

Identification and the First Record of Marine bacteria Mudskippers *Boleophthalmus dussumieri* (Valenciennes, 1837) by 16S rRNA on the Northern Intertidal areas of Persian Gulf, Iran

nerssy nassirabady (✉ resaercherirany@yahoo.com)

Islamic Azad University Ahvaz Branch <https://orcid.org/0000-0001-7354-5640>

N. Negar Ghotbeddin

Islamic Azad University

Laleh Roomiani

Islamic Azad University

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Abstract

Background

Mudskipper is from the Gobiidae family and from the subfamily Oxudercinae. Mudskipper contains four main genera *Boleophthalmus*, *Periophthalmodon*, *Periophthalmus*, and *Scartelaos*. The aim of this research identification of bacterial agent (Marine bacteria) mudskippers *Boleophthalmus dussumieri* on the Shores of the northern intertidal areas of the Persian Gulf (Abadan, Hendijan and Bahrekan), Iran. The mud sediment and water samples (at the depth of one m), and mudskipper fish samples (near shore at the intertidal) were collected from Abadan, Hendijan and Bahrekan in northern coasts of the Persian Gulf, Iran.

Results

A total of 80 aerobic bacteria marine (from the intestines of mudskipper, seawater, and muddy sediments) was identified by biochemical tests and 16S rRNA gene sequence analysis. The bacteria's (Marine bacteria) [Eubacterium] tenue strain DSM 20695, *Praclostridium bifermentans* strain JCM 1386 and *Vibrio hyugaensis* strain 090810a was first identified in the northern intertidal areas of Persian Gulf, Iran.

Conclusions

Bacteria compete with other organisms to get oxygen to the surface layers of the flower bed. They give that the bacterial species common to the fish intestines and sediments is high and due to fish feeding of sediment it can be concluded that the species present in the fish intestine in the present study may be a function of substrate species that needs further studies to prove this.

Background

Mudskipper is widely distributed over the tropical, subtropical, Indian Ocean, western and eastern Atlantic habitats [1, 2]. Mudskippers completely different from fish because they are breathing on land and water [3]. Mudskipper is studied due to their high tolerance to environmental stressors, resistance to organic and inorganic contaminants [4]. These fishes are intimately relevant to mangrove forests in tropical and subtropical regions[5]. Mudskipper for biological studies, environmental, which is a biological indicator for assessing the environment of tropical and subtropical waters [6]. In terms of species distribution the global distribution of mudskipper is in mangrove ecosystems, mudflats in Africa, Madagascar, India's Bengal, South Asia, Northern Australia, southern Japan, mudflats in the Persian Gulf and the Gulf of Kuwait [7]. In contaminated coastal areas, these fishes have the potential for bioaccumulation of pollutants that are directly or indirectly related to human health because they are used in some areas [6]. Mudskipper is actively feeding on tidal habitats. In order to defend themselves, reproduce disturbance of habitat, these fish form channels in the mud. Changes in the habitat of mudskipper have a direct impact

on them, such as temperature, relative humidity, pH and contamination [8]. In this study, mudskipper was found in Intertidal mudflats Abadan, Hendijan, and Bahrekan, Persian Gulf, Iran.

The aim at this research identifies the bacterial agents (Marine bacteria) of *Boleophthalmus dussumieri* feed on the northern intertidal areas of Persian Gulf (Abadan, Hendijan, and Bahrakan), Iran.

Taxonomy Mudskipper *Boleophthalmus dussumieri*

The group presently includes 34 species in seven genera *Periophthalmus*, *Periophthalmodon*, *Boleophthalmus*, *Scartelaos*, *Pseudapocryptes*, *Zappa*, *Apocryptes* [9, 10].

Oxudercinae is sometimes classified inward the family Gobiidae. The new molecular subject does not back this classification [11]. All genera of Mudskipper are subfamily Oxudercinae. The Subfamily Oxudercini includes *Boleophthalmus* (5 species, Table 1) [1].

Table 1
Scientific Classification of *Boleophthalmus dussumieri*

Kingdom Animalia	Animalia
Phylum	Chordata
Superclass	Osteichthyes
Class	Actinopterygii
Superorder	Acanthopterygii
Order	Perciformes
Suborder	Gobiodei
Family	Gobiidae
Subfamily	Oxudercinae
Genus	<i>Boleophthalmus</i> (Valenciennes, 1837)
Species	<i>Boleophthalmus dussumieri</i> (Valenciennes, 1837)
Species	<i>Boleophthalmus birdsongi</i> (Murdy, 1989)
Species	<i>Boleophthalmus boddarti</i> (Pallas, 1770)
Species	<i>Boleophthalmus pectinirostris</i> (Linnaeus, 1758)
Species	<i>Boleophthalmus poti</i> (Polgar, Jaafar & Konstantinidis, 2013)

Species of *Boleophthalmus* (*B. dussumieri*) (Figure. 1) and *Periophthalmus* live in mudflat areas from the Persian Gulf to Pakistan (Murdy, 1989). Adults of all *Boleophthalmus* species typically live in open areas without vegetation in the lower Intertidal areas [12, 13].

Ecological Indicator-inorganic Pollution

Coastal waters widely receive pollutants, heavy metals, and sewage. To determine the effects of heavy metal concentrations, bacterial determinants of fish health, monitoring of coastal contamination of mudskipper are examined. The mudskippers accumulate heavy metals in their gills, skin, liver and also in the digestive system [14].

Materials And Methods

Sample Sites

Bacteria were found in the mud at depths exceeding two meters but most of the samples which were collected for analysis were from the topmost 20 cm. of mud (n = 25, the zone of maximum bacterial activity), water (n = 25) and mudskipper fish (n = 25) samples were collected from different parts 1 m depth, and about 100 m away from the seashore of four-point and mudskipper fish samples (nearshore at the intertidal) including Abadan, Arvand Kenar (30°03'0.00" N, 48°28'0.01" E), Hendijan (30°13'60.00" N, 49°42'59.99" E), Bahrakan

(30° 6' 43.2 66" N, 49° 46' 9.519" E) in Khuzestan Province (Fig. 2), north of Persian Gulf, Iran in April to June 2019.

Extraction of genomic DNA and PCR

A modified method of [15] including thawing and freezing step was applied for environmental bacteria DNA extraction. PCR product concentration on the reaction, 25 µl of the reaction was as follows: 0.5 µl dNTPs, 1X PCR buffer, 0.75 µl MgCl₂, 1.5 U *Taq* polymerase (Gen Favaran, Iran) and 0.25 µl of each forward and reverse primers. Total volume by adding sterile distilled water to 25 µL. Following PCR conditions was employed: 94 °C for 4 min, followed by 30 cycles of 94 °C for 1 min, 68 °C for 2 min and 72 °C for 1 min, with final 7 min extension at 72 °C. In amplifications involving environmental DNA, the mentioned PCR conditioned varied from different annealing temperatures (48–60 °C). The PCR products of the expected size (1500 bp) were gel- purified DNA extraction .

Primers 27F: 5'-AGAGTTTGATCCTGGCTCAG-3', Primers 1392R: 5'-GGTTACCTTGTTACGACTT-3'

Sequence analysis

The sequencing was performed by Gen. Fanavaran Company in Tehran, Iran. The

16S rRNA general of isolates was sequenced directly. Relevant sequences were extracted from Gen Bank using BLASTN [16]. When a pure PCR product of the 16S rRNA gene is obtained (Fig. 3), sequence, and aligned against the bacterial DNA database, then the bacterium can be identified.

Results And Discussion

5.1. A study on morphology fish mudskippers *Boleophthalmus dussumieri*

Based on the results, the mean length of fish species mudskippers *B. dussumieri*

at the stations of Abadan, Hendijan and Bahrekan respectively $13.685 \pm .903$, $16.551 \pm .724$ and $16.595 \pm .993$. The highest average total length is at Bahrekan station and the lowest are at Abadan station. The mean total length of *B. dussumieri* Abadan showed significant difference between Bahrikan and in Hendijan ($P < 0/05$), but there was no significant difference between Hendijan and Bhrekan ($P > .05$).

Average total weight of fish species mudskippers *B. dussumieri* at the stations of Abadan, Hindijan and Bahrekan respectively 8.660 ± 1.956 , 16.671 ± 2.937 and 16.678 ± 2.910 . The highest average total weight was obtained for Bahrekan station and the lowest for Abadan station. The mean total weight of *B. dussumieri* Abadan was significantly different from that of Bahrekan and Hendijan ($P < 0/05$), but there was no significant difference between Hendijan and Bahrekan ($P > .05$) (Table 2).

Table 2
Total length and total weight of species *B. dussumieri*

Region	Number	Standard deviation \pm Average total length	Standard deviation \pm Average total weight
Abadan	25 ^a	$.903 \pm 13.685$ ^a	8.660 ± 1.956
Hendijan	25 ^b	$16.551 \pm .724$ ^b	16.671 ± 2.937
Bahrekan	25 ^b	$16.595 \pm .993$ ^b	16.678 ± 2.910
a : $p > 0/05$, b : $p < 0/05$			

Isolation bacteria of mudflats, Mudskipper and Water sea

Bacterial characterization Based on morphology, chemical techniques, different techniques of cell biology, and Gram staining was done .

Biochemical tests used in this study were as follows: carbohydrate fermentation includes galactose, maltose, mannitol, sucrose, and arabinose, Simmons ' Citrate, MRVP (Methyl Red, Voges-Proskauer), indole, nitrate reduction, gelatinize, ureas, oxidase, catalase, TSI (Triple sugar iron agar) and LIA (lysine iron agar). The capability of growing on TCBS (Thiosulfate-citrate-bile salts-sucrose) agar medium was also tested to meet the nutritional requirements of *Vibrio spp*, as an important genus of light-producing bacteria. Molecular analysis was performed based on the 16S rRNA gene to confirm the identification of the bacterial strains isolated from fish, mud, and seawater (Table 3–6) .

Table 3

16S rRNA all species marine bacteria identification for isolates of areas Study (Abadan, Hendijan, and Bahrekan), Persian Gulf, Iran

No. of isolates	Sampling area	Closest identified species	Percent Identity (%)
1	Muddy sediments	<i>Zobellella denitrificans</i> strain YR3	95.85
2	Muddy sediments	<i>Bacillus sp.</i> BD59S	99.52
3	Muddy sediments	<i>Bacillus licheniformis</i> strain 2J-4	98.06
4	Muddy sediments	<i>Bacillus megaterium</i> strain NCT-2	99.41
5	Muddy sediments	<i>Vibrio metschnikovii</i> strain Vm-4	95.96
12	Muddy sediments/Mudskipper intestine	[<i>Eubacterium</i>] tenue strain DSM 20695]	99.45
16	Muddy sediments	<i>Vibrio parahaemolyticus</i> strain AMI-4	91.38
17	Muddy sediments/Mudskipper intestine	<i>Praclostridium bifermentans</i> strain JCM 1386	97.09
21	Muddy sediments	<i>Bacillus subtilis</i> strain OTG010	99.52
22	Muddy sediments	<i>Brevibacillus brevis</i> strain NCTC2611	99.15
23	Muddy sediments	<i>Bacillus thuringiensis</i> strain B11	97.72
24	Muddy sediments	<i>Lactobacillus rhamnosus</i> strain SCT-10-10-60	96.52
25	Muddy sediments	<i>Bacillus subtilis</i> L1	96.71
26	Muddy sediments	<i>Bacillus wiedmannii</i> bv. <i>Thuringiensis</i> strain FCC41	96.52
35	Water sea	<i>Vibrio harveyi</i> strain AHH C3	99.51
38	Water sea	<i>Vibrio alginolyticus</i> strain 13 - 2	99.41
40	Water sea	<i>Vibrio parahaemolyticus</i> strain B2-1	97.14
41	Water sea	<i>Vibrio alginolyticus</i> strain PC14	94.98
42	Water sea	<i>Vibrio sp.</i> strain mm4	88.69
43	Water sea	<i>Vibrio parahaemolyticus</i> strain B4-4	98.40
44	Muddy sediments	<i>Vibrio alginolyticus</i> strain B4-1	97.90
45	Muddy sediments	<i>Vibrio sp.</i> strain 201707CJKOP-Y201	98.52

No. of isolates	Sampling area	Closest identified species	Percent Identity (%)
46	Water sea	<i>Vibrio metschnikovii</i> strain DL 33–51	97.52
48	Muddy sediments	<i>Vibrio alginolyticus</i> strain Val180620	95.44
50	Muddy sediments	<i>Vibrio alginolyticus</i> strain B3-2	96.11
51	Muddy sediments	<i>Shewanella chilikensis</i> strain 0066	96.10
52	Water sea / Muddy sediments	<i>Photobacterium damsela</i> strain 1PP/SRLAAH/2018	99.23
61	Water sea	<i>Aliivibrio salmonicida</i> strain VS224	98.51
62	Muddy sediments	<i>Vibrio parahaemolyticus</i> strain NIORKP 190	92.24
66	Water sea	<i>Vibrio owensii</i> Strain UMTGB203	98.08
67	Water sea	<i>Vibrio parahaemolyticus</i> strain AP 167	91.73
72	Water sea	<i>Vibrio sp.</i> Strain SAOS-24 MA	96.03
73	Muddy sediments/Mudskipper intestine	<i>Vibrio hyugaensis</i> strain 090810a	98.56

Table 4
Identification marine bacteria with 16S rRNA Sequence from intestines mudskippers *Boleophthalmus dussumieri* in the present study

Species Bacteria	Sampling stations		
	Abadan	Bahrekan	Hendijan
<i>Enterobacter cloacae</i>	*	*	*
<i>Citrobacter sp.</i>	*	*	*
<i>Enterobacter sp.</i>	*	*	*
[<i>Eubacterium</i>] tenue strain DSM 20695]	-	*	*
<i>Praclostridium bifementans</i> strain JCM 1386	-	*	*
<i>Vibrio hyugaensis</i> strain 090810a	-	*	*

Table 5
 Identification marine bacteria with 16S rRNA Sequence from muddy sediments in the present study

Species Bacteria	Sampling stations		
	Abadan	Hendijan	bahekan
<i>Vibrio harveyi</i> strain AHH C3	*	*	*
<i>Shewanella chilikensis</i> strain 0066	-	*	*
<i>Zobellella denitrificans</i> strain YR3	-	*	*
<i>Bacillus</i> sp. BD59S	-	*	*
<i>Bacillus</i> sp. (in: Bacteria) strain HA	-	*	*
<i>Bacillus licheniformis</i> strain 2J-4	-	*	*
<i>Bacillus megaterium</i> strain NCT-2	-	*	*
<i>Bacillus wiedmannii</i> bv. <i>Thuringiensis</i> strain FCC41	-	*	*
<i>Vibrio parahaemolyticus</i> strain AMI-4	-	*	*
[Eubacterium] tenue strain DSM 20695]	-	-	*
<i>Brevibacillus brevis</i> strain NCTC2611	-	-	*
<i>Bacillus thuringiensis</i> strain B11	-	-	*
<i>Lactobacillus rhamnosus</i> strain SCT-10-10-60	-	-	*
<i>Bacillus subtilis</i> L1	-	-	*
<i>Vibrio alginolyticus</i> strain B4-1	-	-	*
<i>Vibrio</i> sp. strain 201707CJKOP-Y201	-	-	*
<i>Vibrio parahaemolyticus</i> strain B4-4	-	-	*
<i>Vibrio alginolyticus</i> strain Val180620	-	-	*
<i>Vibrio alginolyticus</i> strain B3-2	-	-	*
<i>Vibrio</i> sp. M12-1181	-	-	*
<i>Vibrio hyugaensis</i> strain 090810a	-	*	*
<i>Praclostridium bifermentans</i> strain JCM 1386	-	*	*

Table 6

Identification marine bacteria with 16S rRNA Sequence from Water Sea in the present study

Species Bacteria	Sampling stations		
	Abadan	Hendijan	Bahrekan
<i>Vibrio harveyi</i> strain AHH C3	*	*	*
<i>Vibrio parahaemolyticus</i> strain B2-1	*	-	-
<i>Vibrio parahaemolyticus</i> strain B4-4	*	-	-
<i>Potobacterium damselae</i> strain 1PP/SRLAAH/2018	-	-	*
<i>Vibrio alginolyticus</i> strain 13 - 2	-	*	-
<i>Vibrio alginolyticus</i> strain PC14	-	*	-
<i>Vibrio sp.</i> strain mm4	-	*	-
<i>Vibrio sp.</i> Strain SAOS-24 MA	-	*	-
<i>Vibrio metschnikovii</i> strain DL 33-51	-	-	*
<i>Vibrio owensii</i> Strain UMTGB203	-	-	*
<i>Vibrio parahaemolyticus</i> strain AP 167	-	-	*

Marine environments are home to a variety of bacteria species. This is because of the conditions in marine systems, which are neither selective nor inhibitory to specific groups of microorganisms. Marine ecosystems contain many microbes. This is because of the conditions in marine systems, which are neither selective nor to groups of very tiny living things. The three species of mudskipper (*Boleophthalmus dussumieri*, *Periophthalmus waltoni*, *Scartelaos tenuis*) throughout the Persian Gulf are of high ecological value. This study was conducted to identify the bacterial agents of *Boleophthalmus dussumieri*, as well as water pathogens and mud sediments in Abadan, Hendijan and Bahrekan coastal regions of Khuzestan province, Iran. According to the results of the present study, bacterial species in the gut of mudskipper fish in the Abadan region were 3 species, Handijan 6 species, and Bahrekan 6 species. *Enterobacter cloacae*, *Citrobacter sp.*, *Enterobacter sp.* It was observed in all three regions.

Enterobacter cloacae, *Citrobacter sp.*, *Enterobacter sp.*, [Eubacterium] tenue strain DSM 20695], *Praclostridium bifermentans* strain JCM 1386 and *Vibrio hyugaensis* strain 090810a in Hendijan only, *Enterobacter cloacae*, *Enterobacter sp.* Only in Abadan and *Enterobacter cloacae*, *Citrobacter sp.*, *Enterobacter sp.*, *Vibrio hyugaensis* strain 090810a, [Eubacterium] tenue strain DSM 20695], and *Praclostridium bifermentans* strain JCM 1386 were observed only in the Bahrekan. Bacteria were also commonly (*Enterobacter cloacae*, *Citrobacter sp.*, *Enterobacter sp.*) found in Abadan, Hendijan and Bahrekan, Iran.

Most species were gram-negative bacteria in Abadan, gram-negative bacteria and unknown bacteria in Hendijan, and gram-negative bacteria and unknown bacteria in Bahrekan.

Investigation of bacterial contamination of five species of marine fishes *Otolithes ruber*, *Epinephelus coioides*, *Acanthopagrus cuvieri*, *Latjanus malabaricus* and *Pampus argenteus* distribution in Ahvaz and Abadan markets (Khuzestan, Iran). The results showed that fish skin tested for 45/3% had the highest bacterial contamination, then head in the second and third finned fish was contaminated with 24%. Species of bacteria isolated from these species include: *Aeromonas sobri*, *Aeromonas spp.*, *Aeromonas hydrophila*, *Pseudomonas spp.*, *Staphylococcus aureus*, *Acinetobacter lowffii*, *Enterococcus spp.*, *Enterobacter spp.*, *Escherichia coli*. *Aeromonas* species by 17/4% the most abundant bacteria in this study. Then the *Pseudomonas* was next. The least of *Enterococcus* bacteria by 1/3% [17]. The family of bacteria identified with the present study did not match.

Countless species of Gram-negative bacteria species including *Acinetobacter* ☒ *Aeromonas*, *Citrobacter*, *Flavobacterium*, *Pseudomonas* and *Vibrio* and Gram-positive bacteria *Corynebacterium* ☒ *Bacillus* ☐ *Micrococcus* and *Staphylococcus* from Kerry Fish in freshwater [18], isolates as in the present study *Citrobacter* In the intestine of the mudskipper was found in all three regions and also *Vibrio* and Gram-positive bacteria including *Bacillus* were found in mud sediments in the study areas.

Epidermal mucosa in mudskipper contains various bioactive compounds that play an important role in its defense mechanisms. This mucus has antibacterial activity. Fish mucus as a physical barrier by preventing mechanical absorption, no access to parasites, bacteria or viruses [19], the ability to precipitate heavy metals, contributes to the secretion of immunoglobulin [20], and it has the mechanism of electrolyte diffusion in the presence of chloride cells [21]. However, the biochemical and pharmacological effects of mudskipper are not well investigated .

Aguirre et al, 2004, They reported that in the wild fish, bivalves and crustaceans in saline and brackish waters of the species *Vibrio anguillarum* cause a deadly septicemia called vibrioses [22].

Using DNA and 16S rDNA hybridization technology to simultaneously detect eight fish pathogens including *Aeromonas hydrophila*, *Edwardsiella tarda*, *Flavobacterium columnare*, *Lactococcus garvieae*, *Photobacterium damsela*, *Pseudomonas anguilliseptica*, *Streptococcus iniae*, and *Vibrio anguillarum*, commonly identified with aquaculture. The results showed that of the 168 bacterial strains, 81 were fish-related pathogens and 61 strains were related to ecological or phylogenetic factors [23], most of which belonged to the *Vibrionaceae* family, which is consistent with the present study. In the present study 2019, 14 species of *Vibrionaceae* family were isolated from mud and seawater substrates in the study area, in the *Vibrio harveyi* strain AHH C3 muddy Abadan, *Vibrio parahaemolyticus* strain AMI-4 muddy Hendijan and *Vibrio harveyi* strain AHH C3, *Vibrio parahaemolyticus* strain AMI-4, *Vibrio alginolyticus* strain B4-1, *Vibrio sp.* strain 201707CJKOP-Y201, *Vibrio parahaemolyticus* strain B4-4, *Vibrio alginolyticus* strain B3-2 and *Vibrio sp.* M12-1181 Were muddy Bahrakan. From the *Vibrionaceae* family in the present study on seawater in the Abadan area (Arvand Kenar) *Vibrio harveyi* strain AHH C3, *Vibrio parahaemolyticus* strain B4-4, *Vibrio parahaemolyticus* strain B2-1 and in the Hendijan area *Vibrio alginolyticus* strain 13 - 2,

Vibrio harveyi strain AHH C3, *Vibrio sp.* strain mm4, *Vibrio alginolyticus* strain PC14, and *Vibrio sp.* Strain SAOS-24 MA and in the Bahraikan area (fishing dock) *Vibrio harveyi* strain AHH C3 Found.

The most important bacterial diseases include vibriosis, photobacteriosis, furunculosis, marine flexibacteriosis, pseudomonadiosis, streptococciosis, mycobacteriosis, edwardsiellosis and yersiniaosis Which is developing rapidly in the fish farming industry [24]. In the present study, *Vibrio*, *Photobacterium*, and *Bacillus* bacteria were found, which is consistent with the above research.

According to the results of this study, bacterial species in seawater and mud sediments in the Abadan area were 5 species, Hendijan 15 species, and Bahrekan 27 species. Specie

Vibrio harveyi strain AHH C3 and *Vibrio parahaemolyticus* strain B4-4 it was observed in all three regions. Species *Vibrio harveyi* strain AHH C3 only in Hendijan, and species

Vibrio harveyi strain AHH C3 and *Vibrio parahaemolyticus* strain B4-4 only in Abadan, and species *Vibrio harveyi* strain AHH C3 only in Bahrekan were observed. Species

Vibrio harveyi strain AHH C3 common in the Abadan and Bahrekan region, and species *Vibrio harveyi* strain AHH C3 common in Abadan and Hendijan area and *Vibrio harveyi* strain AHH C3 common were observed in Hendijan and Bahrekan. Most species in all three regions were Gram-negative bacteria.

Microbial Community Composition of Wadden Sea Sediments as Revealed by Fluorescence In Situ Hybridization. The results showed that approximately 45% of all bacteria belonged to the cytofaga-flavobacterium branch. The members of this branch were the most abundant in all layers, after which the sulfated bacteria were the most abundant [25], which was not consistent with the above study.

Spatial and Temporal Variation of Phenanthrene-Degrading Bacteria in Intertidal Sediments. The results showed that out of 432 bacteria isolated, 68 groups were similar to *Vibrio* and *Pseudomonas* in the same level (approximately 70%) [26], which was consistent with the above study in *Vibrio* genus only.

Bacterial biodiversity and total number of cultivable bacteria in the tidal zone of the northern coast of the Persian Gulf. The results showed that there is a relatively high number of bacterial populations of the Persian Gulf water and sediments. By morphological and biochemical studies as well as determination of the percentage of guanine and cytosine DNA, Members of the genera *Pseudomonas*, *Vibrio*, *Altromonas*, *Flavobacterium*, *Bacillus*, *Mycobacterium*, and *Alcaligens* were identified [27], which is consistent with the above study.

The Diverse Bacterial Community in Intertidal, Anaerobic Sediments at Sapelo Island, Georgia. The results showed that 99% of the bacterial population had sequence similarity. A quarter of related bacterial communities γ -*Proteobacteria* and other groups include many δ -*Proteobacteria*, *Bacteroidetes* and *Cyanobacteria* [28], were not consistent with the present study.

Phylogenetic diversity of cultural bacteria from Antarctic sandy intertidal sediments. The results showed that with the 16S rRNA gene sequence, Gram-negative bacteria isolated were predominant, while only 16 strains of Gram-positive bacteria were found [29], these results indicate high bacterial diversity of the tidal sediment community in the area and are consistent with the dominant isolate from Gram-negative bacteria in the present study.

Biodiversity of salt-tolerant and salt-tolerant bacteria on the west coast of Lake Urmia. The results showed that of the 217 isolate obtained by 16S rRNA-based culture 52 strains were identified, including: *Halobacillus*, *Halomonas*, *Planococcus*, *Gracilibacillus*, *Bacillus*, *Pontibacillus*, *Paracoccus*, *Marinobacter*, *Providencia*, *Staphylococcus*, *Alkalibacterium*, *Sanguibacter*, *Lysobacter*, *Kocuria*, *Pontibacter*, *Salicola*, *Micrococcus*, *Oceanobacillus*, *Brevundimonas*, *Thalassobacillus*, *Microbacterium* and *Piscibacillus* were found [30], that the *Bacillus* strain is consistent with the above study.

Differences in the present study with other studies can be attributed to differences in environmental factors such as time, location, sex of sediment, temperature, water factors, etc. in different regions. So that [26], reported that spatial and temporal variations affect the diversity and abundance of bacteria. The type of litter sediment is also one of the other effective ecological factors of bacterial abundance [28]. The overall conclusion of this research Intestinal pathogen of mudskipper fished to include *Enterobacter cloacae*, *Citrobacter sp.*, *Enterobacter sp.*, and [Eubacterium] tenue strain DSM 20695], *Praclostridium bifermentans* strain JCM 1386, *Vibrio hyugaensis* strain 090810a which were identified by gene sequence 16S rRNA.

Conclusion

Bacteria compete with other organisms to get oxygen to the surface layers of the flower bed. The results showed that marine bacteria [Eubacterium] tenue strain DSM 20695], *Praclostridium bifermentans* strain JCM 1386, *Vibrio hyugaensis* strain 090810a were first identified in the northern intertidal areas of Persian Gulf, Iran. In aquatic environments *V. sp.* In microbial communities it is often referred to as biofilm [31].

V. sp. can cause biofilm at many living and non-living levels but is mainly found in association with oceanic phytoplankton [32].

The microbial species that make up the microcolonies represent genes that are not expressed when the organisms are released. *Vibrio* genus is pathogenic to humans and other creatures due to its many species and strains. *Vibrio* abundance in sediments and seawater is associated with water temperature and salinity; also increasing temperature has a variable effect on the *Vibrio* abundance associated with the sediment. *Vibrio* bacteria may survive in the sediments in the winter and release in the water column in late spring or early summer when temperatures rise to 20 degrees Celsius. Due to the nutritional activity of the filter, the bacteria software focus on their tissues. Consumption of raw or unprocessed contaminated seafood (and rarely contact between wound and contaminated water) can lead to the

transmission of bacteria to humans. They give that the bacterial species common to the fish intestines and sediments is high and due to fish feeding of sediment it can be concluded that the species present in the fish intestine in the present study may be a function of substrate species that needs further studies to prove this.

Abbreviations

DNA: Deoxyribonucleic acid; bp:Base pair; PCR:Polymerase chain reaction

Declarations

Ethics approval and Consent to participate

The project did not require ethics approval.

Consent for publication

Not applicable.

Availability of data and materials

The 16S rRNA gene sequence datasets analyzed in the current study are available.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

ghotbeddin (Dr) and L.roomiani (Dr) contributed to developing study concept and design.

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Authors' Information

^{1*} Department of Marine Biotechnology, Ahvaz Branch, Islamic Azad University, Ahvaz, Iran

²Department of Fisheries, Ahvaz Branch, Islamic Azad University, Ahvaz, Iran

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Figures

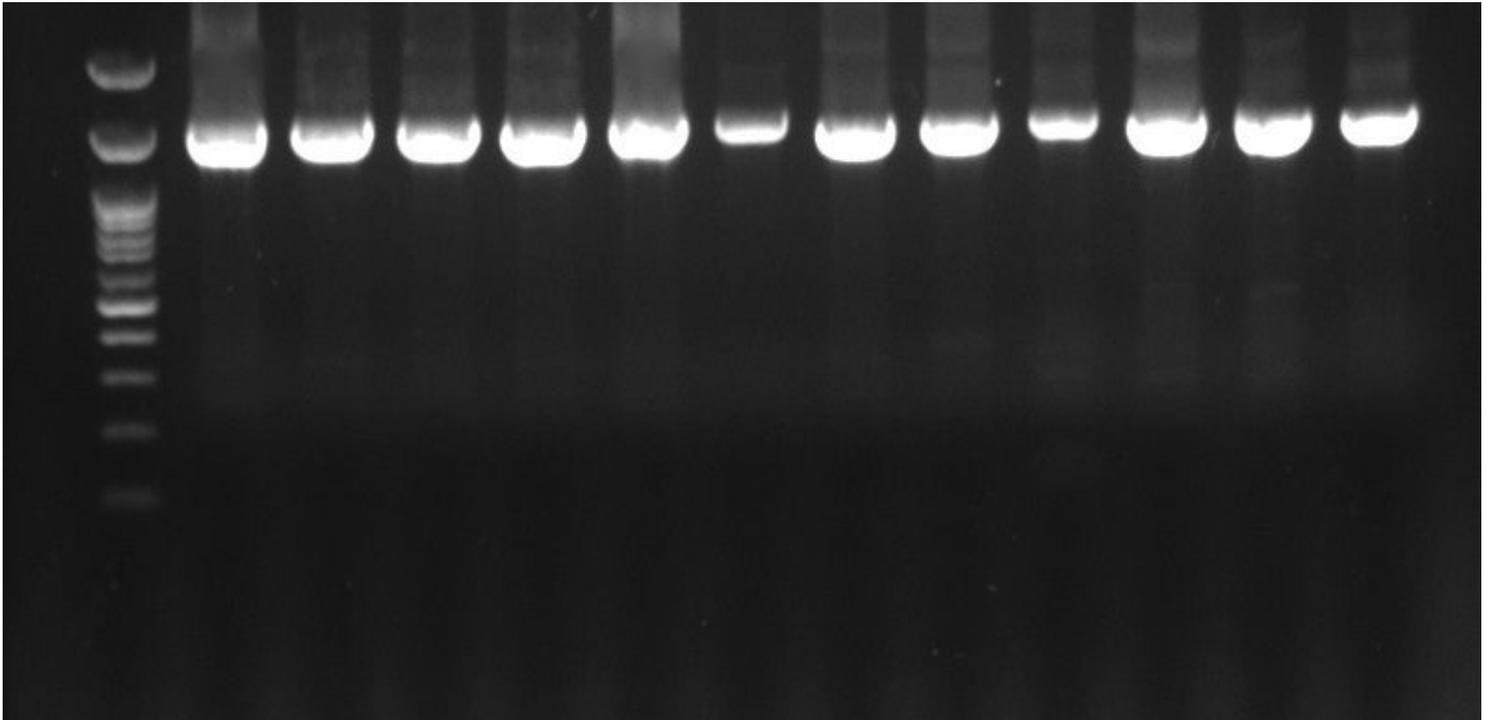


Figure 1

Gene bands 16S rRNA

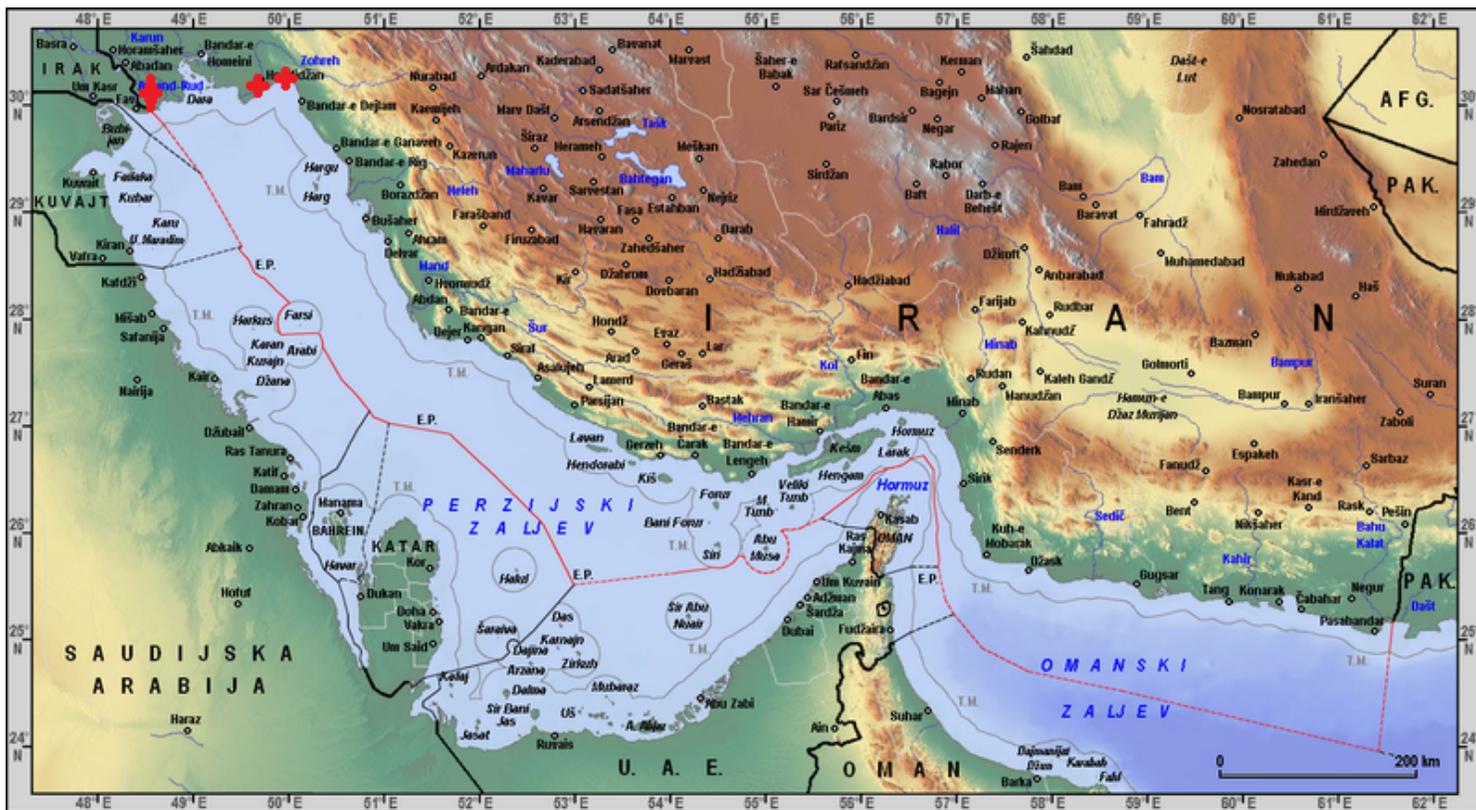


Figure 2

Sampling sites (site 1: Abadan (Arvand kenar), site 2: Hendiyan, site 3: Bahrekan) of Persian Gulf, Iran



Figure 3

Boleophthalmus dussumieri (Valenciennes, 1837) of Bahrekan, Persian Gulf, Iran