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Bio-Corrosion, Sulfate-Reducing Bacteria in the Yucatan Peninsula

Ma Leticia Arena-Ortiz*, Muhilan Mahendhiran, Mariela Reyes-Sosa and Joanna Ortiz-Alcantara

Abstract

Microorganisms colonize the engineering materials and could damage them eventually. Sulfate reducing bacteria (SRB, hereafter) are responsible for corrosion in various metals such as carbon steel, stainless steel, iron and some alloys. Biocorrosion causes huge loss every year which causes various socio and economic complications. In anaerobic environments, SRB are active and thus microbiologically influenced corrosion (MIC) could occur. However, molecular mechanisms of MIC are less understood. Therefore, it is important to recognize the microorganisms at the molecular level and their mechanisms associated to biocorrosion, in order to reduce/prevent damages caused by these organisms. Also, the identification of various genera and species related to biocorrosion is needed. In this article, we determined the presence of SRB related to biocorrosion under anoxic conditions in the Yucatan Peninsula of Mexico. Water and sediment samples were collected from a total of twenty-one sampling sites coming under four environmental types (Freshwater upwelling's, Lagoon, Sea, Sea (Beach) and Wetlands) in Sisal Coastal region of Yucatan State in Mexico. Physicochemical parameters such as pH, salinity, dissolved oxygen, conductivity; total dissolved solids, redox potential and temperature were monitored in situ. 16S ribosomal RNA (rRNA) gene-based sequencing analysis showed that, out of 37 bacterial genera in SRB group, mainly eight anaerobic bacteria were present in both water and sediment samples including *Desulfatibacillum, Desulfatitalea, Desulfobacula, Desulfobulbus, Desulfotignum, Desulfotomaculum, Desulfovibrio* and *Sulfurospirillum.* Principal Component Analysis (PCA) showed that at least six variables were correlated between the selected sampling sites. Hierarchical Cluster Analysis (HCA) indicated a minimum of five groups of environmental variables, including outgroup and two major clusters. This is the first 16S rRNA gene sequence-based study of the presence of sulfate reducing bacteria which could cause biocorrosion in the Yucatan Peninsula of Mexico.

Keywords

16S ribosomal RNA (16S rRNA) gene sequencing; Sulfate-reducing bacteria (SRB), Anaerobe; Microbiologically influenced corrosion (MIC); Yucatan Peninsula; Mexico

Introduction

Corrosion is a chemical action or oxidation which could produce deterioration of the iron and steel. Anaerobic microorganisms endorse iron corrosion, consuming hydrogen as an electron donor from oil facilities [1]. Iron is usually unstable and easily affected by corrosion which could cause severe damages. Corrosion damages and protection measures result in losses of US $ 4 trillion per year all over the world, and also cause various socio-economic complications and human health problems [2-4]. In the Gulf of Mexico, most of the cases of major pipeline failures are caused by corrosion [5]. In industrial sectors, the inferred costs of metal corrosion affect the Gross domestic product (GDP) value of each country from 4% in developing/industrialized countries and 20% of total cost is because of microbial corrosion mechanisms [6,7].

Microbiologically influenced corrosion (MIC) is a serious threat to essential infrastructure in the steel and pipeline industries. In energy industries, microbiologically influenced corrosion in oil and gas pipelines is responsible for more than 20% of the total corrosion expense which could costs billions of dollars loss every year [8-10]. Anaerobic iron corrosion is one of the major devastating damages on infrastructure, such as oil and gas structures in pipeline systems, refineries and storage terminals [9,11,12]. The bacteria which reduce sulfate and iron are called sulfate reducing and iron reducing bacteria respectively [13]. The biocorrosion caused by Sulfate-reducing bacteria (SRB) has been studied over many years. Formation of iron sulfides (FeS) which could lead to iron corrosion by SRB might reduce corrosion in some cases, whereas increase in others [14,15]. Microbes grow on surfaces of various metals and accomplish various metabolic reactions which promote the deterioration of the substrate. Sulfate-reducing bacteria (SRB) causes biocorrosion under anoxic conditions and the activity of these bacteria in some cases creates serious environmental problems [14, 16]. However, their use under carefully controlled conditions could be beneficial, such as purposes both in domestic and industrial and saline wastewater treatment [17,18].

Sulfate reducing bacteria (SRB) are a ubiquitous group of anaerobic bacteria found in sulfate rich environments such as marine, estuarine, sewage, freshwater wetlands, humans and animals [19-21]. SRB are involved in geochemical carbon and sulfur cycles both in land and sea [22-24] and contribute to around 50% of organic matter mineralization in marine sediments [25,26]. These anaerobic bacteria also live in intestinal guts of various animals and humans causing severe damages [27,28]. In anerobic environments SRB performs dissimilatory sulfate reduction in order to obtain energy [29-31]. SRB release Hydrogen sulfide (H_2S) as the final product, after the reduction process of sulfate (electron acceptor) and utilize it for anaerobic respiration [32-34]; this H_2S is toxic, flammable, corrosive and also contributes to corrosion. Moreover, H_2S gas is a serious threat to human beings, transportation pipelines and production places [35] and damages the metals by increasing the iron sulfide concentration which could lead to an increase in the corrosion rate as well. SRB could utilize various organic electron donors for sulfate reduction; for example, *Desulfoluna butyratoxydans*, sulfate-reducing bacterial strain MSL71^T consume formate, butyrate, pyruvate, lactate, malate, ethanol, propanol, butanol, glycerol and H_2 [36]. SRB are also involved in anaerobic degradation of crude oil in sulfate-containing environments [37].

Sulfate-reducing bacteria are classified into five phylogenetic lineages, which consist of 220 species of 60 genera [38]. i)

***Corresponding author:** Ma Leticia Arena-Ortiz, Profesor Titular B, TC, Laboratorio de Estudios Ecogenómicos, UNAM, Parque Científico Tecnológico de Yucatán, Carretera Sierra Papacal-Chuburná, km 5.3 C.P. 97302, Yucatán, México, Tel: (999) 3410867, E-mail: leticia.arena@ciencias.unam.mx

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Desulfobulbus (all delta subgroup) and the genera *Desulfovibrio, Desulfobacterium, Desulfobacter* with mesophic proteobacterias [39], ii) thermophilic G-ve bacteria with the genus *Thermodesulfovibrio*, iii) G+ve *Peptococcaceae* with the genus *Desulfotomaculum*, iv) a genus of *Archaea* named *Archaeoglobus* (22) and v) finally thermophilic autotroph *Thermodesulfobium narugense* of the family *Thermodesulfobiaceae* [40].

The objective of this study was to identify the presence of sulfate-reducing bacteria (SRB) related to biocorrosion in different environmental samples in the Yucatan peninsula of Mexico.

Materials and Methods

Sampling sites

Water and sediment samples were collected from different sites (Freshwater upwellings, Lagoon, Sea, Sea (Beach) and Wetlands) at a total of twenty-one sites near the Sisal Port of Yucatan state in Mexico from March to May and in August 2016 (Table 1). Sampling points were geolocated using a GPS navigation device (Garmin, Olathe, KS, USA). Various physicochemical parameters were used to assess the water quality. Physicochemical data in water including pH, salinity, dissolved oxygen, conductivity, total dissolved solids, redox potential and temperature were collected in situ using a multiparameter probe (YSI, OH, USA, Table 1). Sediment samples were collected in duplicates (20 to 25 cm in depth) using a polypropylene corer of 18 mm diameter and one meter long. The samples were stored in sterile 50 mL conical tubes. Water samples were collected in sterile plastic bottles (3 to 5 L total per site). Samples were transported to the laboratory in an ice box. Pulled column water samples for each sampling site were filtered using a nitrocellulose membrane of 0.45 µm pore size (Millipore, Darmstadt, Germany). Sediment samples and water filters were stored at -20˚C until DNA extraction process.

DNA extraction and sequencing

Total DNA purification was performed with previously reported silica adsorption-based method [41]. DNA was confirmed in a 1% agarose gel, concentration and purity were evaluated using both NanoDrop 2000 (Thermo Scientific, Waltham, MA, USA) and Quantus Fluorometer and the Quantifluor dsDNA system (Promega Corporation, Madison WI, USA). 16S rRNA gene sequencing was performed in the Laboratorio Nacional de Genómica para la Biodiversidad (LANGEBIO, Irapuato, Gto., Mexico). Libraries were prepared using the Nextera XT kit (Illumina, San Diego, CA, USA) and sequenced in a MiSeq instrument (Illumina, San Diego, CA, USA) generating 2 × 300 paired-end reads.

Sequence data analysis

Paired reads were merged using PEAR v1.10.5 [42]. Merged reads were filtered using PRINSEQ-lite v0.20.4 [43], with Q_{20} as quality filter. Primers and adapters were removed using TagCleaner v0.16 [44]. FastQC v0.11.5 (Babraham Institute, UK) was used for quality assessment of raw reads and after the TagCleaner process. One Codex [45] was used for taxonomic assignment. A search to identify bacteria associated to biocorrosion according to previous reports was performed.

Statistical analyses

The physicochemical parameters obtained from environmental sampling sites were analyzed by Primer 6. The environmental variable data were uploaded and then transformed overall by square-root method. Subsequently, Principal Component Analysis (PCA) was performed from the databases of each site to find the correlation between environmental variables. Based on the variation percentage, the most sensible six variables were selected and multivariate analysis was done [46].

In order to find similarities between the samples, we constructed a resemblance matrix with the above-mentioned environmental variables using Primer 6. Subsequently, Hierarchical Cluster Analysis (HCA) of major components was performed [47].

Results

Microbiologically-influenced corrosion (MIC) or biocorrosion causes severe damages in oil and pipeline industries; the causal agent of this problem are Sulfate reducing bacteria [SRB; 14,48,49]. The production of sulfide is highly reactive, corrosive, toxic and causes environmental and economic impact [32,50,51]. In the present study SRB were widely found in both water and sediment samples in the Yucatan peninsula of Mexico. Physicochemical parameters measured in water are presented in Table 2.

Generally, SRB grow optimally in the pH range of 5.5-8.5 and inhabit temperatures that vary from 0 to 100˚C, with optimum temperature of 24-42˚C [38,52]. Although, some SRB like *Desulfonatronovibrio hydrogenovorans* and *Desulfonatronospira thiodismutans* can survive at pH>9.5 and pH<5 respectively [33,53,54]. However, at the time of sampling, the pH and temperature ranged from 6.90 to 9.02 and 25.0 to 35.04˚C respectively, except in one sample from wetlands (water sample 7) where the temperature of water was 78.33˚C, this place is near to the pipeline of the gas station of Sisal, Yucatan (Table 2).

In addition, other parameters such as oxygen percentage, oxygen concentration (mg/L), Redox potential, salt concentration,

Table 1: Samples and sampling sites used in this study.

No	Environment	Sample type (Water/ Sediment)	Location (GPS) North/West
1	Freshwater upwellings	Water	21˚13'8.2554'/89˚53'45.0954"
2	Lagoon	Water and sediment	21˚13'35"/89˚53'44"
3	Lagoon	Water and sediment	21˚13'15"/89˚52'58"
4	Lagoon	Water and sediment	21˚13'08"/89˚52'54"
5	Wetlands	Water and sediment	21˚09'33.7"/90˚02'51.4"
6	Wetlands	Water and sediment	21˚09'30.4"/90˚02'42.4"
7	Wetlands	Water and sediment	21˚09'46.8"/90˚01'52.2"
8	Wetlands	Water and sediment	21˚09'53"/90˚01'28.5"
9 (i)	Sea (Beach)	Water	21˚10'03.8"/90˚01'54.3"
9 (ii)	Sea (Beach)	Sediment	21˚10'03.8"/90˚01'55.9"
10	Sea (Beach)	Water and sediment	21˚10'0.5"/90˚02'1.8"
11	Sea (Beach)	Water and sediment	21˚09'59.7"/90˚02'04.6"
12	Sea (Beach)	Water and sediment	21˚09'59.9"/90˚02'14.3"
13	Sea (Beach)	Water and sediment	21˚09'57.9"/90˚02'18.0"
14	Sea (Beach)	Water and sediment	21˚09'57.8"/90˚02'31.4"
15	Sea (Beach)	Water and sediment	21˚09'57.7"/90˚02'55.9"
16	Sea	Water and sediment	21˚09'34.14"/90˚02'53.92"
17	Freshwater upwellings	Water and sediment	21˚11'24.7"/89˚57'09.2"
18	Freshwater upwellings	Water and sediment	21˚11'52.0"/89˚56'48.0"
19	Wetlands	Water	21˚10'02.1"/90˚00'47.8"
20	Wetlands	Water	21˚11'54.2"/89˚57'09.2"
21	Sea	Water and sediment	21˚20'08.36"/90˚08'08.61"

Table 2: Physicochemical properties of water in the sampling sites.

No	Environment	Oxygen (%)	Oxygen concentration (mg/L)	pH	Redox potential	Temperature (°C)	Salinity	Conductivity(mS/m)	Total dissolved solids (g/L)
1	Freshwater upwellings	4.7	0.35	7.41	77.3	26.64	1.76	3.47	2.19
2	Lagoon	86	5.25	8.67	69.9	31.10	36.03	61.07	35.55
3	Lagoon	109.4	6.4	8.83	33.9	33.3	38.42	67.22	37.72
4	Lagoon	136.5	7.78	9.02	-30.1	35.04	38.40	63.22	37.75
5	Wetlands	27.3	1.78	8.08	117.5	30.01	25.82	44.88	26.39
6	Wetlands	16.7	1.16	8.58	-36.2	26.91	25.76	38.92	24.41
7	Wetlands	51.5	3.61	8.71	-2.6	78.33	19.02	32.69	19.99
8	Wetlands	72.9	4.93	8.57	-94.5	30.32	19.72	35.02	20.69
9 (i)	Sea (Beach)	108	6.9	8.2	41.7	29.30	32.92	54.54	32.76
9 (ii)	Sea (Beach)	106	6.8	8.23	37.8	29.30	32.85	54.23	32.69
10	Sea (Beach)	95.8	5.87	8.46	63.9	30.59	36.57	61.35	36.01
11	Sea (Beach)	95.1	5.83	8.86	50.8	30.61	36.64	61.49	36.08
12	Sea (Beach)	142	9.2	8.16	No data	28.7	33.88	53.81	32.59
13	Sea (Beach)	98.8	6.0	8.57	72.5	30.65	36.59	61.41	36.06
14	Sea (Beach)	127	8.2	8.17	No data	28.7	32.98	54.00	32.82
15	Sea (Beach)	120	7.8	8.07	4.01	27.9	33.01	53.23	32.82
16	Sea	76.0	4.85	8.06	-25.8	29.83	32.46	54.20	32.35
17	Freshwater upwellings	29.0	2.2	6.99	85.3	25.2	2.22	34.47	2.22
18	Freshwater upwellings	4.0	0.3	6.90	67.0	25.0	25.0	63.57	4.13
19	Wetlands	44	3.0	8.12	166.5	30.2	16.51	29.80	17.62
20	Wetlands	107	6.1	8.53	100.6	33.3	36.10	63.52	35.68
21	Sea	109	8.6	8.02	35.5	26.1	32.57	50.88	32.37

conductivity (mS/m) and total dissolved solids (g/L) were shown (Table 2). Percentage of oxygen and oxygen concentration (mg/L) varied in different environments; from very low to high concentrations including Freshwater upwellings (0.3 mg/L) to lagoon (7.78 mg/L) and Sea (Beach; 9.2 mg/L). Salinity, conductivity and total dissolved solids were also presented (Table 2).

Among the five phylogenetic lineages of SRB [38,55], our 16S rRNA gene sequencing analysis showed that eight genera were identified in twenty-one sampling sites of environments such as Lagoon, Freshwater upwellings, Sea and Wetlands in both water and sediment samples; such as *Desulfatibacillum, Desulfatitalea, Desulfobacula, Desulfobulbus, Desulfotignum, Desulfotomaculum, Desulfovibrio* and *Sulfurospirillum* (Figure 1).

Each environment showed different abundance of reads for each genus. *Desulfatibacillum* reads were the most abundant, in lagoon and sea (Figure 1). *Desulfovibrio* reads were the most abundant in freshwater upwellings. In wetlands, the most abundant genera in sequencing reads were *Desulfotignum, Desulfovibrio* and *Desulfatibacilum. Sulfurospirillum* was the least abundant genus, in all the environments followed by *Desulfobacula* and *Desulfotomaculum*.

Desulfotomaculum spp are anaerobic, gram-positive, widely present, heat-resistant spore producing and very diverse in both phylogenetically and physiologically SRB [56-58]. *Desulfotomaculum* genus was widely found in our sampling sites, except lagoon (2w), wetlands (19w), wetlands (20w) and sea (21w). This genus is composed of 30 species and one subspecies [59]. In our samples, we have found *Desulfotomaculum nigrificans* species in just one sampling site (3w lagoon); in sediment samples it was found in two places in wetlands (5s) and sea (21s, data not shown).

Desulfovibrio sp. is a genus of SRB, gram negative, anaerobic bacteria, which create MIC in steel pipeline industries [9]. We have found *Desulfovibrio desulfuricans* ND132 in most of the sampling sites. *D. desulfuricans* species could be detected in soil, fresh water and salt marshes, environment, and human intestinal flora [60,61]. In our study, *Desulfovibrio* genus and its various species were found widely when compared with other genera. *Desulfovibrio alaskensis* was found both in the water and sediment samples from many sites (data not shown). *D. alaskensis* strains are related to petroleum industries [62], this strain might be found in contaminated petroleum regions through the Gulf of Mexico. Similarly, *D. alaskensis* G20 bacteria was isolated from a corrosion site of an oil well in Ventura Country, California [35].

In all twenty-one water sampling sites we have found *Thermodesulfobium narugense* DSM 14796 (*Thermodesulfobium* genus, data not shown). This *T. narugense* is an anerobic, acidophilic and thermophilic autotroph SRB species and classified under *Firmicutes* phylum [40,63], present in the water samples of Freshwater upwellings and in Lagoon. Species: *T. narugense* DSM 14796 is a strain type SRB that was previously isolated from Narugo hot spring of Miyagi, Japan (40). Whereas in sediment samples, *Desulfurobacterium sp.* TC5-1 was found only in Lagoon (2s). *Desulfobulbus sp. Tol-SR* is a species found in all the locations in sediments and in water samples as well (sea 21w, s).

A little variation has been found in water and sediment samples from the same sampling sites. Even at high temperature as 78.33°C, we have found all the eight genera of sulfate reducing bacteria in both water and sediment samples at one place, (Wetlands 7w, s; Table 2). Out of twenty-one sampling sites, we were not able to obtain any data sequences from three sampling sites, such as freshwater upwellings

(1s), wetlands (19s, 20s) in sediment samples. We could not obtain amplicons for the above-mentioned sediment samples, because they had not enough concentration of DNA. Therefore, we analyzed only 21 water samples and 18 sediment samples from distinct environments.

Principal Component Analysis (PCA) from the physicochemical parameters of environmental data sets. Out of eight variables, six were significative and thus considered as principal components, such as oxygen percentage, pH, Temperature, Salinity, Conductivity and Total dissolved solids (Figure 2 and Table 3). Percent variance (% var) and cumulative percent variance (Cum. %) contribution has been showed for each variable. However, the variable Total Dissolved Solids (TDS) g/L did not contribute to the percent variance in this statistical analysis. As indicated in Table 3, oxygen percentage was the principal component among all the variables with the highest percent variance (80.5%) followed by other components.

To complement PCA, a Hierarchical Clustering Analysis (HCA) was carried out (Figure 3) in search of a stricter division of groups, establishing similarities between environmental variables and thus

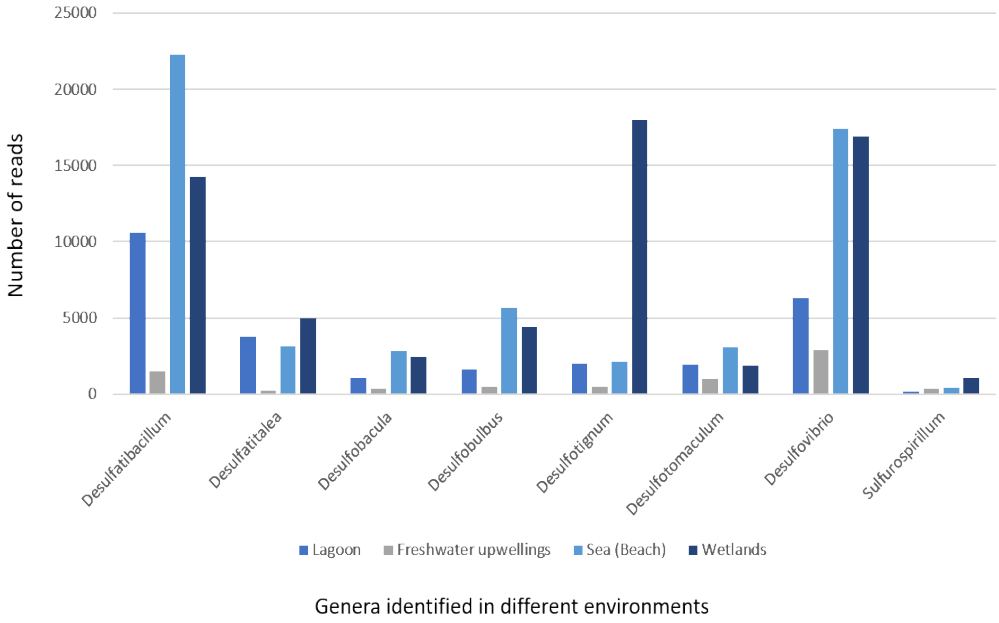

Figure 1: Presence of Sulfate Reducing bacteria (SRB) obtained from 16S rRNA gene sequencing reads from different environmental sampling sites.

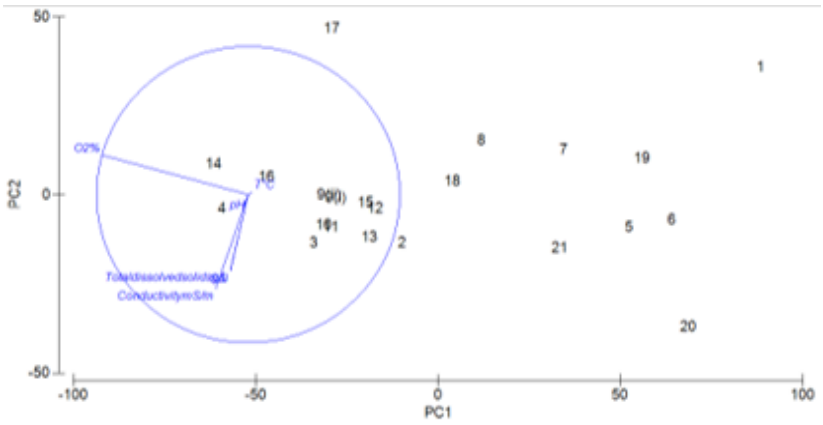

Figure 2: Principal Component Analysis (PCA) of environmental variables.

Table 3: Principal Component Analysis (PCA) of variables from environmental parameters.

No.	Principal Component (PC)	Eigenvalues	% variation	Cum % variation
1	Oxygen (O_2) %	1.96E3	80.5	80.5
2	pH	311	12.8	93.3
3	Temperature (T) ˚C	117	4.8	98.1
4	Salinity (ppm)	44.2	1.8	99.9
5	Conductivity (mS/m)	2.82	0.1	100.0

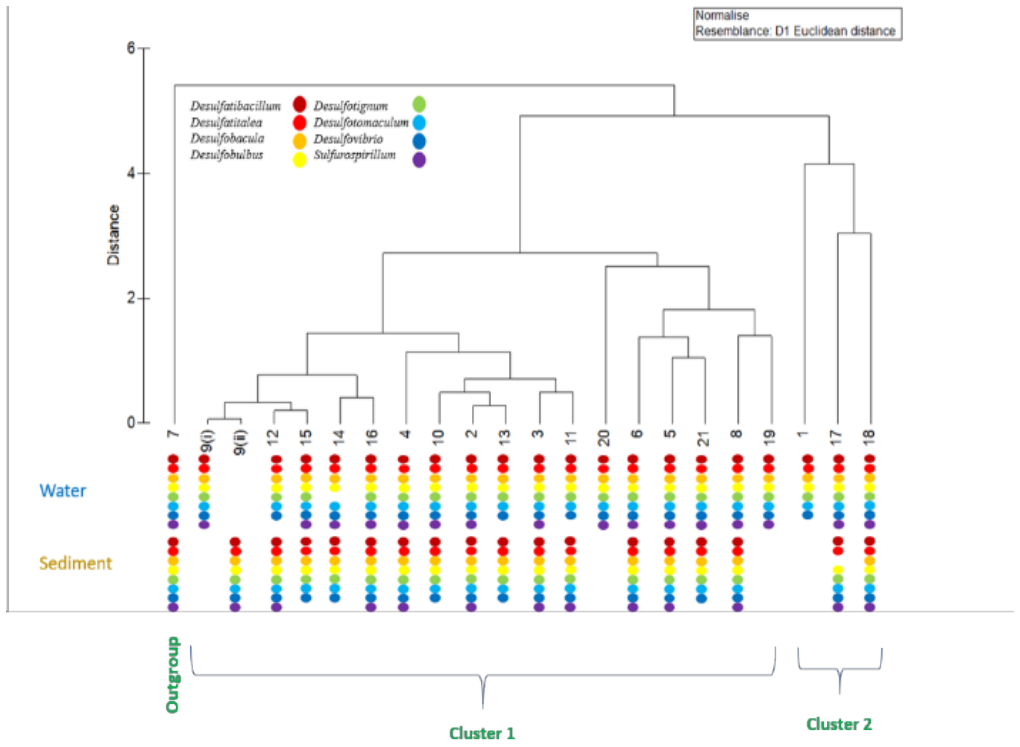

Figure 3: Hierarchical Cluster Analysis (HCA) of environmental samples (water and sediment) with physicochemical parameters.

facilitating the processing of information. HCA showed in Figure 3 that an out group and two major clusters, such as cluster 1 and cluster 2 were obtained. Out group sample (7 wetlands) was collected near to a gas station were the water level was very low. Thus, the temperature was the highest among all the sampling sites (78.33˚C).

Cluster 1 contained three sub-clusters such as sub-clusters 1, 2 and 3. Sub-cluster 1 contained beach and sea samples which had saline water. Sub-cluster 2 included lagoon and beach (sea) samples where salinity was higher. In, sub-cluster 3 most of the samples were from wetlands and just one from sea [21]. In wetlands, the salinity of the water was reduced due to rain fall and thus formed a separate sub-cluster.

Cluster 2 included samples 1, 17 and 18 from freshwater upwelling, where pH values and temperature were relatively low in comparison with other samples. The vegetation was abundant and thus reduced the heat in the ambient. In all the eight SRB genera, *Sulfurospirillum* was not found in some of the water [1,11-13] and sediment samples [10,14,15,21]. It is interesting that even at high temperature (78.33˚C) all the above-mentioned genera were found in both water and sediment samples. Overall, cluster 1 and cluster 2 contained salt water and freshwater respectively (Figure 3).

Thus, statistical analyses such as Principal Component Analysis (PCA) and Hierarchical Cluster Analysis (HCA) showed that samples could be grouped according to the physicochemical parameters measured in water. Eight SRB genera were found in most of the environmental water and sediment samples in all groups.

Discussion

Sulfate-reducing bacteria (SRB) have been considered as typical and ubiquitous in anaerobic environments and one of the most ancient prokaryotes [1,16,51,64]. In tropical mangrove, marine water and sediment samples the temperature is one of the key elements for the healthy microbial niche, metabolic activities and biogeochemical cycle such as carbon and sulfur in the environment [24,65]. Anoxic sulfate-rich environmental conditions such as sea water and ocean salt water promote the survival capacity of SRB. Whereas, in freshwater ambient, the anaerobic metabolic activity would go in minimal level [19]. In the present study, we showed the presence of Sulfate reducing bacteria related to biocorrosion in water and sediment samples from Sisal Port in the Yucatan Peninsula of Mexico.

Our study showed that the optimum temperature was available in most of the sampling sites and other physicochemical parameters also were optimum for the growth of the sulfate reducing bacterial population. Among all the eight genera of SRB present in the samples, *Desulfatibacillum* and *Desulfovibrio* were highly abundant in both water and sediment. The reason behind is that out of 37 bacterial genera in SRB group, *Desulfovibrio* genus is one of the most abundant, opportunists and the second largest in number of species containing genus illustrated as gram-negative bacteria [32,66-68]. In our samples we have found SRB genera such as *Desulfobulbus*, *Desulfotomaculum* and *Desulfovibrio* and their species in the sample next to the gas station according to 16S rRNA gene sequencing analysis; similarly, *Desulfovibrio, Desulfotignum* and *Thermodesulforhabdus* sulfate reducing microorganisms (SRM) including archaeal communities as *Archaeoglobus* genus were found in a high temperature petroleum reservoir by the combined approach of 16S rDNA and 16S rRNA high-throughput sequencing analysis [69]. All eight genera were found in water and sediment of almost all the sampling sites (both freshwater and salt water). Physicochemical parameters did not affect the presence of the bio-corrosion causing SRB in this study.

Laboratory conditions are not similar as in natural environments (Microbiologically-influenced corrosion) for SRB, though various studies have showed that it is possible to culture them under controlled experimental conditions. However, the limitations of the conventional microscopic and culture-based identification techniques allow only a little percentage (less than 1%) of bacteria of the total diversity to be isolated from nature [49,70-72]. Therefore, in this study, 16S rRNA gene sequencing has been used for the identification of sulfate reducing bacteria at the genus level.

Moreover, molecular biology techniques such as Fluorescent *in situ* hybridization (FISH), microarray DNA technology and functional gene markers such as Dissimilatory sulfite reductase (*dsr*AB) and adenosine phosphor sulfate reductase (*aps*A) sequencing analysis could be used for the identification and classification of SRB from different environments. *Dsr*, APS and *Apr* play important roles and act as the key enzymes of dissimilatory pathways such as sulfate reduction and sulfur oxidation [73]. Also, *dsr*AB, *aps*A and other key sulfate reduction genes are conserved in twenty-five [74]. Further studies are needed to understand the genes involved in biocorrosion mechanisms to control the bio-corrosion caused by Sulfate-reducing bacteria.

Molecular related technologies should develop in order to reduce and recover the huge loss in oil and pipeline industries. Apart from this, it is important to understand the complete mechanism of biocorrosion caused by these ancient bacteria. The dilucidation of the genome sequences of these potent microbes have played a positive role in both industrial and agro-health sectors. Moreover, the exploration of the abundant microorganisms in natural resources could lead to their conservation and a better understanding of their roles in ecological niches. To the best of our knowledge, this is the first 16S rRNA sequence-based report to identify the presence of Sulfate-reducing bacteria related to biocorrosion from environmental water and sediment in the Yucatan peninsula of Mexico.

Conclusion

As a conclusion, our study provides evidence of the presence of SRB in the Yucatan peninsula of Mexico, including the genera *Desulfatibacillum, Desulfatitalea, Desulfobacula, Desulfobulbus, Desulfotignum, Desulfotomaculum, Desulfovibrio* and *Sulfurospirillum* which might be involved in biocorrosion mechanisms in various environments. Further genetical and biochemical characterization of these microorganisms will be necessary to dilucidate their role in biocorrosion specifically in the environments studied.

Conflicts of Interest

The authors have declared that no competing interests exist.

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Author Affiliations

Top

Unidad Multidisciplinaria de Docencia e Investigación, Facultad de Ciencias, Universidad Nacional Autónoma de México, Puerto de abrigo s/n, Sisal, Yucatán, México