

Temporal and Spatial Distribution of Sulfate Reducing Bacteria in Shrimp Culture Pond Sediment

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Authors' contributions

This work was carried out in collaboration between all authors. Author DT designed the study, wrote the protocol, and the first draft of the manuscript. Authors MM and RS laid the objectives of the study and critically reviewed the manuscript. Author JAK performed the statistical analysis. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AJEE/2017/35287

Editor(s):

(1) B. P. Mishra, Department of Environmental Science, Mizoram University, Mizoram, India.

Reviewers:

(1) Luis Enrique Ibarra Morales, Sonora State University, Mexico.

(2) Nazura Usmani, Aligarh Muslim University, India.

(3) Anonymous, Niger Delta University, Nigeria.

Complete Peer review History: <http://www.sciencedomain.org/review-history/20137>

Original Research Article

Received 4th July 2017
Accepted 16th July 2017
Published 20th July 2017

ABSTRACT

Sulfate reduction, a key process in aquatic sediments is carried out by a group of anaerobic microorganism called sulfate reducing bacteria (SRB). High numbers of sulphate reducers in shrimp aquaculture pond sediment deteriorates the soil and water quality, causing physiological stress, thereby reducing the immunity of cultured animal. An attempt was made to evaluate the temporal and spatial distribution of SRB horizontally at different locations viz., water pumping area (WPA), sluice gate (SG) and pond center (PC), and vertically from sediment water interface to 10 cm depth in Pacific white shrimp, *Penaeus vannamei* culture ponds. Physico-chemical characteristics of water and soil were correlated with the number of SRB. Distribution of SRB was significantly higher ($p \leq 0.05$) in the pond sediment nearer to SG (874 MPN/g), followed by PC (272 MPN/g) and WPA (99 MPN/g) and at sediment water interface (751 MPN/g) compared to 10 cm depth (114 MPN/g) of

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pond profile. Factors like dissolved oxygen and soil redox potential (oxidation to reduction scale), and organic carbon content in soil had a significant negative and positive correlation with SRB numbers. Phylogenetic relationship of SRB targeting SRB groups showed the presence of *Desulfonema*, *Desulfosarcina*, *Desulfatibaculum*, *Desulfobotulus*, *Desulfomicrobium*, *Desulfococcus*, *Desulfovibrio* and *Clostridium* genera in shrimp culture pond sediments.

Keywords: Sulfate reducing bacteria; sediment-water interface; pond center; sluice gate; brackishwater and shrimp culture pond.

ABBREVIATIONS

SRB : Sulfate Reducing Bacteria
 WPA : Water Pumping Area
 SG : Sluice Gate
 PC : Pond Centre
 SWI : Sediment Water Interface
 MPN : Most Probable Number
 DO : Dissolved Oxygen
 OC : Organic Carbon
 TAN : Total Ammoniacal Nitrogen
 OTU : Operational Taxonomic Units
 DOC : Days of Culture

1. INTRODUCTION

Pond ecosystem is a complex environment in which, microorganism present in water, sediment and gut of the cultured animal interact each other which in turn has impact on growth, survival, nutrient cycling and disease control [1,2]. Walker and Winton, [3] explained that poor soil and water quality along with bacterial and viral pathogens are the main cause for mortalities in shrimp industry. High nutrients load derived from left over feed and fecal materials that accumulate on pond bottom are a major concern, which leads to the formation of toxic compounds like NH₃, NO₂ and H₂S. These toxic compounds deteriorate the water and soil quality, causing physiological stress thereby reducing the immunity of cultured animal [4].

In shrimp culture pond sediments, sulfate reduction is a major process which is carried out by a group of anaerobic microorganisms called sulfate reducing bacteria (SRB). This leads to the formation of hydrogen sulfide, a colorless gas with rotten egg smell and buildup of this toxic substance affects the shrimp health, thereby decreasing the production. Hsu and Chen [5], documented that *P.vannamei* is more susceptible to *Vibrio* sp., and considerable reduction in immune parameters was found under sulfide stress. Generally in organically enriched sediments, the rate of sulfate reduction depends on factors like availability of organic compounds [6], depth related gradient [7] and the quality and

quantity of accumulated organic matter [8]. Oxygen acts as a barrier for the movement of reduced toxic compounds into the water column [9,10]. In aquatic sediments, as oxygen is consumed in 1-5 mm layer, sulfate reduction process becomes dominant in sediment water interface (SWI) and deeper layers [11]. All the factors mentioned above are not uniformly distributed and varies at different places in a pond and also from the neighboring ponds, the cause for variation in sulfate reduction and SRB population.

Several studies have focused on studying the diversity and composition of SRB in environments such as hyper saline lakes [12], freshwater [13], marine sediments [14], estuarine sediments [15] and aquaculture fish ponds [16, 17]. Few reports pertaining to the population of SRB in shrimp culture ponds are available with MPN (Most probable number) quantification [18, 19]. In the previous studies, it was found that higher SRB in the range of 0.8- 4.4 × 10⁹ cells g⁻¹ dry sediment was found in fish farm sediment and it was positively correlated with organic enrichment in the pond sediments [20]. Similarly, SRB in the range of 9,300–42,000 cm⁻³ was detected in the sediment of experimental ponds stocked with penaeid shrimp and fish [21]. Other than this MPN quantification, studies on distribution of SRB in different places of the pond and their phylogenetic relationship in shrimp culture sediments are not available. The fact that only few studies are available with regard to SRB and its distribution in shrimp culture sediments, emphasizes the need for more studies on SRB and the role various pond environmental factors in influencing the process of sulfate reduction. Hence, we made an attempt to study the phylogenetic relationship and distribution of SRB in shrimp culture ponds. In this study, temporal and spatial distribution of SRB horizontally at different places and vertically along the depth in brackishwater shrimp culture ponds. In addition to this, various pond environmental factors that influence the sulfate reducing bacteria was studied.

2. MATERIALS AND METHODS

2.1 Sample Collection

Sediment samples were collected from three brackishwater shrimp culture farms located in Mamallapuram, Tamil Nadu, India. From each farm, four ponds were selected for this study. Pacific white shrimp *Penaeus vannamei* was the cultured species with a stocking density of 40 to 45 nos /m² in each pond and the culture period was 95 to 100 days. All the ponds followed zero water exchange culture with standard management practices. To study the horizontal and temporal distribution of SRB in the culture pond, sediment samples were collected from three locations viz., water pumping area (WPA), sluice gate (SG) and pond center (PC) at different days of culture (DOC) throughout the culture period (22, 37, 51, 65, 80 and the day of harvest). In addition, to study the temporal and vertical distribution of SRB, sediment samples were collected from the above mentioned locations at three time intervals (22 & 51 DOC and harvest time, by inserting PVC core sampler from SWI and cores of 0-0.5 cm, 0.5-1.5 cm, 1.5-2.5 cm, 2.5-5.0 cm, 5.0-7.5 cm and 7.5-10 cm were separated. In order to have a uniform representative sample, soil samples of each core of same depth from all the sampling points in a pond were pooled together. All the samples were transported to laboratory in ice cold condition.

2.2 Sediment and Water Quality Analysis

Measurement of pH, dissolved oxygen (DO) salinity and turbidity in pond water, and redox potential (E_h) in pond sediment was done onsite using multi-parameter water quality analyzer (Hach, USA) at all the sampling places. Water samples were analyzed for total sulfide-S, nitrite-N, nitrate-N, total ammonia nitrogen (TAN) [22] & sulfate-S [23] and sediment samples were analyzed for sulfate-S [23] and organic carbon (OC) content [24] using standard protocols.

2.3 Cultivation and Enumeration of SRB

Cultivation of SRB was done using Postgate medium B with lactate as electron acceptor [25] Resazurin (0.001 g/L) and thioglycolic acid (0.1 ml/L) were added as oxygen indicator and reducing agent, respectively. pH of the medium was adjusted to 7.5 and sterilized by autoclaving at 121°C for 20 min. A 5% ferrous ammonium sulfate was filter sterilized and added separately

at 0.1 ml for every 5.0 ml of the autoclaved medium. Enumeration of viable SRB was done by MPN method using three tube MPN method following FDA-BAM protocol [26]. Headspace oxygen was removed completely by passing oxygen free nitrogen and incubated for the period of two weeks. Formation of black colour precipitate was taken as positive growth and quantification of SRB was done using FDA-BAM table. To study the phylogenetic relationship of SRB, 5 ml of culture from all the highest positive MPN dilutions were transferred to the enrichment media and cultured as mentioned above.

2.4 DNA Extraction and PCR Amplification

Genomic DNA from was extracted using a Power Soil DNA Isolation Kit (Himedia laboratories, India). Primer sets targeting *Desulfotomaculum* (Group-1), *Desulfobulbus* (Group-2), *Desulfobacterium* (Group-3), *Desulfobacter* (Group-4), *Desulfococcus–Desulfonema–Desulfosarcina* (Group-5) and *Desulfovibrio–Desulfomicrobium* (Group-6) suprageneric groups of SRB were used [27]. The amplification reaction mixture contained 1x red dye PCR mix (Ampliqon, Denmark) containing 1mM MgCl₂, 0.4mM dNTPs, and 10 picomoles of each primer. The thermal cycler (Veritii, Applied Biosystems) conditions followed were initial denaturation for 3 min followed by 25 cycles: 94°C for 30 s, 65°C for 30s and 72°C for 30 s with final elongation for 5 min. Amplified products were electrophoresed on 1.5% agarose gel containing Ethidium bromide in 1x TAE buffer @ 120 V for 30 min and visualized using Gel documentation system.

2.5 Cloning and Sequencing

After PCR amplification, unpurified products were purified and cloned with TA (pcrII) cloning vector. The ligation products were introduced into *E.coli* Top10 chemically competent cells, and these cells were plated onto LB medium containing ampicillin and incubated overnight at 37°C. White colonies were randomly selected and screening of positive clones was performed. Clones were analyzed for insert and the purified clones were sequenced using ABI 3730 sequencer.

2.6 Sequence Analysis

Sequences containing chimeras were checked with Decipher [28]. Sequences were aligned using MUSCLE program [29] and aligned

sequences were grouped into Operational Taxonomic Units (OTU) with 97% as the distance cut-off value [30] using RDP (Ribosomal database project) pipeline tool [31]. From each OTU only one representative sequence was taken to construct phylogenetic analysis. Neighbor joining method was used to construct the phylogenetic tree using, MEGA 5.2.2 [32] Bootstrap analysis was performed with 1000 replicates to verify the reliability of the constructed phylogenetic tree.

2.7 Nucleotide Accession Number

Representative sequence from each OTU was published in DDBJ database under the accession numbers AB983657-AB983706.

2.8 Statistical Data Analysis

One- way repeated measures ANOVA was performed to find out the significance in variation of SRB between different places of the pond and days of culture using SPSS 16.0. Pearson correlation analysis was done to find out the relation between physico-chemical parameters of water and soil and SRB population.

3. RESULTS AND DISCUSSION

3.1 Changes in Physico-chemical Parameters of Water and Soil

The average water and soil parameters at different days of culture (DOC) in the culture pond are given in Table 1 and the trend of significant parameters at different sampling places in a pond is shown in Fig. 1 through 4. pH, DO (ppm), TAN (ppm), total sulfide-S (ppm) and sulfate-S (ppm) content in water during the culture period ranged from 6.78-8.31, 5.43-8.69, 0.055-0.174, and 0.004-0.09 and 1367-1626, respectively. There was no significant difference between days of culture with respect to pond water pH, salinity, turbidity, TAN, nitrite-N, nitrate-N and sulfate-S ($p \geq 0.05$), whereas DO and total sulfide content in pond water and, redox potential and organic carbon content in pond soil differed significantly ($p \leq 0.05$) with the progress of culture period (Table 1).

Redox potential in pond soil ranged from 150 to -167 mV during the culture period. Soil redox potential (E_h) which is the indicator of soil health, was in the positive side 150 & 61.6 mV at the start of the culture i.e. at DOC 22 and 37

respectively, and then it gradually decreased to negative values towards the end of the culture (-123 \pm 53 mV). This shows that bottom sediment was in oxidized state during the early phase of culture, which facilitates the aerobic decomposition of organic matter rather than anaerobic decomposition. During the early phase of culture, accumulation of organic carbon and availability of substrates will be less, the reason for the E_h values on oxidation scale, whereas E_h values on reduction scale during the later phase of the culture period, is due to the excess availability of substrates obtained from accumulation of unused feed and fecal material. It is evident by the increase in organic carbon content in pond soil from 0.2% at DOC 22 to 0.41 % at harvest time. Wiyito et al. [4] studied the effect of redox potential in which it was found that negative redox potential generates reduced compounds specifically when the redox value is above -200 mV. It reduces the dissolved oxygen concentration in SWI and increases the sulfide concentration in water column.

3.1.1 Changes in Physico- chemical parameters of water and soil at different places of the pond

When a different place within a pond is taken into account, E_h was highly variable between the three places. Lowest average E_h values of -19.83, -9.3, -167 and -123 mV were observed nearer to SG at DOC 51, 65, 80 and harvest time, respectively (Fig. 1). Similar trend of variation was observed in E_h values at the other two sampling points at different days of culture. Similarly, total sulfide content was highly variable at three places with high value at SG (0.116 ppm) followed by PC (0.094 ppm) at harvest time (Fig. 2). DO content varied between sampling points within the range of 4.37 to 8.34 mg/L. On the whole, low DO values were found nearer to SG at DOC 65 (4.4 mg/L) and DOC 80 (4.37 mg/L) compared to PC at DOC 65 (5.37 mg/L) and DOC 80 (8.21 mg/L) and WPA at DOC 65 (6.42 mg/l) and DOC 80 (8.31 mg/l) (Fig. 3). Organic carbon content in soil ranged from 0.13-0.65% throughout the culture period. Fluctuations were observed between sampling points with lowest organic carbon content at WPA (0.13%) during early days of culture and high nearer to SG (0.65%) at DOC 80 (Fig. 2). Overall, there existed a significant difference ($p < 0.05$) in organic carbon, redox potential, dissolved oxygen and sulfide levels between the three places of the pond. Significantly high organic carbon content (0.49%) and sulfide (0.05 ppm)

and redox potential on reduction scale (-102 mV) and low DO (5.63 ppm) were observed at sluice gate compared to other two sampling places (Table 2).

3.1.2 Changes in Physico-chemical parameters along the depth of pond

In case of vertical distribution, OC was fluctuating along the depth and there was no particular trend observed throughout the culture period. Comparing all the cores, OC content (%) was

found to be high in SWI (0.5 cm) at DOC 22 (0.26 ± 0.03) and at harvest time (0.55 ± 0.03), whereas at DOC 51 high OC was found in 1.5 cm cores (0.61 ± 0.014) compared to 0.26 ± 0.04 in SWI (Fig. 4). Likewise sulfate content in soil was also highly variable along the depth, throughout the culture period. Maximum sulfate concentration (mg/L) was observed in 5.0 cm core at DOC 22 (1218 ± 29.69), 7.5 cm layer at DOC 51 (1733 ± 32.10) & 1.5 cm layer at harvest time (1354 ± 16.37) (Fig. 4).

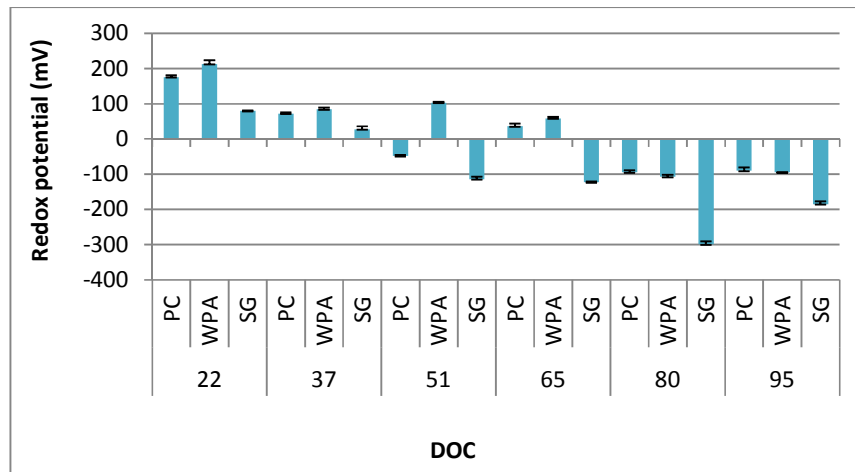


Fig. 1. Changes in soil redox potential at three sampling points during culture period
 Bars represent means \pm SD

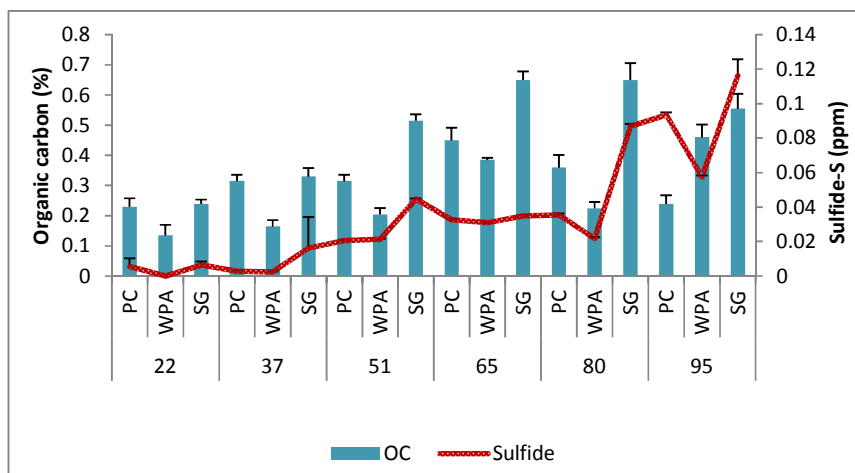


Fig. 2. Changes in sulfide content in water and organic carbon content in soil at three sampling points during culture period
 Bars represent means \pm SD

Table 1. Physico-chemical characteristics of water and soil at different days of culture (DOC)

Parameters	DOC 22	DOC 37	DOC 51	DOC 65	DOC 80	Harvest day
Water						
pH	6.99 ^d ±0.02	8.06 ^a ±0.04	7.41 ^c ±0.09	7.48 ^c ±0.30	8.31 ^b ±0.04	6.78 ^e ±0.01
Dissolved oxygen (mg/L)	7.69 ^a ±0.94	6.6 ^d ±1.46	7.52 ^b ±0.63	5.43 ^f ±0.96	6.9 ^c ±2.2	5.85 ^e ±1.36
Turbidity (NTU)	50 ^c ±0.46	65 ^b ±4.59	45 ^d ±2.19	75 ^a ±4.94	72 ^a ±7.45	73 ^a ±1.98
Salinity (ppt)	16 ^b ±1	18 ^a ±1	16 ^b ±0.0	18 ^a ±1	18 ^a ±1	16 ^b ±1
TAN (ppm)	0.096 ^d ±0.007	0.055 ^f ±0.004	0.133 ^c ±0.001	0.084 ^e ±0.002	0.174 ^a ±0.004	0.152 ^b ±0.020
Nitrite-N (ppm)	0.020 ^b ±0.003	0.025 ^b ±0.001	0.012 ^c ±0.001	0.065 ^a ±0.004	0.007 ^c ±0.002	0.078 ^a ±0.00
Nitrate-N (ppm)	0.007 ^e ±0.001	0.027 ^d ±0.0005	0.03 ^c ±0.001	0.036 ^c ±0.001	0.0569 ^b ±0.0011	0.06 ^a ±0.002
Total sulfide-S (ppm)	0.004 ^e ±0.003	0.007 ^e ±0.007	0.028 ^d ±0.011	0.032 ^c ±0.001	0.048 ^b ±0.034	0.089 ^a ±0.029
Sulfate-S (ppm)	1376 ^d ±65	1626 ^a ±43	1518 ^b ±5	1501 ^b ±37	1367 ^d ±32	1416 ^c ±12
Soil						
Organic carbon (%)	0.20 ^e ±0.05	0.27 ^d ±0.08	0.35 ^c ±0.13	0.49 ^a ±0.12	0.34 ^b ±0.18	0.41 ^b ±0.14
Redox potential (mV)	156 ^a ±68.64	61.66 ^b ±29.7	-19.83 ^d ±54	-9.3 ^c ±46	-167 ^f ±114	-123 ^e ±53

(n=12; mean ± SD); Means bearing different superscript in a row are significantly different ($p \leq 0.05$)

Table 2. Physico-chemical characteristics of water and soil at different sampling places during culture period (Means with the similar superscript in the same row are not significantly different, $p \geq 0.05$)

Parameter	Sampling place		
	Pond center	Water pumping area	Sluice gate
Water			
DO (ppm)	5.08-9.26 (6.78 ^b ±1.51)	6.01-10.59 (8.12 ^a ±1.24)	4.02-7.77 (5.63 ^c ±1.27)
Sulfide (ppm)	0.002-0.094 (0.032 ^b ±0.03)	0-0.058 (0.022 ^c ±0.01)	0.003-0.123 (0.051 ^a ±0.04)
Soil			
Redox potential *(mV)	180 to -99 (8.5 ^b ±99)	221 to -112 (42.61 ^a ±115)	81 to -305 (-102 ^c ±130)
Organic Carbon (%)	0.21-0.48 (0.31 ^b ±0.07)	0.11-0.49 (0.26 ^c ±0.12)	0.23-0.69 (0.49 ^a ±0.16)

* Range is given for redox potential as the values were from oxidation scale (+ve) to reduction scale (-ve)

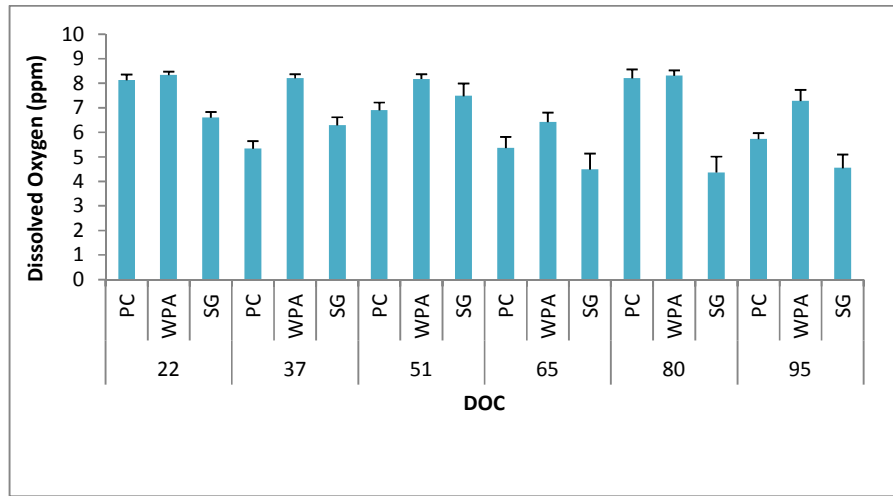


Fig. 3. Changes in dissolved oxygen in water at three sampling points during culture period
 Bars represent means \pm SD

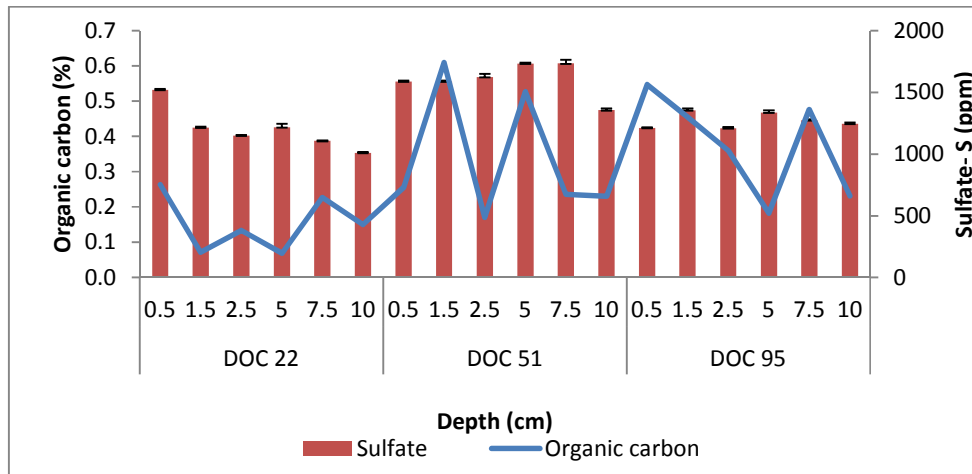


Fig. 4. Variation of sulfate and organic carbon content in soil along the depth of pond during the culture period
 Bars represent means \pm SD

3.2 Enumeration of SRB

3.2.1 Horizontal distribution of SRB at different places of the pond

Distribution of SRB varied between different places of the pond, high numbers registered at SG followed by CP and WPA (Fig. 5). Throughout the culture period, number of SRB was seen fluctuating with no constant trend at different DOC nearer to WPA and PC, whereas the numbers found to be high at SG (>1100 MPN/g) on DOC 51 and it remained constant thereafter. A significant difference ($p \leq 0.05$) was found in means of SRB numbers between three places of the pond and between the days of

culture. Post hoc test revealed significantly high SRB population at SG (874 MPN/g), followed by PC (272 MPN/g) and WPA (99 MPN/g) (Fig. 6). No significant difference was observed with SRB numbers between DOC 51 and 65 & 80 and 95 ($p \geq 0.05$).

3.2.2 Vertical distribution of SRB along the depth of pond

The average number of SRB at DOC 22, 51 and harvest time was 30, 431, 684 MPN/g, respectively (Fig. 7). On DOC 22 from SWI to 10 cm the number of SRB was 53 MPN/g at SWI and decreased up to 0.5 cm (30 MPN/g) and then remained constant throughout 10 cm cores.

At DOC 51, number of SRB was higher in 0.5 and 1.5 cm cores (>1100 MPN/g), decreased from 2.5 to 5.0 cm (150 MPN/g) and further decreased to 30 MPN/g from 7.5 to 10 cm cores. In contrast, at DOC 95, number of SRB was found to be constant (>1100 MPN/g) in 0.5- 2.5 cm cores and then decreased to 290 MPN/g in the remaining cores. A significant difference was found between the numbers of SRB ($p \leq 0.05$) along the depth of the pond except in 0.5 cm and 1.5 cm cores (Fig. 8).

On the whole, number of SRB was found to be high nearer to SG followed by PC and WPA and their distribution along the depth is found to be decreasing with high numbers at SWI. Similar kind of result, with maximum number of SRB in

top 3 cm layer ($6.6 \pm 1.0 \times 10^8$ cells cm^{-3}) and then decreasing numbers below 3cm layer ($1.7 \pm 0.8 \times 10^6$ cells cm^{-3}) was observed in Wadden Sea sediment [33]. Urakawa et al. [7] studied the variation of microbial communities along the depth in marine sediments. They observed large number of SRB in surface layers compared to the deeper depth because of organic matter availability. Generally SRB is expected to be high in deeper sediments due to anaerobic condition in lakes and marine waters. During shrimp culture, unused feeds and waste materials will be deposited on surface sediments. In the presence of sulfate, these complex macromolecules will be utilized by SRB whereas, in absence of sulfate, SRB ferment organic acids through fermentative bacteria by which fermentation compounds like

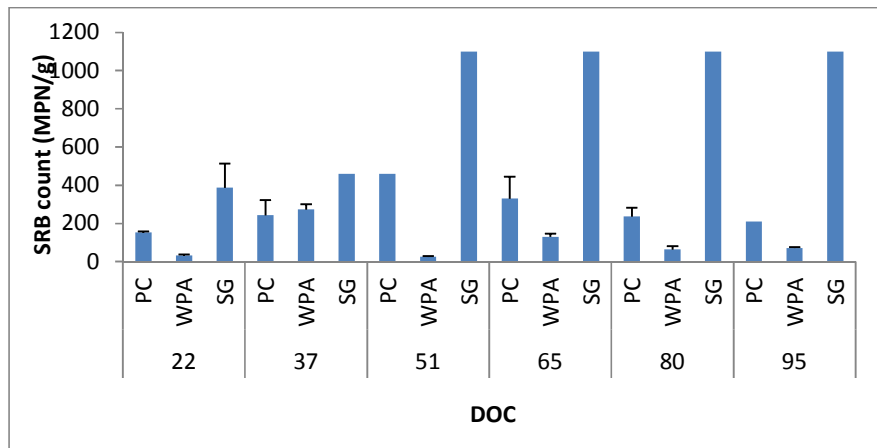


Fig. 5. Horizontal distribution of SRB at different sampling points during culture period. Bars represent means \pm SD

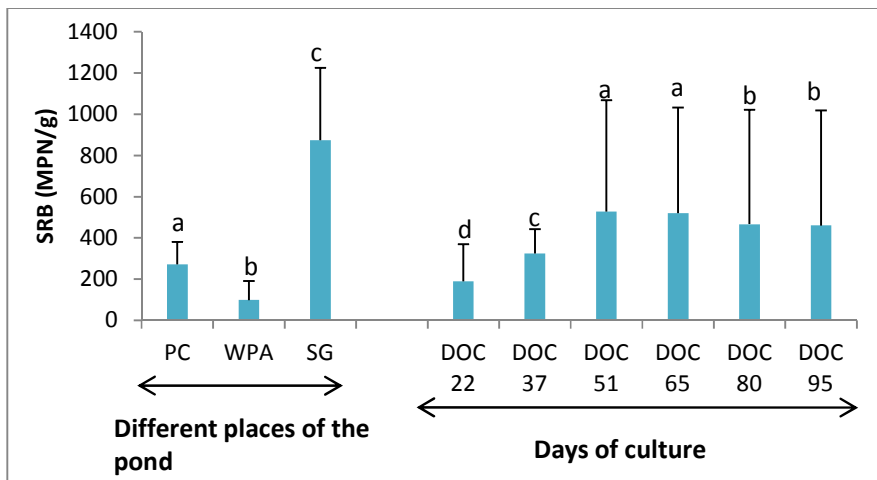


Fig. 6. SRB population at different sampling places and DOC (MPN/g) in three places of the pond and different DOC

(Means with the same letter are not significantly different $p \geq 0.05$. Bars represent means \pm SD)

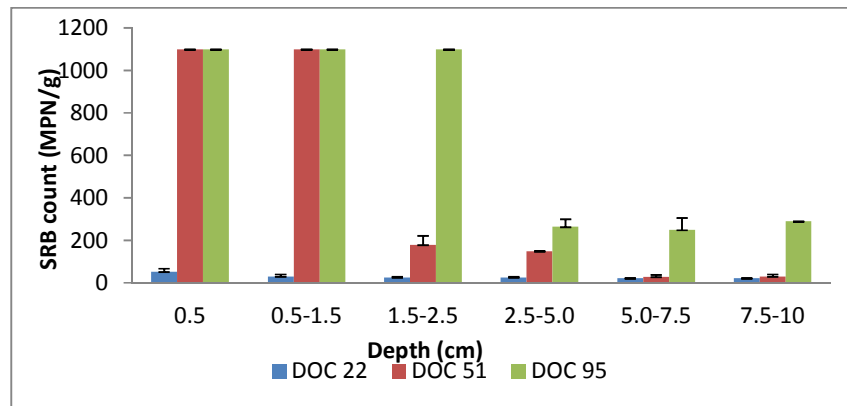


Fig. 7. Vertical distribution of SRB (MPN/g) along the depth of pond during culture period
Bars represent means ± SD

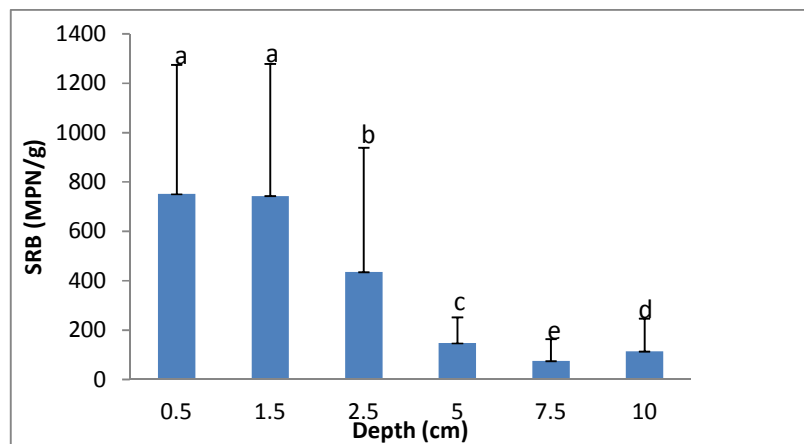


Fig. 8. SRB population (MPN/g) along the depth of pond (Means with the same letter are not significantly $p \geq 0.05$)
Bars represent means ± SD

lactate, acetate and propionate will be produced. Holmer and Storkholm [34] observed high sulfate reduction rate in surface layers of fish farmed sediments, where accumulation of organic matter was high. Thus, SWI provides ideal condition for the anaerobic dissimilatory sulfate reduction and fermentative growth of SRB. Presence of sulfide levels of 0.004, 0.028 and 0.09 ppm during DOC 22, 51 and harvest time, respectively (Fig. 2) indicates the effective sulfide production in the pond sediment.

3.3 Correlation between SRB and Physico-chemical Parameters of Pond Water and Soil

Significant negative correlation was found between SRB numbers and dissolved oxygen ($r = - 0.633$) and redox potential values from oxidation to reduction scale ($r = - 0.672$). A

significant positive correlation was found between SRB numbers and organic carbon content ($r = 0.812$) and sulfide in water ($r = 0.525$). In case of vertical distribution, significant positive correlation was found between organic carbon in soil and SRB ($r = 0.651$) and a weak correlation ($r = 0.109$) was observed with sulfate. Many studies have reported that organic carbon as a main limiting factor in shaping the abundance and distribution of SRB. Kondo et al [35] studied SRB from Japanese fish farm sediments with different level of organic enrichment in which fish pond with high organic pollution found to be more diverse in SRB. Kawahara et al [17] observed that organic enrichment influences the bacterial communities and clones related to SRB were found to be in higher frequency from organically enriched surface sediments (0-4 cm) of fish farm in Wakasa Bay of Japan. Santander et al. [36]

studied the bacterial communities in milk fish cages from Philippines in which they observed many sulfate reducing bacteria and other spore forming genera. They further explained that organic load derived from higher fish feed and its left over constituents, created reduced environment through which anaerobic bacteria flourish. It is evident from this study that organic matter accumulated in the form of unused feed and faecal materials play a major role in sulfate reduction.

3.4 PCR Amplification

DNA was isolated from highest positive (>1100/g) MPN dilutions and amplification of partial fragments of 16S-rDNA genes using group specific primer yielded expected base pair in all the enrichment cultures for group 5 & 6. No bands were found in groups 1, 2, 3 and 4. More than 100 clones in group 5 & 6 were screened for an insert. Twenty seven clones in group 5 and 43 clones in group 6 were positive. All the 70 clones were sequenced in which eight sequences were found to be chimeric and removed from further analysis. The remaining clones were grouped into 50 OTU's (16 in group 5 & 34 in group 6) using 0.03% as distance cutoff value.

3.5 Phylogenetic Analysis

Neighbor joining method was performed to visualize the phylogenetic relationship of clones isolated from shrimp farm sediments, with clones isolated from other habitats available in NCBI database with *Desulfuromonas acetoxidans* (AY188891) as outgroup. Group 5 (*Desulfococcus-Desulfonema-Desulfosarcina*) formed five clusters comprising *Desulfococcus*, *Desulfonema*, *Desulfosarcina*, *Desulfatiferula* and *Desulfobotulus* (Fig. 9).

Cluster 1 had five phylotypes (DCC12, DCC18, DCC11, DCC22 (n=2), DCC13) which shared phylogenetic relationship with *Desulfobotulus sapovarans* (NR-044601) isolated from hyper saline sodalake sediment. Cluster 2 consist of four phylotypes (DCC21 (n=3), DCC16, DCC20, DCC15) related to *Desulfatiferula olefinivorans* (NR_043971) isolated from brackishwater sediment of oil refinery which can utilize only sulfate as electron acceptor and C₁₄-C₂₄ fatty acids as electron donor [37]. Cluster 3 had two phylotypes DCC19 and DCC25 that formed monophyletic relationship with *Desulfococcus biacutus* (NR_025406) and environmental clone (EU917051) recovered from crude oil gathering

system of China [38]. DCC25 formed a separate lineage within *Desulfococcus* group. Cluster 4 had six clones (DCC1 (n=5) and DCC4) which is related to *Desulfonema magnum* (NR_025990) isolated from anaerobic mud of sea water lagoon. This is one of the gliding filamentous sulfate reducing bacteria in deltaproteobacter, which can oxidize acetate and aliphatic acids [39]. Cluster 5 had three phylotypes (DCC14, DCC17 and DCC5 (n=4) which formed a separate lineage from bacterial clone (FJ786119) isolated from shrimp farming sediment within *Desulfosarcina* sp., (FJ416305).

Group 6 formed three distinct clusters comprising *Desulfomicrobium* sp., *Desulfovibrio* sp., *Clostridium* sp., (Fig. 10) in which cluster 1 with 14 phylotypes namely DSV7, 14, 5, 4, 10, 3, 1 (n=2), 8, 15, 12 (n=2), 6 and 24 formed a separate lineage within *Desulfomicrobium* sp., and clones DSV2 and DSV9 shared its relationship with *Desulfomicrobium* sp., (AY548759).

Cluster 2 had 14 phylotypes namely DSV30, DSV29 & DSV31 formed a monophyletic clade with *Desulfovibrio* sp., (AJ251630), *Desulfovibrio inopinatus* (NR025038) and *Desulfovibrio desulfuricans* (NR074858) respectively. DSV27, 35 and DSV21 formed monophyletic clade with *Desulfovibrio piezophilus* (NR_102518), *Desulfovibrio* sp., (KF733439) and *Desulfovibrio salexigens* (NR102801) respectively. Other clones (DSV28, 25, 22, 17, 19, 18, 16, and 26) formed independent cluster within *Desulfovibrio* group.

Desulfovibrio spp., which belongs to deltaproteobacter, is dominant in organic rich marine habitats. In the presence of sulfate, fermentation products like lactate, malate and fumarate can be used as electron donors and even in the absence of sulfate, it can utilize pyruvate and formate [40]. Saas et al [41] studied the vertical distribution of SRB in the oligotrophic lake sediments, in which many strains related to *Desulfovibrio* sp., and *Desulfomicrobium* sp., were found in oxic-anoxic layers and these bacteria, being catalase positive organism, shows higher oxygen tolerance capacity and they are well adapted to live near sediment water interface. *Desulfovibrio* has also been isolated commonly from corals affected by Black Band disease [42,43]. Around eleven clones related to *Desulfovibrio desulfuricans* (with 97% similarity) were isolated from diseased corals in Northern Red sea [44]. Interestingly two clones DSV17 &

DSV19 isolated in this study were similar to *Desulfovibrio* sp., isolated from coral montipora in Japan.

Cluster 3 had six clones (DSV32, 36, 34, 23, 20 and 33) in which DSV32 and DSV23 formed monophyletic cluster with *Clostridium* sp., (AB470961) and *Clostridium aestuarii* (DQ126679) isolated from tidal flat sediment which is closely related to type species *Clostridium butyricum*. DSV36 & DSV34 formed independent lineage within family Clostridiales, a group of spore forming bacteria under phylum

Firmicutes which have the potential to switch to an energy conserving metabolism with low sulfate or even with no sulfate [15]. Tamminen et al, [45] also observed clones similar to Clostridia from Rainbow trout fish farms with black muddy sediment near Baltic Sea. It is further explained that clones related to Clostridia, more likely to have originated from fish gut micro biota. Moreover, this is possible because many of the soil probiotics used in aquaculture contains *Clostridium butyricum* as one of the essential component.



Fig 9. Phylogenetic tree showing representative 16SrRNA gene sequences related to Group-5 isolated from shrimp cultured sediments (shown in bold). Number of clone sequenced in each phylotype is given in the parentheses

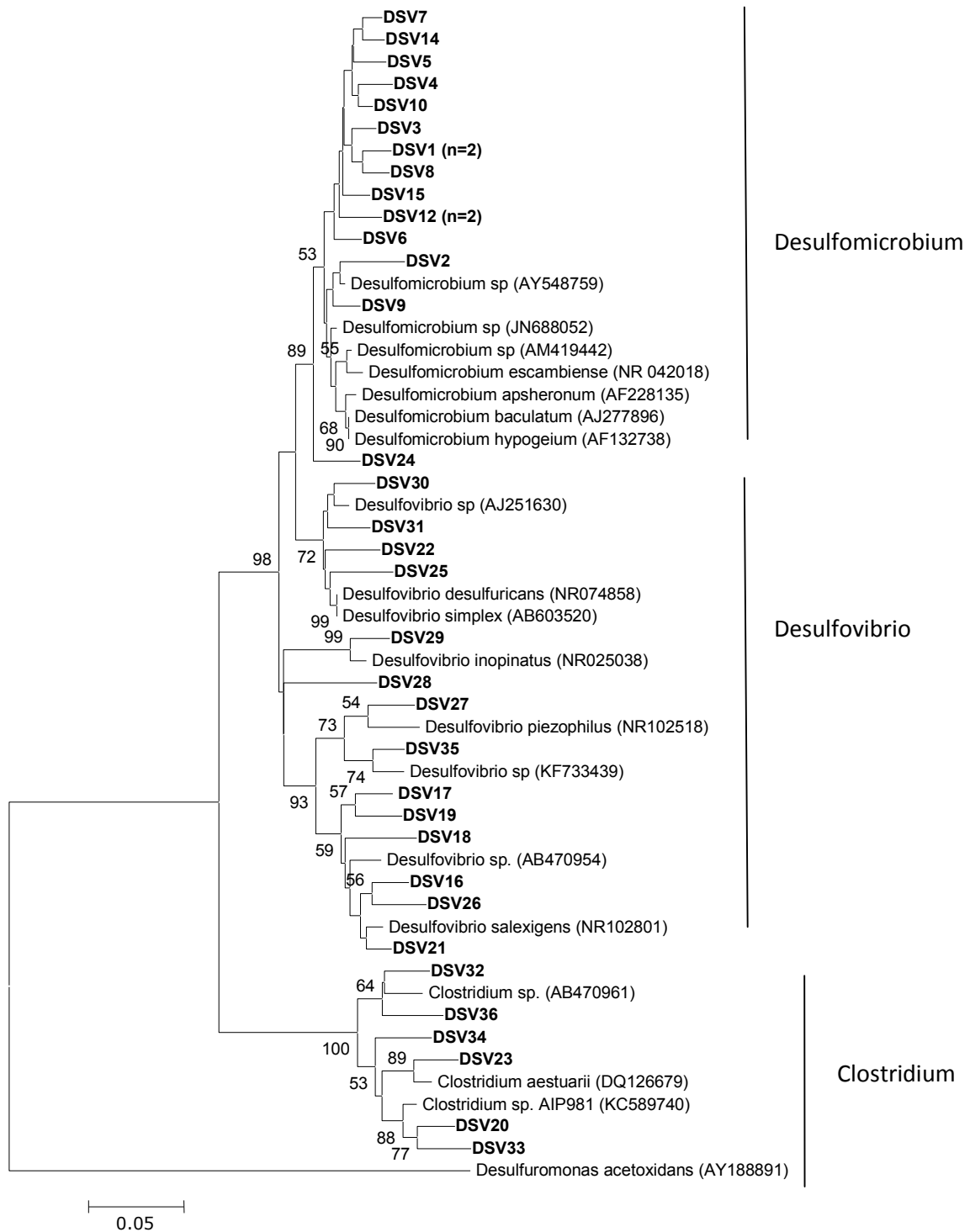


Fig. 10. Phylogenetic tree showing representative 16SrRNA gene sequences related to Group 6 isolated from shrimp cultured sediments (shown in bold). Number of clone sequenced in each phylotype is given in the parentheses

It is interesting to note that Clones related to group *Desulfotomaculum* (Group-1), *Desulfobulbus* (Group-2), *Desulfobacterium* (Group-3), *Desulfobacter* (Group-4) which are reported to have isolated from both marine and fresh water sediments are completely absent in this study. This is possibly because of substrate availability and organic enrichment in the shrimp culture sediments. Kawahara et al, [17] suggested that composition and activity of SRB is influenced by amount of organic enrichment in aquaculture. Castine et al, [46] studied the effect of organic load in tropical finfish cage farm in which, they found genus related to *Desulfovibrio*, *Desulfobacter*, *Desulfococcus*, *Desulfonema* in higher abundance. They further suggested that anaerobic zones created by organic matter load plays a key role in selection of bacteria involved in sulfate reduction. Understanding the microbial interaction in pond bottom is necessary in shrimp aquaculture because more than any other aquatic species, shrimp dwell on the bottom and ingest pond-bottom soil [47]. Avnimelech [48] estimated that 50% of the pond bottom in shrimp culture is covered by reduced sediment with a typical black color and smell of hydrogen sulfide which affects the shrimp growth, activity and health.

Abraham et al, [19] studied the population of SRB in shrimp culture systems of India, in which significant difference was found in population of SRB in semi intensive and traditional ponds because of varying degree of substrate availability and anaerobic processes. Suplee and Cotner [18] studied sulfide fluxes in shrimp ponds over a period of 17 months during which they found organic matter availability and its reactivity was the predominant factor in determining the sulfide fluxes in shrimp pond. They also compared sulfate reduction in old and newly constructed shrimp ponds, in which significant difference was observed between two ponds because of higher organic matter deposition in old ponds over the years.

Farm management practices which includes stocking, feeding, and inputs application during the culture period plays a key role in shaping up the microbial community in pond bottom. Generally in shrimp culture sediments, as the days of culture increases, pond bottom becomes more and more reduced due to application of feed rich in protein, accumulation of nutrients, unused feed and fecal materials. This provides suitable environment for anaerobic microorganism to flourish and in addition to this,

brackishwater shrimp ponds contain high level of sulfate in sea water which provides enormous scope for sulfate reduction to take place. Moreover, in organic matter rich sediments, methanogenic archaea compete with SRB for common substrates like acetate, H₂ and other organic compounds. Since, SRB has more affinity towards these common substrates, they generally out compete methanogens which further favours the process of sulfate reduction [49].

Despite high saline sediments having huge scope for sulfate reduction; there are studies which demonstrated sulfide production in low saline aquatic sediments [50,51]. Liu et al, [52] quantified the sulfate reducing prokaryotes in paddy sediments. They observed sulfate reduction in rice paddy sediments equal to marine sediments and it is further mentioned that in low sulfate environments, sulfate reduction happens via fermentative growth of SRB. This indicates that sulfate reduction will be an equally important process even in low saline shrimp culture sediments as the organic matter accumulation and anaerobic condition are same vertically from SWI.

4. CONCLUSION

In this study, we evaluated the distribution of SRB horizontally and vertically and its phylogenetic diversity brackishwater shrimp culture ponds. In conclusion, SRB was higher nearer to SG followed by PC and WPA and at sediment water interface compared to deeper depths. Factors like dissolved oxygen in water, redox potential and organic carbon content in soil had a key role in sulfate reduction and were correlated with SRB numbers. Genera like *Desulfonema*, *Desulfosarcina*, *Desulfatibaculum*, *Desulfobotulus*, *Desulfomicrobium*, *Clostridium*, *Desulfococcus* and *Desulfovibrio* were found to be present in brackishwater shrimp culture sediments. Future investigations with regard to the role of various organic matter sources on sulfate reducing bacteria communities will certainly help in understanding the process of sulfate reduction and its mitigation in shrimp culture sediments.

ACKNOWLEDGEMENTS

The authors are thankful to the Indian Council of Agricultural Research (ICAR) for funding the study through NICRA project (National Innovations in Climatic Resilient Agriculture) and

to Director, CIBA for providing the necessary facilities to carry out the research.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Cheng YF, Zhou QL, Xie J, Ge XP, Zhu WY, Liu B. Microbial community analysis in crab ponds by denaturing gradient gel electrophoresis. *World Journal of Microbiology & Biotechnology*. 2010;26(5):825–31.
2. Zeng Y, Ma Y, Wei C, Jiao N, Tang K, Wu Z, et al. Bacterial diversity in various coastal mariculture ponds in Southeast China and in diseased eels as revealed by culture and culture-independent molecular techniques. *Aquaculture Research*. 2010; 41(9):172–86.
3. Walker PJ, Winton JR. Emerging viral diseases of fish and shrimp. *Veterinary Research*. 2010;41(6).
4. Wiyoto, Sukenda, Harris E, Nirmala K, Djokosetiyanto D. Water quality and sediment profile in shrimp culture with different sediment redox potential and stocking densities under laboratory condition. *Ilmu Kelautan*. 2016;21(2):65–76.
5. Hsu SW, Chen JC. The immune response of white shrimp *Penaeus vannamei* and its susceptibility to *Vibrio alginolyticus* under sulfide stress. *Aquaculture*. 2007;271(1–4):61–9.
6. Schubert CJ, Ferdelman TG, Strotmann B. Organic matter composition and sulfate reduction rates in sediments off Chile. *Organic Geochemistry*. 2000;351–61.
7. Urakawa H, Yoshida T, Nishimura M, Ohwada K. Characterization of depth-related population variation in microbial communities of a coastal marine sediment using 16S rDNA-based approaches and quinone profiling. *Environmental Microbiology*. 2000;2(5): 542–54.
8. Warner GF, Domaniewski JCJ. Fish farming and the environment. *Biologist*. 1993;40(5):202–5.
9. Boyd CE and Queiroz F. The role and management of best management practices in Aquaculture ponds. *INFOFISH International*. 2014;22–28. Available:www.infofish.org
10. Wang C, Shan B, Zhang H, Rong N. Analyzing sediment dissolved oxygen based on microprofile modeling. *Environmental Science and Pollution Research*. 2014;21(17):10320–8.
11. Meysman FJR, Galaktionov OS, Glud RN, Middelburg JJ. Oxygen penetration around burrows and roots in aquatic sediments. *Journal of Marine Research*. 2010;68:309–36.
12. Kjeldsen KU, Loy A, Jakobsen TF, Thomsen TR, Wagner M, Ingvorsen K. Diversity of sulfate-reducing bacteria from an extreme hypersaline sediment, Great Salt Lake (Utah). *FEMS Microbiology Ecology*. 2007;60(2):287–98.
13. Mubmann M, Ishii K, Rabus R, Amann R. Diversity and vertical distribution of cultured and uncultured *Deltaproteobacteria* in an intertidal mud flat of the Wadden Sea. *Environmental Microbiology*. 2005;7(3):405–18.
14. Purdy KJ, Nedwell DB, Martin Embley T, Takii S. Use of 16S rRNA-targeted oligonucleotide probes to investigate the distribution of sulphate-reducing bacteria in estuarine sediments. *FEMS Microbiology Ecology*. 2001;36(2–3):165–8.
15. Leloup J, Fossing H, Kohls K, Holmkvist L, Borowski C, Jørgensen BB. Sulfate-reducing bacteria in marine sediment (Aarhus Bay, Denmark): Abundance and diversity related to geochemical zonation. *Environmental Microbiology*. 2009;11(5):1278–91.
16. Kondo R, Butani J. Comparison of the diversity of sulfate-reducing bacterial communities in the water column and the surface sediments of a Japanese meromictic lake. *Limnology*. 2007;8(2): 131–41.
17. Kawahara N, Shigematsu K, Miyadai T, Kondo R. Comparison of bacterial communities in fish farm sediments along an organic enrichment gradient. *Aquaculture*. 2009;287(1–2):107–13.
18. Suplee MW, Cotner JB. Temporal changes in oxygen demand and bacterial sulfate reduction in inland shrimp ponds. *Aquaculture*. 1996;145(1–4):141–58.
19. Abraham TJ, Ghosh S, Nagesh TS, Sasmal D. Distribution of bacteria involved in nitrogen and sulphur cycles in shrimp

- culture systems of West Bengal, India. *Aquaculture*. 2004;239(1-4):275-88.
20. Kawahara NAK, Higematsu KOS, Iura SAM, Iyadai TOM, Ondo RYK. Distribution of sulfate-reducing bacteria in fish farm sediments on the coast of southern Fukui Prefecture, Japan. *Plankton and Benthos Research*. 2008;3(1):42-5.
 21. Rao PSS, Karunasagar I, Otta SK, Karunasagar I. Incidence of bacteria involved in nitrogen and sulphur cycles in tropical shrimp culture ponds. *Aquaculture International*. 2000;8(5):463-72.
 22. APHA. Standard methods for the examination of water and wastewater. American Public Health Association, 22nd edn. Washington, DC; 2012.
 23. Tandon HL. Methods of analysis of soils, plants, waters, fertilisers & organic manures. Fertiliser Development and Consultation Organisation; 2005.
 24. Walkley A, Black IA. An examination of the degtjareff method for determining soil organic matter, and a proposed modification of the chromic acid titration method. 1934;1;37(1):29-38.
 25. Postgate, JR The sulphate-reducing bacteria. Cambridge University Press, London; 1984.
 26. Sutton S. The most probable number method and its uses in enumeration, qualification, and validation. *Journal of Validation Technology*. 2010;16(3):35-8.
 27. Daly K, Sharp RJ, McCarthy AJ. Development of oligonucleotide probes and PCR primers for detecting phylogenetic subgroups of sulfate-reducing bacteria. *Microbiology*. 2000;146(7):1693-705.
 28. Wright ES, Yilmaz LS, Noguera DR. Decipher, a search-based approach to chimera identification for 16S rRNA sequences. *Applied and Environmental Microbiology*. 2012;78(3):717-25.
 29. Edgar RC. Muscle: Multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res*. 2004; 32(5):1792-1797.
 30. Stackebrandt E, Goebel BM. Taxonomic note: A place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol*. 1994;44(4):846-9.
 31. Cole JR, Chai B, Marsh TL, Farris RJ, Wang Q, Kulam SA, et al. The Ribosomal Database Project (RDP-II): Previewing a new autoaligner that allows regular updates and the new prokaryotic taxonomy. *Nucleic Acids Research*. 2003; 2:442-443.
 32. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology and Evolution*. 2011;28(10):2731-9.
 33. Brossa E, Rabus R, Böttcher ME, Könneke M, Finke N, Schramm A, et al. Community structure and activity of sulfate-reducing bacteria in an intertidal surface sediment: A multi-method approach. *Aquatic Microbial Ecology*. 2002;29(3):211-26.
 34. Holmer M, Storkholm P. Sulphate reduction and sulphur cycling in lake sediments: A review. *Freshwater Biology*. 2001;46:431-51.
 35. Kondo R, Shigematsu K, Kawahara N, Okamura T, Yoon YH, Sakami T, et al. Abundance of sulphate-reducing bacteria in fish farm sediments along the coast of Japan and South Korea. *Fisheries Science*. 2012;78(1):123-31.
 36. Santander-de Leon SM, Reichardt W, Peralta-Milan S, Diego-McGlone S, Lourdes M, Nuñal SN, Wei H, Yoshikawa T, Okunishi S, Maeda H. Bacterial community composition of sediments from a milkfish *Chanos chanos* Forsskal farm. *Aquaculture Research*. 2016;47(8):2569-81.
 37. Laureau C, Labat C, Joulian C, Matheron R, Hirschler-Réa A. *Desulfatiferula olefinivorans* gen. nov., sp. nov., a long-chain n-alkene-degrading, sulfate-reducing bacterium. *International Journal of Systematic and Evolutionary Microbiology*. 2007;57(11):2699-702.
 38. Liu Y, Nikolausz M, Jin P. Abundance and diversity of sulphate-reducing bacteria within a crude oil gathering and transferring system in China. *Annals of Microbiology*. 2008;58(4):611-5.
 39. Fukui M, Teske A, Abmus B, Muyzer G, Widdel F. Physiology, phylogenetic relationships, and ecology of filamentous sulfate-reducing bacteria (genus *Desulfonema*). *Archives of Microbiology*. 1999;172(4):193-203.
 40. Widdel F, Bak F. The Prokaryotes. The Prokaryotes 2nd ed. 1992;IV:3352-3378.
 41. Sass H, Cypionka H, Babenzien HD. Vertical distribution of sulfate-reducing bacteria at the oxic-anoxic interface in

- sediments of the oligotrophic Lake Stechlin. FEMS Microbiology Ecology. 1997;22(3):245-55.
42. Cooney RP, Pantos O, Le Tissier MD, Barer MR, Bythell JC. Characterization of the bacterial consortium associated with black band disease in coral using molecular microbiological techniques. Environmental Microbiology. 2002;4(7): 401-13.
 43. Bourne DG, Muirhead A, Sato Y. Changes in sulfate-reducing bacterial populations during the onset of black band disease. The ISME Journal. 2011;5(3):559–64.
 44. Barneah O, Ben-Dov E, Kramarsky-Winter E, Kushmaro A. Characterization of black band disease in Red Sea stony corals. Environmental Microbiology. 2007;9(8): 1995–2006.
 45. Tamminen M, Karkman A, Corander J, Paulin L, Virta M. Differences in bacterial community composition in Baltic Sea sediment in response to fish farming. Aquaculture. 2011;313(1–4):15–23.
 46. Castine SA, Bourne DG, Trott LA, McKinnon DA. Sediment microbial community analysis: Establishing impacts of aquaculture on a tropical mangrove ecosystem. Aquaculture. 2009;297 (1–4):91–8.
 47. Boyd CE. Water quality management and aeration in shrimp farming. Fisheries and allied aquaculture. Departmental series. Alabama Agricultural Experiment Site, Auburn University, Alabama. 1989;2.
 48. Avnimelech Y. Sludge accumulation in the shrimp pond bottom: Significance and management. Asian Shrimp News, 1995; (4th quarter):2.
 49. Mitterer RM. Methanogenesis and sulfate reduction in marine sediments: A new model. Earth and Planetary Science Letters. 2010;295(3–4):358–66.
 50. Holmer M, Kristensen E. Seasonality of sulfate reduction and pore water solutes in marine fish farm sediment: the importance of temperature and sedimentary organic matter. Biogeochemistry. 1996;32(1):15–39.
 51. Pallud C, Van Cappellen P. Kinetics of microbial sulfate reduction in estuarine sediments. Geochimica et Cosmochimica Acta. 2006;70(5):1148–62.
 52. Liu XZ, Zhang LM, Prosser JI, He JZ. Abundance and community structure of sulfate reducing prokaryotes in a paddy soil of southern China under different fertilization regimes. Soil Biology and Biochemistry. 2009;41(4): 687–94.

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