes have the potential to enhance the efficiency and sustainability of industrial processes by facilitating the creation of novel products. This can lead to more cost-effective and environmentally friendly applications (Finore et al. 2014; León et al. 2014). The structure of marine bacterial communities varies across locations due to multiple factors, including variations in human activities, seasonal changes, salinity, inorganic nutrient levels, depth, nearby habitats, oxygen levels, particulate organic carbon, algal dominance and sand mining operations (Suh et al. 2014; Campbell et al. 2015; Terahara et al. 2016; Yergeau et al. 2017).

Seagrasses are marine flowering plants classified as angiosperms that can complete their life cycle either entirely or partially submerged in seawater (Aboud and Kannah 2017). They are prevalent in coastal areas of both temperate and tropical oceans. Seagrass meadows play a crucial role as global carbon sinks, boost coastal biodiversity, and help prevent coastal erosion (Duarte et al. 2025). They provide habitat for a wide range of organisms, including endangered species such as seahorses, dugong, turtles, and manatees. They also serve as nursery areas for a diverse array of fish species. Additionally, seagrasses play a crucial role in protecting coastlines from storm-induced erosion and capture millions of tons of carbon dioxide annually (Duarte et al. 2025). Seagrasses host significant microbial populations within their rhizomes, roots and leaves (Garcias-Bonet et al. 2016, Khalid et al. 2021). For example, Jensen et al. (2007) illustrated that Epsilonproteobacteria, including sulfur-oxidizing bacteria such as *Arcobacter* and *Sulfurimonas,* as well as Gammaproteobacteria and Actinomycetota, which are significant colonizers of *Zostera marina* roots. Moreover, Deltaproteobacteria seem to be prevalent in the rhizosphere. Furthermore, Cúcio et al. (2016) demonstrated that the root epiphytic bacterial communities of seagrasses (*Z. marina*, *Zostera noltii* and *Cymodocea nodosa*) exhibited significant differences from the communities found in the surrounding sediment and seawater. Consistent with these findings, Fahimipour et al. (2017) demonstrated a significant distinction between eelgrass root microbial communities and sediment communities, attributed to the elevated presence of the genus Sulfurimonas on the root

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surface as opposed to the sediment. Bacterial communities fulfil crucial functions within seagrass meadows, especially in the process of material recycling (Duarte et al. 2025). The organism, along with its symbiotic partners, forms an interconnected community that sustains each member and contributes to their collective survival and success (Seymour et al. 2025). Specifically, *Thalassia hemprichii*, commonly known as Sickle Seagrass, typically inhabits shallow coastal waters of the Indian Ocean, Red Sea, and western Pacific Ocean. It plays a vital ecological role by forming dense underwater meadows that serve as both habitat and food sources for a wide variety of marine organisms. *Syringodium isoetifolium*, also known as Noodle Seagrass, occurs in shallow, sandy or muddy coastal areas of the Indian and Pacific Oceans. This species contributes to nutrient cycling while providing essential habitat for marine life (Brazas and Lagat 2022).

One of the bacterial groups that have biotechnological potential and are dominating seagrasses are Actinomycetota species (Jensen et al. 2007; Borowitzka et al. 2015). Actinomycetota are highly significant due to their extensive diversity and established capacity to generate potential secondary metabolites. For example, the seagrass *T. hemprichii* has been shown to associate with ten genera of Actinomycetota (Karuppiah et al. 2014). The GenBank 16S rRNA data revealed a comparatively greater diversity of seagrass-associated Actinomycetota, encompassing 15 families from three subclasses: *Actinobacteridae*, *Acidimicrobidae* and *Nitriliruptoridae* (Karuppiah et al. 2014). The symbionts found in *T. hemprichii* include genes encoding polyketide synthase (PKS) and nonribosomal peptide synthetase (NRPS), indicating that the Actinomycetota could serve as an antibacterial agent (Wu et al. 2012).

Investigating the complete bacterial community in marine environments is best achieved through high-throughput next-generation sequencing (NGS) technology targeting the taxonomically informative 16S rRNA gene. This approach is highly effective because it allows the classification of individual reads into specific taxa (Salipante et al. 2014). Furthermore, a metagenomics approach is capable of revealing the entire spectrum of community members in the association, as it is believed that culturable microbes represent less than 1%, while the remaining 99% are considered unculturable microbes (Retnowati et al. 2021). Recent advancements in NGS technology have not only allowed for more detailed characterization of bacterial genomes but also facilitated more comprehensive taxonomic identification of intricate microbiomes (Cao et al. 2017). The NGS approach has been widely employed to study microbial communities across diverse marine environments, including Antarctic ecosystems (Aislabie & Deslippe 2022), the Georgetown Coast in Malaysia, the Gulf of Mexico, and Malipo Beach in South Korea (Hinthong et al., 2024), as well as the central-eastern Arabian Sea (Singh et al. 2024). To the best of our knowledge, no research has yet employed the NGS approach in studying seagrass ecosystems in the western Indian Ocean region. Hence, this study aimed to characterize the bacterial communities associated with the seagrasses *Thalassia hemprichii* and *Syringodium isoetifolium* along the coast of Dar es Salaam, Tanzania, and to analyze their composition and diversity using next-generation sequencing (NGS) techniques.

Materials and Methods

Sample collection

Samplings were done during the dry season in August 2022 at Mjimwema (approximately latitude 06°50’S and longitude 39°21’E) in Dar es salaam, Tanzania (Figure 1). The sampling site is characterized by a sandy/muddy intertidal flats with seagrass beds extending to Kendwa Islands (Hamisi et al. 2004). Samples of the seagrasses *T. hemprichii* and *S. isoetifolium* were collected by uprooting whole plant from near shore waters during low tide at Approximately 10 m intervals within the seagrass dominated by each species, resulting in 5 sampling points per species. Prior to sampling, standard identification guidebook (Richmond 2011) was used to identify the two seagrass species in the field. The samples were packed separately (leaves, roots and rhizosphere sediment) to avoid cross contamination in sterile polyethylene bags and stored in cool box for transportation to the Department of Molecular Biology and Biotechnology laboratory, UDSM for further analysis. Environmental parameters, namely: salinity, pH and temperature were measured *in-situ* at each sampling point to provide basic contextual information about the sampling sites. Salinity was measured using a salt refractometer (SPER 300011 Scientific) while pH and temperature were measured using HANNA instrument (Woonsocket RI USA).

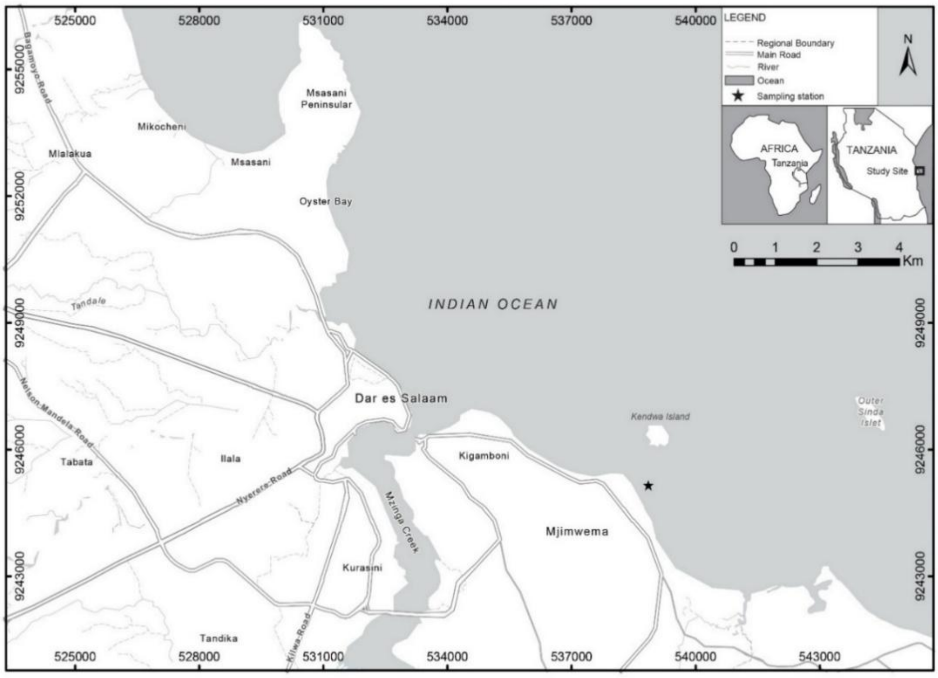


Figure 1: A map showing the sampling station ⋆ at Mjimwema, Dar es Salaam, Tanzania

DNA extraction

Community DNA was extracted from five replicates per sample type (leaves, roots and sediments), resulting in a total of 30 DNA extracts. The roots and leaves samples were rinsed with sterile water and crushed into small pieces using mortar and pestle before undergoing DNA extraction using the ZymoBIOMICS^{TM} DNA Miniprep Kit (Cat. No.: D4300) according to the manufacturer's instructions. DNA quality and quantity were assessed using a Nanodrop One instrument (Thermo Fisher Scientific, USA A sterile DNA/RNA free water sample was included as a negative control during DNA extraction and Nanodrop concentration measurement on the showed 0.0 ng/µl.

Pacific Bioscience sequencing

For sequencing, pooled genomic DNA was forwarded to Inqaba Biotechnical Industries, a commercial NGS service provider (https://inqababiotec.co.za/). The samples were sequenced using the Sequel system by PacBio (www.pacb.com). The genomic DNA samples were subjected to polymerase chain reaction (PCR) amplification using the universal primer pair 27_F/1492_R, which targeted the 16S rRNA gene. These primers were designed with PacBio M13 adaptor sequences at both the 5' and 3' ends for barcoding each amplicon. Following amplification, the amplicons were barcoded using PacBio M13 barcodes via limited cycle PCR for multiplexing. The barcoded amplicons were then quantified, pooled equimolarly, and subjected to purification using Ampure PB beads.

Analysis of the sequence data

The raw subreads were processed via the SMRTlink (v11.0) Circular Consensus Sequences (CCS) algorithm to generate highly accurate reads (>QV40). Subsequently, these high-quality reads were processed using vsearch GNU/Linux (https://github.com/torognes/vsearch), and QIIME (version 1.8.0) was used for operational taxonomic unit (OTU) and taxonomic information retrieval (Bibi and Azhar 2021). Taxonomic designations for the major sequences of each OTU were assigned using the Silva database. Microbial alpha diversity (richness and evenness) were assessed through the Shannon, Simpson, Chao1 indices and rarefaction curves. Beta diversity was computed to assess microbial communities across various samples The weighted UniFrac distance metric was utilized to calculate phylogenetic beta diversity. Principal coordinate analysis (PCoA) was performed to analyse genetic dissimilarity and relationships among the samples.

Nucleotide sequence accession numbers

The Pacific Bioscience reads were deposited in the Sequence Read Archive (https://www.ncbi.nlm.nih.gov/sra/PRJNA1062700) under accession numbers SAMN39308639, SAMN39308640, SAMN39308641, SAMN39308642, SAMN39308643 and SAMN39308644 for *Thalassia hemprichii* roots, *Syringodium isoetifolium* roots, *Thalassia hemprichii* sediment, *Syringodium isoetifolium* sediment, *Thalassia hemprichii* leaves and *Syringodium isoetifolium* leaves, respectively.

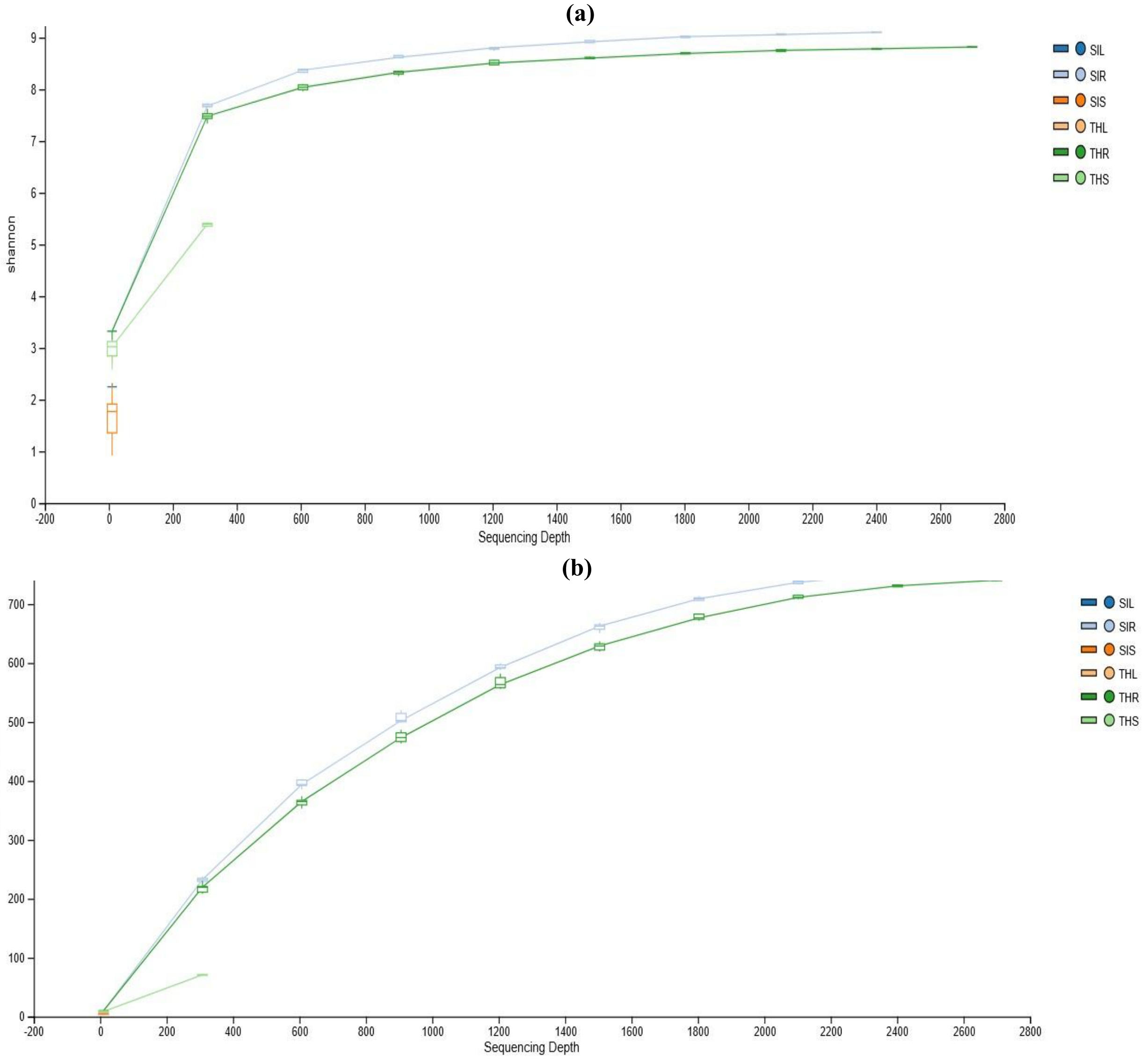
Results

Bacterial diversity indices and statistical analysis

A total of 212,747 raw sequences were acquired from the analysis of 16S rRNA gene sequences in seagrass leaf, root and sediment samples using Pacific Biosciences (PacBio) technology as seen in Table 1. Significant levels of bacterial species were observed along different parts of the seagrasses, with *T. hemprichii* roots showing the highest diversity (117 OTUs), *S. isoetifolium* roots followed by (109 OTUs). Lower diversity counts (28 and 24 OTUs) were reported for *S. isoetifolium* rhizosphere sediment and leaves, respectively (Table 1). The Chao1 metric, revealed high values for *T. hemprichii* roots and *S. isoetifolium* roots (Table 1). High values of Shannon's diversity 9.12 and 8.82 were documented for roots of seagrass *T. hemprichii* and *S. isoetifolium,* respectively, while low values (2.30) were detected for the *S. isoetifolium* leaves, which exhibited minimum bacterial diversity. Rarefaction analysis demonstrated satisfactory sequence coverage values for roots, with rhizosphere sediment seagrass samples following closely (Figure 2). The Principal Coordinate Analysis (PCoA) plot illustrates distinctions between the two seagrass samples, as depicted in Figure 2 whereby the PCoA plot effectively segregates the seagrass samples and highlights their distinct clustering patterns. The average salinity, pH, and temperature recorded were 33 ± 1, 8.45 ± 0.1, and 27 ± 1 °C, respectively. DNA extracts obtained showed quality (UV260/280) values ranging from 1.93 to 2.06 for *T. hemprichii* and from 1.87 to 1.93 for *S. isoetifolium*. Nanodrop readings of DNA concentrations from leaves, roots, and sediments ranged between 18.0–35.3 ng/µL for *T. hemprichii* and 31.8–39.4 ng/µL for *S. isoetifolium*.

Table 1: Summary of the diversity indices of the studied seagrass species

Seagrass sample	Total reads	Total OTU	Shannon	Chao1	Simpson
T. hemprichii roots	72725	117	9.12	752	0.997
S. isoetifolium roots	67909	109	8.82	741	0.994
T. hemprichii rhizosphere sediment	21646	53	5.43	73	0.959
S. isoetifolium rhizosphere sediment	13816	28	2.78	31	0.607
T. hemprichii leaves	22591	32	4.59	32	0.945
S. isoetifolium leaves	14060	24	2.30	5	0.793



Key:
🟥 *T. hemprichii* roots
🟦 *S. isoetifolium* roots

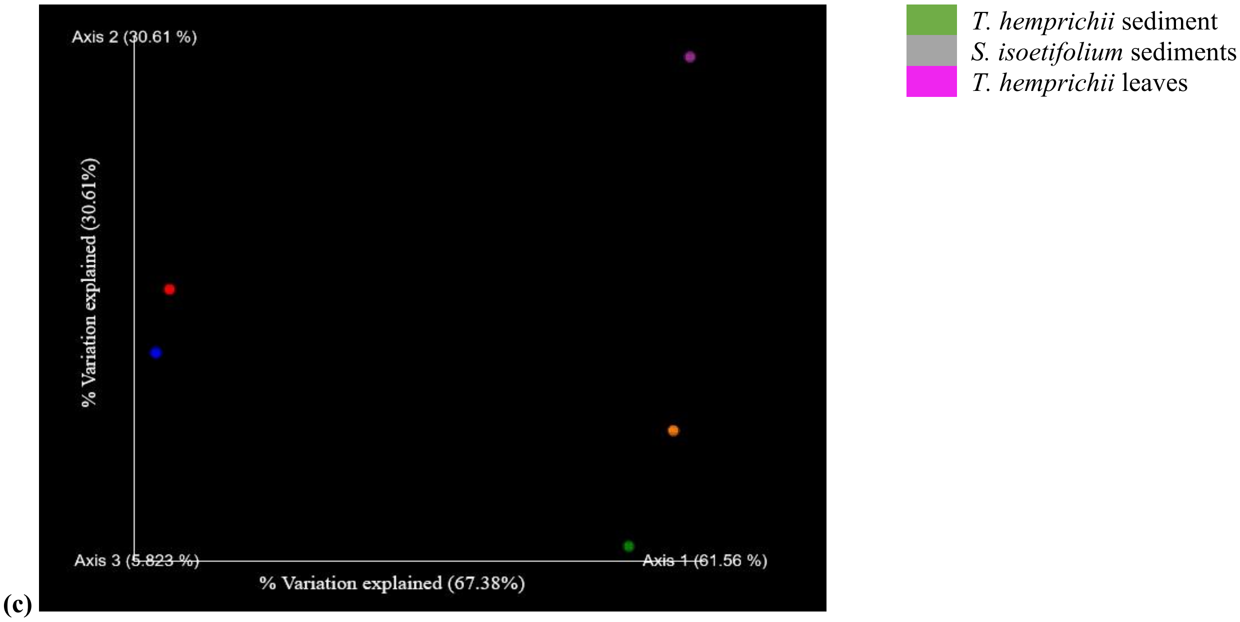


Figure 2: Microbial diversity and community structure of seagrass-associated bacteria: (a) Shannon diversity index, (b) observed features rarefaction curves, and (c) Principal Coordinates Analysis (PCoA) plot."

Diversity of the microbial community

Bacterial diversity at the phylum level

Sequence reads of the 16S rRNA gene from two seagrass samples showed that *T. hemprichii* had more bacterial phyla (45) compared to the *S. isoetifolium* (41 phyla). The phylum Proteobacteria was the dominant phylum in all the seagrasses species especially on the leaves (99.23% and 82.71%), followed by rhizosphere sediment (33.16% and 42.78%) and roots (24.85% and 25.68%) of the studied seagrasses (*S. isoetifolium* and *T. hemprichii,* respectively) as seen in Figure 3. Campilobacterota was observed to be the second abundant phylum in the seagrasses species mainly on the sediment with relative abundance of 33.10% and 20.04% in *T. hemprichii* and *S. isoetifolium* respectively. The third most abundant phylum was Planctomycetota, which dominated the roots of *T. hemprichii* (13.34%) and *S. isoetifolium* (9.32%). Notably, a large number of phyla were unknown, with relative abundances ranging from 12.92% in the sediment to 0.22% in the leaves of *S. isoetifolium*. Phylum Acidobacteriota was observed only in the *T. hemprichii*, the remaining phyla were observed mainly in the roots and sediment and were less abundant or absent in the two samples, as shown in Figure 3 and appendix 1. Other phyla comprise of total of 25.09% and 31.83% of relative abundance for *T. hemprichii* and *S. isoetifolium,* respectively where by Actinomycetota stood out as a prominent phylum among others as shown in appendix 1.

Bacterial diversity at the class level

The number of classes (97) in *T. hemprichii* was slightly greater than that in the 95 classes in *S. isoetifolium* meadow. The class Gammaproteobacteria was dominant, especially on the leaves (99.11% and 81.66%), followed by the rhizosphere sediment (28.44% and 41.04%) and roots (20.58% and 21.48%) of the studied seagrasses *S. isoetifolium* and *T. hemprichii,* respectively (Figure 4). Campylobacteria was the next most dominant class, particularly in the sediment, with relative abundances of 33.13% and 20.04% in the seagrasses *T. hemprichii* and *S. isoetifolium,* respectively. The classes Bacteroidia and Clostridia were the third most abundant classes in the roots (12.80% and 7.96%, respectively) and sediment (12.14% and 8.74%, respectively) of *S. isoetifolium* and *T. hemprichii*, respectively. Unknown classes were also highly abundant in these seagrasses, with relative abundances ranging from 14.05% in sediment to 0.33% in leaves. Among the two seagrass classes, Desulfobulbia was detected on *S. isoetifolium,* and Phycisphaerae was detected only on *T. hemprichii*. The other bacterial classes were observed in leaves, followed by sediment and roots, with less than 5% relative abundance, as shown in Figure 4 and appendix 2.

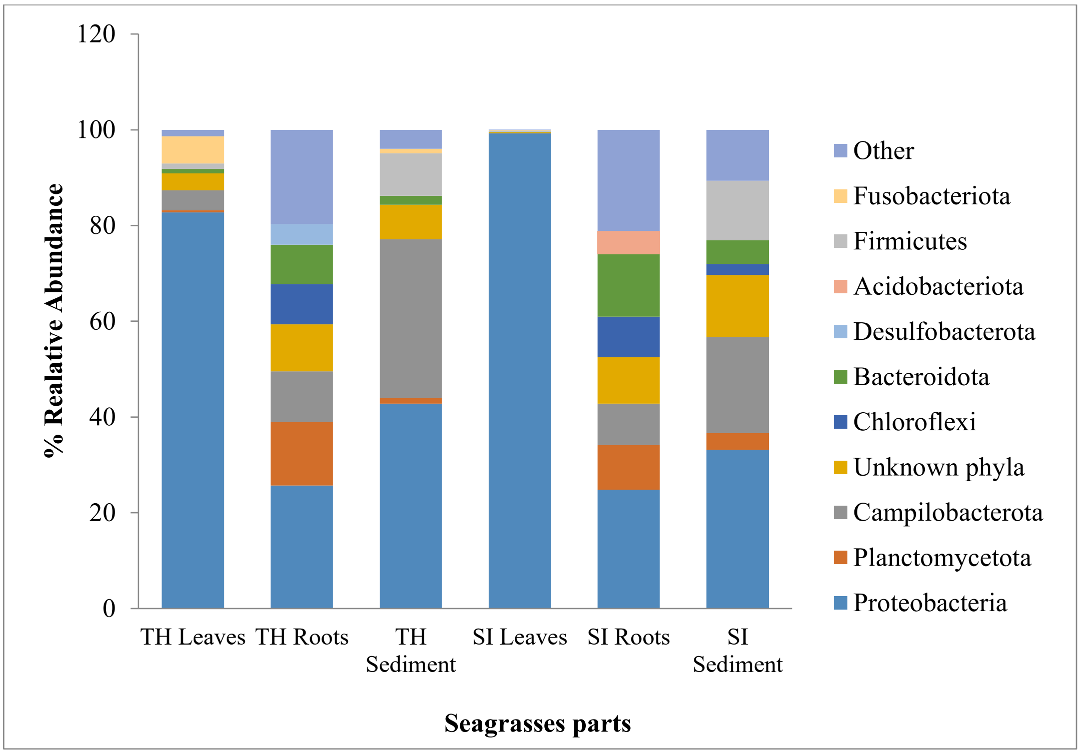


Figure 3: The relative abundance and taxonomic classification of the top bacterial phyla identified in samples from the seagrass species *T. hemprichii* (TH) and *S. isoetifolium* (SI)

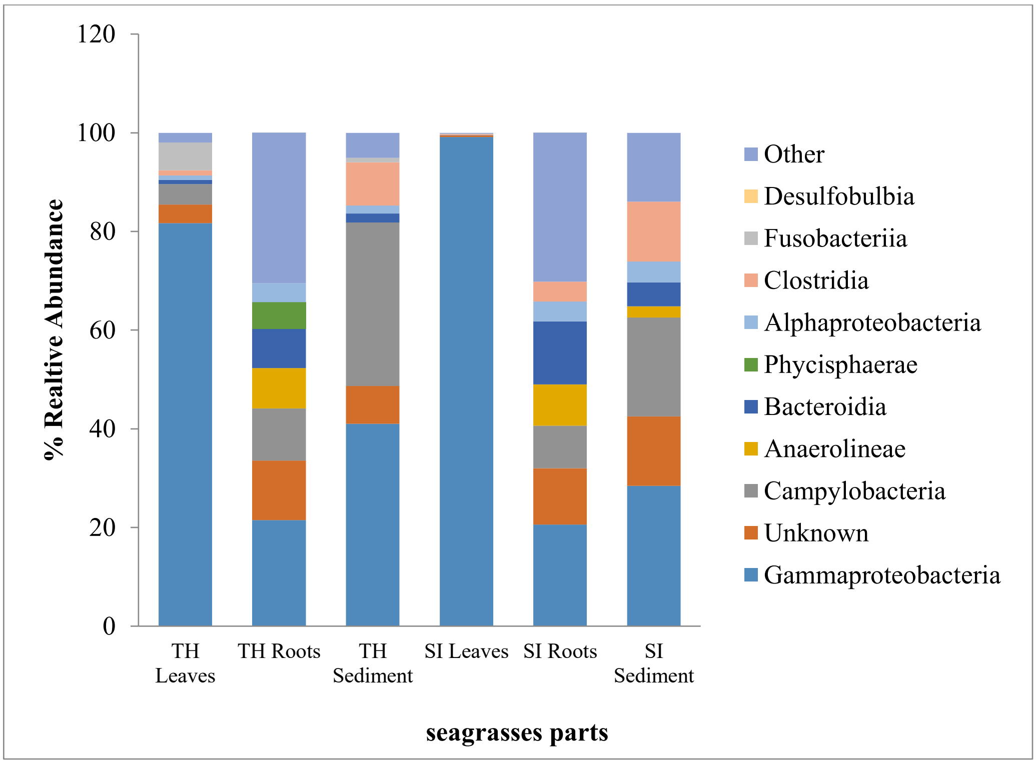


Figure 4: The relative abundance of taxonomic classification of the top bacterial classesidentified in samples from the seagrass species *T. hemprichii* (TH) and *S. isoetifolium* (SI)

Bacterial diversity at the order level

The seagrass *S. isoetifolium* meadow consisted of 196 orders, while the *T. hemprichii* meadow contained 194 orders. The dominant order on these seagrasses was Vibrionales, particularly on the leaves, with abundances of 98.91% and 76.32%, followed by rhizosphere sediment (18.08% and 36.36%), and finally roots, with abundances of 8.01% and 7.86% in the seagrasses *S. isoetifolium* and *T. hemprichii,* respectively (Figure 5). Campylobacterales was more abundant in the sediment (20.04% and 10.59%) of *S. isoetifolium* and *T. hemprichii,* respectively, than in other parts of these seagrasses. Likewise, the unknown orders formed high relative abundances ranging from 20.27% in the sediment to 0.45% in the leaves. The remaining bacterial orders were less abundant or not present in the same seagrass, as shown in Figure 5 and appendix 3.

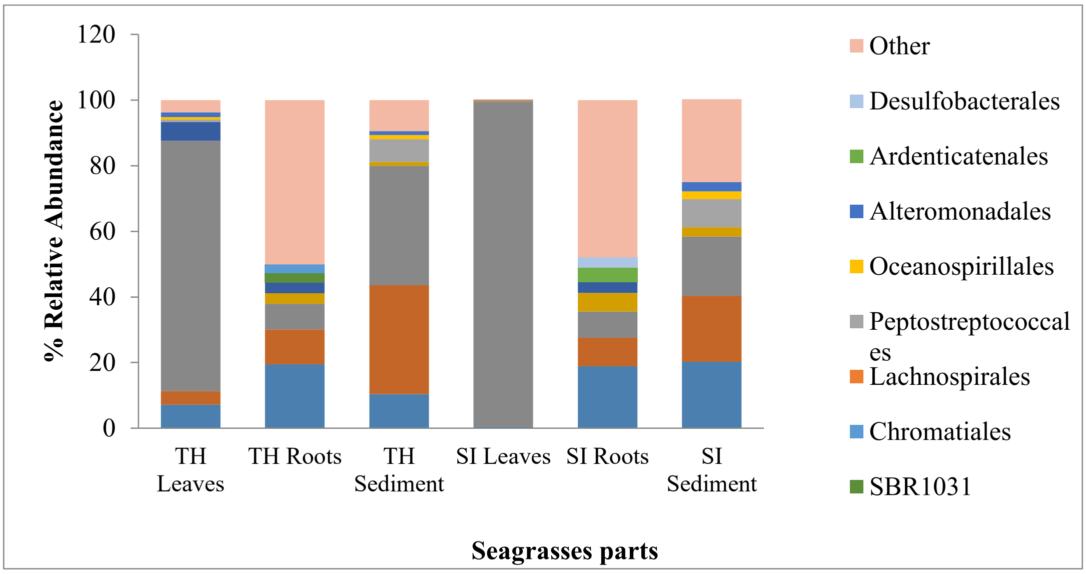


Figure 5: The relative abundance of taxonomic classification of the top bacterial orders identified in samples from the seagrass species *T. hemprichii* (TH) and *S. isoetifolium* (SI)

Bacterial diversity at the family level

There were more families of seagrass *S. isoetifolium* (289) than seagrass *T. hemprichii* (252 families). Vibrionaceae was the most dominant family on both seagrasses, represented mostly on leaves (98.91% and 76.37%), followed by on sediment (18.08% and 36.41%), and finally on roots, with abundances of 8.02% and 7.88% in *S. isoetifolium* and *T. hemprichii,* respectively. The second most dominant family in the sediment was Arcobacteraceae, with relative abundances of 32.31% and 19.43% in *T. hemprichii* and *S. isoetifolium,* respectively (Figure 6). An unknown family was also observed to dominate these seagrasses, especially in the roots, with relative abundances of 21.71% and 21.69% in *T. hemprichii* and *S. isoetifolium,* respectively. The remaining families were less than 6% or were absent in some samples, as revealed by the appendix 4.

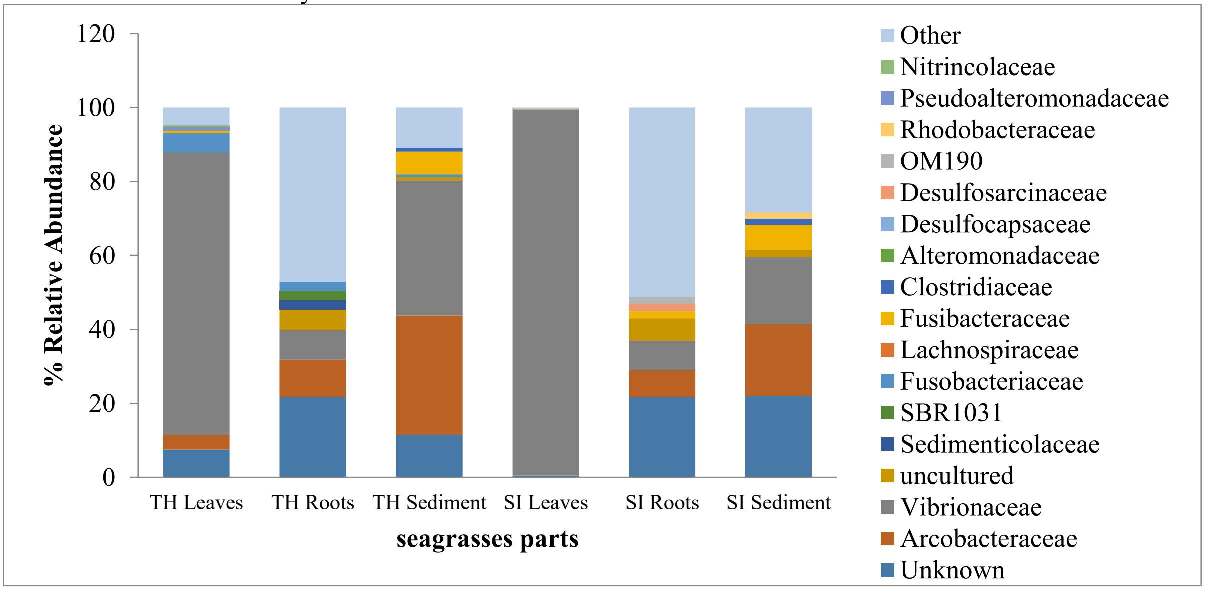


Figure 6: The relative abundance of taxonomic classification of the top bacterial families identified in samples from the seagrass species *T. hemprichii* (TH) and *S. isoetifolium* (SI)

Bacterial diversity at the genus level

A greater number of bacterial genera (361) were detected in the seagrass *S. isoetifolium* meadow than in the *T. hemprichii* meadow, with 305 bacterial genera. The genus *Vibrio* was dominant in both seagrass species, mainly in the leaves, with high relative abundances of 91.99% and 63.64%, followed by the sediment (28.40% and 11.78%, respectively) and leaves (5.55% and 4.79%, respectively) in *S. isoetifolium* and *T. hemprichii* (Figure 7). The unknown genus ranked as the second most prevalent among these seagrasses, exhibiting a relative abundance ranging from 37.01% in the sediment to 7.20% in the leaves. The genera *Alteromonas* (0.02%) and *Hypnocyclicus* (1.52%) were detected only in *S.*

isoetifolium, while the genus *Malaciobacter* (2.41%) was detected only *in T. hemprichii*. The remaining bacterial genera were less abundant or not present in the same samples, as shown in appendix 5.

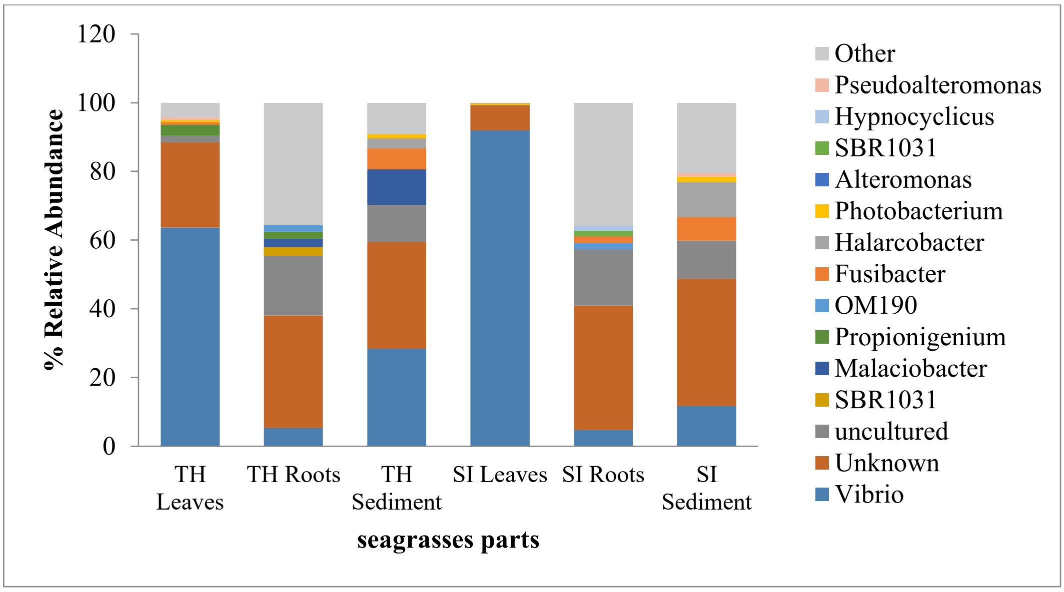


Figure 7: The relative abundance of taxonomic classification of the top bacterial genera identified in samples from the seagrass species *T. hemprichii* (TH) and *S. isoetifolium* (SI)

Discussion

Distinct variations in bacterial communities were observed across different sample types, leaves, roots and rhizosphere sediments of *Thalassia hemprichii* and *Syringodium isoetifolium* meadows. This result is consistent with previous studies on other seagrass species, such as *Zostera marina* and *Zostera japonica* (Crump et al. 2018) and *Z. marina*, *Zostera noltii* and *Cymodocea nodosa* (Cúcio et al. 2007), which also reported microbial community composition varying with sample type and location. In particular, species diversity was significantly higher in roots and rhizosphere sediments, reflecting the influence of root-associated nutrients, biomass, and metal concentrations in promoting bacterial abundance (Wei et al. 2017). The elevated diversity in sediments likely results from the release of readily degradable sugars, amino acids, and small organic acids from roots, as well as localized oxygenation in otherwise anaerobic sediments (Jensen et al. 2007). Although this study did not perform functional assays to directly measure microbial activity, the observed patterns strongly suggest that root and rhizosphere environments are hotspots for diverse microbial communities in these seagrasses.

The prevalence of the Proteobacteria phylum in the leaves, roots and sediment of both seagrasses aligns with findings from previous studies on seagrasses. This similarity is notable in the research conducted by Cúcio et al. (2016), who reported that Proteobacteria was the predominant phylum in the rhizomes of the seagrasses *Z. noltii*, *C. nodosa* and *Z. marina,* with proportions ranging from 65% to 68%. Proteobacteria play a significantrole in maintaining the stability of the microbial community, given their ability to support host defence mechanisms, nitrogen fixation and nitrification processes (Mohamed et al. 2010). Furthermore, the other dominant phyla surrounding the studied seagrasses were Planctomycetota, Campilobacterota, Chloroflexi, Bacteroidota, Desulfobacterota, Acidobacteriota, Firmicutes and Fusobacteriota. A high abundance of Planctomycetota was reported in the seagrass *Posidonia oceanica* (Kohn et al. 2020). These slow-growing bacteria are highly adaptable to diverse habitats, including extreme environments, and are capable of producing a variety of bioactive compounds (Graça et al. 2016). Planctomycetes are commonly linked with phytoplankton or other aquatic phototrophs, such as seagrasses or macroalgae (Bangtsson et al. 2012; Vollmers et al. 2017). They play a role, either directly or indirectly, in global biogeochemical cycles (Peeter and vanNifrik 2019). Furthermore, the phyla Campylobacterota and Desulfobacterota are known for their decomposition of organic matter and have been identified in marine sediments of seagrass meadows (Markovski et al. 2022). Chloroflexi play a vital role by fermenting carbohydrates and breaking down complex polymeric organic compounds into lowmolecularweight substrates. This process supports their own growth as well as that of other bacterial populations (Speirs et al. 2019). In addition, Chloroflexi have been detected in the phyllosphere of other seagrass species, such as *Halophila stipulaceae* and *Z. marina*, albeit at lower abundances (Bengtsson et al. 2017). According to Wei et al. (2007), the presence and co-occurrence of Bacteroidota and Firmicutes are essential for stabilizing microbial communities, as they help reduce resource competition through cooperative interactions or functional specialization. In the bacterial communities of the seagrasses *T. hemprichii* and *S. isoetifolium*, the phylum Fusobacteriota was also found to dominate the seagrass meadow, as previously reported by Zhang et al. (2021) in seagrass roots of *T. hemprichii* and *E. acoroides.* Various seagrass species harbor bacterial communities composed primarily of distinct bacterial species. In our investigation, the phylum Acidobacteria was exclusively identified in the seagrass *T. hemprichii*. This phylum represents a newly identified group of bacteria that is consistently detected across diverse habitats worldwide. Acidobacteria are notoriously challenging to culture while the existing information relies solely on the analysis of the 16S rRNA gene sequence (Ward et al. 2009). The bacteria identified are engaged in a symbiotic relationship with seagrasses, converting atmospheric nitrogen (N_2) into compounds usable by plants to support their growth. Additionally, these prolific and active bacterial communities serve as the primary consumers of seagrassgenerated organic matter and play crucial roles in enhancing seagrass productivity through nutrient recycling processes (Laverock et al. 2018). Among the phyla reported in this study have been shown to be economically very important although they occurred in less abundance in these seagrasses. For example, Actinomycetota species are known for producing more than 20,000 natural products that have extensive applications in the pharmaceutical and agrochemical industries (Donald et al. 2022).

Gammaproteobacteria were the dominant class in leaves, roots and sediments, highlighting their central role in seagrass-associated microbial communities. These bacteria act as root colonizers that oxidize sulfide using oxygen and nitrate as electron acceptors, mitigating the toxicity of sulfide to seagrasses (Loria et al. 2016; Campbell et al. 2006). Similar protective roles of sulfur oxidizing Gammaproteobacteria have been reported in other plants; for instance, *Beggiatoa* was shown to protect rice from hydrogen sulfide (Joshi & Hollis 1977). In addition to Gammaproteobacteria, Phycisphaerae was detected exclusively in *Thalassia hemprichii*. This class comprises largely uncultured bacteria of the phylum Planctomycetes, typically found in marine and soil environments, suggesting potential novel functional roles in this seagrass species. Furthermore, Desulfobulbia was observed solely in *Syringodium isoetifolium*. Members of this class are Gram-negative anaerobes that participate in sulfate reduction, contributing to sulfur cycling within the sediment (Widdel & Pfennig 1982). Although the study did not directly measure microbial activity, the consistent detection of these classes across samples supports their ecological relevance in maintaining seagrass health.

The Vibrionaceae family was the most abundant in both *Thalassia hemprichii* and *Syringodium isoetifolium*, followed by Arcobacteraceae. Members of Arcobacteraceae are widespread in aquatic environments, with certain species associated with diseases in animals and humans (Venâncio et al. 2022). The potentially pathogenic genus *Vibrio* was detected across all seagrass parts, consistent with previous reports of virulent *Vibrio* species, including *V. cholerae*, in coastal Tanzania (Dalusi et al. 2015a, b). Globally, *Vibrio* species inhabit diverse marine environments and associate with corals, seagrasses, sponges, zooplankton, shellfish, fish, and humans, with at least 12 species being pathogenic to humans (Wright & Naim 2021; Famers et al. 2003; Johnson et al. 2012), highlighting their relevance for public health.

Additionally, the genera *Alteromonas* and *Hypnocyclicus* were found exclusively in *S. isoetifolium*, while *Malaciobacter* was observed in *T. hemprichii*. *Alteromonas* species, widely distributed in marine environments, exhibit hydrolytic activity and rapidly utilize sudden organic matter inputs (López-Pérez et al. 2014). *Malaciobacter* (formerly *Arcobacter*), part of the aerotolerant Epsilonproteobacteria, is moderately halophilic and thrives in organic-rich aquatic habitats such as sewage (Pérez-Cataluña et al. 2018). While the precise ecological role of *Malaciobacter* in seagrass meadows remains unclear, its consistent detection suggests adaptation to high-organic environments. Although this study did not assess microbial pathogenicity or functional activity directly, the observed patterns provide important insights into seagrass associated bacterial communities and their potential ecological and public health significance.

Conclusion

This study provides the first comprehensive analysis of bacterial communities associated with the seagrasses *Thalassia hemprichii* and *Syringodium isoetifolium* in the Western Indian Ocean, addressing the hypothesis that different seagrass species and tissues harbour distinct microbial communities. Our findings demonstrate that *T. hemprichii* supports greater bacterial diversity and richness than *S. isoetifolium*, with roots exhibiting the highest microbial richness, highlighting the importance of below ground tissues in seagrass microbiomes. The observed dominance of Proteobacteria particularly Gammaproteobacteria, Vibrionaceae and *Vibrio* across both seagrass species suggests these bacteria play crucial roles in nutrient cycling, detoxification and growth promotion, directly supporting seagrass health and resilience. These results have broader relevance beyond the Western Indian Ocean, as seagrass ecosystems globally face threats from climate change, coastal development and pollution. Understanding their associated microbial communities can inform conservation strategies, sustainable coastal management and the harnessing of marine microbes for biotechnological applications. The detection of bacteria capable of producing bioactive compounds, enzymes and plant beneficial metabolites underscores their potential in agriculture, pharmaceuticals, environmental remediation and industrial biotechnology. Based on these findings, future research should focus on functional characterization of these microbial communities, genome mining for biosynthetic gene clusters, and the development of applications in marine agriculture, biocontrol and sustainable ecosystem management. Such studies will not only expand our understanding of seagrass microbe interactions but also provide a foundation for leveraging marine microbial diversity for global biotechnological innovations.

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Conflict of interest

The authors declare no conflicts of interest, as they are not affiliated with any organization or entity with any financial or nonfinancial interest in the subject matter discussed in this paper.

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