

Table S1 Environmental parameters of seawater around the coral samples (Expressed as mean value and standard error, mean±SE).

	Spring	Summer
	Mean ± SE.	Mean ± SE
Temperature (°C)	24.63±0.32	25.83±0.45
Salinity (‰)	33.46±0.31	35.01±0.09
pH	8.12±0.01	8.11±0.01
Ammonium (µg L <sup>-1</sup> )	36.92±0.57	12.95±0.12
Nitrate (µg L <sup>-1</sup> )	17.93±1.53	55.70±0.13
Nitrite (µg L <sup>-1</sup> )	2.28±0.38	2.25±0.06
Phosphate (µg L <sup>-1</sup> )	12.18±0.88	5.30±0.66
Chlorophyll a (µg L <sup>-1</sup> )	1.81±0.19	1.43±0.11
COD (mg L <sup>-1</sup> )	0.25±0.01	1.53±0.09
DO (mg L <sup>-1</sup> )	6.03±0.05	6.96±0.05

Table S2 The richness and diversity information of *nifH* sequences from three coral species (n=3) in two seasons. (Expressed as mean value and standard error, mean±SE).

	<i>G. astreata</i>			<i>P. decussata</i>			<i>P. lutea</i>		
	spring (mean±SE)	summer	P t-test	spring (mean±SE)	summer	P t-test	spring (mean±SE)	summer	P t-test
Chao 1	406±76	220±120	0.087	551±329	199±91	0.148	408±96	273±142	0.246
OTUs	298±64	181±91	0.14	415±227	127±53	0.1	317±75	191±97	0.149
Shannon (H')	4.43±0.31	3.74±0.74	0.212	4.17±0.64	3.24±0.30	0.085	4.34±0.31	3.71±0.52	0.156
Simpson E	0.14±0.08	0.14±0.04	0.951	0.07±0.03	0.12±0.06	0.299	0.12±0.06	0.13±0.10	0.891

Table S3 The percentage of the diazotrophic variable OTUs accounted for the total sequences (Expressed as mean value and standard error, mean±SE).

	spring	summer
<i>G. astreata</i>	17.11±3.97	38.45±5.12
<i>P. decussata</i>	13.92±1.56	24.85±3.79
<i>P. lutea</i>	26.81±1.84	32.62±8.11

Table S4 The overlap of variable diazotrophic communities among three coral species.

	<i>G. astreata</i>		<i>P. decussata</i>		<i>P. lutea</i>		<i>NiJH</i> nearest relative (Prot-Acc number-% similarity)	
	Spring (%)	Summer (%)	Spring (%)	Summer (%)	Spring (%)	Summer (%)		
OTU1363	0.043	0.773	/	/	0.013	0.863	<i>Rhodopseudomonas palustris</i> (ABJ08453-90%)	Alphaproteobacteria
OTU3604	0.793	<b>6.571</b>	/	/	0.107	<b>14.507</b>	<i>Rhodopseudomonas palustris</i> (ABJ08453-92%)	Alphaproteobacteria
OTU3305	0.133	<b>8.173</b>	/	/	0.21	<b>2.067</b>	<i>Gluconacetobacter diazotrophicus</i> (ACI51349-87%)	Alphaproteobacteria
OTU3752	0.193	<b>1.765</b>	0.067	0.003	/	/	<i>Azospirillum lipoferum</i> (CBS86044-91%)	Alphaproteobacteria
OTU657	0.073	0.773	/	/	0.003	0.187	<i>Desulfovibrio aespoeensis</i> (ADU62037-93%)	Deltaproteobacteria
OTU978	0.23	0.018	/	/	0.13	0.04	<i>Desulfovibrio aespoeensis</i> (ADU62037-95%)	Deltaproteobacteria
OTU890	0.003	0.44	/	/	0.613	0.003	<i>Desulfuromonas acetoxidans</i> (EAT15955-96%)	Deltaproteobacteria
OTU884	0.003	0.677	/	/	0.31	0.017	<i>Desulfuromonas acetoxidans</i> (EAT15955-94%)	Deltaproteobacteria
OTU619	0.203	<b>1.609</b>	/	/	<b>4.54</b>	0.483	<i>Desulfuromonas acetoxidans</i> (EAT15955-95%)	Deltaproteobacteria
OTU667	/	/	0.317	0.003	0.053	<b>1.427</b>	<i>Desulfonatronospira thiodismutans</i> (EFI35493-90%)	Deltaproteobacteria
OTU668	/	/	0.33	0.06	0.78	0.157	<i>Halorhodospira halophila</i> (ABM61068-94%)	Gammaproteobacteria
OTU991	<b>1.223</b>	0.03	/	/	<b>1.427</b>	0.177	<i>Halorhodospira halophila</i> (ABM61068-93%)	Gammaproteobacteria
OTU775	0.007	0.451	/	/	0.08	0.007	Verrucomicrobiae bacterium (EDY82020-96%)	Verrucomicrobia