

# Potential Contribution of Coastal Upwelling to Carbon Sink Through Interaction Between Cyanobacteria and Microbial Eukaryotes

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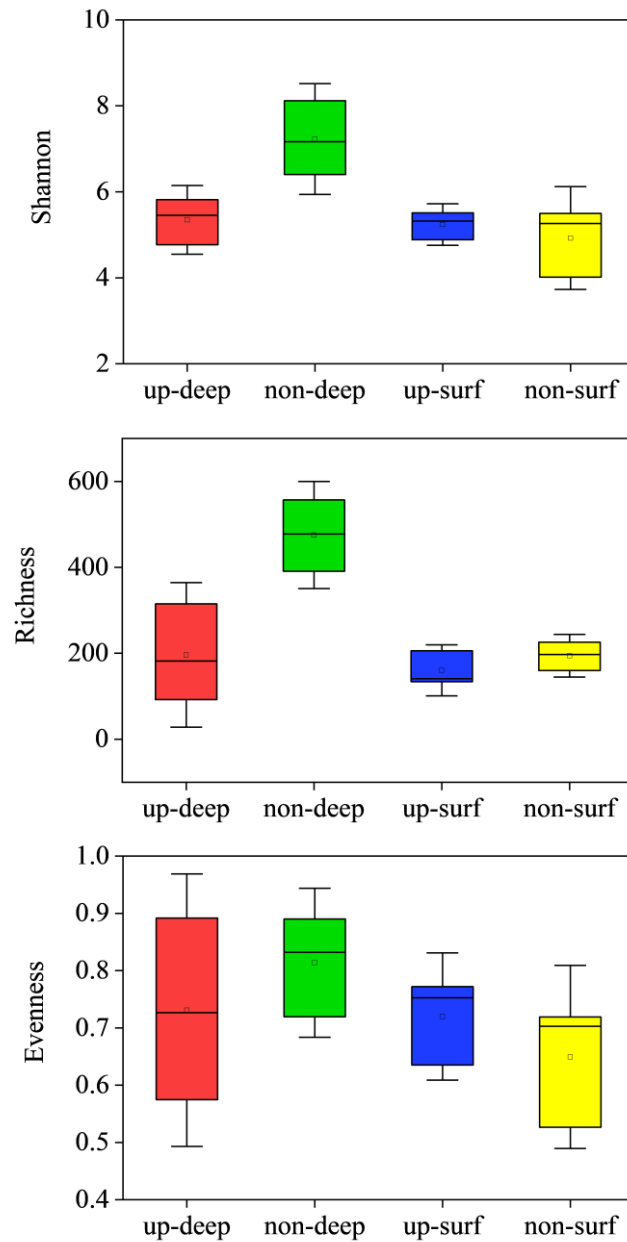
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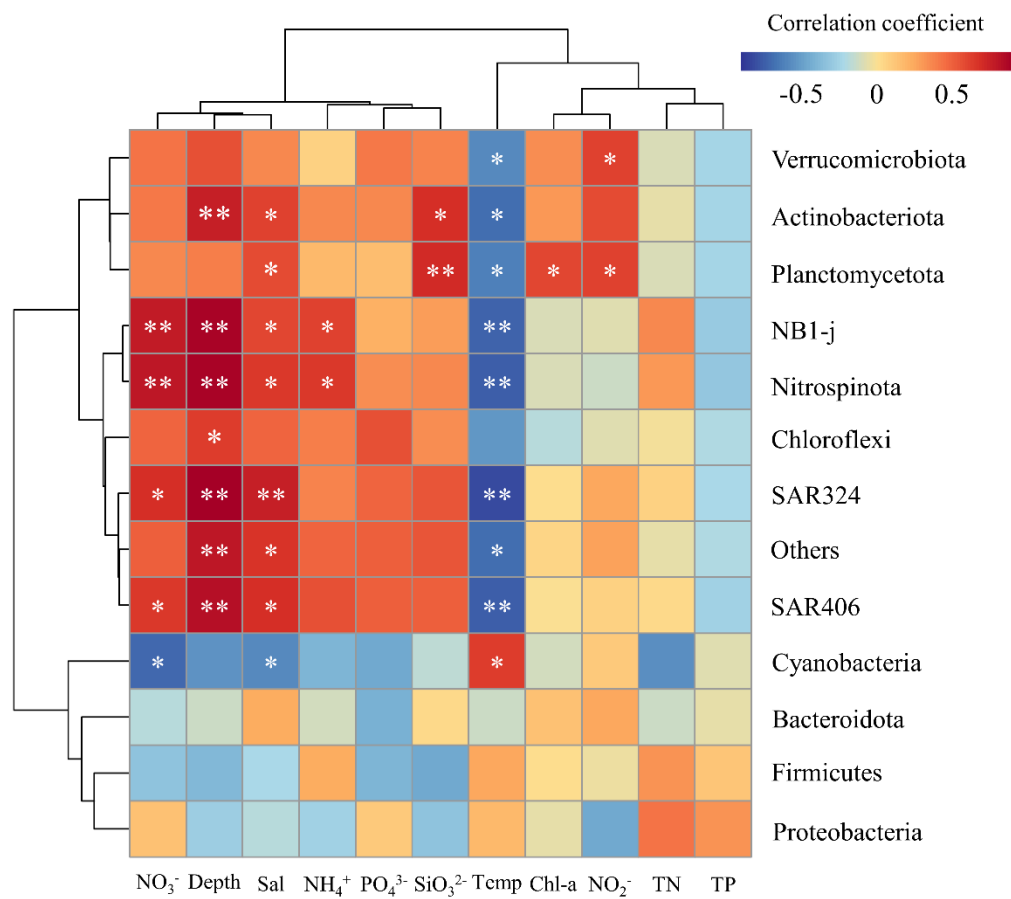
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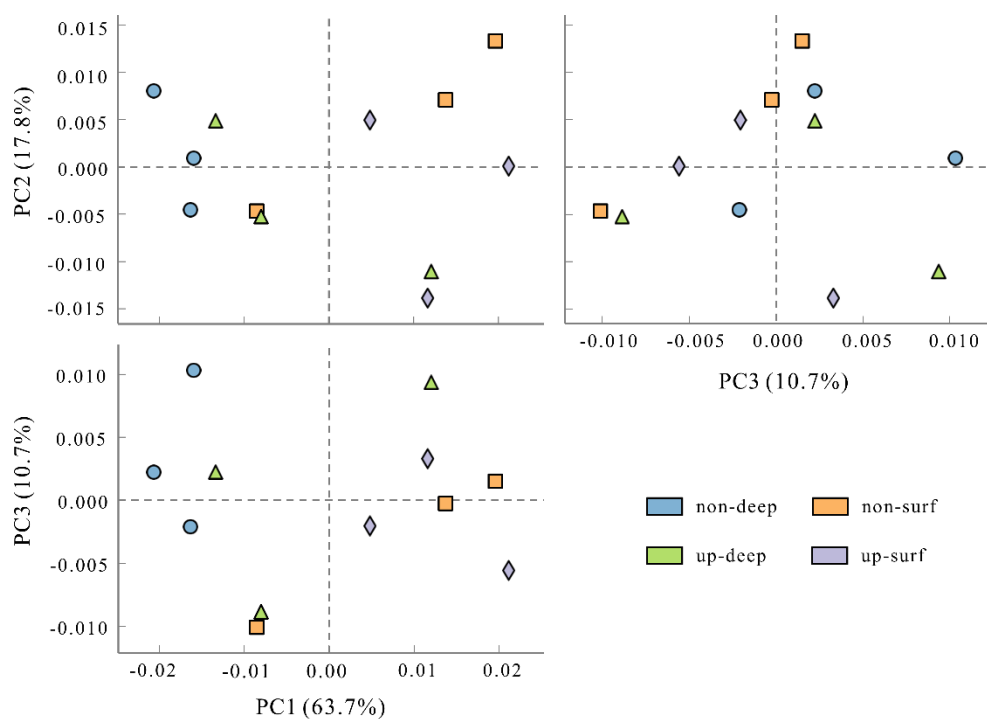
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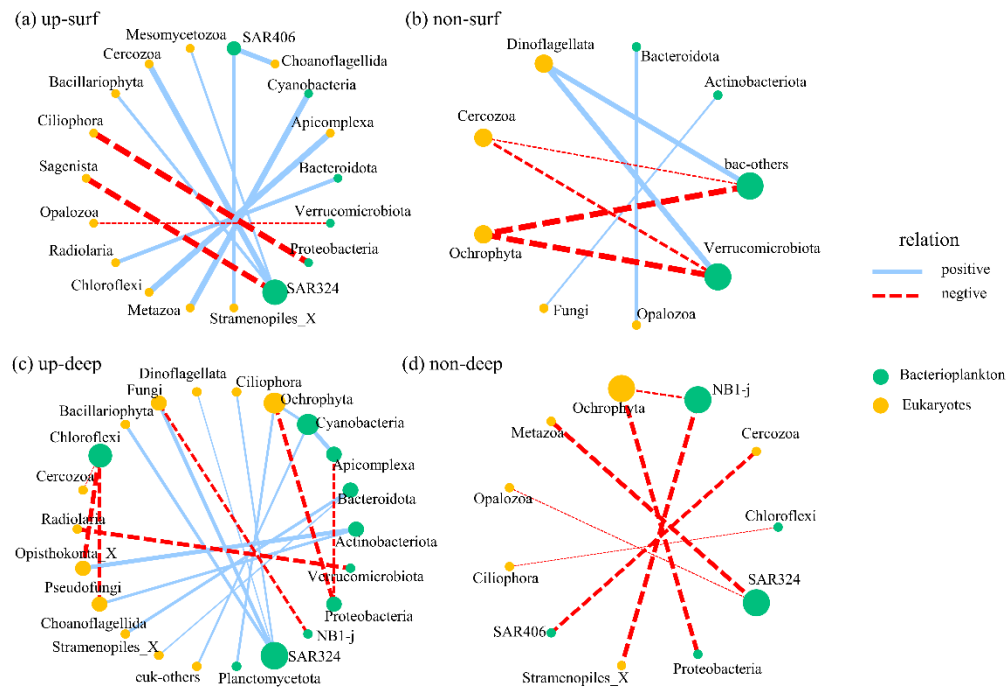
**Figure S1.** Shannon (a), Richness (b), and Evenness (c) for the bacterial communities from different habitats. Labels “non-deep”, “non-surf”, “up-deep” and “up-surf” represent non-upwelling deep water, non-upwelling surface water, upwelling deep water, and upwelling surface water, respectively. The boxes represent the ranges of the first and third quartiles, the line and small square inside each box represent the median and mean values, and the ends of the whiskers represent the lowest and highest datums (mean  $\pm$  1.5 SD).



**Figure S2.** Correlations between environmental parameters and bacterial phyla. Asterisks indicate  $p < 0.05$  and the color bar is based on the scale of Pearson's correlation coefficients.



**Figure S3.** Principal component analysis based on the predicted KEGG pathways. Labels “non-deep”, “non-surf”, “up-deep” and “up-surf” represent non-upwelling deep water, non-upwelling surface water, upwelling deep water, and upwelling surface water, respectively.



**Figure S4.** A network analysis of associations between bacterioplankton and microbial eukaryotes in (a) upwelling surface water, (b) non-upwelling surface water, (c) upwelling deep water, (d) non-upwelling deep water. The bacterioplankton phyla and microbial eukaryotes phyla are represented by circles with distinctive colors. The size of the nodes represented the relative abundances of each microbe. The blue and red lines between the nodes represent positive or negative correlations, respectively. The thickness of the line represents the strength of correlation.

**Table S1.** Location, depth, temperature, and salinity of environmental samples

Region	Station	Longitude	Latitude	Samples	Depth(m)	Temperature(°C)	Salinity(‰)
Upwelling	1	111.1940	20.0005	S1	3	26.06	33.55
				D1	40	21.72	34.35
	2	111.1001	19.7002	S2	3	26.9	34.00
				D2	30	20.88	34.44
	3	110.6998	18.9024	S3	3	26.48	34.09
				D3	75	19.44	34.54
Non-upwelling	4	111.9399	19.9916	S4	3	29.02	33.81
				D4	80	20.52	34.40
	5	111.9012	19.4811	S5	3	29.44	33.66
				D5	100	18.93	34.57
	6	111.1017	18.4994	S6	3	30.2	34.00
				D6	150	16.42	34.59

**Table S2.** Potential environmental factors for the bacterial phyla composition revealed by RDA

Name	Explains %	pseudo-F	P	P(adj)
Depth*	57.2	13.4	0.002	0.011
Temperature	49.6	9.8	0.002	0.011
Salinity	45.2	8.3	0.004	0.01467
NO <sub>3</sub> <sup>-</sup>	36.7	5.8	0.012	0.033
SiO <sub>3</sub> <sup>2-</sup>	30.2	4.3	0.016	0.0352
NH <sub>4</sub> <sup>+</sup>	25.1	3.3	0.048	0.088

Note: The listed environmental factors were significant in terms of simple effects; The asterisk indicates the association was significant in terms of conditional effect.