SUPPORTING INFORMATION

Diversity, distribution and nitrogen use strategies of bacteria in the South China Sea basin

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Table of contents

Table S1. Specific primer sequences in *Prochlorococcus*

Gene	F (5'-3')	R (5'-3')
amt1	ACCTGYTGGATTGCYTGGTCT	AAGTCKGGATAWGCYTCCAT
ureC	GTAATAGCTGGTGAGGGGCA	CCCGGAGTACAAGTAGTGGC
glnA	CCCCTAACTGGTCCAAGTCC	ACCAGCCATCATCATTGCAC
gltS	CACCGATCTGACGATCCTGG	TCGACAACTGGACCGTGAAG
AAT	TCTGAGCGGTCAAGCGATTT	CCTGGTACTTGATCGGGGTG
urtA	CWGGWCCYTGWGGRGCATCRA	ACTAYGGYGCTTGGAACTACAT
nirA	TAGAAGACTGCGTGAAGCCG	AGTGGATTGCCGGTTACGTT
IdiA	CCGAGCAGGTGAGCAGTTAT	ACTGGTTGTAGACACTGCGG

Table S2. Efficient sequencing information statistics of 16S rRNA samples

Sample	Reads	Base	Mean	Min	Max	OTU	Cover.	Ace	Shannon
SEATS_sur	63804	27571230	432.12	387	454	468	99.85	517	3.50
SEATS_68m	70929	31447507	443.36	332	466	394	99.83	470	3.27
SEATS_200m	77982	34696980	444.93	298	462	741	99.74	867	3.04
SEATS_750m	72767	32471293	446.23	278	515	633	99.74	756	2.72
SS1_sur	81677	35129984	430.10	291	462	496	99.87	555	2.63
SS1_105m	93821	40314095	429.69	338	493	488	99.91	530	3.29
SS1_200m	80679	35127502	435.39	366	462	893	99.84	956	5.03
SS1_750m	71756	31308923	436.32	305	467	843	99.94	857	4.78
A2_surface	61845	26649347	430.90	270	464	506	99.85	559	3.01
B1_sur	64261	27721347	431.38	365	492	479	99.83	539	3.38
C1_sur	83617	36018895	430.76	347	464	461	99.86	545	3.02
Total	823138	358457103	435.47	325	473	1427	99.85	517	3.50

Table S4. Efficient sequencing information statistics of nifH samples

Sample	Reads	Base	Mean	Min	Max	OTU	Cover.	Ace	Shannon
SEATs_sur	10090	4358673	431.97	268	533	128	99.58	196	2.45
SEATs_68m	16019	6739420	420.71	205	530	149	99.89	155	2.73
SEATs_200m	10370	4366260	421.04	214	532	221	99.91	222	4.48
SEATs_750m	13919	5940517	426.79	204	551	170	99.90	174	3.47
SS1_sur	12974	5493021	423.38	223	549	230	99.53	280	3.04
SS1_105m	13192	5620397	426.04	210	533	119	99.84	131	2.59
SS1_200m	13201	5577525	422.50	243	552	150	99.81	162	2.56
A2_sur	19717	7721344	391.60	207	553	215	99.87	226	3.43
B1_sur	11603	4816444	415.10	233	523	217	99.65	243	3.21
C1_sur	10484	4326312	412.65	219	533	212	99.65	234	3.60
Total	131569	54959913	417.72	223	539	749	99.76	202	3.16

Table S7. T test of correlation analysis between microbial community diversities and environmental factors

			T	Salinity	Chl a	NO_2^-	NO_3^-	PO_4^{3-}	SiO_3^{2-}	DO
Bacterial diversity	OTUs	Correlation	-0.518	0.2	-0.700*	-0.1	0.648*	0.778**	0.591	-0.793**
		P-value	0.102	0.555	0.016	0.77	0.031	0.005	0.056	0.004
	Ace	Correlation	-0.445	0.077	-0.773**	-0.3	0.563	0.689*	0.573	-0.692*
		P-value	0.17	0.821	0.005	0.37	0.072	0.019	0.066	0.018
	Shannon	Correlation	-0.327	0.465	-0.273	0.1	0.181	0.243	0.2	-0.323
		P-value	0.326	0.15	0.417	0.77	0.594	0.472	0.555	0.332
	PCoA axis 1	Correlation	-0.909**	0.761**	-0.6	0	0.915**	0.843**	0.800**	-0.692*
		P-value	0	0.007	0.051	1	0	0.001	0.003	0.018
	Bray-Curtis	Correlation	0.7974**	0.2829*	0.09156	-0.1544	0.7653**	0.7**	0.7374**	0.6728**
		P-value	0.002	0.043	0.265	0.837	0.001	0.002	0.003	0.002
Diazotrophic diversity	OTUs	Correlation	0.394	-0.565	-0.333	-0.522	-0.2	-0.089	-0.079	0.225
		P-value	0.26	0.089	0.347	0.122	0.579	0.807	0.829	0.532
	Ace	Correlation	0.697*	-0.863**	-0.176	-0.522	-0.627	-0.464	-0.491	0.413
		P-value	0.025	0.001	0.627	0.122	0.052	0.176	0.15	0.235
	Shannon	Correlation	-0.079	-0.316	-0.285	-0.29	0.162	0.225	0.333	-0.061
		P-value	0.829	0.374	0.425	0.416	0.656	0.531	0.347	0.868
	PCoA axis 1	Correlation	-0.685*	0.766**	-0.127	0.406	0.769**	0.676*	0.648*	-0.529
		P-value	0.029	0.01	0.726	0.244	0.009	0.032	0.043	0.116
	Bray-Curtis	Correlation	0.5637*	0.2271	0.2194	0.2652	0.5452*	0.5185*	0.5415*	0.5045*
		P-value	0.012	0.053	0.138	0.286	0.013	0.017	0.018	0.016