

長江洪水對東海中超微浮游植物生態之影響

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利用新穎分子指標技術以及雙雷射 (激發波長488-nm與633-nm) 流式細胞儀分析, 首度對於東海水域聚球藻族群 (*Synechococcus* spp.) 生態進行深入的探討。我們發現以往在長江口附近被誤認為原核綠藻 (*Prochlorococcus*) 的超微浮游植物族群, 事實上應該是屬於在海洋生態系中極少被研究的富含藻藍素 (phycocyanin) 的聚球藻。經由藻藍蛋白操作子基因 (phycocyanin operon) 序列多樣性分析, 這群富含藻藍素的聚球藻可以進一步分為4個亞群 (ECS-1到ECS-4), 以及附屬於富含藻紅素聚球藻 (phycoerythrin) 的ECS-PE這一群。進一步與各個水文因子進行相關性分析, 發現水體濁度是影響這4個亞群富含藻藍素聚球藻在東海分布的主要環境因子。此外, 我們也發現大量的陸源污染物可能隨著長江大洪水注入東海海域, 進而抑制了海洋常見的富含藻紅素聚球藻的生長。預估這樣的研究成果, 將為日後研究海洋浮游植物生態與全球環境變遷之關係提供極具參考價值的資訊。此研究成果已發表於國際頂尖期刊「Microbial Ecology」(IF=3.277, 7% in Marine and Freshwater Biology)。

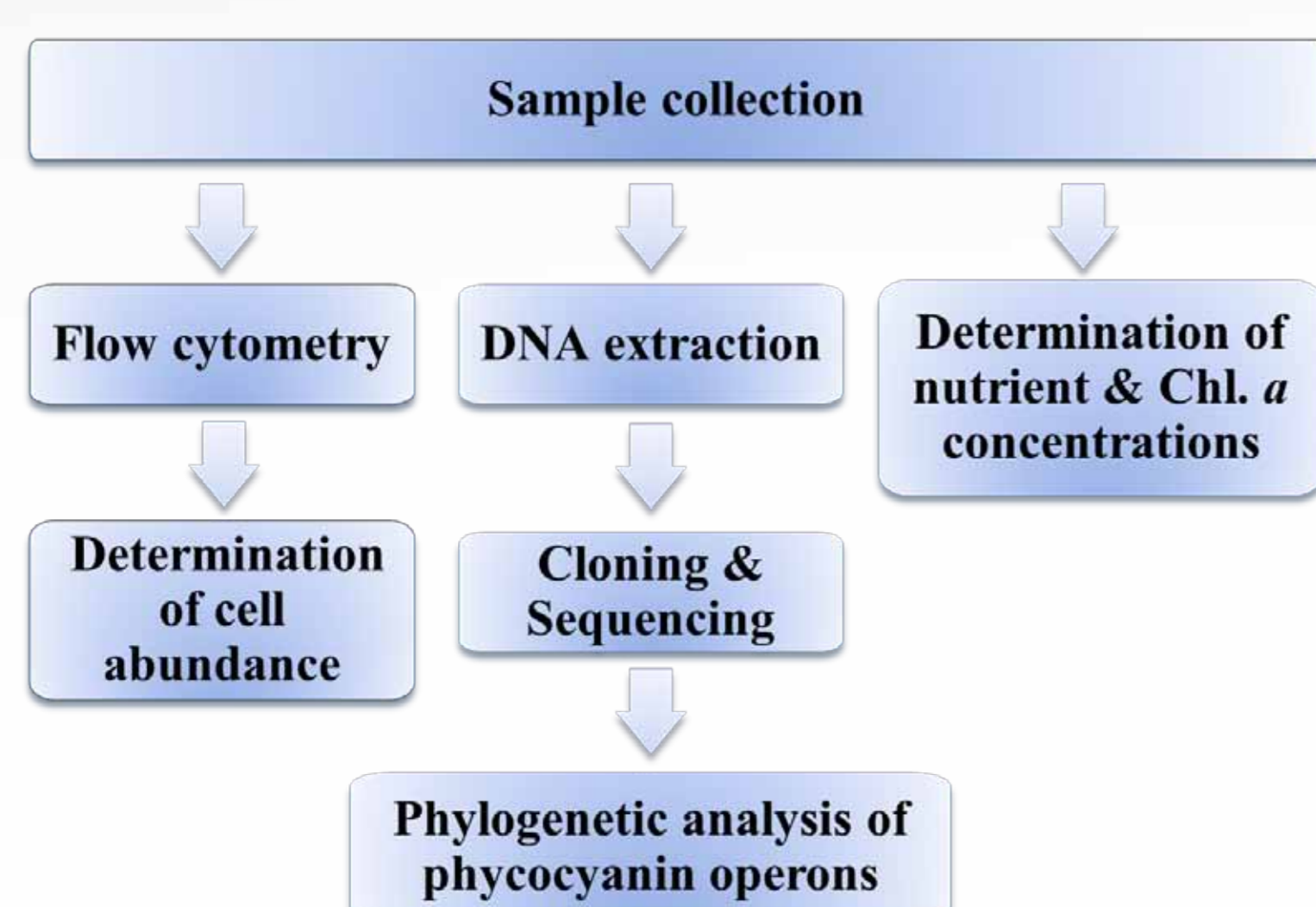


Table 1. Hydrographic features of the Changjiang dilution water coverage (salinity ≤ 31 PSU) during the summers 2009 and 2010. Each parameter is presented as the mean value ± 1 standard deviation. n: station number; DIN: dissolved inorganic nitrogen ($\text{NH}_4 + \text{NO}_2 + \text{NO}_3$); DIP: dissolved inorganic phosphate; Chl. a: chlorophyll a. **: significant difference at a level of $p < 0.01$ (Student's t-test).

	2009 (n=7)	2010 (n=20)
Coverage area ($\times 10^3$ km ²)	43	160
Temperature ($^{\circ}\text{C}$)	25.0 \pm 0.9	24.9 \pm 1.6
Transparency (%)	69.9 \pm 4.9	78.4 \pm 4.4**
DIN (μM)	4.90 \pm 9.79	12.04 \pm 11.97
DIP (μM)	0.13 \pm 0.07	0.24 \pm 0.38
Chl. a (mg m^{-3})	2.51 \pm 1.69	2.10 \pm 1.56

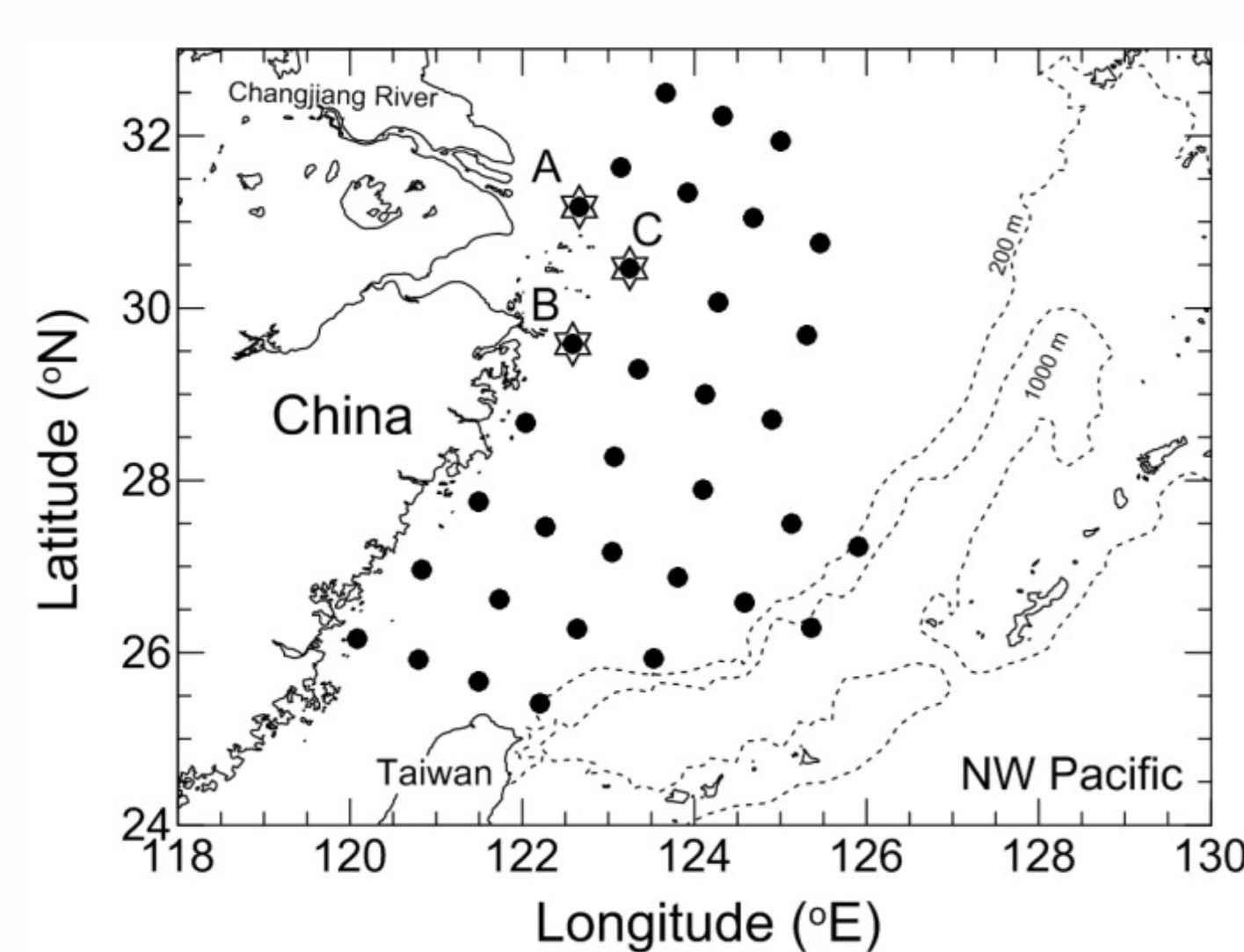


Figure 1. Location of observation stations on the East China Sea during the summers of 2009 and 2010.

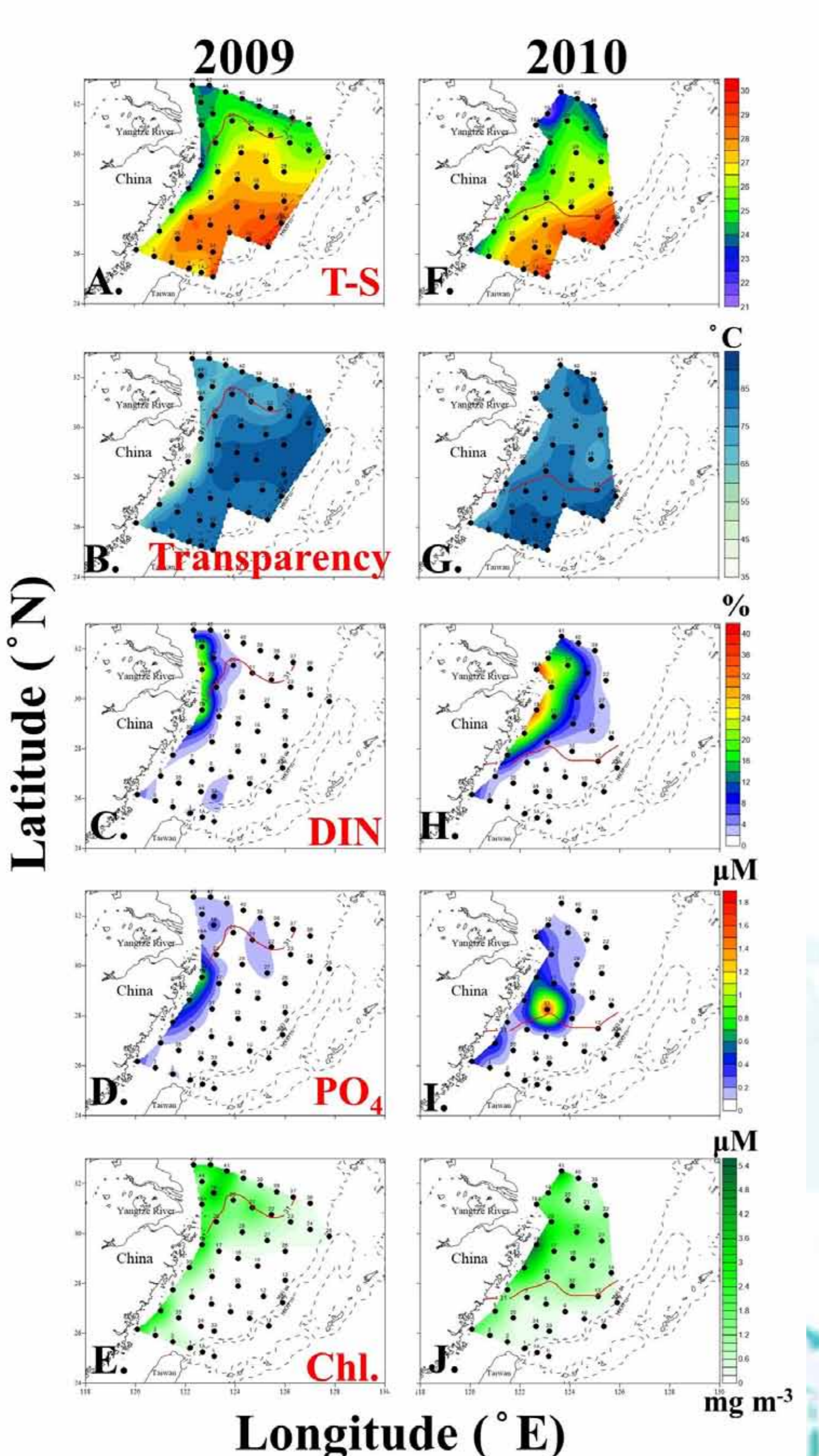


Figure 2. Distribution of (A, F) temperature-salinity, (B, G) transparency, (C, H) dissolved inorganic nitrogen ($\text{NH}_4 + \text{NO}_2 + \text{NO}_3$, μM), (D, I) dissolved inorganic phosphate (μM), and (E, J) chlorophyll a (mg m^{-3}) over the surface of the East China Sea during the summers of 2009 and 2010.

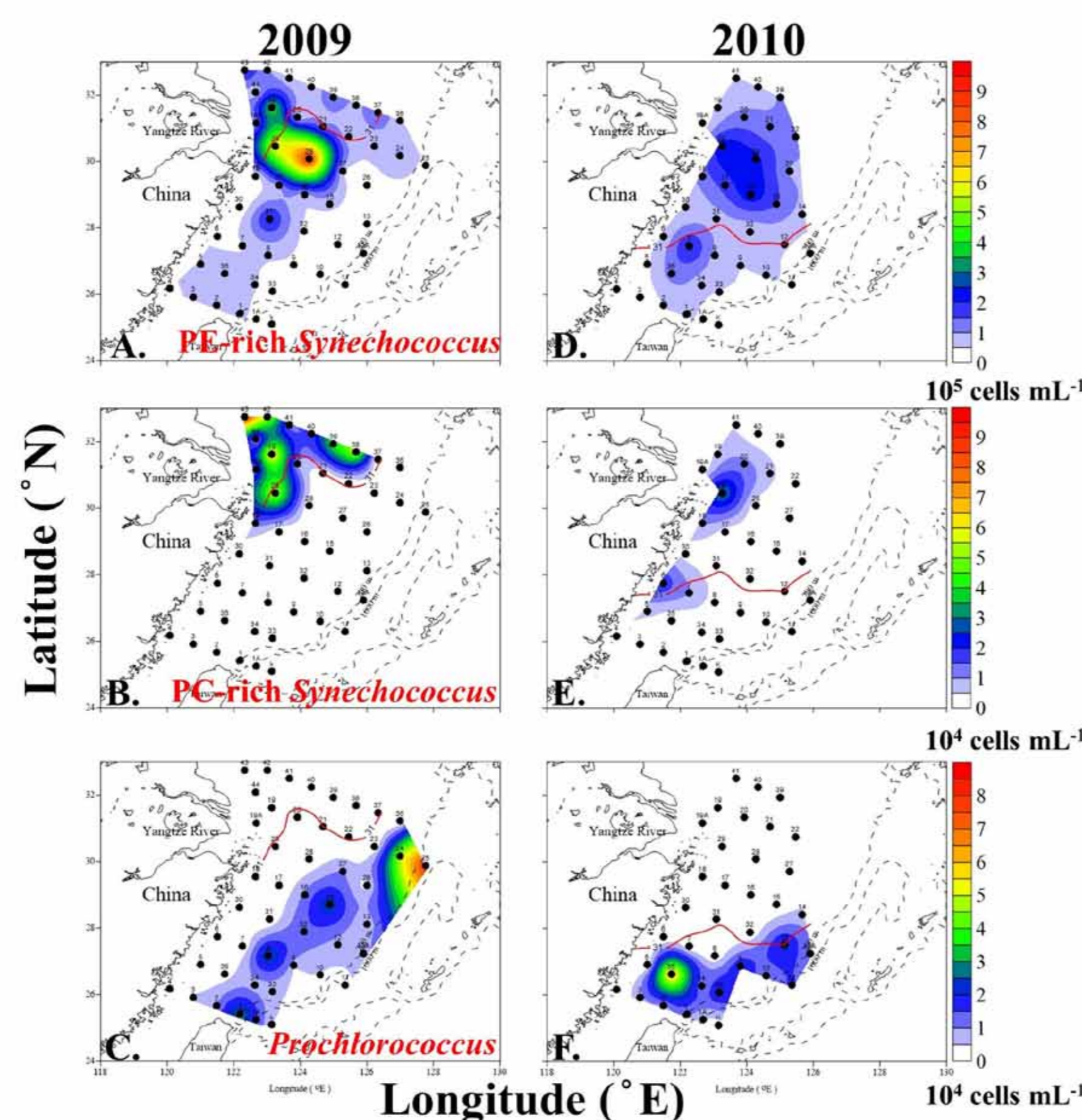


Figure 3. Distribution of picocyanobacterial abundance on the surface of the East China Sea: (A, D) Phycocyanin-rich *Synechococcus*, (B, E) phycocyanin-rich *Synechococcus*, and (C, F) *Prochlorococcus*. The bold dashed lines represent the isohaline of salinity 31, indicating the outer boundary of the CDW-affected area.

Table 2. Pearson correlations observed between picocyanobacterial abundances and hydrographic factors during the summers of 2009 and 2010 (n=68). DIN: dissolved inorganic nitrogen ($\text{NH}_4 + \text{NO}_2 + \text{NO}_3$); DIP: dissolved inorganic phosphate.

	Temperature	Salinity	Transparency	DIN	DIP
Syn.					
PE-rich	-0.198	-0.130	-0.065	-0.003	-0.031
PC-rich	-0.404**	-0.260*	-0.290**	0.105	0.071
Pro.	0.290**	0.314**	0.293**	-0.236*	-0.218*

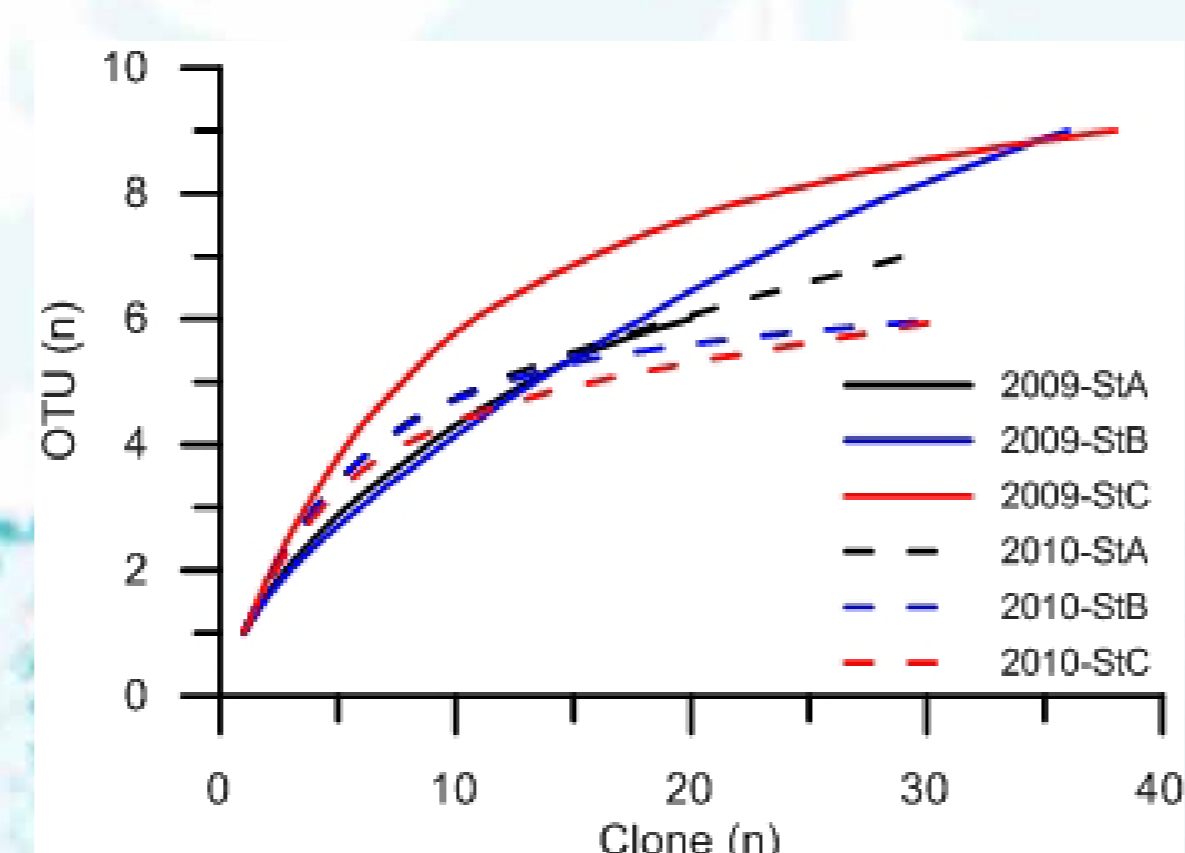


Figure 4. Rarefaction curves inferred from *cpcBA*-ITS and *rpcBA*-ITS sequences obtained from the surface of the East China Sea during the summers of 2009 and 2010. DNA samples were collected from stations A, B, and C (Fig. 1). Operational taxonomic units (OTU) were defined at the level of 90% sequence identity.

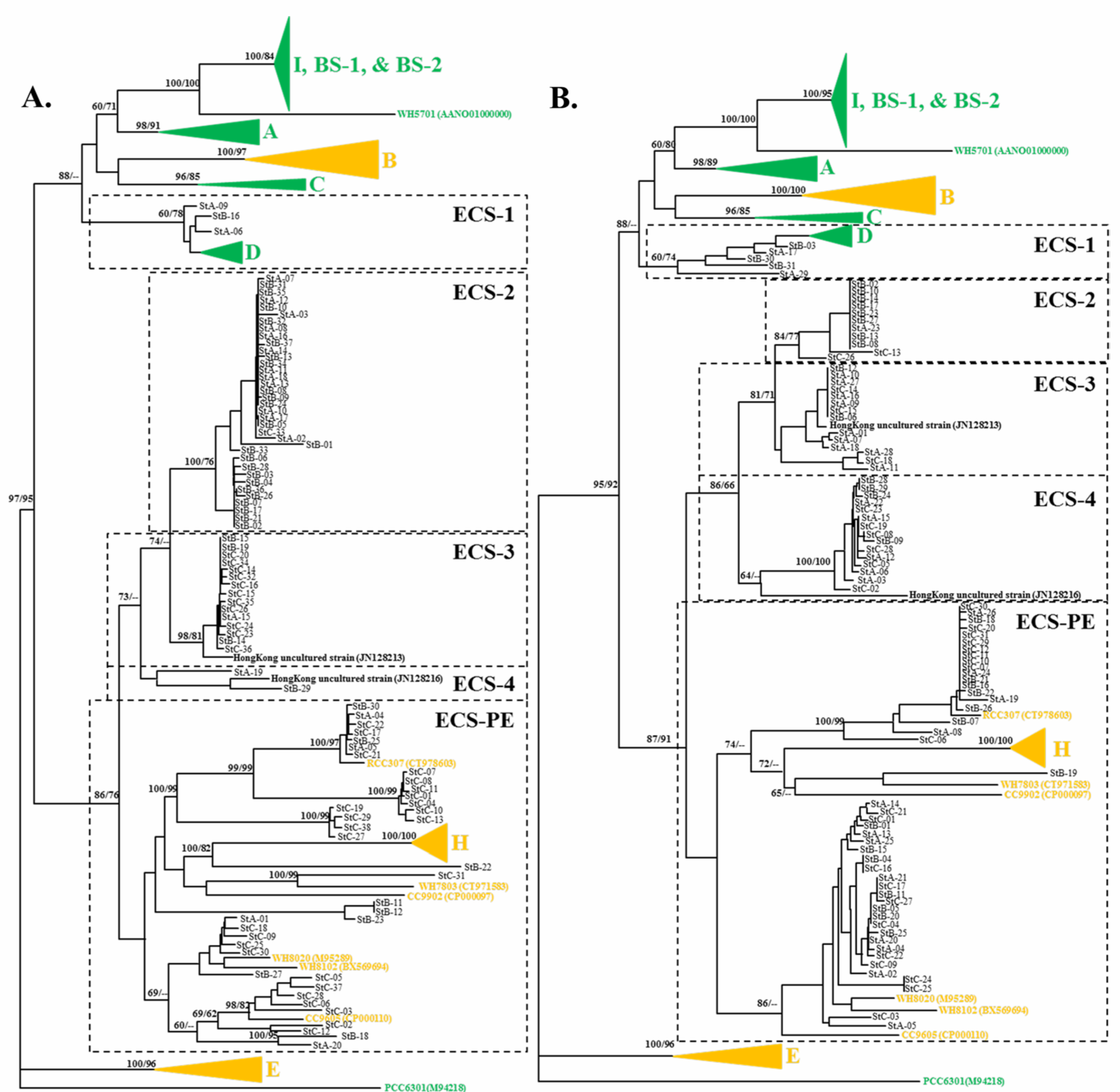


Figure 5. Neighbor-joining tree inferred from *cpcBA*-ITS and *rpcBA*-ITS sequences obtained from the East China Sea (ECS) during the summer of 2009 (A) and 2010 (B). DNA samples were collected from stations A, B, and C (Fig. 1). The effects of sampling error on tree inference and the stability of branch nodes were tested by a bootstrap analysis with 1000 repetitions. Bootstrap values of ≥ 60 are displayed on the branches. The freshwater PC-rich strain of *Synechococcus* PCC6301 served as the root. The length of the scale bar on the lower-left indicates a 0.1 nucleotide substitution unit.

Table 3. Distribution of *Synechococcus* analyzed by the phylogeny of the phycocyanin operon (as shown in Figures 6 and 7) on the surface of the East China Sea during the summers of 2009 and 2010. The percentage of phycocyanin operon sequences belonging to a specific clade is included in parentheses.

Station	Salinity (PSU)	Transparency (%)	<i>cpcBA</i> -ITS				<i>rpcBA</i> -ITS	Total clones
			ECS-1	ECS-2	ECS-3	ECS-4	ECS-PE	
2009								
A	30.38	62.5	2 (10%)	12 (60%)	1 (5%)	1 (5%)	4 (20%)	20 (100%)
B	31.25	60.4	1 (3%)	23 (64%)	3 (8%)	1 (3%)	8 (22%)	36 (100%)
C	32.10	77.2	0	1 (3%)	11 (29%)	0	26 (68%)	38 (100%)
2010								
A	27.84	75.4	2 (7%)	1 (4%)	9 (31%)	5 (17%)	12 (41%)	29 (100%)
B	24.98	69.9	3 (10%)	8 (26%)	2 (6%)	4 (13%)	14 (45%)	31 (100%)
C	25.44	75.0	0	2 (6%)	3 (10%)	6 (19%)	20 (65%)	31 (100%)

Conclusion

In comparison with previous studies, this study was the first to completely describe the distributions of both PE- and PC-rich *Synechococcus* in the ECS by flow cytometric enumeration and molecular phylogenetic analysis. Furthermore, PE- and PC-rich *Synechococcus* ecology was affected by a well-described disastrous flood that happened in the Changjiang River basin. Based on our findings, we suggest that anthropogenic pollutants carried in with the floodwater and increased transparency within the CDW expansion appear to be the factors that transiently changed the *Synechococcus* ecology after the flood.