Revista Argentina de Microbiología 57 (2025) 171–181

REVISTA ARGENTINA DE MICROBIOLOGÍA

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ORIGINAL ARTICLE

Bacterial richness assessment in water and sediments in the northern coast of the Yucatan Peninsula

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Received 26 June 2024; accepted 29 October 2024
Available online 5 December 2024

KEYWORDS
Bacterial communities;
Coastal ecosystems;
Pathogens;
Xenobiotic degraders

Abstract Given the importance of the coastal environments and the multiple ecological services that they provide, it is important to explore and understand the interactions that occur within them. The microbiome is a key factor for the understanding of the dynamics of these fragile sites. A metagenomic study based on the profiling of the 16S ribosomal gene was carried out in order to assess the bacterial diversity present in the northern coastal zone of the Yucatan Peninsula. The results showed that water and sediment samples share some similarities regarding the bacterial genera found, only differing in the quantitative part. Through a PCO (principal coordinates) analysis clear differences between sediment and water samples could be observed. The highest relative diversity was found in wetland and lagoon sediment samples, respectively. It was observed that 3–8% of the total sequence reads belonged to opportunistic genera such as: *Vibrio* in the sea samples and *Capnocytophaga* in the other environments. Salinity and pH were the factors which contributed the most to the differences among the communities in the various environments in the coastal zone. There is an important similarity in the sediments across the different environments within the studied coastal zone. The data presented herein contribute to setting a baseline for research in the coastal region of the Yucatan Peninsula.

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https://doi.org/10.1016/j.ram.2024.10.009

PALABRAS CLAVE
Comunidades bacterianas;
Ecosistemas costeros;
Patógenos;
Degradadores de xenobióticos

Evaluación de la riqueza bacteriana en agua y sedimentos en la costa norte de la península de Yucatán

Resumen Dada la importancia de los ambientes costeros y de los múltiples servicios ecológicos que proporcionan, es importante conocer y comprender las interacciones que se llevan a cabo en ellos. El microbioma que los caracteriza es un factor clave para entender la dinámica de estos sitios frágiles. Se realizó un estudio metagenómico basado en el perfil del gen 16S ribosomal con el fin de evaluar la diversidad bacteriana en la zona costera norte de la península de Yucatán. Las muestras de agua y de sedimento tuvieron algunas similitudes con respecto a los géneros bacterianos identificados, diferenciándose solo en términos cuantitativos. A través de un análisis de coordenadas principales se pudieron observar claras diferencias entre las muestras de sedimentos y de agua. La mayor diversidad relativa se encontró en los sedimentos de humedal y laguna, en ese orden. Entre el 3 y el 8% del total de las lecturas de secuencia correspondieron a géneros oportunistas, como *Vibrio* en muestras de mar y *Capnocytophaga* en los demás ambientes. El pH y la salinidad fueron los factores que más contribuyeron a las diferencias entre las comunidades en los distintos ambientes evaluados. Concluimos que existe una importante similitud en el microbioma de los sedimentos al comparar diferentes ambientes dentro de la zona costera estudiada. Los datos aquí presentados contribuyen a establecer una línea de base para la investigación en la región costera de la península de Yucatán.

Introduction

Organisms such as bacteria, archaea, protists and unicellular fungi represent the largest proportion of marine biomass, and are responsible for 98% of primary production[36]. These communities account for more than 10^5 cells per milliliter in the ocean's surface water[5,36] and their role in biogeochemical processes, including the carbon and nitrogen cycles, is critical for life in all the environments[22].

The microbial diversity in coastal environments is influenced by several factors such as: sediment type, water salinity, biomass contribution (terrestrial, marine) and the effect of regional hydrogeography on freshwater input. These environments are highly dynamic, ecologically important and a key factor in the economic development of a country. Coastal environments exist in fragile equilibrium, which can be affected by the interaction of continental, marine, hydrological and ecological dynamics. In particular, the coasts of the Yucatan Peninsula experience a convergence of marine, estuarine and freshwater environments, as well as multiple anthropogenic components.

The predominant sediment type in the continental platforms is permeable sand[6]; these types of sediments could act as a biocatalytic filter for various materials carried by the atmosphere, including dissolved organic compounds and/or particulate matter[13]. It is known that sandy sediments rapidly recycle the organic matter and may play an important role in global biogeochemical cycles[17,21]. Previous studies in fine-grained sediments have shown that the molecular diffusion in them limits the aerobic and suboxic microbial metabolism to a thin superficial layer[25]. In contrast, the high permeability of sands allows rapid water exchange through pores, facilitating transport of microbial substrates and metabolic residues out of the sediments. Inter-grain pores are the site of constant particle exchange from turbulent current flow and water advection, which can induce substantial organic matter flows[38]. Hydrodynamic forces can therefore produce high microbial metabolic rates in permeable sands while supporting low microbial abundance and organic matter content[7].

Little is known about the microorganism community structure in permeable sediments[21]. Some researchers have studied it using biomarkers and fluorescent *in situ* hybridation (FISH)[7,31], while others have used denaturing gradient gel electrophoresis (DGGE)[37]. It is still unknown if the biofilms associated with sand grains could trap microorganisms from terrestrial sources or from the water column, or if these biofilms function as a source of diversity in oceans[17]. Coastal sediments are a transition zone between land and sea, are characterized by high mixing rates and may therefore harbor many rare types of bacteria[17]. To date, few studies have addressed the structure and ecology of microbial communities in coastal sediments[5,17,29], and even fewer have addressed microbial communities in the water column. However, their clear importance in potential biotechnological applications has placed greater attention on microorganisms. This has also been promoted by the advent of culture-independent technologies such as next generation sequencing (NGS), which complements data on microbial community diversity and their ecological and metabolic functions in different environments. For example, freshwater inputs can harbor various types of chemolithotrophic bacteria, as well as rare microbial uncultured phyla[32].

Biotic interactions affect microbial organisms, but the specific properties of lacustrine ecosystems can also influence the establishment of a set of typical and unique microbes[32]. The formation of freshwater microbial communities is affected by regional factors such as local climate, biochemical interactions in the catchment zone and the

massive introduction of bacteria in bodies of water with low hydrological retention times.

Bodies of freshwater are discontinuous habitats and several factors intrinsic to them such as internal variation, trophic condition, pH, organic matter composition, phytoplankton and trophic network structure can modify the microbial community structure by selecting for a set of specific ecotypes[32].

Although coastal zones exist within a fragile equilibrium and dynamics, they are ecologically, economically and socially important. Understanding their microorganism taxonomic richness is vital for effectively protecting and sustainably using these zones. In the present study, NGS was used for the assessment of the bacterial diversity present in the sediments and waters of a portion of the coastal zone (different environments) of the northwestern Yucatan Peninsula near Sisal, Yucatan, Mexico. The aim of the study was to identify differences between the microbial diversity of the water and sediment as well as between the different environments within the study area.

Materials and methods

Sampling sites

The study area encompassed approximately 20 km of the northwest coast of the Yucatan Peninsula, near the port town of Sisal, Yucatan, Mexico. Located on a sand barrier island at the southeastern edge of the Gulf of Mexico, Sisal is bordered by wetlands and mangroves on all sides except the seafront. Samples were collected on the beach in front of Sisal (21°09′55″ N; 90°01′50″ W), in the wetlands immediately to the southeast, in La Carbonera lagoon (approx. 16 km northeast of Sisal) (21°13′0″ and 21°14′0″ N; 89°53′0″ and 89°54′0″ W), and on the open ocean (Fig. 1). The sand on the Sisal beach ranges from fine to medium-grain with shell deposits. The wetlands adjacent to the town are seasonally flooded areas with mostly calcareous soils and secondary soils with a thick texture and strong sodic chemistry[20]. Compared to other wetlands on the Yucatan coast, the Sisal wetlands receive very little freshwater discharge, meaning that the soils are hypersaline with low nutrient concentrations[20]. All the samples were collected during the rainy season (August 2016). La Carbonera lagoon covers approximately 5 km^2, and is a convergence site for marine water from an inlet and freshwater upwellings and subterranean currents. These dynamics result in a wide variety of ecological niches providing resources for multiple fish and bird species.

Sample processing

Water and sediment samples were collected, placed in sterile containers, stored on ice and transported to the

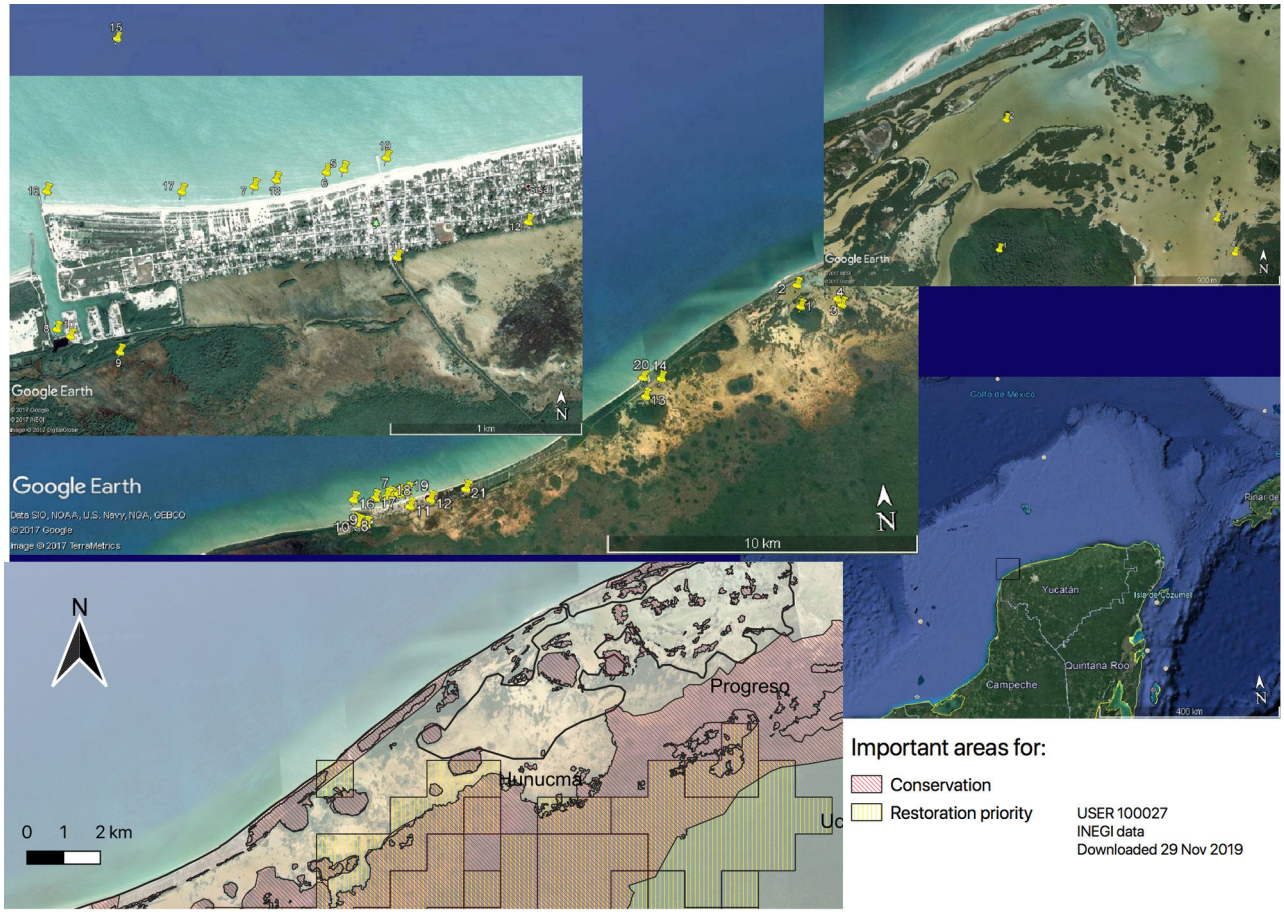

Figure 1 Study area and sampling points. According to official data from Mexico, there are priority areas for conservation and restoration in the wetland.

Ecogenomics laboratory (Universidad Nacional Autonoma de Mexico [UNAM], Sisal, Yucatan). From a total of 42 samples collected, 16 were from the coastline (sea), 12 from the wetlands, 12 from La Carbonera lagoon (including 6 from freshwater springs) and 2 from the open ocean at a depth of 10 m setoff (sea). Three-liter samples were taken in the open ocean and in the Sisal wetlands, while five-liter samples were taken at fresh water springs in La Carbonera lagoon. Sediment samples (50 ml) were collected in duplicate using 50 ml Falcon tubes, and carefully limited to the first 20–25 cm of sediment. Seven environmental parameters were measured at each collection site: temperature, oxygen concentration, pH, salinity, conductivity, dissolved solids and REDOX potential (556 Multiprobe System YSI). Water samples were filtered with a 0.45 μm pore filter in a Büchner-type filtration device. The filters were then stored (−20 °C) for later DNA extraction. Sediment samples were homogenized and a 0.5 g sample was placed in a 1.5 ml tube for later DNA extraction. Each sample was considered a replicate for each sampling site.

DNA extraction

DNA extraction was performed according to the protocol[34]. The DNA integrity was assessed by electrophoresis, quantification was performed using a fluorometer (Quantus™ Promega) and DNA quality was determined with a NanoDrop (Thermo Fisher Scientific).

DNA amplification and sequencing

High-fidelity Taq-polymerase (KAPA HiFi Ready Mix) was used to amplify the 16S region (V4–V5), with the following primers: Forward: 5′-TCGTCGGCAGCGTCGATGTGTATAAGAGACAG-3′; Reverse: 5′-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-3′.

The amplified fragments were sent to the National Biodiversity Genome Laboratory (Laboratorio Nacional de Genómica para la Biodiversidad – LANGEBIO, Irapuato, Guanajuato, Mexico). Libraries were prepared using the Nextera XT kit (Illumina, San Diego, CA, USA). The libraries were sequenced in a MiSeq (Illumina, San Diego, CA, USA) by pair-end read (2 × 300 pb).

Taxonomical and functional analysis

The quality control of the reads obtained from the sequencing of each sample was assessed using the FASTQC software. Subsequently, the reads with a quality value (Q) above 20 on the PHRED = 33 scale were selected with the Trimmomatic software.

Taxonomical identification of the sequenced reads was performed on the One Codex platform; this program compares a reading to the K-mer (31 bp sequences) of a database reference sequence and classifies it when the highest proportion of the 100% K-mer is attained[34]. This platform is highly accurate and contains 114 000 complete microbial genomes, including 62 000 distinct bacterial genomes, is constantly updated, and supported by the National Center for Biotechnology Information (NCBI). The sequences can be consulted in the supplementary material (Table S1).

The functional annotation was performed by processing the sequences using the Quantitative Insights In to Microbial Ecology program (QIIME, v1.8.0)[8]. The sequences were grouped using the UCLUST algorithm contained in QIIME, and the OTU assignment was performed using the GreenGenes database (gg_13_5_otus) with a 97% identity. The OTU table normalization was performed with the ''normalize_table.py'' algorithm contained in QIIME.

The OTU table obtained from QIIME was exported as a BIOM file for use in PICRUSt[33]; the copy number normalization was performed with the algorithm ''normalize_by_copy_number.py'' within PICRUSt. The metagenomic functional prediction was subsequently performed and the functions were annotated according to the Kyoto Encyclopedia of Genes and Genomes (KEEG) database terms[27].

Statistical analyses

Multivariate analyses and the Shannon index were performed using the Primer vs7 ecology statistics package to determine data distribution patterns. Abundance data transformation was performed ($\log x + 1$) prior to the multivariate analysis. Environmental parameters were standardized and normalized before the analysis. A cluster analysis was performed based on the similarity coefficient and an association distance matrix based on the Bray–Curtis index. A principal coordinate analysis (PCO), hierarchical cluster analysis (Cluster), matched resemblance matrices testing (RELATE), SIMPROF-test (similarity profile) were performed to evaluate graph similarities between samples, using bacterial communities at the genus level[4,10] and permutational multivariate analysis of variance (PERMANOVA)[3]. The following factors were considered: environment (lagoon, freshwater upwellings, sea and wetland) and sample (water and sediment). The SIMPER routine was applied to identify the environmental variables and taxonomic groups that contributed most to intersample similarity or dissimilarity. The abundance of pathogens and xenobiotic functions were represented graphically using a shade plot[9].

Results

The sequencing results produced a total of 9 284 199 reads, of which 8 407 670 were filtered ($Q \geq 30$). One Codex identified 7 652 798 reads (90.6%). A total of 2 009 543 reads (i.e. 23.9% of the filtered reads) were classified at the genus level.

A PCO and clustered analysis were performed taking into consideration all the identified genera in the One Codex database (Fig. 2). However, this analysis only explains 50% of the variance. The results of these analyses, along with the PERMANOVA (Table 1), indicate a statistically mean interaction, therefore the environmental differences depend on the sample type (water, sediment). In Figure 2, it can be observed that the differences among environments are greater in water samples, while in sediments there are minor differences. According to the RELATE analysis (Table 2), the results showed significant correlations with the sample type and environmental factors ($p < 0.001$).

Through SIMPER, 58.7% of differences were obtained among the water and sediment populations; more than 50% of these differences could be attributed to the 30 most abun-

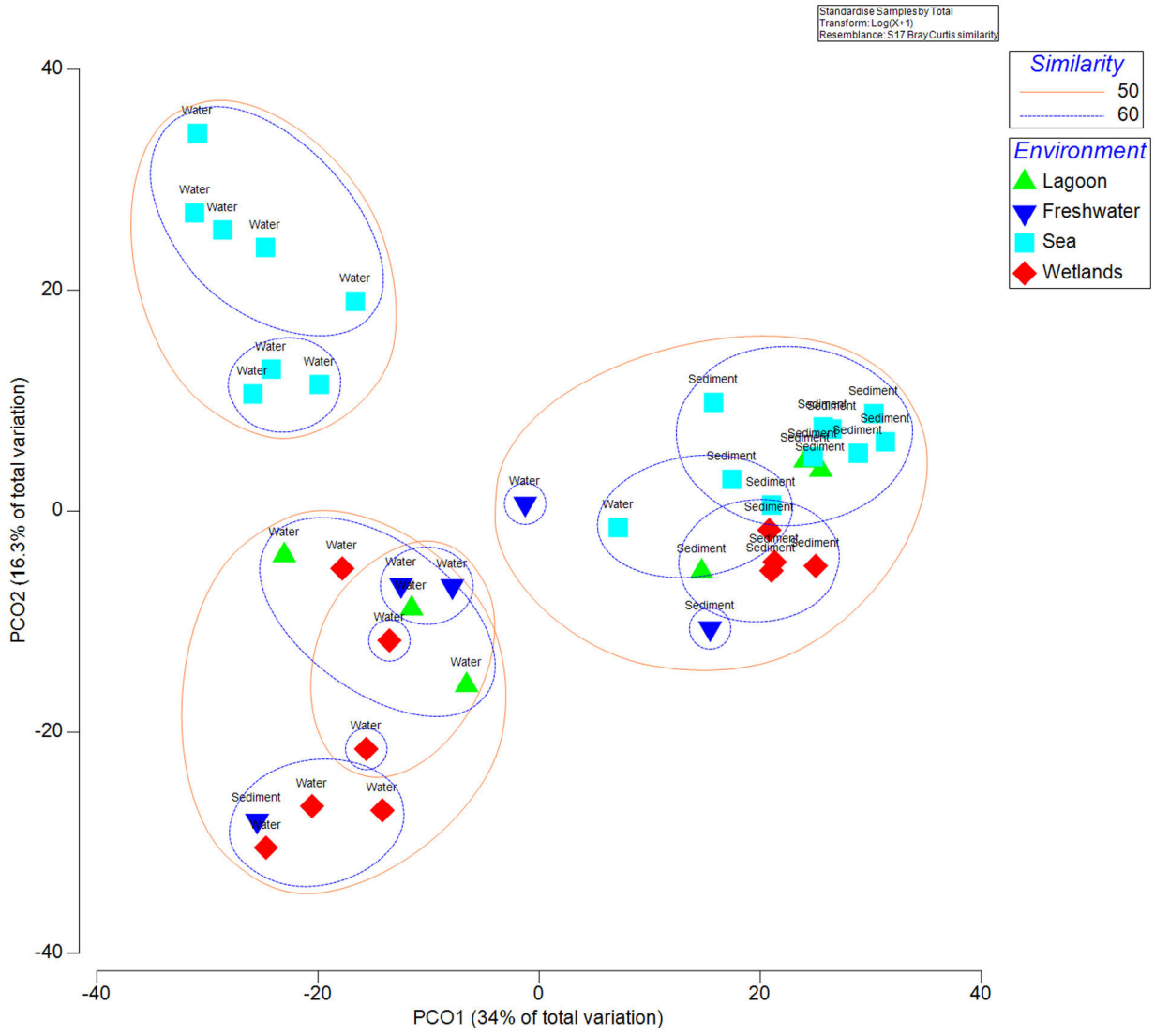

Figure 2 Principal coordinate analysis (PCO) between water and sediment in each environment. The samples correspond to the Bray–Curtis similarity based on hierarchically agglomerative clustering and the SIMPROF-test.

Table 1 Permutational multivariate analysis of variance (PERMANOVA) based on Bray–Curtis similarity, standardized and log + 1 transformed abundances of genera.

PERMANOVA						
Factor: Environment (En) fixed; Sample (Sa) random						
Source	df	SS	MS	Pseudo-F	P (perm)	Unique perms
En	3	9583.6	3194.5	1.1666	0.2936	7828
Sa	1	7645.5	7645.5	10.834	0.0001	9926
En * Sa	3	8214.7	2738.2	3.88	0.0001	9873
Res		21878	705.73			
Total		53710				

dant genera (supplementary material Table S2) according to the SIMPER results. It is noteworthy that most of the genera found in water were also found in sediments and vice versa; therefore, the differences mainly account for abundances, as can be seen in the supplementary material (Table S2) (difference ratio). In order to understand the subdivision formed in the water samples, a SIMPER analysis was conducted with the environmental parameters (conductivity, salinity, dissolved oxygen, temperature, pH and total dissolved solids).

Table 2 Testing matched resemblance matrices (RELATE) based on Bray–Curtis similarity, standardized and log + 1 transformed abundances of genera.

RELATE (correlation method Spearman rank)		
Within levels of factor	Environment	Sample
Sample statistic (average Rho)	0.549	0.671
Significance level of sample statistic	0.1%	0.1%
Number of permutations	999	999
Number of permuted statistic greater than or equal to Rho	0	0

The results showed that the similarities among the sea water samples mainly corresponded to the oxygen concentration in the water column. There is also a similarity among the lagoon water samples; where the contribution is also from the oxygen concentration. The freshwater samples showed differences, largely due the conductivity and pH. The wetland samples showed differences among themselves due to temperature and oxygen concentration. The differences between freshwater and lagoon samples are due to total dissolved solids, whereas the differences between freshwater and wetland samples are due to electric conductivity and total dissolved solids. When comparing freshwater and sea samples, the differences are attributed to three parameters: total dissolved solids, salinity and pH. Among the lagoon and wetland samples, temperature followed by oxygen concentration are the factors that account for the difference in these environments. The differences between wetlands and sea are due to oxygen concentration followed by temperature. The complete and more detailed results are shown in the supplementary material (Table S3).

Environmental analysis within the environments in the coastal area

The highest number of reads was registered in the sea samples followed by wetlands. With regard to the total average diversity, the highest number was found in the sediment samples of the wetlands (384 OTUs at the genus level and a Shannon index of 4.627), followed by lagoon sediments (381 OTUs at genus level and 4.625 Shannon index) and in third place the lagoon water samples (341 OTUs at the genus level and a Shannon index of 4.466).

Some of the identified phenotypes in the samples were: acidogenic–acetogenic bacteria, denitrifying bacteria, nitrogen fixing bacteria, carbon fixing bacteria, sulfate reducing bacteria (SRB), sulfur oxidizing bacteria (SOB), iron oxidizing bacteria (IOB), iron reducing bacteria (IRB), nitrate reducing bacteria (NRB), hydrogenophobic bacteria, polyphosphate accumulating organism (PAO), ammonium oxidizing bacteria (AOB), methanogen archaea, methanotrophic bacteria and methylotroph bacteria (supplementary material Table S4).

Some genera that are present only in one of the studied environments could be identified through the representation of results as presence and absence data. For example, in the lagoon samples the following genera were present: *Cladophialophora*, *Enterobacter*, *Enterorhabdus*, *Haemophilus*, *Holdemania*, *Kingella*, *Knoxdaviesia*, *Metarhizium*, *Niebella*, *Pantoea*, *Segniliarus*, *Selenomonas*, *Thiobacillus* and *Tolypocladium*. In the freshwater samples, *Chitinophaga*, *Edwardsiella*, *Isoprericola*, *Methylocystis*, *Phyllobacterium*, *Talassobacter*, *Talassospira* and *Yonghaparkia* were found only in these samples. In the sea samples, the only genera present were: *Actinokineospora*, *Aggregatibacter*, *Aminobacterium*, *Candidatus Riesia*, *Gallionella*, *Gorillibacterium*, *Halogeometricum*, *Klebsiella*, *Methanocella*, *Microbispora*, *Mitsuokella*, *Parvimonas*, *Serratia*, *Shigella*, *Streptacidiphilus*, *Trichoderma* and *Trichophyton* (*Actinoplanes*, *Agrobacterium*, *Borreliella*, *Desulfomicrobium*, *Dorea*, *Ensifer*, *Escherichia*, *Haloarcula*, *Halobacterium*, *Haloferax*, *Halolamina*, *Methanobacterium*, *Methanocaldococcus*, *Orientia*, *Plantibacter*, *Pseudocardia*, *Roseburia*, *Roseivivax*, *Sodalis*, *Sporomusa*, *Tatlockia*, *Terrabacter*, *Terriglobus*, *Thermodesulfovibrio* and *Thermofilum*).

Potential pathogens

The total number of reads revealed that 3–8% (Fig. 3) of them belonged to pathogens and etiological agents among the studied environments, according to bibliographic research. The highest percentage of pathogenic genera was found in the wetland samples (supplementary material Table S5). These findings are important given that in this coastal environment, crabs and other shellfish are typically consumed in this region. It is worth mentioning that most of these genera affect the human population, but also the presence of other pathogens that affect plants, animals, corals, ciliates and insects were found. The lowest number of described pathogenic genera was found in the sea samples; in this environment the highest relative abundance belonged to the *Vibrio* genus (more in water). In the lagoon samples the highest relative abundance at the genus level belonged to *Capnocytophaga* (more in water), in the freshwater samples the genera *Burkholderia* (more in water) and *Capnocytophaga* (more in water) showed high relative abundance; and in the wetlands *Arcobacter* and *Capnocytophaga* (more in water) showed high relative abundance.

Organisms with biotechnological capabilities (xenobiotic degradation, polyhydroxy alkane production (PHA) and medical relevance)

A bibliographic search was performed and several genera with described biotechnological capabilities were identified among the population present in the samples, which

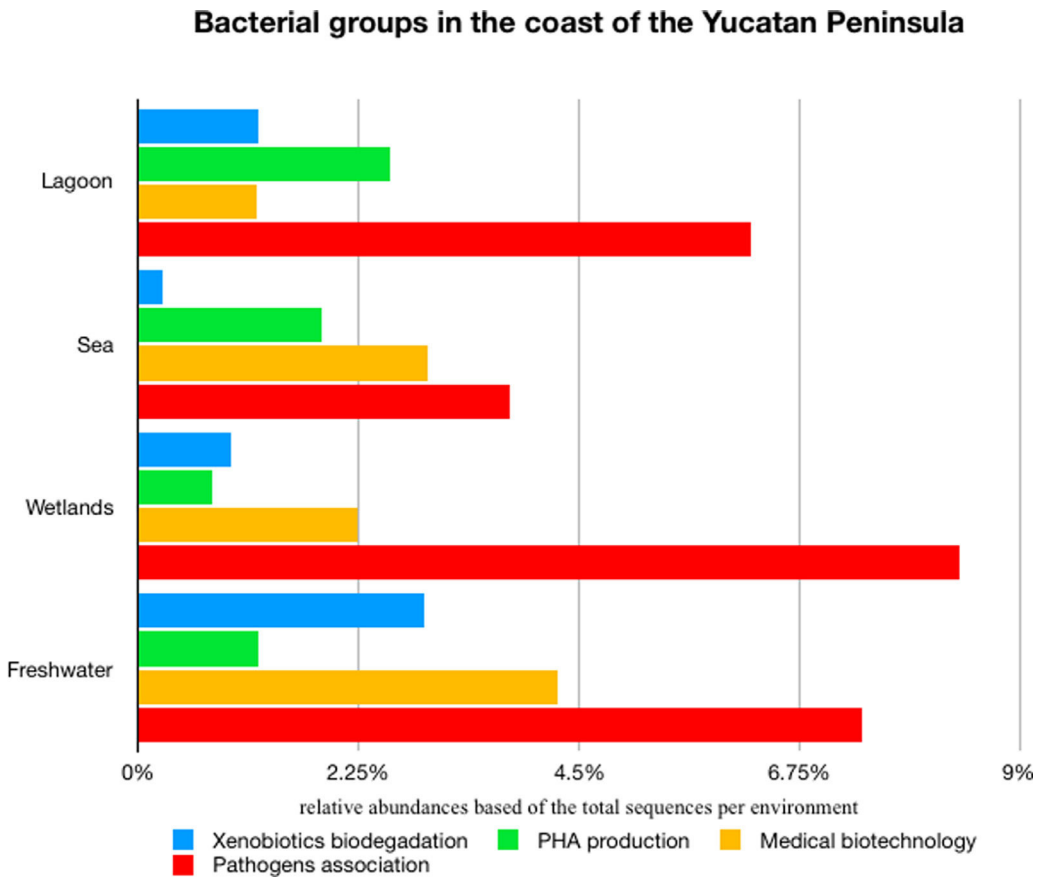

Figure 3 Relative abundances of the main bacterial groups in the Sisal coast Yucatan.

included genera attributed to the degradation of xenobiotic compounds other than hydrocarbons, genera related to the production of bacterial PHAs and several genera of great interest in medical biotechnology.

In the case of xenobiotics, 31 genera could be registered in the database of the organisms present among the different samples in the Yucatan coastal zone. The abundance of each genus was low; however, it should be noted that 3% of the total genus sequences in freshwater samples were associated with xenobiotic degradation (Fig. 3). In the case of the genus with the capabilities for producing PHAs, there is a record of 20 different genera, especially in the lagoon environment (3% of the total reads in this environment). A total of 59 genera with medical biotechnological relevance were found, mainly in freshwater (4% of the relative abundance) and sea (3% of the relative abundance) environments (Fig. 3).

Predicted metabolic functions related to pathogenesis and xenobiotic compound degradation

The metabolic functions other than those related to cell maintenance and metabolism were related to bacterial infections and the degradation of xenobiotic compounds (Fig. 4). Among the predicted functions, the degradation of benzoate, aminobenzoate, caprolactam and chloroalkane was the most represented. These results, along with the PERMANOVA analysis (degradation of xenobiotic compounds data, Table S6) showed a statistically significant interaction due the sample type (water, sediment).

Regarding the pathogenic associated functions, the presence of the several genera such as *Vibrio* (supplementary material Fig. S1A), *Bordetella* (supplementary material Fig. S1B) and *Helicobacter* (supplementary material Fig. S1C). The PERMANOVA analysis (pathogenic associated functions data, Table S7) did not show mean differences in the interaction; however, the sample type (water, sediment) is determinant in the differences. The function PCO is shown in the supplementary material (Fig. S2).

Discussion

In the exposed results, there is a clear difference among the samples which came from the water column and those who came from sediments. However, according to the results of the present study, the differences among the sampling matrices were related more to the abundances found. This indicates that the identification performed to the microbial community in the sands of the coastal zone of Yucatan is qualitatively similar to those present in the water column. Even permeable sand sediments (sea) showed similarity (50%) to the fine wetland and lagoon sediments due to the dominant populations; however, in each environment there are different minority populations.

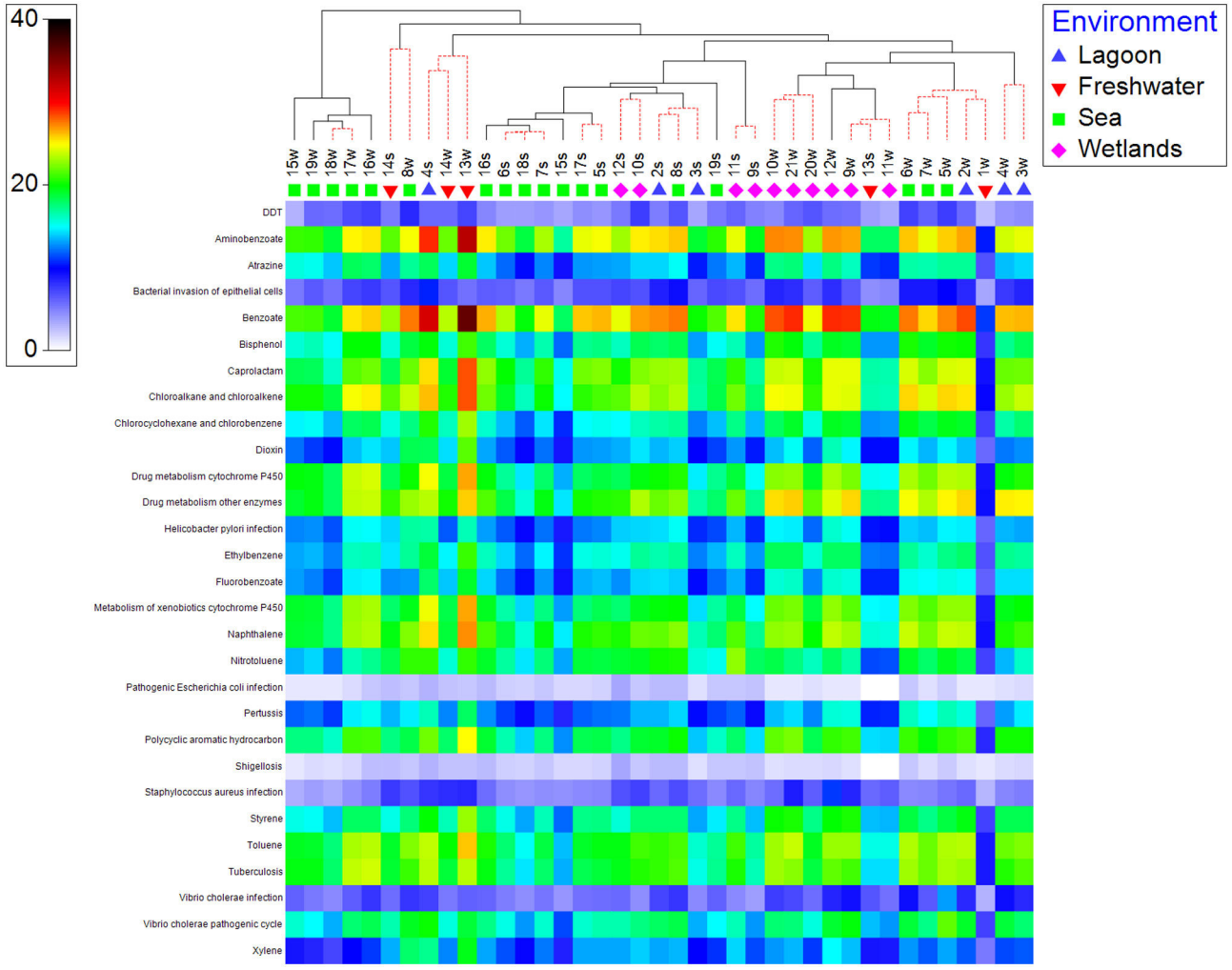

Figure 4 Shade plot of the samples (columns) according to the functional activities. The depth of spectrum shading is linearly proportional to the fourth root of the reads. The order of the samples corresponds to similarity based on a hierarchical agglomerative clustering and the SIMPROF-test. Water (w), sediment (s), numbers represent sampling points.

Previous studies conducted in population dynamics in sediments and water samples (freshwater and seawater) showed that the changes in the communities were not related to temperature changes, but instead the shifting salinity was the main factor for these changes among environments[17]. Similar observations were reported in coastal wetlands[28] and in a bibliographic report of coastal communities in Mexico by Torres-Alvarado et al.[40].

In freshwater and seawater environments, the main factor that propelled the changes in the bacterial communities were total dissolved solids, salt content, and pH. Salt content and pH are parameters with a strong correlation regarding the changes in bacterial communities in part of the coastal area of China[12,42]. Salinity is a crucial factor that impacts biogeochemical processes in the structures and activities of estuarine wetlands and microbial communities[42]. In this study the changes in salinity and pH agree with previous reports of coastal environments.

The similarities between the bacterial communities among the environments are largely related to oxygen concentration. In general, it could be said that the analyzed sediments shared the same microbial communities as those found in the water column, at phylum and class level, which differ from the results reported by Gobet et al.[17]. The differences among the results could be attributed to the fact that this study details the community at the genus level, whereas the current databases still lack more detailed environmental genus annotations.

Several studies have identified human pathogens in the waters of coastal areas[39]. In Mexico the studies of human pathogens in coastal areas are limited to those found in the General Law of Ecological Balance and Environment Protection (LGEEPA), therefore, there is no detailed information regarding the potential pathogens present in coastal areas in Mexico. Torres-Alvarado et al.[40], details the total content of fecal coliforms found in diverse zones within the Mexican coastal area.

The present results showed the presence of diverse potential pathogens as observed in bibliographic data, and also the functional prediction showed functions associated with pathogenic activity in a low proportion (less than 3%).

Thus a more detailed study regarding the pathogenic species and their viability could be of great importance.

Groups of putative pathogens associated with plastic contamination, such as *Vibrio* and *Pseudomonas*, have been found in marine water samples and other saltwater bodies around the world[24]. The high relative presence of *Vibrio* in the sea and wetland samples is important for public health. A study conducted on marine products from the Yucatan coastal area found 11 of the 12 species of *Vibrio* of clinical importance[30]. In another study that reported the detection of pathogenic bacteria in samples of fish for human consumption from the Yucatan Peninsula, the presence of *Vibrio*, *Pseudomonas* and other pathogens was found[23].

Recent studies related to *Vibrio cholerae* mention that associations with this pathogen are increasing and are among the most important emergent diseases associated with climate change[41]. The presence of the genera and the associated pathogenic functions found, could represent a potential risk in the studied area. Froelich and Daines[16], mention that the increase in the temperature and salinity are the main parameters in the concentration changes and the virulence rate in several *Vibrio* species in the water column and shellfish. Given the current environmental data, it could be recommended the continual screening of this pathogen in fishing and recreational areas.

According to official data from the Secretary of Health in its epidemiological bulletin[14] in Yucatan 17 675 cases were registered of gastrointestinal infections unrelated to *Salmonella* and *Shigella*, in addition to 73 967 cases of acute respiratory infections other than pulmonary tuberculosis, this makes necessary to propose more detailed studies, regarding these types of pathogens in the environment and their relationship with the registered health cases. Recent health reports from the Yucatan National Human Rights Commission, gastrointestinal and respiratory diseases were registered as the most prevalent conditions in the state[11]. The pathogenic bacteria described in this study and the most abundant, are related to both gastrointestinal conditions (*Arcobacter*, *Campylobacter*, *Vibrio*) as well as respiratory (*Acinetobacter*, *Burkholderia*, *Pseudomonas*) (supplementary material Table S5). Likewise, the results of this study with respect to the diseases reported in the graph of functions (Fig. 4) are detailed among gastrointestinal infections: *V. cholerae* infection, *Helicobacter pylori* infection, *Escherichia coli* infection and shigellosis. Among respiratory infections: tuberculosis, pertussis and *Staphylococcus aureus* infection are among the respiratory infections.

The *Mycobacterium* genus, which causes tuberculosis was found not only in the taxonomic description but also in the associated metabolic function, which highlights the relevance of studies with molecular techniques that provide important insights regarding the presence of potential environmental pathogens. In Mexico, tuberculosis is not only a lung disease, as cutaneous tuberculosis accounts for up to 2% of the extra-pulmonary forms of these disease[35]. Moreover, these pathogens can survive in inanimate objects for months[2].

The results found in this study could suggest potential risks for public health. Other pathogenic genera such as *Acinetobacter*, *Alcaligenes*, *Bacillus*, *Burkholderia*, *Comamonas*, *Pseudomonas* and *Vibrio* could develop other capacities of biotechnological use, such as those related to hydrocarbon degradation[34]. In the tables included in this manuscript, it was observed that bacterial genera with a diverse array of metabolic capacities, including those considered opportunistic pathogens, may be found in the coastal area. An important fact from the study area is the presence of pesticides (unpublished data) and other xenobiotics that have been found during the monitoring and observations conducted by the Sisal coastal observatory of LANRESC[19], which could be related to some genera mentioned in this manuscript. A recent study performed in the Sisal zone by Guillen-Chable et al.[18], has reported the presence of medicinal compounds (drugs), which agrees with the observations of this study (Fig. 4). The presence of this type of compounds could pose a health risk due the increase of drug resistance genes in the pathogenic population. It is worth mentioning that the presence of multi-resistant strains to antibiotics was found in the same study. Among the genera found in this study with species that have potential biomedical applications, we can mention *Alistipes* (mainly in sediment and present in other environments) which has been reported to have protecting characteristics against colitis[15] and *Cellulophaga* (marine sediment) which has potential as an antagonist to *Pseudomonas aeruginosa*[26], *Chondromyces* (mainly in sediment) which has been reported to have antibacterial, antifungal and cytotoxic activity, due a wide array of bioactive compounds with biomedical potential[43] and *Cohnella* (wetland sediment), genus described with potential for the thermostable chitinase production, a compound of interest in the biotechnology, biomedicine, agriculture and nutritional area[1]. Many of the bacterial communities at the genus level community were not identified.

Conclusions

Due to their distinctive characteristics, the coastal environments around the town of Sisal, Yucatan, Mexico are a substantial source of bacterial diversity. Most of the groups identified in the present study have been reported previously in marine environments. Bacterial diversity is similar between coastal environments, the differences depend on the communities present in water and sediment. pH and salinity are the factors among those analyzed that determine the differences found between environments. There is important similarity in the sediments across the different environments within the studied coastal zone. The differences between water and sediments are due to microbial abundances in dominant populations. This data constitutes a baseline for future studies in the region and will be vital to understand the biological processes occurring in these ecosystems.

Ethical approval

This article does not contain any studies conducted by the authors involving human participants or animals.

Data access statements

No new data were generated during the study.

Funding

The research reported here was financed (payment of sequences and field expenses) by the LANRESC-CONACyT 271544, CONACyT PN-212745 and PAPIIT-IT202418, and a CONACyT graduate studies scholarship (reference 258678).

Conflict of interest

The authors state that there is no conflict of interests (non-financial and no competing interests).

Acknowledgement

Technical assistance was provided by Dr. Joanna María Ortíz Alcántara.

Appendix A. Supplementary data

Supplementary data associated with this article can be found in the online version available at https://doi.org/10.1016/j.ram.2024.10.009.

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