

Huge anthropogenic microbial load during southwest monsoon season in coastal waters of Kakinada, Bay of Bengal.

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Abstract

To examine the influence of anthropogenic activities on the marine ecosystem near the coastal waters of the port city, Kakinada, a study was conducted to investigate the abundance of heterotrophic, indicator and pathogenic bacteria during the spring inter monsoon (SIM) and southwest monsoon (SWM) seasons. A drastic change in the marine bacteria due to the input of allochthonous bacteria during SWM was noticed. An order of magnitude higher abundance of indicators (*Escherichia coli* and *Enterococcus faecalis*) and bacterial pathogens (*Proteus mirabilis* and *Pseudomonas aeruginosa*) was observed during SWM. In contrast, Chlorophyll-*a*, heterotrophic bacterial abundance, *Aeromonas hydrophila* and *Klebsiella pneumoniae* were higher during SIM. A significant increase in some of the indicator and pathogenic bacterial abundance due to moderate rainfall suggests that the improper drainage system in the city could spread these bacteria, posing a considerable threat to both environment and human health.

Keywords: Heterotrophic, indicator & pathogenic bacteria; sewage; SIM & SWM seasons; anthropogenic activities; 16S rRNA gene sequence analysis.

1. Introduction

Coastal waters, which are transitional areas between land and ocean, include estuaries, inland water bodies, bays, salt marshes, beaches, mangrove forests, intertidal zone, coastal wetlands, etc. These areas are significant for their extensive ecosystem functionality and the services they provide. Nearly 2.4 billion people exist within 100 km of the coast (Factsheet, 2017). Coastal areas help in the livelihood of many people, which include fisher folk; industries related to fish production, preservation and export; several businesses related to maritime and recreational activities. Two-thirds of the world's major cities are located in coastal regions. Industries tend to be near these regions for their water requirements and uncomplicated discharge of wastes. These areas are also prone to high pollution as they are used as dumping zones.

Various monitoring methods and indicators are used to track the extent and change in pollution levels. *Escherichia coli* and *Enterococcus faecalis* are good indicators of faecal contamination and anthropogenic pollution from domestic and animal wastes and sewage (Sumampouw and Risjani, 2014; Rochelle-Newall et al., 2015). Indicator bacteria also act as a proxy for other pathogenic bacteria, and studies have shown their positive correlation (Hussain, 2019; Korajkic et al., 2018; Sudharani et al., 2018; Wu et al., 2011). According to the World Health Organization (WHO, 1996), mortality from water-related diseases is higher than 5 million people yearly. Deaths due to inadequate water, sanitation and hygiene in 2016 were 1.8 million people (WHO, 2018). Cholera, caused by the pathogenic bacterium *Vibrio cholerae*, is responsible for 21,000 to 1,43,000 deaths worldwide among all water-borne diseases (weekly epidemiological report, WHO, 2018). Other bacteria like *Aeromonas hydrophila*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Salmonella*, *Shigella* and *Staphylococcus aureus* are responsible for various diseases in humans and animals. The occurrence and number of both an indicator and pathogenic bacteria are affected by different factors. Sewage discharge into the coastal waters by different means, such as domestic, agricultural, industrial or port-related activities, is a significant cause of the increasing abundance of coliforms, faecal pollution indicators and bacterial pathogens (Caruso et al., 2004; Grøndahl-Rosado et al., 2014; Islam et al., 2017; Shehane et al., 2005; Tolouei et al., 2019; Tryland et al., 2014). A study by Sudharani et al. (2018) in Visakhapatnam offshore waters on the east coast of India indicates the effect of atmospheric forcing, coastal upwelling and monsoon on the abundance of heterotrophic, various indicators and pathogenic bacteria. These bacteria are found to be higher in number during the southwest monsoon. A study on the estuaries along the East coast of India found that the abundance of heterotrophic bacteria correlated with the magnitude of riverine discharge bringing organic matter and nutrients (Prasad et al., 2015).

In a country like India, which has a coastline of 7516.6 km, around 95% of trading by volume and 70% by value are carried out by maritime transport (Dasgupta, 2018). Kakinada, a minor port in Andhra Pradesh on the east coast of India, has been strategically placed between 2 major ports, Visakhapatnam and Chennai and includes an anchorage and a deep-water port. In this region, anthropogenic activities, such as industrial waste, domestic wastewater, and sewage and shipping, pollute the coastal ecosystem and affect the Coringa mangrove sanctuary (ICMAM, 2001; COMAPS report, 2018). Variability in water quality and microalgal diversity with time series measurements during different seasons was also observed in the Kakinada coastal water (Shaik et al., 2015).

Few studies performed on Kakinada coastal waters focus on the distribution of pathogenic bacteria, most of which are on the associated bacteria from shrimp farms. The shrimp quality is low due to the high microbial load (Kamat et al., 2005). *Vibrio* species isolated from diseased shrimp were found to be resistant to various antibiotics (Jayasree et al., 2008). To know the effect of land-driven and ship-borne discharge in this marine ecosystem, a fundamental study on the microorganisms of these waters must be available. However, there are no such data regarding the influence of anthropogenic activities on the spatial and temporal distribution of these bacteria in the offshore region of Kakinada. Therefore, the current study provides information on the abundance and variation of indicators and selected pathogenic bacteria in the waters off Kakinada city during dry and wet periods (corresponding to spring inter monsoon and southwest monsoon). To assess the effect of tidal variations on water quality, time series data were acquired at one station and single-time sampling was carried out from 4 surrounding stations twice, at high tide and low tide, as part of this study.

2. Materials and methods

2.1. Study area and sampling methods

Stations in this study were chosen near Kakinada port, situated along the coast of the East Godavari district of Andhra Pradesh. This port is a natural harbour. The Coringa mangrove patch (India's second-largest mangrove forest) is south of this port. A natural sandbar from the mangrove runs parallel to the Kakinada coastal region, making it safe from the impact of the cyclones or tsunamis generated in the Bay of Bengal. Various materials like iron ore, steel, coal, feldspar, fertilisers, forest products, bulk LPG etc., are exchanged between different countries through the Kakinada port. The port is a part of the proposed "Petroleum, Chemical and Petrochemical Investment Region" and a Special Economic Zone. The presence of agricultural and aquaculture activities, fertiliser industries and oil refineries nearby, port activities and other anthropogenic inputs has increased the pollution

load into the sea near this region. Bacterial pollution indicators, some waterborne pathogens, and physicochemical parameters can give an accurate picture of the pollution level. Therefore, stations were chosen near the opening of this bay into the open ocean waters to monitor the seasonal changes occurring in the bacterial load.

2.2. Sample collection

Five stations were sampled during the spring inter monsoon (SIM) (April 2019) and the southwest monsoon (SWM) (August 2019) comprising one central station (KC1) and 4 adjacent stations (KC2, KC3, KS1, KN1) (Fig. 1). Time-series (TS) measurements were performed at the central station KC1 at 3-hour intervals up to 36 h based on the local tide table of the sampling area (Fig. 2). Similarly, high-tide and low-tide (HT and LT) samplings were performed from the adjacent 4 stations. Samples collected during increasing tide were HT samples and decreasing tide as LT samples. Water samples were collected from both surface (1 m) and bottom (9 m), from the central and other 4 surrounding stations, using a 10 L pre-cleaned Niskin bottle (General Oceanics).

2.3. Physicochemical parameters

Salinity and temperature were recorded employing a portable conductivity, temperature and depth (CTD) profiler (SBE 19 plus, Sea-Bird Electronics, USA). Bubble-free water samples were collected in acid-washed glass bottles to analyse dissolved oxygen (DO) and biological oxygen demand (BOD). DO samples were immediately fixed with Winkler's reagents A and B. After five days of incubation at 20 °C, BOD samples were fixed with Winkler's reagents. Both samples were analysed by the Winkler titration method (Strickland and Parsons, 1972). For nutrient analysis (nitrate (NO₃), nitrite (NO₂), silicate (SiO₄), phosphate (PO₄), total nitrogen (TN) and total phosphate (TP)), water samples were collected in acid-washed plastic bottles and fixed immediately by 2 to 3 drops of mercuric chloride (0.2 M). Nutrients were analysed in the laboratory using standard spectrophotometric methods (Grasshoff et al., 1983). The Potentiometric (Metrohm, Zofingen, Switzerland) Gran-titration method was used to measure pH, following the standard operating procedures suggested by the Department of Energy (DOE, 1998). For chlorophyll-*a* measurement, water samples were filtered through Whatman GF/F filter paper of size 0.7 µm. Filter papers were soaked in 90% acetone at 4 °C overnight, and Chlorophyll-*a* concentration was determined by High-Performance Liquid Chromatography (HPLC, Agilent Technologies, USA). A C8 column was used, and chlorophyll-*a* peak was detected at 660 nm in the HPLC. The rainfall data of Kakinada city was obtained from the World Weather online web page (<https://www.worldweatheronline.com/kakinada-weather-averages/andhrapradesh/in.aspx>)(Supplementary Fig. S1). The overall rainfall (3-hour

precipitation accumulation) in and around the Kakinada region during the sampling time of the SWM season was obtained from Earth (<https://earth.nullschool.net/>)(Supplementary Fig. S2). It was presented as a 3-hour precipitation accumulation in that region.

2.4. Phytoplankton analysis

One litre of the water sample was preserved with 1 to 2 ml of Lugol's solution. Preserved samples were settled for 24 h and concentrated to 10 ml using a mesh of 20 µm size. Triplicate volumes (1 ml) of the concentrated sample were analysed under an inverted microscope. The diatoms and dinoflagellates were identified according to Tomas (1997).

2.4. Bacteriological parameters

Replicates of 100 ml of water were collected, stored at +4 °C and analysed for the target bacteriological parameters. Heterotrophic bacterial counts (HBC) were determined on R2A agar (HiMedia, M1743), total coliforms (TC) on MacConkey agar (HiMedia, M081B), *Escherichia coli* (EC), *Enterococcus* like organisms (ELO), *Klebsiella* like organisms (KLO), *Proteus* like organisms (PrLO), and *Staphylococcus like organisms* (SLO) on HiCrome Universal Differential agar (HiMedia, M1600), *Aeromonas like organisms* (ALO) on *Aeromonas* isolation agar (HiMedia, M884), *Salmonella* spp. and *Shigella* spp. (SSLO) on Xylose-Lysine deoxycholate (XLD) agar (HiMedia, M031), *Vibrio* spp. (TV) on Thiosulphate citrate bile salt sucrose (TCBS) agar (HiMedia, M189), *Pseudomonas like organisms* (PsLO) on *Pseudomonas* agar (HiMedia, M120). A 100 µl of the sample was spread on the respective agar plates. In case of higher growth, 10X dilution (1 µl of sample in 99 µl of autoclaved sea water) was re-spread. The plates were incubated at 37 °C for 24–48 h, and colonies were counted. Following the description of colony morphology on each media, presumptive positive colonies for the above-mentioned bacterial species were considered for counting. Results were reported as Colony-Forming Units (CFU) per ml of sample of heterotrophic bacteria, bacterial indicators and selected pathogens were determined by following Sudharani et al. (2018) and Prasad et al. (2015).

2.5. Phylogenetic analysis

Isolation of genomic DNA, polymerase chain reaction (PCR) amplification (Rotor-Gene Q, Qiagen), and sequencing of the 16S rRNA gene were performed as described by Surendra et al. (2012). The V3-V4 region of the 16S rRNA gene sequence was amplified and sequenced using V3V4F (3'-CCTACGGGNGGCWGCAG-5') and V3V4R (3'-GACTACHVGGGTATCTAATCC-5') primers and subjected to EzBioCloud (<http://ezbiocloud.net/>) search (Yoon et al., 2017) to find the nearest taxa. The closest 16S rRNA gene sequences of the type strains of different genera were downloaded

from NCBI (<http://www.ncbi.nlm.nih.gov>) and aligned using the CLUSTAL-W tool of MEGA version 6 (Tamura et al., 2013). The neighbor-joining method was used to construct the phylogenetic tree using MEGA 6. Two trees were established at the phylum level (*Firmicutes* and *Proteobacteria*). A total of 42 and 129 sequences and 460 and 297 positions were in the final datasets of trees related to the phyla *Firmicutes* and *Proteobacteria*, respectively. A bootstrap analysis of 1000 replicates was performed to infer the robustness of the phylogenetic tree, and the evolutionary distances were calculated using the Kimura-2-parameter (Kimura, 1980). The trees were drawn to scale, with branch lengths of the same units as those of the evolutionary distances used to infer the phylogenetic tree. All positions containing gaps and missing data were eliminated from the data (Complete deletion option).

2.6. Statistical analyses

To determine any significant difference in the physical and chemical parameters between the two seasons, parametric One-Way ANOVA (analysis of variance) was performed with Past 4.03 software. For bacteriological parameters, a non-parametric Kruskal–Wallis test was performed. The non-parametric Spearman's r_s correlation coefficient was calculated for each pair of variables. The significant threshold value was set up at $p < 0.05$. The impact of physicochemical parameters on bacteriological parameters was determined using principal component analysis (PCA) using Past 4.03 software (Hammer et al., 2001). Before PCA analysis, all the values were transformed according to the formula; New value (X') = $(X - \text{Mean})/\text{Stdev}$.

3. Results

3.1. Physicochemical parameters

The average surface temperature was 29.3 °C during SIM and 27.6 °C in SWM; the average subsurface temperature was 27.8 °C in SIM and 25.7 °C in SWM (Table 1). The sampling points showed significant temperature differences between SIM and SWM periods inferred by ANOVA ($p < 0.05$) (Table 1). The salinity variation between the two periods showed a maximum of 1 ppt. Surface and subsurface salinity values were comparable during the SIM period; however, during SWM, differences in salinity of 1–2 ppt were recorded (Table 1). Dissolved oxygen (DO) values varied from 3.6 to 8.9 mg/ml in the surface layer during SIM and 6.3 to 9.9 mg/ml during the SWM period (Fig. 3b). DO concentrations were significantly higher during the SWM period compared to SIM. Subsurface water showed lower DO concentrations than surface water during SIM, whereas the difference between the depths was low during SWM. Biological oxygen demand (BOD) values varied from 0.5 to 6.4 mg/ml in surface layers during SIM and 0.5 to 2.8 mg/ml during the SWM

period (Fig. 4b). BOD values of both depths are much higher during the SIM period compared to SWM (p-value < 0.05, Table 1). Nitrate (NO₃), nitrite (NO₂), phosphate (PO₄), silicate (SiO₄), TN, and TP concentrations were in the range of 0.16 to 2.67, 0.01 to 0.93, 0.01 to 2.92, 3.31 to 6.98, 4.09 to 5.91 and 1 to 1.83 μM respectively during SIM. During SWM, they ranged from 0.04 to 3.24, 0.15 to 0.71, 0.01 to 1.05, 0.67 to 5.96, 3.75 to 5.96, and 1 to 1.77 μM, respectively. Nitrate, phosphate and silicate concentrations were higher in the SIM period than in SWM. Nitrate concentration differences in the surface layers were significant between the SWM and SIM; however, the subsurface layer concentrations were comparable (Table 1). In the case of phosphate and silicate, the surface and subsurface values significantly differed between SIM and SWM (Table 1). Nitrate concentrations were comparable between surface and subsurface samples during SIM; however, the difference was noticeable during the SWM period. The vertical difference between phosphate and silicate concentrations was comparable during both periods. Variations in total nitrogen (TN) and total phosphorus (TP) between the periods were not significant. Overall, the SIM period was found to be nutrient-rich, warmer and higher saline than SWM. Spatial differences in the hydrographical parameters were comparable among the stations (KC1, KC2, KC3, KS1, and KN1).

Like other parameters, chlorophyll-*a* concentration also differed between the seasons (Fig. 3a). Chlorophyll-*a* concentration was higher in the SIM period compared to SWM (Table 1, Fig. 3a). Maximum of chlorophyll-*a*, i.e., 13.9 mg/l was found during the SIM period, and the maximum during SWM was 8.5 mg/l. Two noticeable features were found in the study site, a high abundance of *Coscinodiscus* with mixed diatom bloom (2.4×10^4 /L) during the SIM and heterotrophic red *Noctiluca* (dinoflagellate) bloom (1.2×10^4 /L) during the SWM period (unpublished data). The average rainfall data of the Kakinada city region showed very little to no rainfall during SIM and heavy rainfall during the SWM period (Supplementary Fig. S1). Although rainfall starts in June, the peak time is in September. During the sampling time of SIM season, there was no rainfall, but during SWM, moderate rainfall occurred (Supplementary Fig. S2).

3.2. Bacteriological parameters

Heterotrophic bacteria count (HBC) was lower in SWM than SIM (Fig. 4a). It ranged from 0.05 to 3.4×10^3 and 0.3 to 15.3×10^3 CFU/ml during SWM and SIM seasons, respectively. HBC positively correlated with BOD (Fig. 4). Indicator bacteria (IB) were observed at most stations during both seasons. Total coliform (TC), *Escherichia coli* (EC), and *Enterococcus* like organisms (ELO) counts were higher during SWM compared to SIM (Fig. 5a, 5b and 5c, respectively). The average values of TC, EC and ELO during SWM were 5×10^2 , 3.3×10^3 and 1.3×10^3 CFU/ml and during SIM were 1.6×10^2 , 6.9×10^2 and 1.4×10^2 CFU/ml respectively. EC numbers differed significantly between the

two seasons in both water depths (Table 2). Another enteric and pathogenic bacterium *Klebsiella* like organism (KLO), was found to be present in more significant numbers during SIM (highest: 1.7×10^3 CFU/ml) compared to SWM (highest: 4×10^2 CFU/ml) (Fig. 6b). The variation in KLO between the two seasons was significant ($p < 0.05$) (Table 2). *Proteus* like organisms (PrLO) were observed at three stations and in lower numbers during SIM compared to the SWM season (Fig. 7a). *Staphylococcus* like organisms (SLO) were found at two stations with low numbers in both the SIM and SWM seasons (Fig. 8c). Pathogenic bacteria (PB) such as *Salmonella* and *Shigella* like organism (SSLO) (Fig. 8a) and total *Vibrio* (TV) (Fig. 8b) were found at several sampling points and almost similar in both seasons. *Aeromonas* like organism (ALO) and SSLO range during SIM were 0 to 7.8×10^2 and 0 to 4.8×10^2 CFU/ml, respectively. During SWM, they were 0 to 2×10^2 and 0 to 8×10^2 CFU/ml, respectively. ALO, numbers were found to be significantly higher during SIM than SWM with a $p < 0.0001$ (Fig. 6a) (Table 2). Total *Vibrio* (TV) were in the range of 0 to 8.3×10^2 CFU/ml during SIM; they ranged from 0 to 9.5×10^2 CFU/ml during SWM (Fig. 8b). A significant difference in *Pseudomonas* like organism (PsLO) counts was seen between both seasons, which was significant ($p < 0.0001$) (Table 2). PsLO was found to be 100 times higher during SWM (range: 0 to 2×10^5 CFU/ml) compared to SIM (range: 0 to 4.7×10^3 CFU/ml) (Fig. 7b). The numbers of EC and PsLO at the other four stations showed a difference compared with other bacterial groups targeted in this study. EC and PLO counts were higher in high-tide samples compared to low-tide (Fig. 9).

3.3. Phylogenetic analysis

Phylogenetic analysis of all 16S rRNA gene sequences (144) generated in this study indicated that they belong to the two different phyla, *Firmicutes* (36 sequences), Proteobacteria (*Aeromonadaceae*, *Enterobacteriaceae* and *Yersiniaceae*) (73 sequences) and Proteobacteria (*Pseudomonadaceae*, and *Vibrionaceae*) (35 sequences) (Figs. 10a, b, c). Among the 36 sequences of the phylum *Firmicutes*, 20 sequences belong to the family *Enterococcaceae*, and the rest belong to the family *Staphylococcaceae* (Fig. 10a). Within the family *Enterococcaceae*, the strains were found to be close to *Enterococcus faecalis* and *Enterococcus faecium*. The sequence similarity among our sequences with closely related type strains was between 97.89 and 100%. Within the family *Staphylococcaceae*, the strains were found to be close to the *Staphylococcus aureus*, *Staphylococcus saprophyticus* and *Staphylococcus sciuri*. The sequence similarity among our sequences with closely related type strains was between 97.89 and 100%. Among the 108 sequences of the phylum *Proteobacteria*, 35 sequences belonged to the family *Aeromonadaceae*, 36 sequences belonged to the family *Enterobacteriaceae*, 19 sequences belonged to the family *Pseudomonadaceae*, 16 sequences belonged to the family *Vibrionaceae*, and two sequences belonged to the family *Yersiniaceae* (Figs. 10b, c).

Within the family *Aeromonadaceae*, the strains were found to be close to the *Aeromonas caviae*, *Aeromonas hydrophila*, *Aeromonas enteropelogenes*, *Aeromonas sobria* and *Aeromonas veronii*. The sequence similarity of our sequences with closely related type strains was between 97.12% and 100%. Within the family *Enterobacteriaceae*, the strains were found close to the *Enterobacter aerogenes*, *Enterobacter cancerogenus*, *Enterobacter tabaci*, *Escherichia coli* and *Klebsiella pneumoniae*. The sequence similarity among our sequences with closely related type strains was between 98.35 and 100%. Within the family *Pseudomonadaceae*, the strains were close to the *Pseudomonas alcaligenes*, *Pseudomonas balearica*, *Pseudomonas fluorescens* and *Pseudomonas fluvialis*. The sequence similarity among our sequences with closely related type strains was between 97.66 and 100%. Within the family *Vibrionaceae*, the strains were found to be close to the *Vibrio alginolyticus*, *Vibrio brasiliensis* and *Vibrio hepatarius*. The sequence similarity among our sequences with closely related type strains was between 97.19 and 100%. Within the Yersiniaceae family, the strains were found to be close to the *Yersinia pestis*. The sequence similarity among our sequences with closely related type strains was between 98.83 and 99.53%.

3.4. Statistical analysis

Multivariate analysis of various hydrographical, chemical and bacterial parameters is presented in the PCA plot, which shows two separate clusters: one cluster with the SWM measurements and the other with SIM measurements (Fig. 11). The first two components in Fig. 11 explain a 37.03% variance in the data (PC1: 23.54% and PC2: 13.49%). Increasing gradients of hydrographical parameters, temperature, salinity, nitrate, phosphate, and silicate, were oriented on the right-hand side of the plot along with observations of SIM measurements, in agreement with their higher values during SIM compared to SWM. The orientation of the ALO, TV, KLO, and HBC and the increasing direction with Chl-*a*, BOD and nutrients show a positive correlation. The axis of TC, SSLO, EC, ELO, and PsLO, oriented in the opposite direction of salinity and temperature during the SWM season, agrees with their abundance during the SWM season.

4. Discussion

4.1. Variation in physicochemical parameters during the SIM season

The bottom water temperature of the sampling stations during SIM was slightly lower than surface water though salinity values didn't differ much. Nutrients like nitrate, silicate and phosphate concentrations were higher in surface and bottom water, whereas bottom water DO values were lower than the surface. Nitrate inversely correlated with nitrite ($r = -0.73$, $p < 0.001$ surface; $r = -0.45$, $p < 0.05$ bottom) (Supplementary Tables 1 and 2). It indicates that nitrite reduction happens as the

nitrate concentration increases, which shows that remineralisation occurs during this season. Salinity correlated positively with phosphate and total phosphorus in the surface and total nitrogen in the bottom ($r = 0.54$, $p < 0.01$; $r = 0.44$, $p < 0.05$; $r = 0.56$, $p < 0.01$ respectively) (Supplementary Table 1 and 2). Nitrate inversely correlated with pH ($r = -0.50$, $p < 0.05$) in the surface water (Supplementary Table 1 and 2), indicating that with an increase in nitrate concentration, pH value decreases. A mixed diatom bloom was observed during the sampling with abundant *Coscinodiscus*, supported by higher silicate values in this water. Higher chlorophyll-*a* values (highest: 13.9 mg/l) of these samples confirm the occurrence of bloom. Chl-*a* correlated positively with silicate on the surface and with the temperature at the bottom ($r = 0.51$, $p < 0.05$) (Supplementary Tables 1 and 2), indicating that high silicate and temperature trigger the growth of phytoplankton. The DO concentration of the bottom water was found to be lower than that of the surface, suggesting the degradation of organic matter in the bottom water. The increased nutrient concentration might be due to the regeneration of the nutrients, which might be due to the possible high bacterial activity evident from the high BOD and low DO values in the bottom waters during this season. There was no rainfall during the sampling time, and rainfall during this season is deficient (Supplementary Fig. S1).

4.2. Variation in physicochemical parameters during the SWM season

During SWM salinity of the surface water is lower than that of bottom water, suggesting a possible effect of freshwater influx due to sewage discharge, rainfall, and land runoff (riverine inflow). Still, the latter is unsubstantial as the Godavari River water inflow does not directly enter the bay connected through the Coringa mangrove forest. It shows that agricultural and riverine influence increases as a significant part of the Godavari River discharge enters the open ocean as flash floods and due to sandbar, which covers the whole city area and the current direction (EICC towards north). The DO concentration was high in surface and bottom water, indicating good aeration. BOD values were comparatively lower (highest: 1.3 mg/l) than SIM, indicating low heterotrophic bacterial activity. Nutrient concentrations were low compared to the SIM season, especially silicate, as the riverine input was low (Table 1). Phosphate correlated positively with nitrate + nitrite and nitrate ($r = 0.56$, $p < 0.05$; $r = 0.60$, $p < 0.05$) (Supplementary Tables 3 and 4). The low silicate concentration shows a limited riverine influence in this region. Silicate correlated inversely with temperature and nitrate ($r = -0.55$, $p < 0.05$; $r = -0.57$, $p < 0.05$) (Supplementary Tables 3 and 4). The average Chl-*a* concentration (surface water: 3.2 mg/l, bottom water: 4.15 mg/l) in these waters was low compared to the SIM. During the sampling period, the bloom of the heterotrophic dinoflagellate, red *Noctiluca*, was observed. These organisms graze upon plankton, diatoms, other dinoflagellates, fish eggs and even bacteria (Kirchner et al., 1996; Nakamura, 1998). The low Chl-*a* concentration of these waters

can be attributed to the grazing of phytoplankton by *Noctiluca*. According to the study by D'Silva et al. (2012), algal blooms along the East and West coasts of India provide information on the onset of *Noctiluca* blooms, which are succeeded by diatom bloom. During SIM, diatom blooms are observed, preceded by *Noctiluca* blooms during SWM. The average pH of this water was 8.0 for the surface and 7.9 for the bottom water, which was a little basic. *Noctiluca* releases ammonia into the surrounding water, increasing in a later stage of the bloom (Baliarsingh et al., 2016), which explains the higher pH in the water column during SWM. A parametric one-way ANOVA test for physicochemical parameters between 2 seasons suggested significant variation in values of different physical and chemical parameters with $p < 0.05$ (Table 1). According to the average rainfall data, the rain starts in May (very few). Still, high rainfall happens from June onwards, peaking from July to September and decreasing in December (Supplementary Fig. S1).

4.3. Variation in microbiological parameters during SIM season

R2A agar plates were used for heterotrophic bacterial counts, which support the growth of slow-growing bacteria resulting in higher diversity than numbers. HBC during the SIM season were higher than in SWM. These bacteria help break down organic matter into simpler compounds and release nutrients into the environment (Azam et al., 1983; Landa et al., 2014; Taylor et al., 1985). Due to mixed diatom bloom, the activity of HBC in the water column is enhanced, as evidenced, by the lower DO values and higher BOD in the water column. Heterotrophic bacteria use for their growth both dissolved and particulate organic matter, both derived from phytoplankton. The maximum BOD value of these waters was 6.38 mg/l suggesting a high level of bacterial activity, which the high DOC and POC support during the phytoplankton bloom formation and senescence as the bacteria use up oxygen while performing respiration for the degradation of organic matter (Jouanneau et al., 2014; D'Silva et al., 2012). HBC is inversely correlated with total phosphorus ($r = -0.57$, $p < 0.01$) in bottom water (Supplementary Table 2). As low indicator bacterial abundance is found, high HBC and BOD suggest the prevalence of autochthonous compared to allochthonous bacteria. Indicator bacterial low abundance supports this in the water column during this season. These bacteria show that untreated/low-treated sewage water from either land (domestic or industrial), ship-borne discharges, or fisherfolk activities are evident. Although this bacterial abundance is low (1.0×10^3 CFU/ml for *E. coli* and 1.4×10^2 CFU/ml for *E. faecalis*), it is much above the standard limit (5 CFU/ml for *E. coli* and 0.35 CFU/ml for *E. faecalis*) in marine recreational waters (EU Directive 2006/7/EC, 2006; Lévesque and Gauvin, 2007). Cells of *Escherichia coli* and *Vibrio cholerae* might go into a specific condition known as the viable but non-culturable state in marine waters (Caruso et al., 2003; Li et al., 2014). As a result, the CFU detected on the respective media may underestimate the actual number

of bacteria in the sample. TC positively correlated with silicate and Chl-*a* ($r = 0.45$, $p < 0.05$; $r = 0.52$, $p < 0.05$) in the bottom water (Supplementary Table 2), indicating that TC is high where phytoplankton abundance is high. Although TC is generally thought to be allochthonous, some parts are also from marine biota, and simultaneously, these microbes withstand the salinity of seawater and can survive and proliferate (Piccolomini et al., 1987). EC positive correlation with total phosphorus ($r = 0.49$, $p < 0.05$) in the surface water (Supplementary Table 1) indicates that EC is high where the total phosphorus concentration is high. ELO in the bottom water positively correlated strongly with EC ($r = 0.84$, $p < 0.001$) (Supplementary Table 2), indicating that if EC is high, the possible occurrence of ELO is also high as both are enteric bacteria. Similar to the indicator bacteria, other pathogenic bacteria such as *Proteus mirabilis* like organisms and *Pseudomonas* like organisms counts were low. The *Salmonella* sp., *Shigella* sp., and *Staphylococcus* like organisms and total *Vibrio* counts were high or low similar to the SWM season. PrLO inversely correlated with salinity ($r = -0.52$, $p < 0.05$) (Supplementary Table 1) in the surface water indicates that they are allochthonous bacteria and inhibited by salinity. PrLO is positively correlated with HBC ($r = 0.72$, $p < 0.001$) (Supplementary Table 1) in the surface water, indicating that they are part of heterotrophic bacteria. PsLO inversely correlated with nitrate + nitrite, nitrate, total phosphate and Chl-*a* ($r = -0.57$, $p < 0.01$; $r = -0.50$, $p < 0.05$; $r = -0.43$, $p < 0.05$; $r = -0.51$, $p < 0.05$) (Supplementary Table 1) in the surface water indicating that they are allochthonous bacteria and their abundance increases when phytoplankton abundance decreases. PsLO in the bottom water positively correlated with HBC ($r = 0.48$, $p < 0.05$) (Supplementary Table 2), indicating that they are part of heterotrophic bacteria. SSLO positively correlated with Chl-*a*, TC, and ALO ($r = 0.43$, $p < 0.05$; $r = 0.71$, $p < 0.001$; $r = 0.81$, $p < 0.001$) (Supplementary Table 1 and 2), indicating that SSLO abundance is related to them. TV positively correlated with silicate, TC, EC, ELO, ALO and SSLO ($r = 0.43$, $p < 0.05$; $r = 0.74$, $p < 0.001$; $r = 0.68$, $p < 0.001$; $r = 0.67$, $p < 0.01$; $r = 0.57$, $p < 0.01$; $r = 0.57$, $p < 0.01$) (Supplementary Table 1 and 2) indicated that TV abundance was related to them. There is no standard limit for the PB in marine waters; care must be taken during and after recreational activities. Interestingly PB such as ALO and KLO were present in most of the stations of SIM samples, and their abundance was higher than in the SWM season. These bacteria are commonly present in marine waters (Podschn et al., 2001; Barati et al., 2016; Dumontet et al., 2000; Mukhopadhyay et al., 2008; Prasad et al., 2015; Sudharani et al., 2018). ALO is a fish pathogen that causes serious infections in freshwater and marine fishes (Akmal et al., 2020). ALO inversely correlated with DO ($r = -0.46$, $p < 0.05$) in the surface water (Supplementary Table 1), indicating that ALO is facultative and can grow in a low DO environment too. ALO positively correlated with silicate, Chl-*a* and TC ($r = 0.43$, $p < 0.05$; $r = 0.52$, $p < 0.05$; $r = 0.92$, $p < 0.001$) in the surface water (Supplementary Table 1) indicating that they are

autochthonous bacteria and their abundance increases in the presence of DOC, which is released from the phytoplankton. Similarly, TC related to Chl-*a* ALO is related to both Chl-*a* and TC. In the aquatic ecosystem, KLO acts as the main vector of drug-resistance genes to clinically significant bacteria (Wyres and Holt, 2018). KLO positively correlated with ELO and ALO ($r = 0.51$, $p < 0.05$; $r = 0.52$, $p < 0.05$) in the surface water (Supplementary Table 1), indicating that KLO is high in parallel with high ELO and ALO abundance. Both organisms can cause serious life-threatening human infections, such as septicemia, meningitis, pneumonia, endocarditis and urinary tract infections (O'Beirne and Francis, 2003; Wang et al., 2020).

4.4. Variation in microbiological parameters during the SWM season

HBC counts during SWM are low compared to the SIM season. It is supported by results as follows: (a) The presence of *Noctiluca* bloom during SWM, which grazes on bacteria (Kirchner et al., 1996; Nakamura, 1998); (b) the low BOD values in the water column during SWM, which supports low heterotrophic bacterial activity; (c) low chl-*a* concentration. The presence of indicator bacteria, such as *Escherichia coli*, *Enterococcus faecalis* and pathogenic bacteria, such as *Proteus* like organisms and *Pseudomonas* like organisms an order of magnitude higher than SIM season can be attributed to rainfall, because of heavy anthropogenic microbial load (land-driven), during the monsoon as rainwater drains the sewage, which, drastically changes the bacterial diversity of the marine water then results in the low abundance of culturable heterotrophic bacteria and their activity in terms of BOD. HBC is inversely correlated with nitrite ($r = -0.68$, $p < 0.01$) in the bottom water (Supplementary Table 4). Generally, nitrite concentration in marine water is low, and the higher concentration shows its intrusion from sewage, which also releases land-driven bacteria HBC-positive correlation with BOD ($r = 0.79$, $p < 0.01$) (Supplementary Table 4) in the bottom water indicates that if BOD is high; HBC is also high. Low BOD indicates a low HB activity. IB, such as EC and ELO, was observed to be an order of magnitude higher compared to the SIM samples. EC and ELO are considered excellent indicators of faecal contamination and sewage pollution, and their numbers increase during high discharge after rainfall (Serrano et al., 1998; Wheeler et al., 2002; Wyer et al., 1995). High numbers of EC and EF during the SWM season in our study show the effect of land runoff from coastal settlements during SWM and the possible effect of anthropogenic activity. Average rainfall data show that most of the land-driven microbial load in the city had to be washed away during June and July. Moderate rainfall was noticed during the sampling time (Supplementary Fig. S2). But a huge abundance of allochthonous bacteria noticed during the sampling time (mid-August) shows that the city's drainage system is improper. With moderate rainfall itself, human waste enters the coastal water directly. It shows that the accumulated drainage

during the monsoon's starting period may make the coastal water uninhabitable to the local biota. IB counts have also been observed in the coastal and offshore waters of several coastal cities on the east coast of India, indicating the release of untreated sewage (Clark et al., 2003; DebRoy et al., 2012; Patra et al., 2009; Prasad et al., 2015; Sudharani et al., 2018). IB indicates the possible presence of PB in those water samples (Piccolomini et al., 1987; Rozen and Belkin, 2001). Very few PB, such as ALO and KLO, were observed during this season, which supports their natural presence in the marine water. Besides this, ALO prefers warmer temperatures as the temperature values are lower than 2 °C compared to the SIM season. ALO in the surface water positively correlated with HBC, TC and ELO ($r = 0.58$, $p < 0.05$; $r = 0.50$, $p < 0.05$; $r = 0.63$, $p < 0.01$) (Supplementary Table 3), indicating that they co-exist together. KLO is inversely correlated with silicate ($r = -0.53$, $p < 0.05$) in the surface water (Supplementary Table 3). KLO correlated positively with ELO ($r = 0.96$, $p < 0.001$) in the bottom water (Supplementary Table 4). SLO and TV were observed to be nearly the same as the SIM seasons, except for TV in bottom water during this season. But the mere presence of these bacteria in marine coastal waters is alarming. They are present in both dry and wet seasons, being members of the autochthonous marine microflora. A drastic increase in the PB, such as PrLO and PsLO, is an order of magnitude higher than the SIM season was also seen. *Proteus* spp. are recognised as human opportunistic pathogens isolated from clinical sources such as urine and wounds. These bacteria are highly proteo- and ureo- lytic and are commensals of the intestines and several wild and domestic fauna, which may be hosts of *Proteus* spp., and play a task of commensals or parasites (Drzewiecka, 2016). *Proteus* spp. can cause pneumonia, sepsis, and wound infections (mostly in hospitalised patients) (Schaffer and Pearson, 2015). PsLO is generally found in soil and has broad fundamental niches, which include coastal marine habitats, soil, marshes, plant and animal tissues, rhizospheres, freshwater, skin flora, and most artificial environments throughout the world. They have high metabolic diversity, intrinsic and acquired antibiotic resistance, resistance to multiple drugs, and inherently superior antibiotic resistance mechanisms. They have a relationship with severe health problems, hospital-acquired diseases such as ventilator-associated pneumonia and various sepsis syndromes and can adapt to varied physical conditions (Goldberg, 2000; Pirnay et al., 2009). The substantial increase in PsLO during SWM (>100 times) over SIM season shows that a huge anthropogenic microbial load is entering the marine ecosystem, drastically changing marine biodiversity during this season. The most significant difference in numbers was seen in PLO and PsLO counts ($p < 0.0001$) during this season compared to SIM. Guimarães et al. (1993) found that PsLO counts were notably higher in freshwater than in marine water. It also supports the high number of these bacteria during SWM when the freshwater intrusion into the coastal water is greater. In another study, it was established that there is a strong positive correlation between EC and PsLO,

similar to this study, where both the number of EC and PsLO were found to be high during SWM (Januário et al., 2020). PsLO in the surface water positively correlated with EC ($r = 0.91$, $p < 0.001$) (Supplementary Table 3), which indicates that a high abundance of EC shows the possible occurrence of high PsLO. A study by Nallathambi et al. (2002) of Port Blair Bay, Andaman, determined numbers of PA and faecal coliforms were high when there were *Noctiluca* blooms, similar to this study during SWM. SSLOs were found in most stations during both times, but their numbers were higher during SWM. Among the *Vibrio*, *Vibrio cholerae* like organisms were found in both seasons. During SWM, *Vibrio parahaemolyticus* like organisms were also found along with *V. cholera* like organisms, but the occurrence of *Vibrio vulnificus* like organisms were very low during both seasons. TV positively correlated with TC ($r = 0.68$, $p < 0.01$) in the bottom water (Supplementary Table 4), indicating that a high abundance of TC shows the possible occurrence of high TV. Statistical analysis of these bacterial numbers from 2 seasons was also found to be significant in the case of EC, KLO, ALO, TV and PsLO ($p < 0.05$) (Supplementary Table 3).

4.5. Phylogenetic analysis

Using the sequence similarity threshold value of 97%, 16S rRNA gene sequence similarities of the 144 sequences were categorised into 22 phylotypes (Figs. 10a, b and c). Taxonomic analysis indicated that 36 (5 phylotypes) were Gram-positive, and 108 (17 phylotypes) were Gram-negative. Although the sequences obtained were clustered with the type strains and fell within the clade, some sequences clustered separately. It shows the possible novel taxa among them. We find four clusters in the *Enterococcus faecium* clade; one sequence is entirely outside the cluster. In the *Enterococcus faecalis*, we find two clusters. Coming to the family *Staphylococcaceae*, we find 4 clusters and two sequences clustered outside. In the case of *Aeromonadaceae*, 7 clusters were observed. In *Enterobacteriaceae*, seven clusters were observed. In *Pseudomonadaceae*, six clusters were observed, and in *Vibrionaceae*, three clusters were found. The phylogenetic analysis showed that the identified CFU based on the culturable method matched with molecular identification with few exceptions. All the sequences related to *Escherichia coli* were clustered with the same species and were closely related. All the CFU identified as *Enterococcus* were clustered with *Enterococcus faecalis* and *E. faecium*. *E. faecium* is a commensal in the gastrointestinal tract of humans and animals, but it may also be pathogenic, causing diseases such as endocarditis or neonatal meningitis (Agudelo Higuera and Huycke, 2014). In the case of CFU identified as *Aeromonas*, the sequences were close to those of *A. caviae*, *A. enteropelogenes*, *A. hydrophila*, *A. sobria* and *A. veronii*. *A. caviae* can cause diarrhoea in children (Beatson et al., 2011). *A. sobria* is generally widespread in the environment and causes gastroenteritis in humans and septicemia in fish (Zhang et al., 2021). *A.*

veronii is an important pathogen that causes freshwater fish sepsis and ulcer syndrome (Li et al., 2020). In the case of CFU identified as *Enterobacter aerogenes*, the sequences were close to those of *E. aerogenes*, *E. cancerogenus* and *E. tabaci*. *E. aerogenes* is a significantly opportunistic and multi-resistant bacterial pathogen to humans (Davin-Regli and Pagès, 2015). *E. cancerogenus* is an opportunistic human pathogen (Wei et al., 2013). In the case of colonies identified as *Klebsiella*, the sequences were close to the same but formed 4 clusters. In the case of colonies identified as *Pseudomonas* the sequences were close to *P. alcaligenes*, *P. balearica*, *P. fluorescens* and *P. fluvialis*, but not close to *P. aeruginosa*. *P. alcaligenes* is a rare opportunistic human pathogen (Martino et al., 1990). *P. fluorescens* does not cause human disease and usually affects patients with compromised immune systems (e.g., patients on cancer treatment) (Gershman et al., 2008). In the case of colonies identified as *Staphylococcus*, the sequences were close to those of *S. aureus*, *S. saprophyticus* and *S. sciuri*. *S. saprophyticus* is a common cause of community-acquired urinary tract infections (Kuroda et al., 2005). *S. sciuri* is an important human pathogen responsible for endocarditis, peritonitis, septic shock, urinary tract infection, pelvic inflammatory disease and wound infections (Chen et al., 2007). In cases of colonies identified as *Vibrio*, the sequences were close to those of *V. alginolyticus*, *V. brasiliensis* and *V. hepatarius*. *V. alginolyticus* is one of the most common pathogenic marine *Vibrio* species and has caused severe seafood-poisoning or fatal extra-intestinal infections in humans, such as necrotising soft-tissue infections, bacteremia, septic shock, and multiple organ failures (Fu et al., 2016). *V. brasiliensis* is a shrimp pathogen isolated from the Pacific white shrimp *Penaeus vannamei* (Li et al., 2021). We found two sequences which were clustered and close to *Yersinia pestis*. We could not identify the *Proteus mirabilis* and *Salmonella*, *Shigella* like organisms using 16S rRNA gene sequence analysis. Other bacteria identified, such as *E. tabaci*, *P. balearica*, *P. fluvialis* and *V. hepatarius*, were not found to be pathogenic. *E. tabaci* is a recently identified bacterium isolated from a tobacco stem (Duan et al., 2015). *P. balearica* is a denitrifying and environmental bacterium mostly isolated from polluted environments worldwide (Bennasar et al., 1996). *P. fluvialis* is a recently identified bacterium isolated from the Ganges, India (Sudan et al., 2018). *V. hepatarius* was isolated from aquatic animals and the marine environment (Thompson et al., 2003).

4.6. Impact of tidal variation on bacterial abundance

TC, EC, and PsLO counts differed between high- and low-tide samples during both seasons. EC counts were high in all sampling stations during high-tide in SIM. Similarly, during the SWM season, all high-tide samples (except one station) showed higher counts than low-tide samples (Fig. 9). PrLO counts also showed a similar trend during the SIM and SWM seasons. Studies by Solo-

Gabriele et al. (2000) from a coastal waterway in Florida and Shibata et al. (2004) from 2 beaches (Hobie and Crandon beach) showed a positive impact of tidal height on the abundance of IB, which supports our results. Mixing during high tide in the shallow height of the water column can result in a higher bacterial load because of the resuspension of sediment and bottom waters. Not much difference was seen in HBC and other PB counts (KLO, PrLO, PsLO, TV, ALO, and SSLO) during high- and low-tide.

5. Conclusion

Seasonal studies during the dry and wet seasons with different physical and atmospheric events on the Bay of Bengal west coast reveal that SWM and SIM significantly impact nutrient cycling and phytoplankton biomass, which further impacts the heterotrophic, indicator and pathogenic bacterial abundance in the water column. HBC showed significant temporal and spatial variations along with the different stations near Kakinada coastal waters due to diverse physical and biogeochemical phenomena. Higher HBC and BOD were noticed during the SIM period due to the increased availability of nutrients to phytoplankton, which releases elevated dissolved organic carbon into the water, boosting heterotrophic bacterial metabolism. Indicator bacteria abundance was noticed in the entire study area during both SWM and SIM, with a vast abundance during SWM. TC, EC and ELO were an order of magnitude higher during SWM, possibly due to the influence of land-driven discharge accompanied by precipitation during this season. We found a correlation between IB and PB; wherever IB presence is observed, PB occurrence is also observed, but it is inconsistent; this implies that not all untreated discharges to the coastal water due to land driving or due to shipping traffic, fisher folk's activities in the sea might not contribute to PB. Coliforms (TC, EC and ELO) and potentially pathogenic bacteria such as PrLO and PsLO were noticed in huge numbers, an order of magnitude higher than the SIM season. Anthropogenic impact near coastal water with untreated/partial discharges from land and direct discharges by large ships and fishing activity makes various harmful bacteria thrive. It leads to declining marine water quality and affects coastal human population health. This study reveals the significant impact of the monsoon on the water column biogeochemistry and the phytoplankton, heterotrophic, indicator and pathogenic bacteria in the coastal Bay of Bengal. This study also emphasises that the city's drainage system is improper. With moderate rain, a substantial anthropogenic discharge enters the coastal water, which may cause a menace. Further studies must examine the microbial source tracking of the enteric bacteria and how these allochthonous microbes influence the marine (autochthonous) bacterial abundance and its impact on the other ecosystem components. Regular monitoring of these waters and further studies

must identify the possible source of pollution, which is required to establish effective policies for sewage discharge and their pre-treatment before being released into the coastal waters.

Authors' contributions

STNR: Conceptualization, Project administration, Methodology, Writing - Review & Editing; KMSR: Writing - Review & Editing of physicochemical parameters; JL: Writing - Review & Editing of biological parameters; Swarnaprava Behera: Supervision, Methodology, Writing - original draft, Review & Editing. Sravani, M., Satyanarayana Reddy, T., Vivek Rachuri: Formal analysis, Visualisation, Investigation, Data curation.

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Figure legends:

Fig. 1. The study area (Kakinada city, port and sampling stations) indicates the time-series station (KC1) and other surrounding stations (KC2, KC3, KN1 and KS1)

Fig. 2. Local tide table in the study area during the sampling periods

Fig. 3. Temporal variation of Chl-*a* (a) and DO (b) in surface and bottom waters during SIM and SWM seasons at TS and high- and low-tide sampling points (average value is shown as a straight line)

Fig. 4. Temporal variation of HBC (a) and BOD (b) in surface and bottom waters during SIM and SWM seasons at TS and high- and low-tide sampling points (average value is shown as a straight line)

Fig. 5. Temporal variation of total coliforms (a), *Escherichia coli* (b) and *Enterococcus* like organisms (c) in surface and bottom waters during SIM and SWM seasons at TS and high- and low-tide sampling points (average value is shown as a straight line)

Fig. 6. Temporal variation of *Aeromonas* like organisms (a) and *Klebsiella* like organisms (b) in surface and bottom waters during SIM and SWM seasons at TS and high- and low-tide sampling points (average value is shown as a straight line)

Fig. 7. Temporal variation of *Proteus* like organisms (a) and *Pseudomonas* like organisms (b) in surface and bottom waters during SIM and SWM seasons at TS and high- and low-tide sampling points (average value is shown as a straight line)

Fig. 8. Temporal variation of *Salmonella/Shigella* like organisms (a), *Staphylococcus* like organisms (b) and total *Vibrio* (c) in surface and bottom waters during SIM and SWM seasons at TS and high- and low-tide sampling points (average value is showed as a straight line)

Fig. 9. High tide and low-tide variation in the numbers of *Escherichia coli* and *Pseudomonas aeruginosa* both during SIM and SWM seasons

Fig. 10. Phylogenetic trees based on 16S rRNA gene sequences showing the relationship of sequences related to the phyla Firmicutes (a), Proteobacteria (*Aeromonadaceae*, *Enterobacteriaceae* and *Yersiniaceae*) (b), and Proteobacteria (*Pseudomonadaceae*, and *Vibrionaceae*) (c) obtained from water samples collected from the Kakinada time-series station, with their nearest phylogenetic relatives. Phylogenetic trees were constructed by the neighbor-joining method. Numbers at nodes are bootstrap values. Bootstrap support values of more than 50% are shown at the nodes. *Bacillus subtilis* IAM 12118^T (AB042061) was used as an out-group taxon for (a) and *Caulobacter vibrioides* CB51^T (AJ009957) was used as an out-group taxon for (b), and (c), respectively. The bar represents 0.01, 0.02 and 0.02 substitutions per alignment position in (a), (b) and (c).

Fig. 11. Principal Component Analysis (PCA) of physicochemical and bacteriological parameters (HBC, heterotrophic bacterial counts, TC: total coliforms, EC: *Escherichia coli*, ELO: *Enterococcus* like organisms, ALO: *Aeromonas* like organisms, KLO: *Klebsiella* like organisms, PrLO: *Proteus* like organisms, PsLO: *Pseudomonas* like organisms, SS: *Salmonella* and *Shigella* like organisms, TV: total *Vibrio*) of time-series station (KC) (red dots represent SWM samplings and violet dots represent SIM samplings)

Supplementary Fig. S1. The average rainfall data of Kakinada city

Supplementary Fig. S2. The three-hour precipitation accumulation data of the sampling period during the SWM season

Supplementary Fig. S3. Microscopic pictures of *Coscinodiscus* with other diatoms (during April 2019) and Red *Noctiluca* (during August 2019)

Table 1. Mean values and standard deviation of physicochemical parameters of all stations combined during SIM and SWM periods and Parametric One-Way ANOVA test of physicochemical parameters between SIM and SWM season (ns: non-significant (p-value > 0.5), *significant, **highly significant)

Name	Spring Inter Monsoon		South West Monsoon		P - value	
	Surface	Bottom	Surface	Bottom	Surface	Bottom
Temperature (°C)	29.34 ± 1.09	27.79 ± 0.4	27.65 ± 0.8	25.72 ± 0.5	<0.0001**	<0.0001**
Salinity	34.15 ± 0.24	34.75 ± 0.2	33.41 ± 0.6	34.41 ± 0.1	<0.0001**	<0.0001**
NO₃ (µM)	1.46 ± 0.72	1.37 ± 0.58	0.65 ± 0.51	1.06 ± 1.05	<0.0001**	ns
NO₂ (µM)	0.38 ± 0.27	0.41 ± 0.25	0.43 ± 0.14	0.47 ± 0.14	ns	ns
SiO₄ (µM)	5.26 ± 0.92	5.39 ± 0.05	3.18 ± 1.28	3.71 ± 1.16	<0.0001**	<0.0001**
PO₄ (µM)	0.62 ± 0.46	1.02 ± 0.8	0.36 ± 0.28	0.41 ± 0.36	<0.05*	<0.05*
TN (µM)	5.15 ± 0.52	5.43 ± 0.45	5.15 ± 0.61	5.37 ± 0.47	ns	ns
TP (µM)	1.25 ± 0.22	1.32 ± 0.22	1.24 ± 0.12	1.34 ± 0.17	ns	ns
DO (mg/l)	6.66 ± 1.49	4.63 ± 1.65	7.6 ± 3.03	6.8 ± 2.74	ns	<0.0001**
BOD (mg/l)	3.40 ± 1.49	2.14 ± 1.37	0.78 ± 0.83	0.83 ± 0.8	<0.0001**	<0.05*
pH	7.48 ± 0.15	7.48 ± 0.15	8.01 ± 0.09	7.97 ± 0.09	<0.0001**	<0.0001**
Chlorophyll-<i>a</i>	7.49 ± 3.09	5.11 ± 2.7	3.16 ± 2.03	3.97 ± 2.25	<0.0001**	ns

Table 2. Non-parametric Kruskal–Wallis test of bacteriological parameters between SIM and SWM season (ns: non-significant (p-value > 0.5), *significant, **highly significant)

Parameter	Surface		Bottom	
	H-value	p-value	H-value	p-value
Heterotrophic bacterial counts	1.4	ns	0.0034	ns
Total coliforms	0.48	ns	3.13	ns
<i>Escherichia coli</i>	6.88	<0.05*	11.29	<0.005**
<i>Enterococcus</i> like organism	0.19	ns	0.01	ns
<i>Aeromonas</i> like organism	17.53	<0.0001**	15.28	<0.0001**
<i>Klebsiella</i> like organism	12.44	<0.05*	6.8	<0.05*
<i>Proteus</i> like organism	2.25	ns	0.06	ns
<i>Pseudomonas</i> like organism	24.49	<0.0001**	25.3	<0.0001**
<i>Salmonella</i> and <i>Shigella</i> like organism	0.06	ns	1.02	ns
Total <i>Vibrio</i>	4.3	<0.05*	1.09	ns

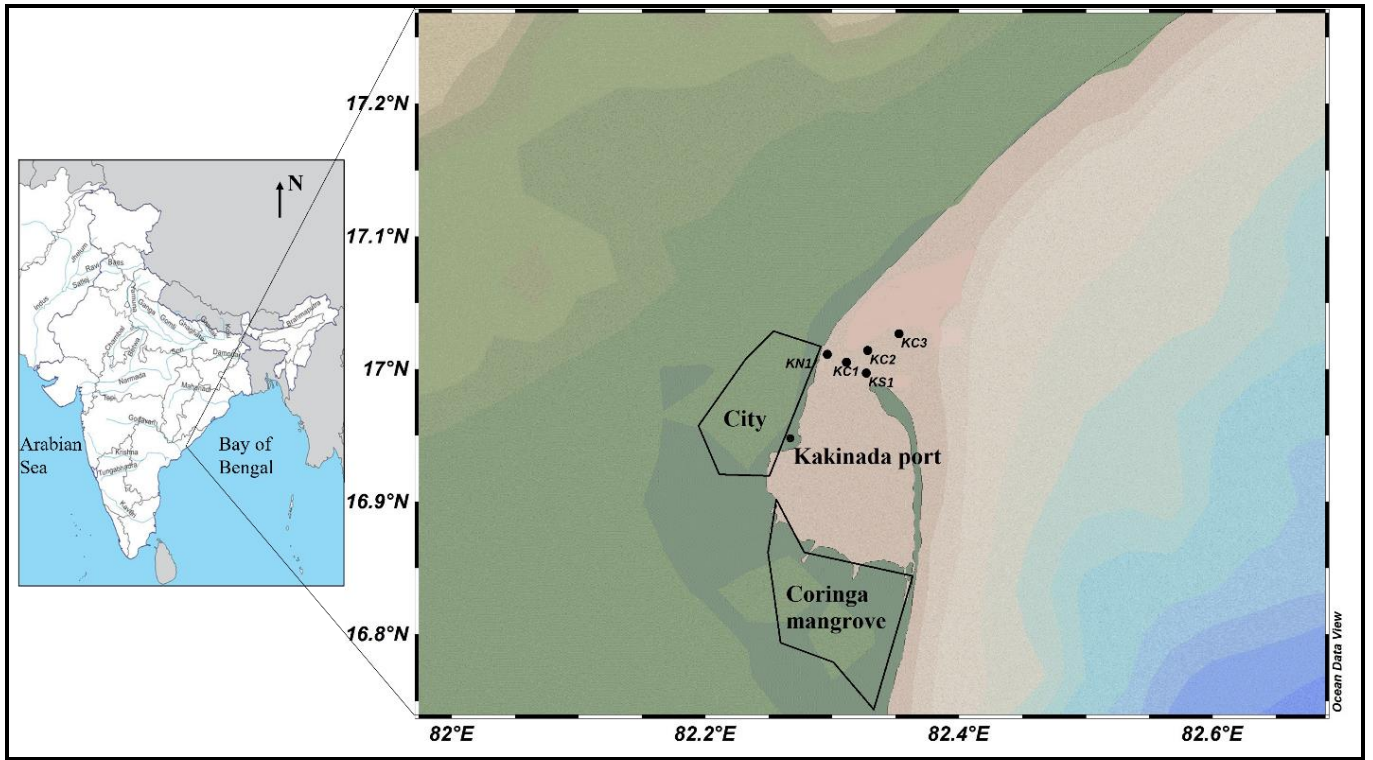


Fig. 1

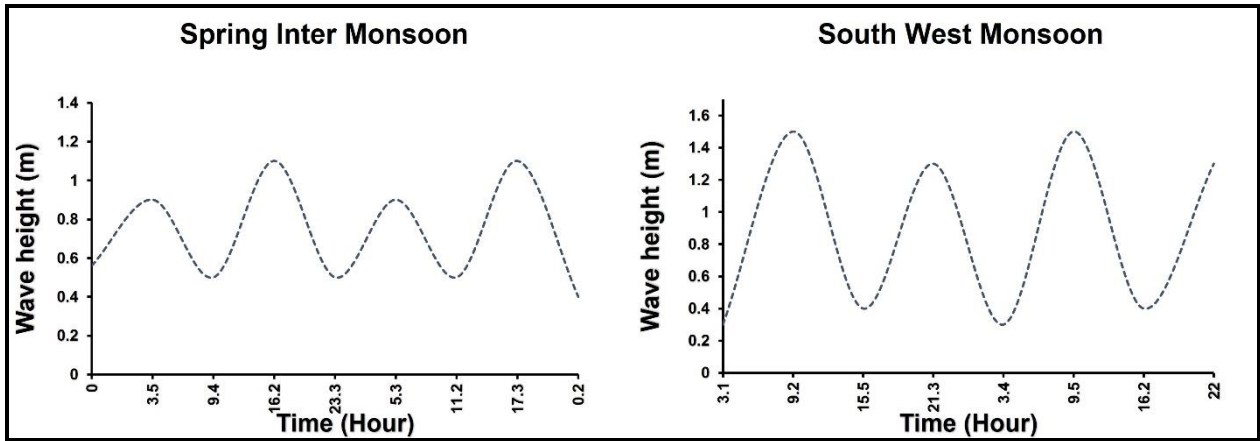


Fig. 2

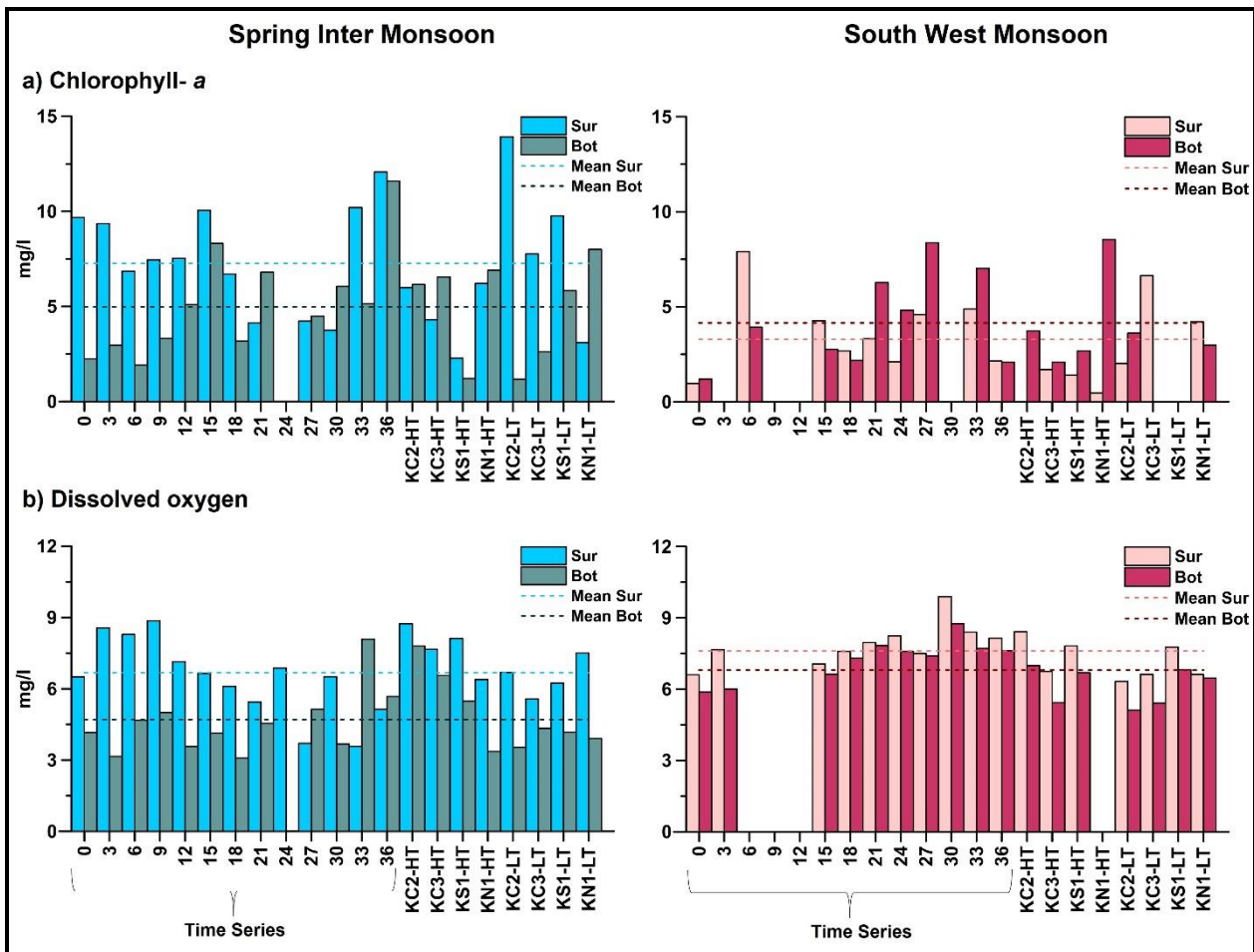


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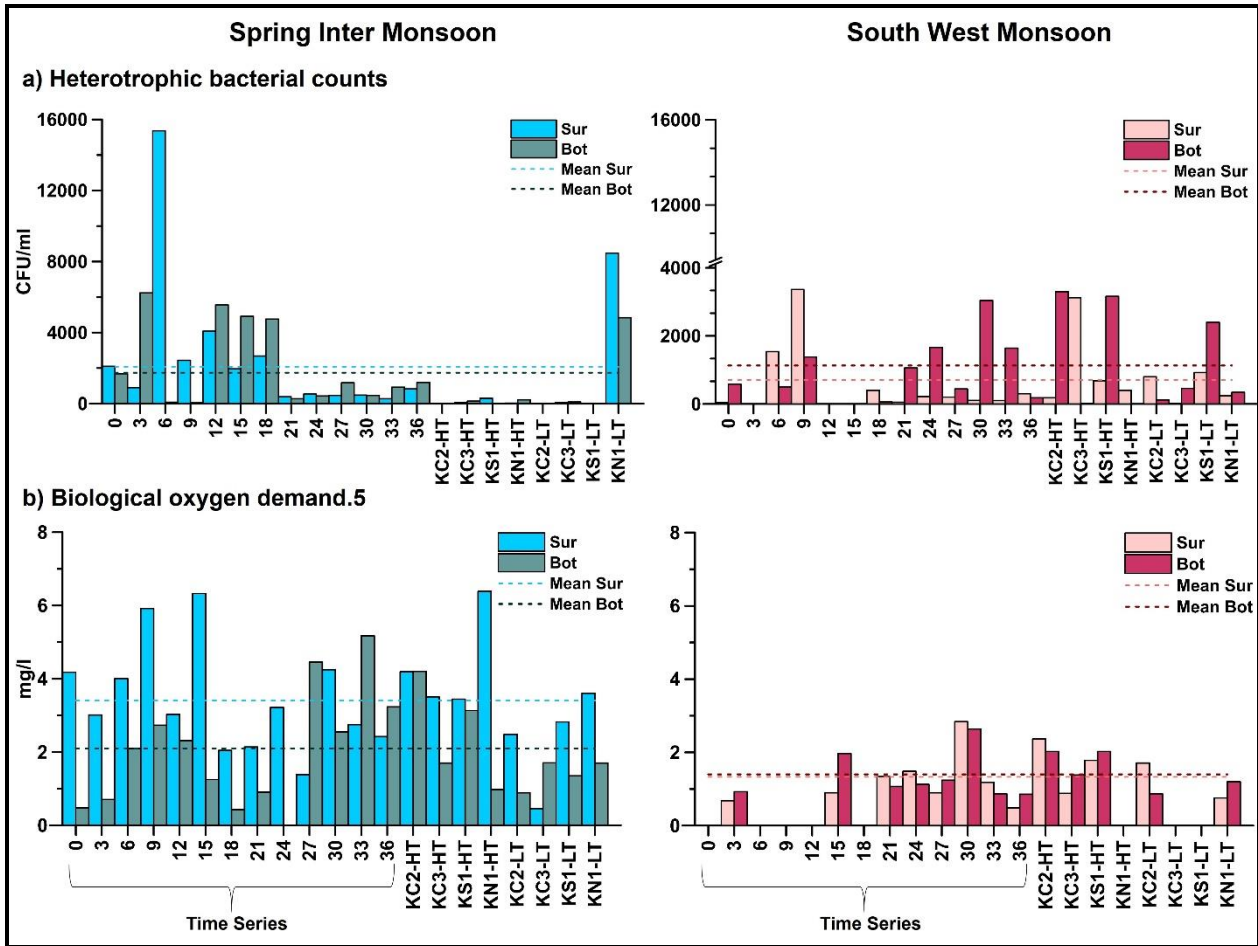


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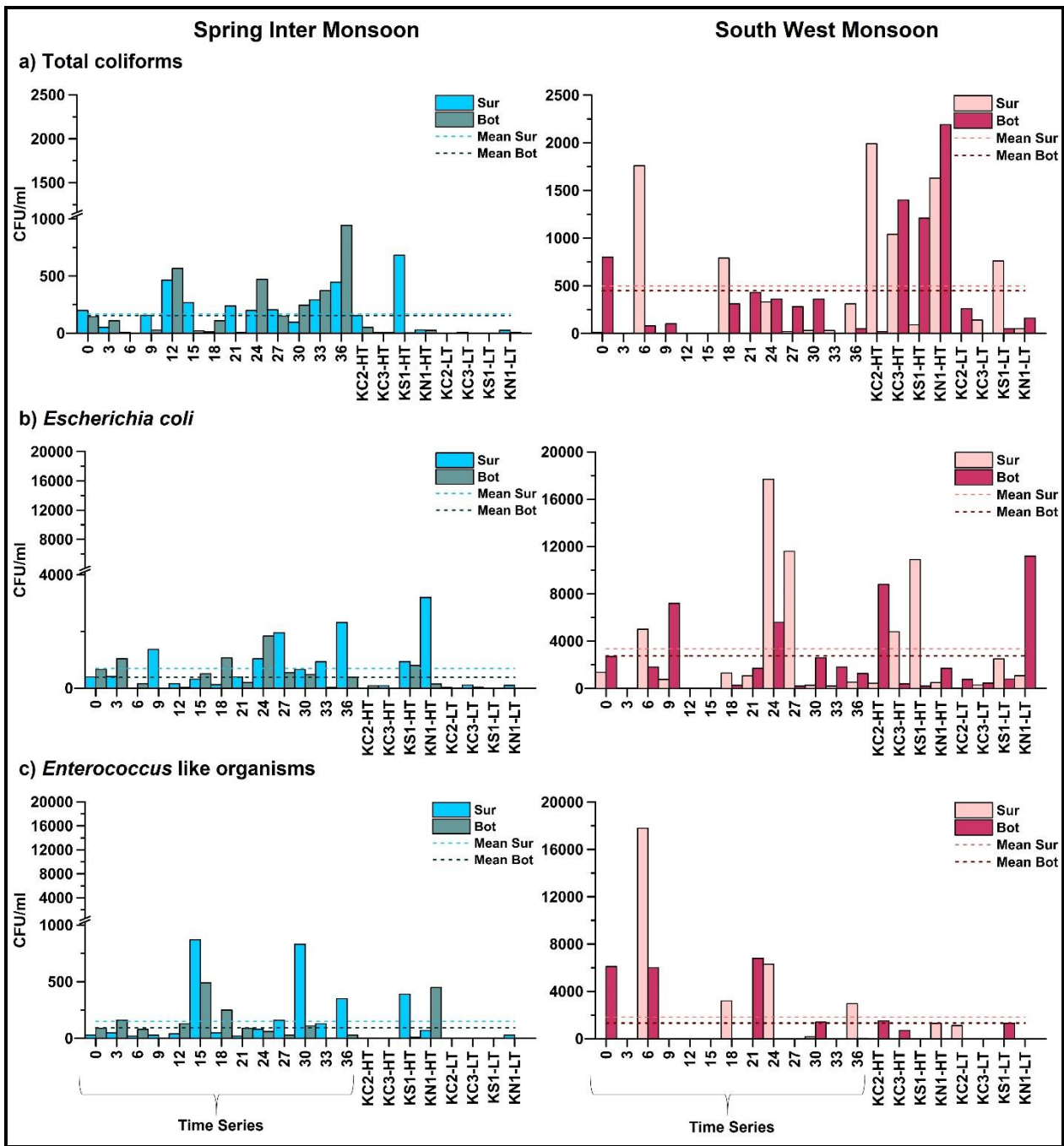


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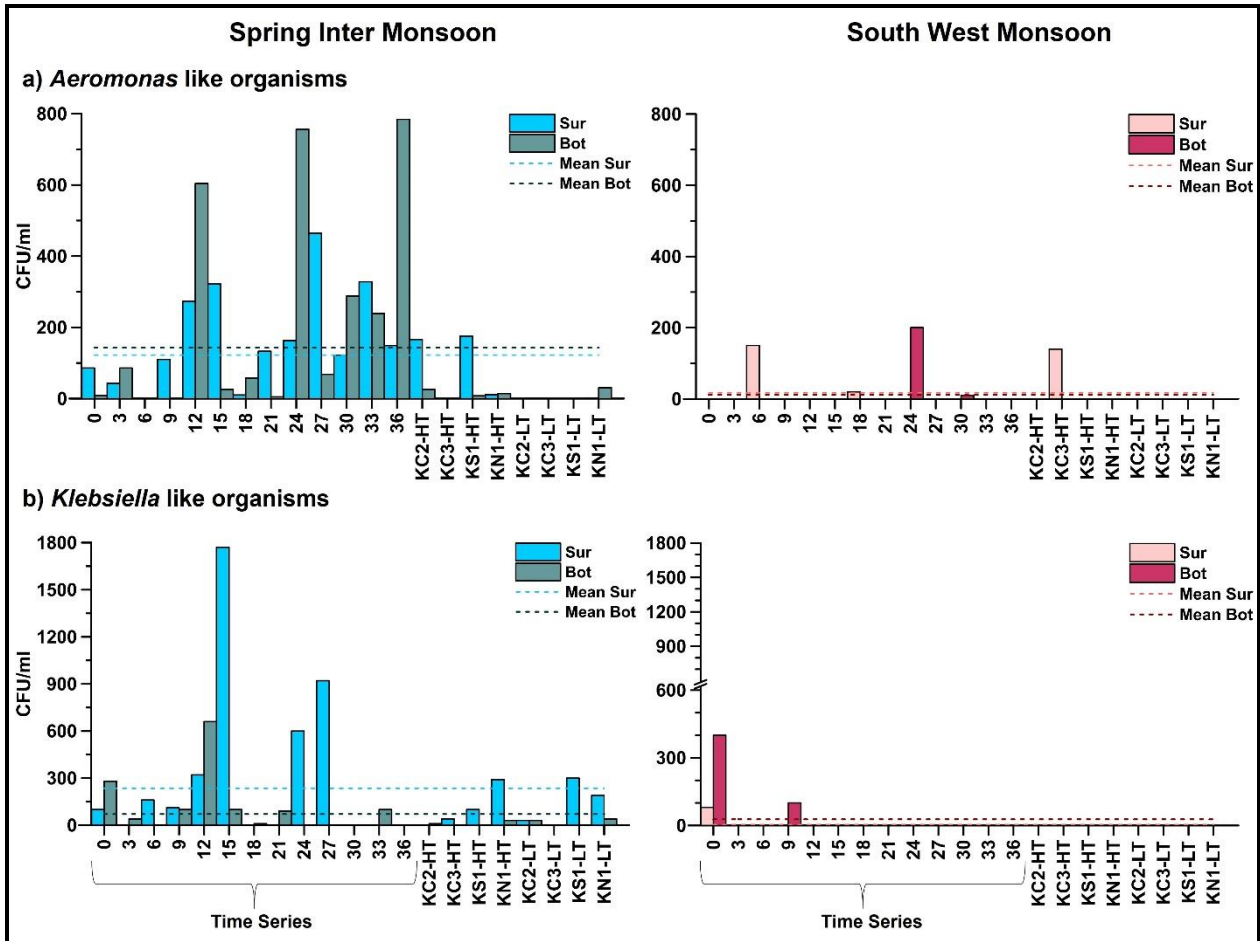


Fig. 6

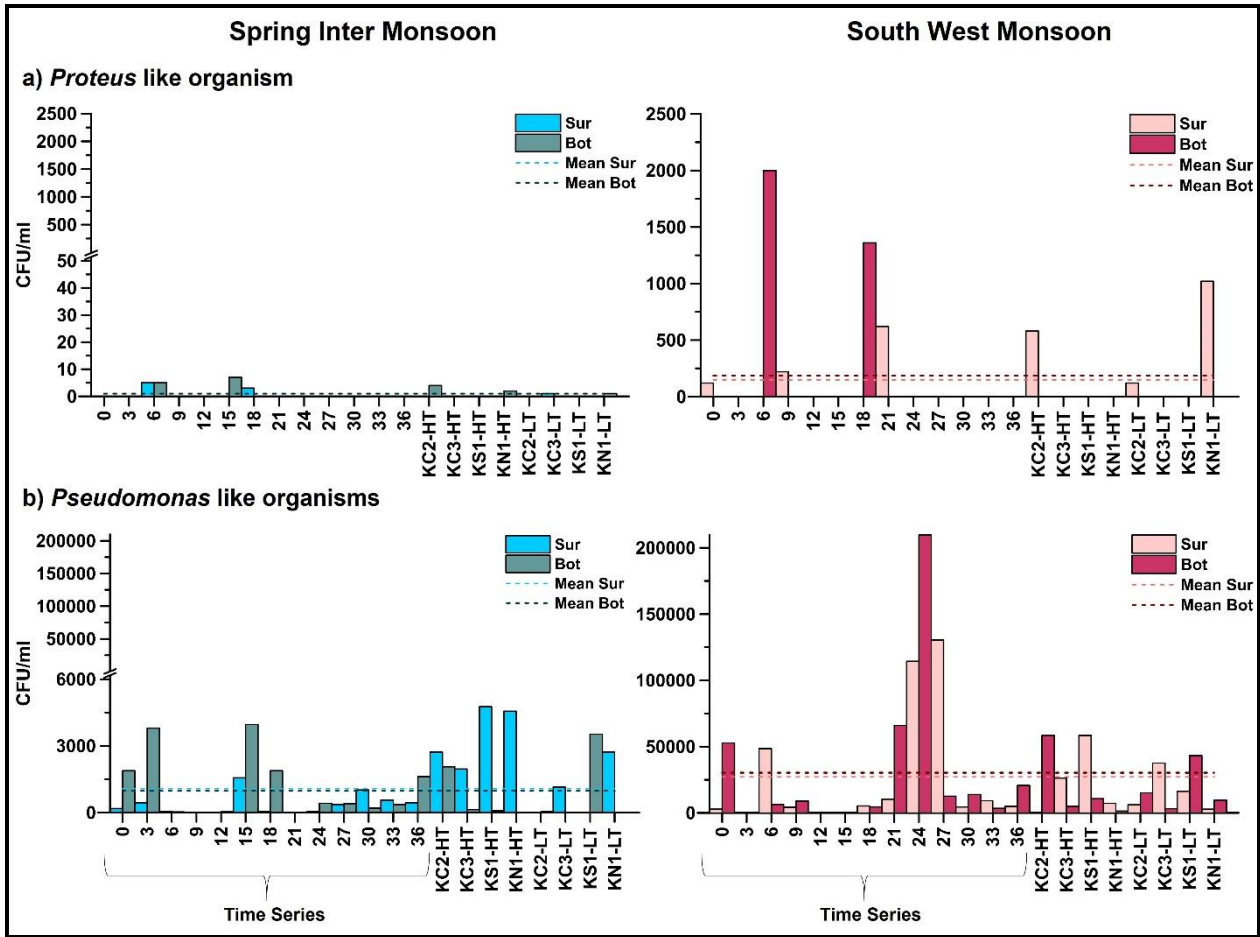


Fig. 7

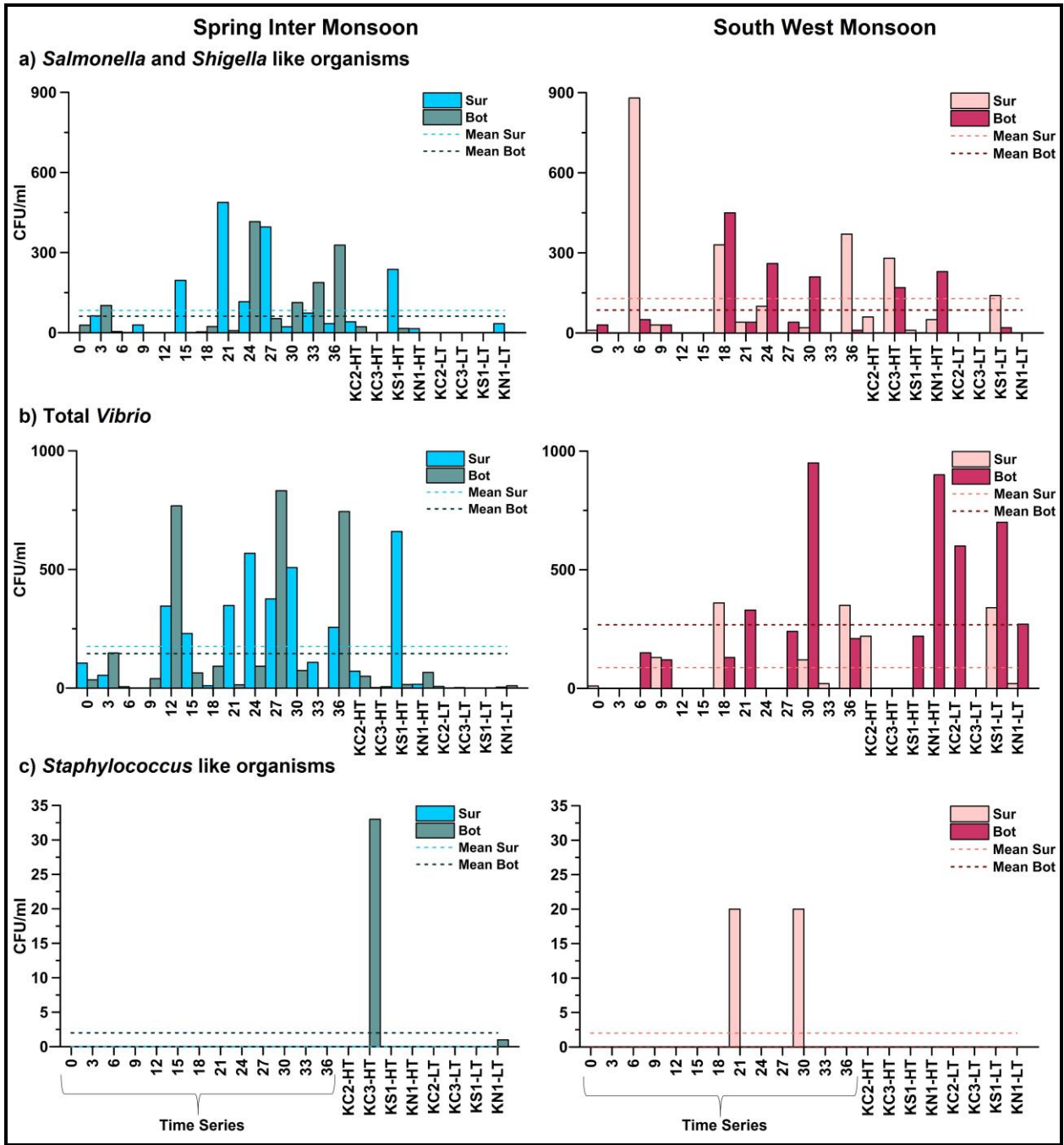


Fig. 8

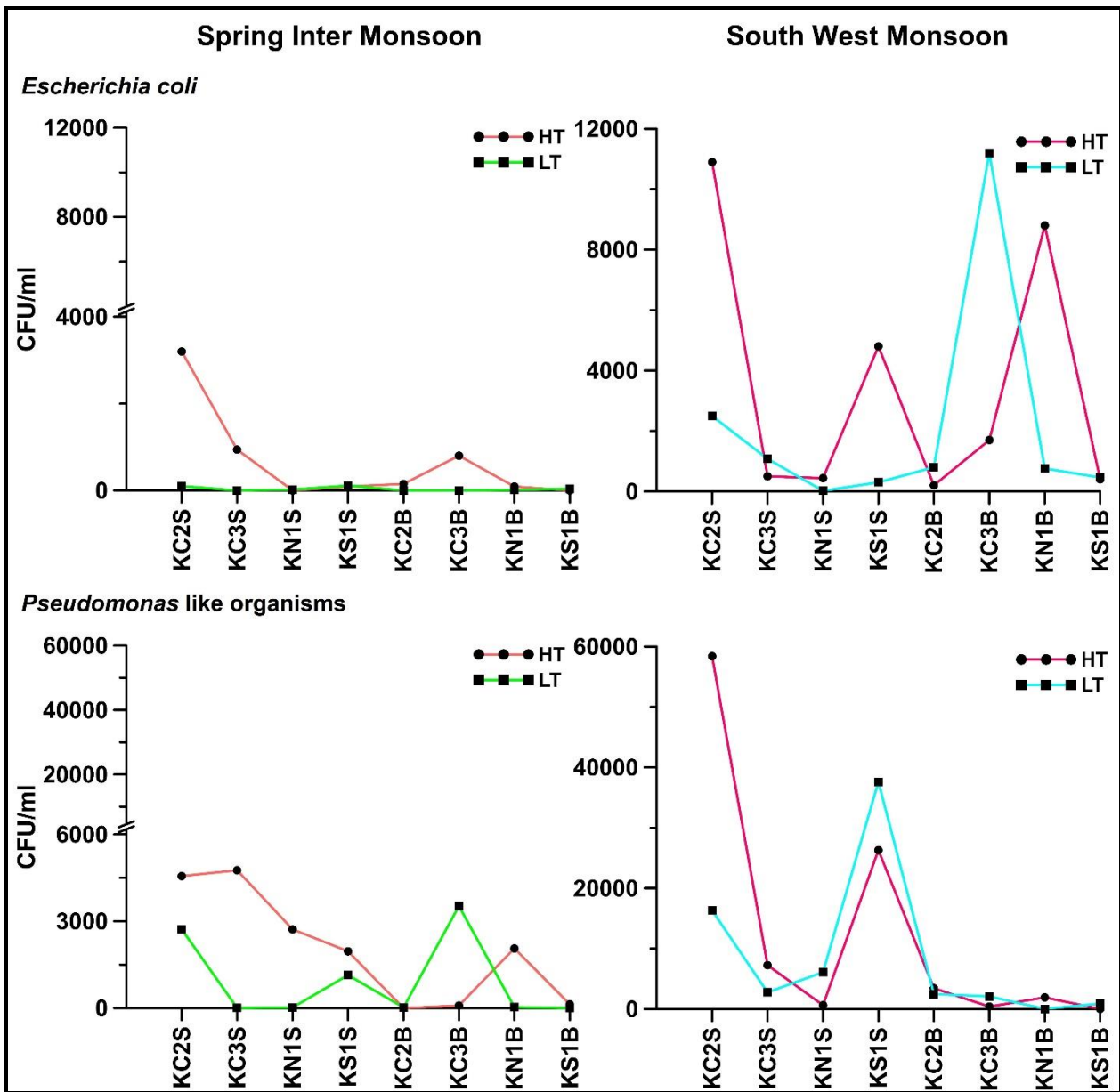


Fig. 9

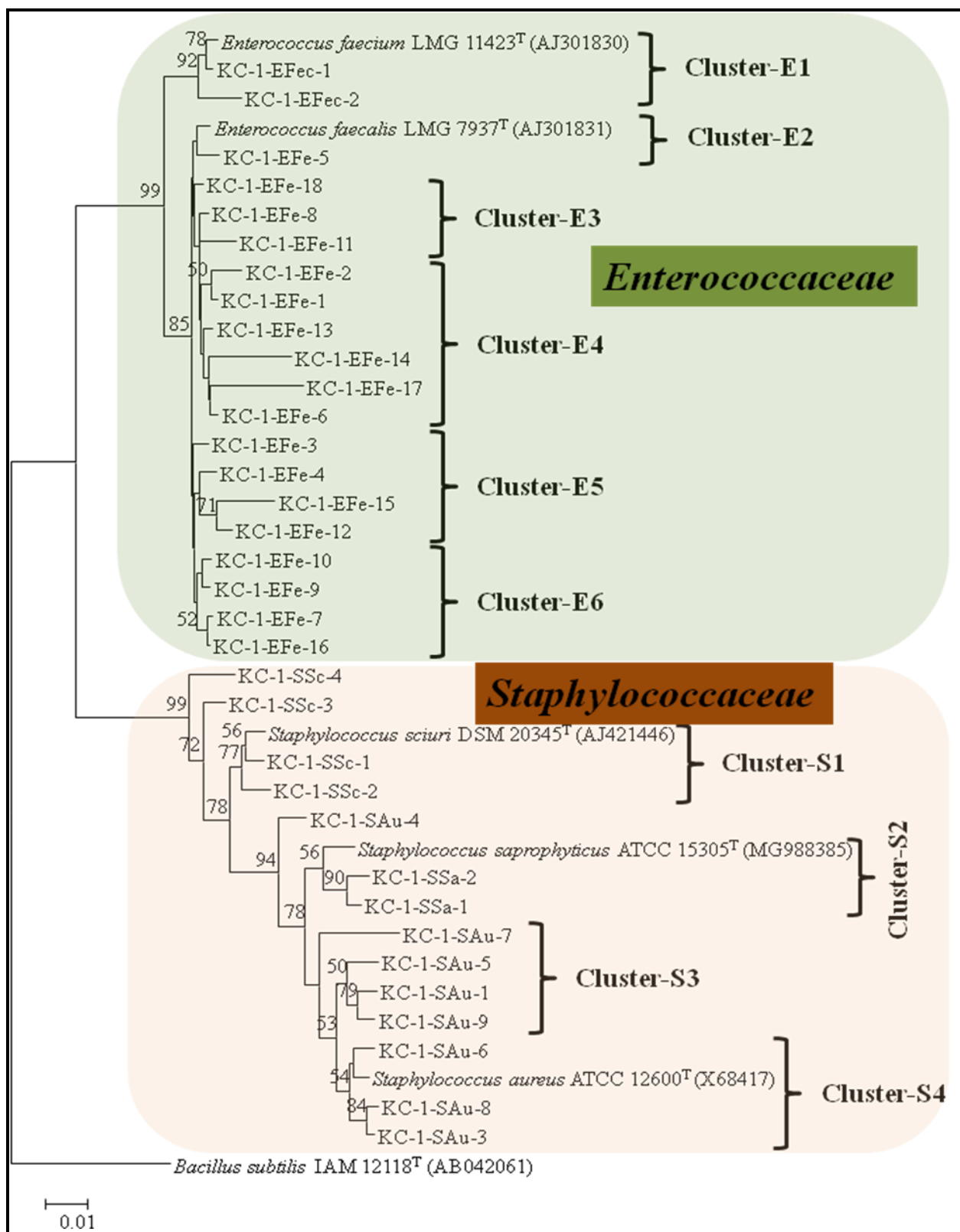


Fig. 10a

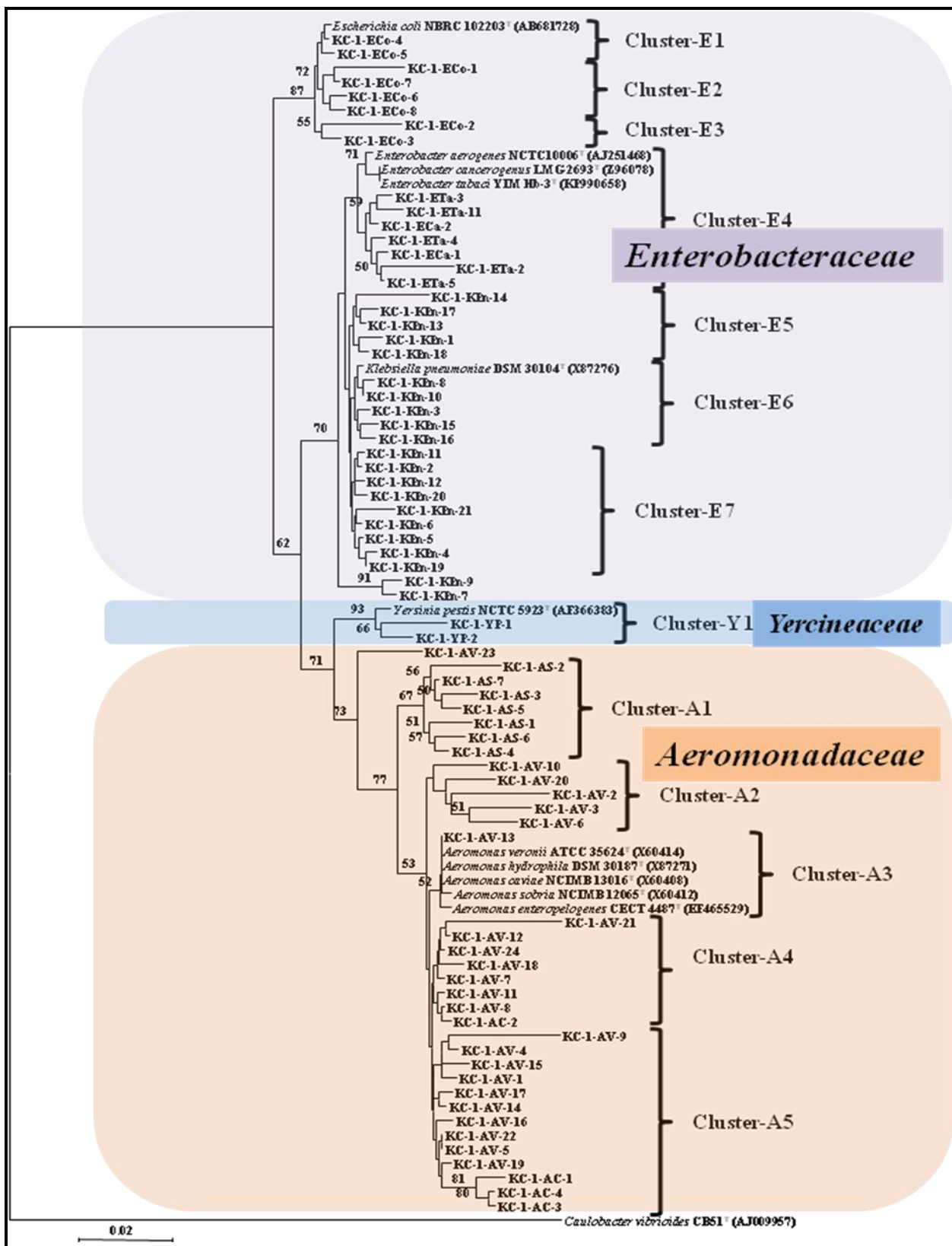


Fig. 10b

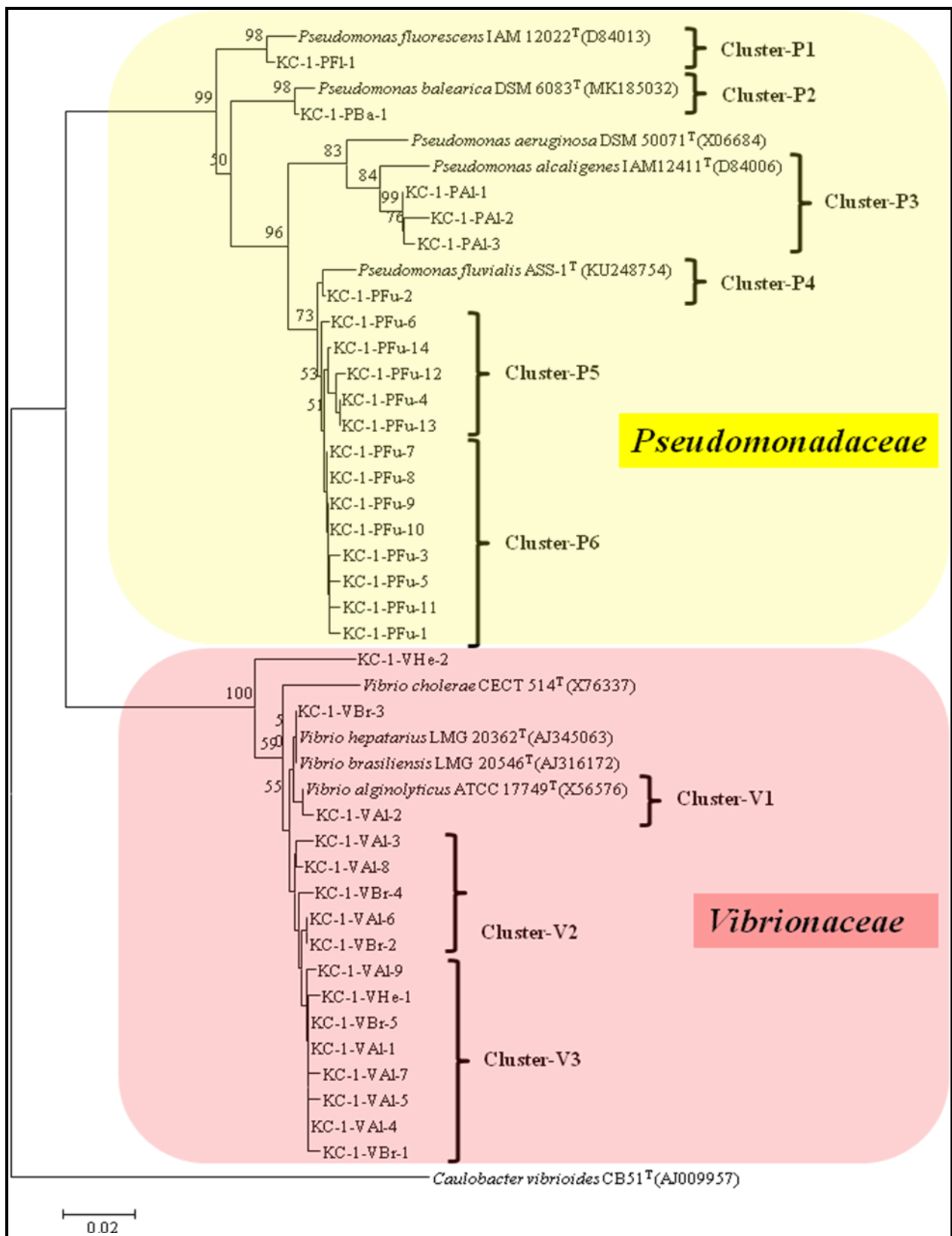


Fig. 10c

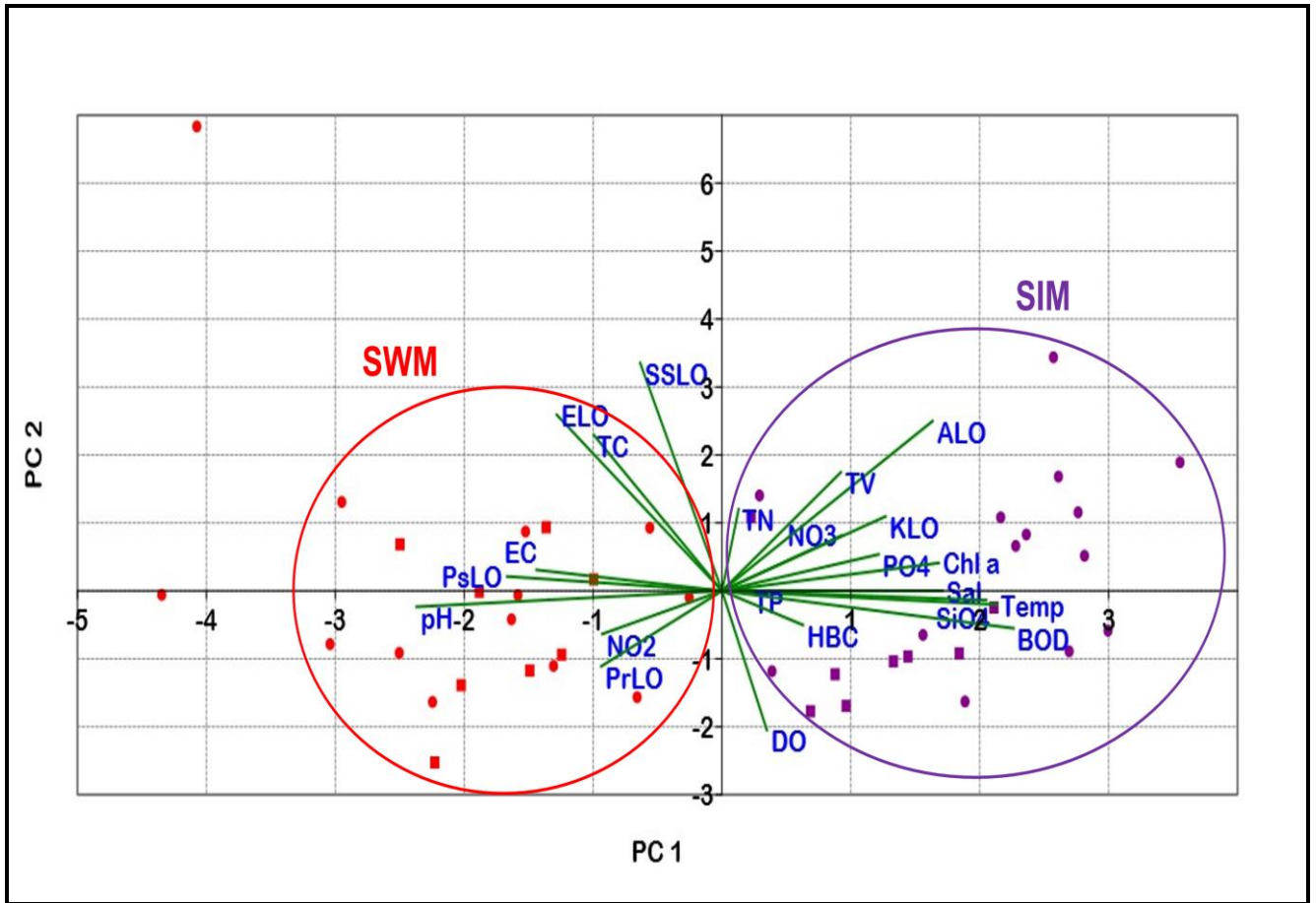


Fig. 11

Supplementary Table S1. Correlations among various components of surface water during SIM

	Temp (oC)	Salinity (ppt)	NO3+N02 (uM)	NO3 (uM)	N02 (uM)	PO4 (uM)	SIO4 (uM)	TN (uM)	TP (uM)	DO (mg/l)	BOD 5 (mg/l)	pH	Chl-a (mg/l)	HBC (CFU/ml)	TC (CFU/ml)	EC (CFU/ml)	ELO (CFU/ml)	ALO (CFU/ml)	KLO (CFU/ml)	PrLO (CFU/ml)	PsLO (CFU/ml)	SSLO (CFU/ml)	SLO (CFU/ml)	TV (CFU/ml)
Temp (oC)		0.378	0.533	0.555	0.767	0.201	0.260	0.096	0.088	0.761	0.136	0.861	0.557	0.762	0.128	0.284	0.121	0.884	0.972	0.838	0.861	0.386	0.621	0.573
Salinity (ppt)	0.20		0.536	0.382	0.295	0.010	0.424	0.778	0.048	0.461	0.793	0.446	0.329	0.087	0.114	0.241	0.984	0.761	0.119	0.012	0.971	0.493	0.226	0.685
NO3+N02 (uM)	-0.14	-0.14		0.000	0.031	0.916	0.468	0.847	0.446	0.991	0.416	0.053	0.386	0.511	0.897	0.141	0.989	0.963	0.868	0.542	0.006	0.992	0.438	0.669
NO3 (uM)	-0.13	-0.20	0.94		0.000	0.645	0.202	0.753	0.409	0.973	0.620	0.027	0.302	0.586	0.947	0.431	0.795	0.653	0.613	0.458	0.019	0.968	0.423	0.562
N02 (uM)	0.07	0.23	-0.46	-0.73		0.314	0.055	0.237	0.486	0.911	0.745	0.041	0.342	0.914	0.664	0.404	0.509	0.194	0.317	0.473	0.474	0.900	0.589	0.507
PO4 (uM)	0.28	0.54	0.02	0.10	-0.23		0.181	0.992	0.715	0.060	0.260	0.796	0.299	0.098	0.262	0.249	0.948	0.244	0.155	0.248	0.848	0.880	0.107	0.703
SIO4 (uM)	-0.25	0.18	0.16	0.28	-0.41	0.30		0.764	0.519	0.137	0.421	0.050	0.018	0.791	0.817	0.656	0.083	0.760	0.742	0.607	0.180	0.643	0.508	0.170
TN (uM)	0.37	-0.07	-0.04	0.07	-0.27	0.00	0.07		0.143	0.960	0.323	0.848	0.586	0.641	0.637	0.091	0.343	0.068	0.796	0.993	0.177	0.364	0.921	0.295
TP (uM)	0.38	0.44	-0.18	-0.19	0.16	0.08	-0.15	0.33		0.571	0.200	0.853	0.544	0.487	0.265	0.025	0.730	0.368	0.662	0.565	0.597	0.905	0.725	0.490
DO (mg/l)	-0.07	-0.17	0.00	-0.01	0.03	-0.41	-0.33	-0.01	0.13		0.022	0.974	0.400	0.082	0.583	0.154	0.619	0.031	0.499	0.541	0.241	0.100	0.806	0.471
BOD 5 (mg/l)	0.33	0.06	-0.18	-0.11	-0.07	-0.25	-0.18	0.23	0.29	0.49		0.552	0.869	0.469	0.990	0.268	0.124	0.913	0.132	0.633	0.078	0.390	0.998	0.717
pH	0.04	-0.19	-0.45	-0.50	0.47	0.06	-0.45	-0.05	0.05	0.01	-0.15		0.687	0.950	0.713	0.463	0.826	0.766	0.728	0.533	0.219	0.361	1.000	0.680
Chl-a (mg/l)	-0.14	0.22	0.20	0.24	-0.22	0.24	0.51	0.13	-0.14	-0.19	-0.04	-0.10		0.474	0.812	0.742	0.668	0.937	0.914	0.965	0.019	0.222	0.156	0.284
HBC (CFU/ml)	0.07	-0.38	0.15	0.13	-0.03	-0.37	0.06	0.11	0.16	0.39	0.17	-0.02	-0.17		0.394	0.222	0.543	0.342	0.977	0.000	0.694	0.325	0.729	0.244
TC (CFU/ml)	-0.33	0.35	-0.03	0.01	-0.10	0.25	-0.05	0.11	0.25	-0.12	0.00	0.09	0.06	-0.20		0.461	0.227	0.002	0.722	0.271	0.559	0.045	0.065	0.000
EC (CFU/ml)	0.24	0.26	-0.32	-0.18	-0.19	0.26	0.10	0.38	0.49	-0.31	0.25	0.18	-0.08	-0.28	0.17		0.46	0.295	0.547	0.215	0.152	0.531	0.446	0.495
ELO (CFU/ml)	0.34	0.00	0.00	0.06	-0.15	0.01	-0.38	0.22	-0.08	-0.11	0.34	-0.05	-0.10	-0.14	0.27	0.17		0.0966	0.016	0.417	0.378	0.504	0.574	0.035
ALO (CFU/ml)	0.03	0.07	-0.01	0.10	-0.29	0.26	0.07	0.41	0.21	-0.46	-0.02	-0.07	0.02	-0.22	0.62	0.23	0.36		0.013	0.186	0.637	0.004	0.378	0.005
KLO (CFU/ml)	-0.01	-0.34	0.04	0.11	-0.22	-0.31	-0.07	0.06	-0.10	-0.15	0.33	-0.09	0.03	0.01	0.08	0.14	0.51	0.52		0.548	0.880	0.150	0.592	0.405
PrLO (CFU/ml)	-0.05	-0.52	0.14	0.17	-0.16	-0.26	0.12	0.00	-0.13	0.14	-0.11	0.15	-0.01	0.72	-0.25	-0.28	-0.18	-0.29	-0.14		0.296	0.413	0.659	0.282
PsLO (CFU/ml)	-0.04	0.01	-0.57	-0.50	0.16	0.04	-0.30	-0.31	-0.12	0.26	0.38	0.30	-0.51	-0.09	0.13	0.32	0.20	-0.11	0.03	-0.23		0.971	0.562	0.759
SSLO (CFU/ml)	-0.19	-0.15	0.00	-0.01	0.03	-0.03	-0.10	0.21	-0.03	-0.36	-0.19	0.22	-0.28	-0.23	0.43	0.14	0.15	0.58	0.32	-0.18	-0.01		0.326	0.006
SLO (CFU/ml)	-0.11	0.27	0.17	0.18	-0.12	0.35	0.15	0.02	0.08	-0.06	0.00	0.00	0.32	-0.08	0.40	-0.17	-0.13	0.20	-0.12	0.10	-0.13	0.22		0.166
TV (CFU/ml)	-0.13	0.09	0.10	0.13	-0.15	0.09	-0.30	0.24	0.16	-0.16	-0.08	-0.10	-0.25	-0.27	0.74	0.15	0.45	0.57	0.19	-0.24	0.07	0.57	0.31	

Temp: temperature; TN: total Nitrogen; TP: total Phosphorus; DO: dissolved oxygen; BOD: Biological oxygen demand; Chl-a: Chlorophyll-a; HBC: heterotrophic bacterial counts, TC: total coliforms, EC: *Escherichia coli*, ELO: *Enterococcus* like organisms, ALO: *Aeromonas* like organisms, KLO: *Klebsiella* like organisms, PrLO: *Proteus* like organisms, PsLO: *Pseudomonas* like organisms, SS: *Salmonella* and *Shigella* like organisms, TV: total *Vibrio*

Supplementary Table S2. Correlations among various components of bottom water during SIM

	Temp (oC)	Salinity (ppt)	NO3+N02 (uM)	NO3 (uM)	N02 (uM)	PO4 (uM)	SIO4 (uM)	TN (uM)	TP (uM)	DO (mg/l)	BOD 5 (mg/l)	pH	Chl-a (mg/l)	HBC (CFU/ml)	TC (CFU/ml)	EC (CFU/ml)	ELO (CFU/ml)	ALO (CFU/ml)	KLO (CFU/ml)	PrLO (CFU/ml)	PsLO (CFU/ml)	SSLO (CFU/ml)	SLO (CFU/ml)	TV (CFU/ml)
Temp (oC)		0.314	0.230	0.230	0.774	0.863	0.445	0.071	0.845	0.672	0.509	0.538	0.018	0.908	0.736	0.950	0.592	0.781	0.271	0.980	0.567	0.664	0.324	0.753
Salinity (ppt)	-0.22		0.793	0.891	0.830	0.781	0.161	0.007	0.521	0.308	0.072	0.523	0.835	0.543	0.693	0.374	0.302	0.953	0.929	0.721	0.228	0.945	0.918	0.479
NO3+N02 (uM)	0.27	-0.06		2E-08	0.997	0.666	0.231	0.548	0.448	0.184	0.081	0.839	0.537	0.795	0.725	0.192	0.418	0.594	0.581	0.687	0.365	0.815	0.768	0.170
NO3 (uM)	0.27	-0.03	0.89		0.034	0.553	0.055	0.458	0.840	0.122	0.195	0.851	0.263	0.406	0.658	0.427	0.898	0.210	0.881	0.258	0.197	0.450	0.253	0.668
N02 (uM)	-0.06	-0.05	0.00	-0.45		0.645	0.072	0.651	0.291	0.471	0.593	0.982	0.220	0.141	0.083	0.433	0.183	0.082	0.448	0.084	0.297	0.221	0.045	0.077
PO4 (uM)	0.04	-0.06	0.10	0.13	-0.10		0.561	0.412	0.952	0.149	0.916	0.893	0.470	0.683	0.818	0.938	0.986	0.604	0.126	0.258	0.264	0.190	0.013	0.672
SIO4 (uM)	0.17	-0.31	0.27	0.41	-0.39	-0.13		0.637	0.964	0.197	0.808	0.977	0.270	0.722	0.036	0.088	0.093	0.045	0.858	0.441	0.718	0.206	0.013	0.048
TN (uM)	-0.39	0.56	-0.14	-0.17	0.10	0.18	-0.11		0.563	0.271	0.173	0.671	0.902	0.969	0.840	0.593	0.610	0.930	0.336	0.679	0.069	0.577	0.604	0.705
TP (uM)	-0.04	0.14	0.17	0.05	0.24	-0.01	0.01	0.13		0.416	0.118	0.027	0.584	0.009	0.454	0.923	0.565	0.387	0.925	0.116	0.043	0.559	0.765	0.623
DO (mg/l)	-0.10	0.23	-0.30	-0.35	0.17	0.33	-0.29	0.25	0.19		0.000	0.537	0.572	0.056	0.724	0.273	0.054	0.879	0.520	0.647	0.679	0.152	0.169	0.479
BOD 5 (mg/l)	-0.15	0.40	-0.39	-0.29	-0.12	0.02	0.06	0.31	0.35	0.71		0.313	0.407	0.173	0.080	0.563	0.680	0.137	0.717	0.955	0.251	0.056	0.736	0.098
pH	-0.15	-0.16	-0.05	-0.05	0.01	-0.03	0.01	0.10	0.51	0.16	0.25		0.186	0.710	0.595	0.701	0.084	0.788	0.407	0.447	0.784	0.853	0.805	0.284
Chl-a (mg/l)	0.51	0.05	0.14	0.26	-0.28	0.17	0.25	0.03	-0.13	0.13	0.19	-0.33		0.790	0.016	0.346	0.152	0.017	0.761	0.492	0.536	0.048	0.579	0.080
HBC (CFU/ml)	-0.03	-0.14	0.06	0.20	-0.34	-0.10	0.08	0.01	-0.57	-0.44	-0.33	0.10	0.07		0.749	0.794	0.568	0.733	0.054	0.427	0.031	0.642	0.507	0.61
TC (CFU/ml)	0.08	-0.09	-0.08	0.10	-0.38	0.05	0.45	-0.05	0.17	0.08	0.39	0.13	0.52	0.08		0.121	0.350	0.000	0.228	0.208	0.810	0.000	0.495	0.000
EC (CFU/ml)	-0.01	-0.20	-0.29	-0.18	-0.18	-0.02	0.37	-0.12	-0.02	-0.25	0.13	-0.09	0.22	-0.06	0.34		8E-07	0.418	0.574	0.605	0.707	0.862	0.730	0.001
ELO (CFU/ml)	0.12	-0.23	-0.18	-0.03	-0.29	0.00	0.37	-0.11	-0.13	-0.43	-0.10	-0.41	0.32	0.14	0.21	0.84		0.780	0.924	0.362	0.695	0.578	0.572	0.008
ALO (CFU/ml)	-0.06	-0.01	0.12	0.28	-0.38	0.12	0.43	0.02	0.19	0.04	0.34	0.07	0.52	0.08	0.92	0.18	0.06		0.217	0.268	0.682	0.000	0.541	0.016
KLO (CFU/ml)	-0.25	-0.02	-0.12	-0.03	-0.17	-0.34	-0.04	-0.22	0.02	-0.15	-0.08	0.20	-0.07	0.44	0.27	-0.13	-0.02	0.27		0.741	0.812	0.455	0.645	0.314
PrLO (CFU/ml)	-0.01	0.08	0.09	0.25	-0.38	0.25	-0.17	0.09	-0.34	0.11	-0.01	-0.19	0.16	0.19	-0.28	-0.12	0.20	-0.25	-0.07		0.126	0.297	0.660	0.363
PsLO (CFU/ml)	0.13	-0.27	0.20	0.29	-0.23	0.25	-0.08	-0.39	-0.43	-0.10	-0.26	-0.07	0.14	0.48	-0.05	-0.08	0.09	-0.09	-0.05	0.34		0.885	0.536	0.644
SSLO (CFU/ml)	-0.10	0.02	0.05	0.17	-0.27	0.29	0.28	0.13	0.13	0.32	0.42	-0.05	0.44	-0.11	0.71	0.04	-0.13	0.81	-0.17	-0.23	0.03		0.588	0.468
SLO (CFU/ml)	0.22	0.02	-0.07	-0.25	0.43	0.52	-0.52	0.12	0.07	0.31	-0.08	-0.06	0.13	-0.16	-0.15	-0.08	-0.13	-0.14	-0.10	-0.10	-0.14	-0.12		0.584
TV (CFU/ml)	0.07	-0.16	-0.30	-0.10	-0.38	-0.10	0.43	-0.09	0.11	-0.16	0.37	0.26	0.39	0.12	0.68	0.67	0.55	0.51	0.22	-0.20	-0.10	0.16	-0.12	

Temp: temperature; TN: total Nitrogen; TP: total Phosphorus; DO: dissolved oxygen; BOD: Biological oxygen demand; Chl-a: Chlorophyll-a; HBC: heterotrophic bacterial counts, TC: total coliforms, EC: *Escherichia coli*, ELO: *Enterococcus* like organisms, ALO: *Aeromonas* like organisms, KLO: *Klebsiella* like organisms, PrLO: *Proteus* like organisms, PsLO: *Pseudomonas* like organisms, SS: *Salmonella* and *Shigella* like organisms, TV: total *Vibrio*

Supplementary Table S3. Correlations among various components of surface water during SWM

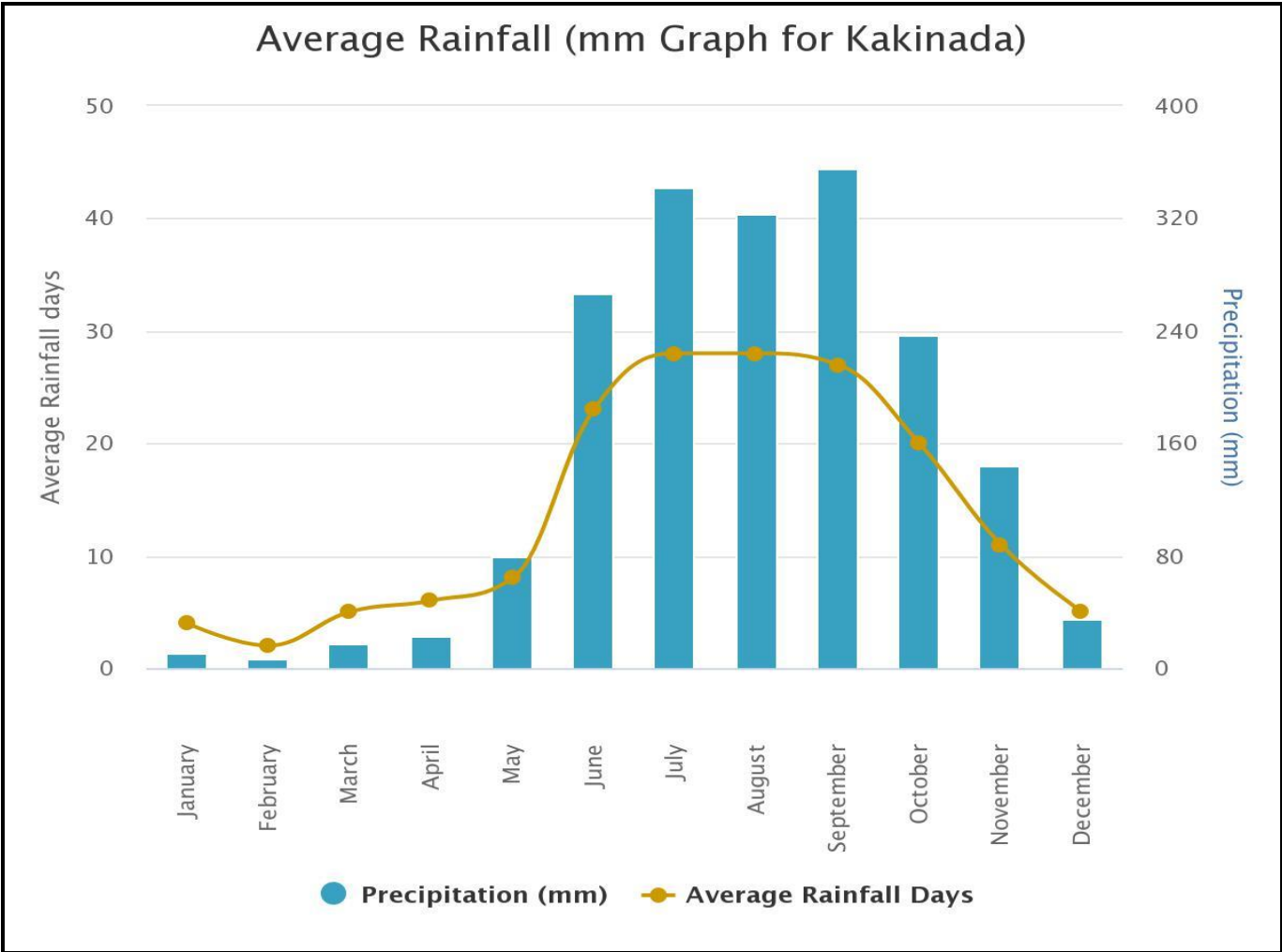
	Temp (oC)	Salinity	NO3+N02 (uM)	NO3 (uM)	N02 (uM)	PO4 (uM)	SIO4 (uM)	TN (uM)	TP (uM)	DO (mg/l)	BOD 5 (mg/l)	pH	Chl- <i>a</i> (mg/l)	HBC (CFU/ml)	TC (CFU/ml)	EC (CFU/ml)	ELO (CFU/ml)	ALO (CFU/ml)	KLO (CFU/ml)	PrLO (CFU/ml)	PsLO (CFU/ml)	SSLO (CFU/ml)	SLO (CFU/ml)	TV (CFU/ml)
Temp (oC)		0.050	0.620	0.695	0.667	0.457	0.261	0.747	0.363	0.688	0.720	0.524	0.661	0.195	0.723	0.847	0.184	0.498	0.088	0.833	0.759	0.633	0.867	0.947
Salinity (ppt)	-0.47		0.541	0.564	0.865	0.996	0.469	0.883	0.354	0.246	0.860	0.242	0.978	0.383	0.270	0.596	0.658	0.429	0.773	0.716	0.495	0.782	0.354	0.408
NO3+N02 (uM)	0.13	-0.17		6E-07	0.192	0.021	0.754	0.044	0.571	0.433	0.711	0.377	0.537	0.258	0.103	0.722	0.625	0.060	0.424	0.201	0.896	0.154	0.756	0.745
NO3 (uM)	0.11	-0.16	0.91		0.077	0.011	0.332	0.006	0.406	0.261	0.786	0.071	0.791	0.226	0.161	0.918	0.837	0.078	0.302	0.953	0.810	0.272	0.733	0.779
N02 (uM)	0.12	0.05	-0.33	-0.44		0.202	0.850	0.416	0.033	0.721	0.050	0.404	0.703	0.865	0.605	0.512	0.662	0.920	0.929	0.887	0.516	0.916	0.897	0.481
PO4 (uM)	0.20	0.00	0.56	0.60	-0.33		0.482	0.064	0.476	0.651	0.780	0.148	0.303	0.077	0.904	0.173	0.521	0.286	0.997	0.100	0.416	0.871	0.338	0.608
SIO4 (uM)	0.30	0.19	0.08	0.25	0.05	0.18		0.106	0.601	0.457	0.825	0.880	0.647	0.480	0.555	0.504	0.800	0.827	0.028	0.625	0.610	0.799	0.829	0.798
TN (uM)	-0.09	0.04	-0.51	-0.65	0.22	-0.47	-0.42		0.992	0.286	0.659	0.291	0.081	0.735	0.489	0.930	0.141	0.187	0.634	0.719	0.679	0.184	0.290	0.915
TP (uM)	0.24	0.25	-0.15	-0.22	0.53	-0.19	-0.14	0.00		0.409	0.127	0.804	0.528	0.525	0.307	0.444	0.776	0.887	0.918	0.873	0.711	0.606	0.837	0.068
DO (mg/l)	0.11	0.31	-0.23	-0.32	-0.10	-0.13	0.22	0.31	-0.24		0.039	0.005	0.943	0.248	0.677	0.803	0.591	0.330	0.281	0.575	0.969	0.875	0.031	0.237
BOD 5 (mg/l)	-0.12	0.06	-0.13	-0.09	-0.60	-0.10	0.08	-0.16	-0.52	0.58		0.942	0.255	0.489	0.450	0.772	0.696	0.452	1.000	0.868	0.612	0.157	0.184	0.914
pH	0.16	0.29	-0.24	-0.46	0.22	-0.38	-0.04	0.28	0.07	0.67	-0.02		0.471	0.113	0.634	0.787	0.986	0.213	0.503	0.600	0.941	0.842	0.277	0.657
Chl- <i>a</i> (mg/l)	-0.12	-0.01	-0.19	-0.08	-0.12	-0.31	-0.14	0.50	0.19	-0.02	-0.40	-0.20		0.893	0.772	0.816	0.077	0.259	0.302	0.793	0.491	0.153	0.961	0.612
HBC (CFU/ml)	0.33	-0.23	0.29	0.31	-0.04	0.44	-0.18	0.09	0.17	-0.32	-0.23	-0.40	-0.04		0.510	0.998	0.619	0.013	0.514	0.594	0.750	0.227	0.363	0.935
TC (CFU/ml)	0.09	-0.28	0.41	0.36	-0.14	-0.03	0.15	-0.18	-0.26	0.12	0.25	-0.12	0.09	0.17		0.765	0.058	0.033	0.473	0.878	0.661	0.018	0.296	0.426
EC (CFU/ml)	-0.05	0.14	0.09	0.03	0.17	0.35	0.17	-0.02	-0.20	0.07	-0.10	0.071	-0.07	0.00	-0.08		0.291	0.685	0.695	0.282	0.000	0.841	0.438	0.222
ELO (CFU/ml)	-0.34	0.12	0.13	0.05	0.11	-0.17	-0.07	0.37	-0.07	0.15	-0.13	0.00	0.49	0.13	0.45	0.26		0.005	0.678	0.376	0.297	0.000	0.562	0.795
ALO (CFU/ml)	0.18	-0.21	0.47	0.44	-0.03	0.27	-0.06	0.34	-0.04	-0.27	-0.25	-0.32	0.32	0.58	0.50	0.10	0.63		0.717	0.427	0.735	0.000	0.596	0.464
KLO (CFU/ml)	-0.43	0.08	-0.21	-0.27	-0.02	0.00	-0.53	0.12	0.03	-0.30	0.00	-0.17	-0.30	-0.16	-0.18	-0.10	-0.11	-0.09		0.922	0.533	0.597	0.735	0.573
PrLO (CFU/ml)	-0.06	-0.10	-0.33	-0.02	0.04	-0.41	0.13	-0.09	-0.04	-0.16	-0.06	-0.14	0.08	-0.13	-0.04	-0.27	-0.22	-0.20	-0.02		0.193	0.311	0.423	0.742
PsLO (CFU/ml)	-0.08	0.18	0.03	-0.06	0.17	0.21	0.13	0.11	-0.10	0.01	-0.17	0.02	0.20	-0.08	-0.11	0.91	0.26	0.09	-0.16	-0.32		0.875	0.458	0.140
SSLO (CFU/ml)	-0.12	-0.07	0.36	0.28	0.03	0.04	-0.07	0.34	-0.13	0.04	-0.46	-0.05	0.40	0.30	0.55	0.05	0.87	0.78	-0.13	-0.25	0.04		0.521	0.377
SLO (CFU/ml)	-0.04	0.24	-0.08	-0.09	-0.03	-0.25	0.06	0.27	0.05	0.56	0.43	0.28	0.01	-0.23	-0.26	-0.19	-0.15	-0.13	-0.09	0.20	-0.19	-0.16		0.773
TV (CFU/ml)	-0.02	-0.21	0.09	0.07	-0.18	0.13	0.07	-0.03	-0.45	0.33	0.04	0.12	-0.15	-0.02	0.20	-0.30	-0.07	-0.18	-0.14	-0.08	-0.36	0.22	-0.07	

Temp: temperature; TN: total Nitrogen; TP: total Phosphorus; DO: dissolved oxygen; BOD: Biological oxygen demand; Chl-*a*: Chlorophyll-*a*; HBC: heterotrophic bacterial counts, TC: total coliforms, EC: *Escherichia coli*, ELO: *Enterococcus* like organisms, ALO: *Aeromonas* like organisms, KLO: *Klebsiella* like organisms, PrLO: *Proteus* like organisms, PsLO: *Pseudomonas* like organisms, SS: *Salmonella* and *Shigella* like organisms, TV: total *Vibrio*

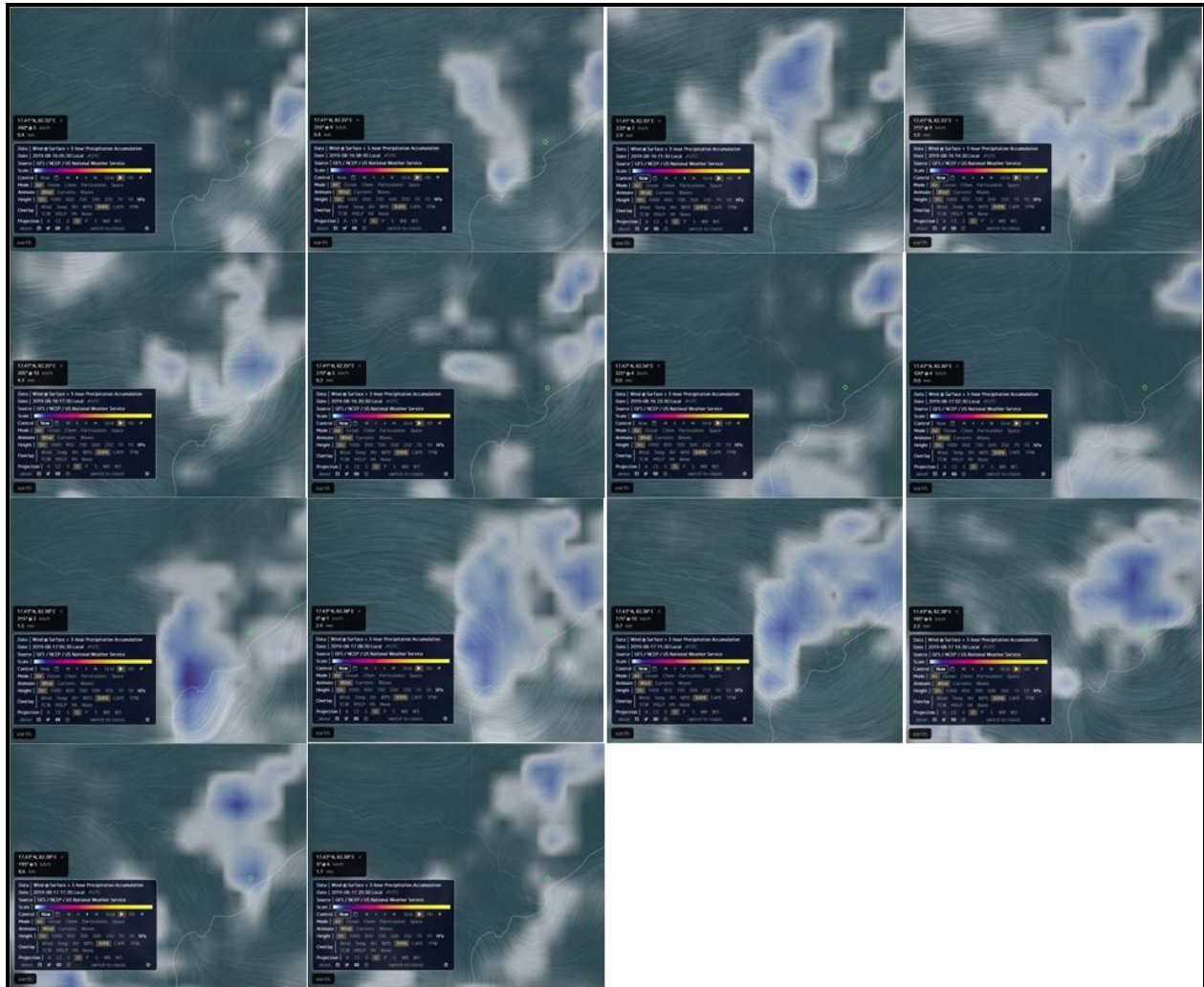
Supplementary Table S4. Correlations among various components of bottom water during SWM

	Temp (oC)	Salinity	NO3+N02 (uM)	NO3 (uM)	N02 (uM)	PO4 (uM)	SIO4 (uM)	TN (uM)	TP (uM)	DO (mg/l)	BOD 5 (mg/l)	pH	Chl- <i>a</i> (mg/l)	HBC (CFU/ml)	TC (CFU/ml)	EC (CFU/ml)	ELO (CFU/ml)	ALO (CFU/ml)	KLO (CFU/ml)	PrLO (CFU/ml)	PsLO (CFU/ml)	SSLO (CFU/ml)	SLO (CFU/ml)	TV (CFU/ml)
Temp (oC)		1E-07	0.973	0.934	0.361	0.633	0.042	0.472	0.185	0.008	0.722	0.001	0.154	0.346	0.398	0.867	0.546	0.634	0.633	0.230	0.967	0.683	1.000	0.460
Salinity	-0.91		0.660	0.607	0.257	0.945	0.082	0.584	0.663	0.066	0.977	0.003	0.333	0.755	0.195	0.494	0.517	0.795	0.626	0.273	0.432	0.985	1.000	0.223
NO3+N02 (uM)	0.01	-0.13		0.000	0.240	0.514	0.051	0.963	0.581	0.266	0.275	0.476	0.067	0.081	0.288	0.836	0.027	0.699	0.013	0.812	0.556	0.797	1.000	0.857
NO3 (uM)	0.02	-0.14	0.98		0.569	0.531	0.027	0.473	0.494	0.448	0.711	0.762	0.087	0.428	0.703	0.559	0.021	0.569	0.006	0.786	0.503	0.936	1.000	0.886
N02 (uM)	0.26	-0.32	0.32	0.16		0.884	0.773	0.098	0.852	0.551	0.155	0.054	0.211	0.005	0.323	0.580	0.851	0.918	0.684	0.232	0.382	0.176	1.000	0.207
PO4 (uM)	-0.14	-0.02	-0.18	-0.18	-0.04		0.147	0.874	0.085	0.452	0.037	0.550	0.745	0.568	0.169	0.328	0.544	0.544	0.331	0.645	0.374	0.627	1.000	0.156
SIO4 (uM)	-0.55	0.48	-0.51	-0.57	-0.08	0.39		0.824	0.436	0.297	0.730	0.311	0.371	0.977	0.868	0.468	0.494	0.126	0.349	0.056	0.136	0.457	1.000	0.796
TN (uM)	0.20	-0.15	-0.01	0.20	0.46	-0.05	-0.07		0.201	0.016	0.875	0.051	0.525	0.424	0.051	0.682	0.668	0.571	0.639	0.149	0.700	0.897	1.000	0.482
TP (uM)	-0.36	0.12	-0.16	-0.19	-0.05	0.48	0.23	-0.34		0.124	0.278	0.653	0.595	0.750	0.337	0.438	0.842	0.413	0.952	0.229	0.428	0.292	1.000	0.123
DO (mg/l)	0.63	-0.47	-0.35	-0.22	0.19	-0.24	-0.33	0.65	-0.45		0.308	0.001	0.062	0.094	0.288	0.711	0.428	0.432	0.359	0.685	0.408	0.283	1.000	0.299
BOD 5 (mg/l)	0.12	0.01	-0.44	-0.13	-0.55	0.74	0.15	0.06	-0.41	0.31		0.460	0.272	0.004	0.407	0.734	0.873	0.689	1.000	1.000	0.701	0.399	1.000	0.203
pH	0.70	-0.66	-0.21	-0.08	0.53	0.17	-0.29	0.51	-0.13	0.76	0.24		0.011	0.507	0.662	0.552	0.179	0.726	0.211	0.876	0.720	0.159	1.000	0.065
Chl- <i>a</i> (mg/l)	0.39	-0.27	-0.57	-0.49	0.41	0.11	0.30	0.20	0.17	0.53	-0.36	0.64		0.983	0.600	0.680	0.221	0.818	0.200	0.543	0.965	0.969	1.000	0.055
HBC (CFU/ml)	0.24	-0.08	-0.46	-0.21	-0.68	0.16	0.01	0.22	-0.09	0.45	0.79	0.17	-0.01		0.486	0.363	0.661	0.591	0.681	0.316	0.314	0.475	1.000	0.527
TC (CFU/ml)	0.22	-0.33	0.29	0.10	0.27	0.37	-0.05	-0.50	0.26	-0.29	0.28	0.11	0.15	-0.18		0.299	0.611	0.878	0.665	0.513	0.668	0.181	1.000	0.002
EC (CFU/ml)	0.04	0.18	0.06	0.15	-0.16	-0.27	-0.20	-0.11	-0.21	0.10	0.12	-0.16	-0.12	0.23	-0.26		0.956	0.383	0.751	0.497	0.267	0.513	1.000	0.632
ELO (CFU/ml)	-0.16	0.17	0.57	0.55	0.05	-0.17	-0.19	0.12	-0.05	-0.22	0.05	-0.34	-0.35	-0.11	0.13	-0.01		0.755	0.000	0.937	0.622	0.616	1.000	0.618
ALO (CFU/ml)	0.12	0.07	0.11	0.15	-0.03	-0.17	-0.41	0.15	-0.22	0.22	-0.14	0.09	0.07	0.14	-0.04	0.22	-0.08		0.764	0.727	0.000	0.146	1.000	0.669
KLO (CFU/ml)	-0.12	0.13	0.62	0.63	0.11	-0.27	-0.26	0.13	-0.02	-0.26	0.00	-0.32	-0.36	-0.10	0.11	0.08	0.96	-0.08		0.683	0.736	0.594	1.000	0.599
PrLO (CFU/ml)	-0.31	0.28	-0.07	-0.07	0.33	0.13	0.50	0.38	-0.32	0.11	0.00	-0.04	-0.18	-0.25	-0.17	-0.17	-0.02	-0.09	-0.10		0.479	0.147	1.000	0.657
PsLO (CFU/ml)	0.01	0.20	0.17	0.17	-0.24	-0.25	-0.40	0.10	-0.21	0.23	-0.13	-0.09	0.01	0.25	-0.11	0.28	0.12	0.91	0.09	-0.18		0.445	1.000	0.464
SSLO (CFU/ml)	0.11	0.01	0.07	0.02	0.37	-0.14	-0.21	0.04	-0.28	0.30	0.28	0.36	-0.01	-0.18	0.33	-0.16	-0.13	0.36	-0.13	0.36	0.19		1.000	0.266
SLO (CFU/ml)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		1
TV (CFU/ml)	0.19	-0.31	-0.05	-0.04	0.35	0.39	0.07	-0.19	0.40	0.29	0.42	0.46	0.52	-0.16	0.68	-0.12	-0.13	-0.11	-0.13	-0.11	-0.18	0.28		0

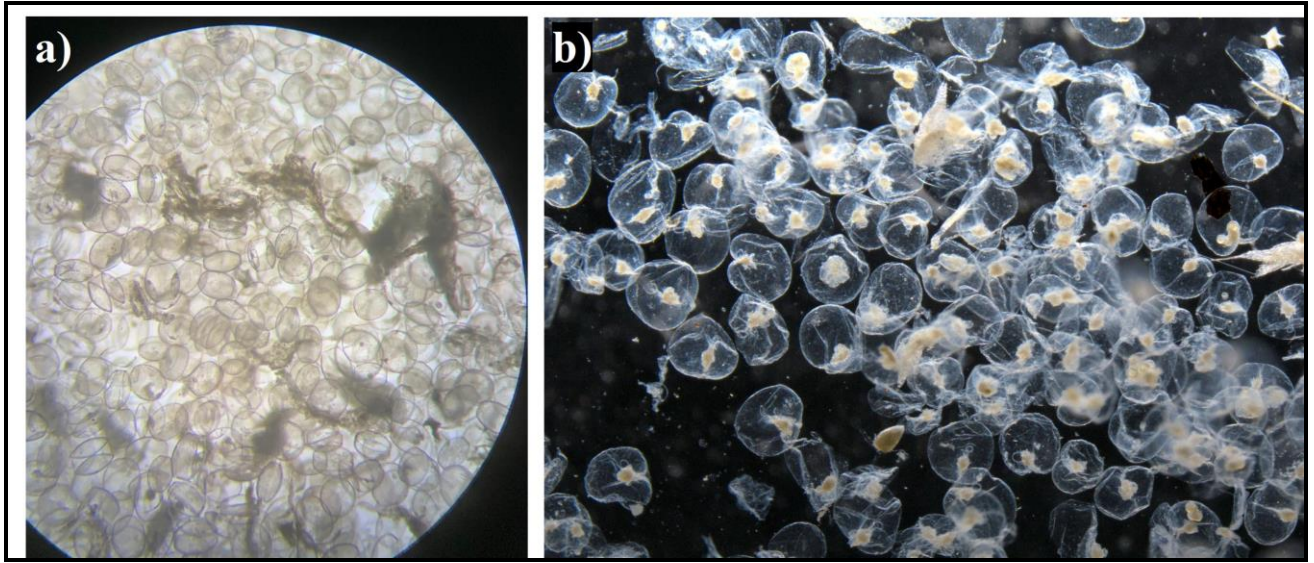
Temp: temperature; TN: total Nitrogen; TP: total Phosphorus; DO: dissolved oxygen; BOD: Biological oxygen demand; Chl-*a*: Chlorophyll-*a*; HBC: heterotrophic bacterial counts, TC: total coliforms, EC: *Escherichia coli*, ELO: *Enterococcus* like organisms, ALO: *Aeromonas* like organisms, KLO: *Klebsiella* like organisms, PrLO: *Proteus* like organisms, PsLO: *Pseudomonas* like organisms, SS: *Salmonella* and *Shigella* like organisms, TV: total *Vibrio*



Supplementary Fig. S1



Supplementary Fig. S2



Supplementary Fig. S3