

## **Supplementary Material**

**Figure S1.** Principal coordinate analysis (PCoA) of periphytic algal communities

**Figure S2.** The values and trend of environmental parameters

**Figure S3.** Co-occurrence network of the periphytic algal communities

**Figure S4.** Redundancy analysis in H1 and H2

**Figure S5.** Environmental heterogeneity determines the action of the ecological processes assembling the periphytic algal community

**Table S1.** Latitude and longitude of sampling sites

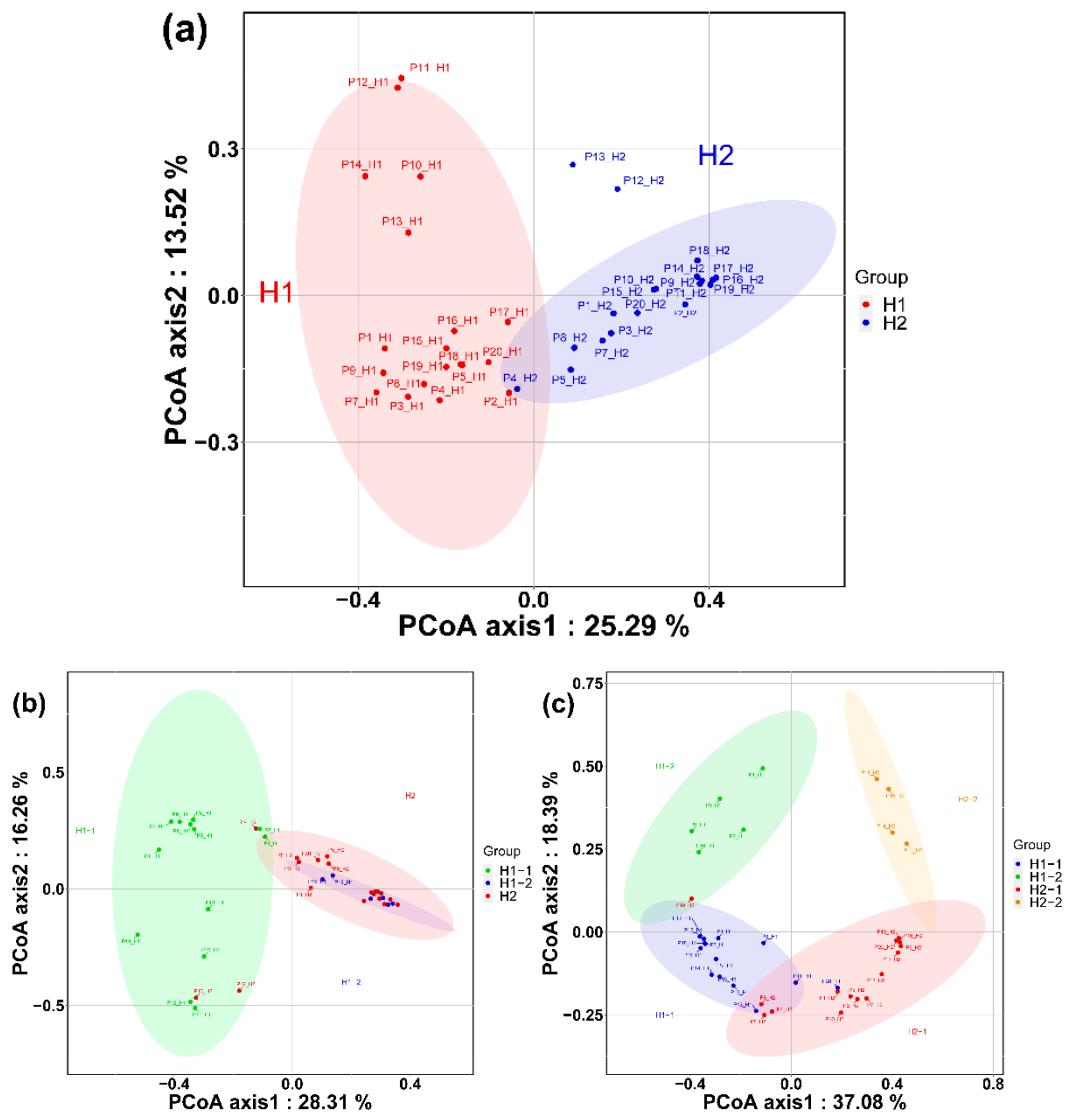
**Table S2.** Environmental heterogeneity and community structure heterogeneity

**Table S3.** Coefficient of variation (CV%) of each environmental parameter

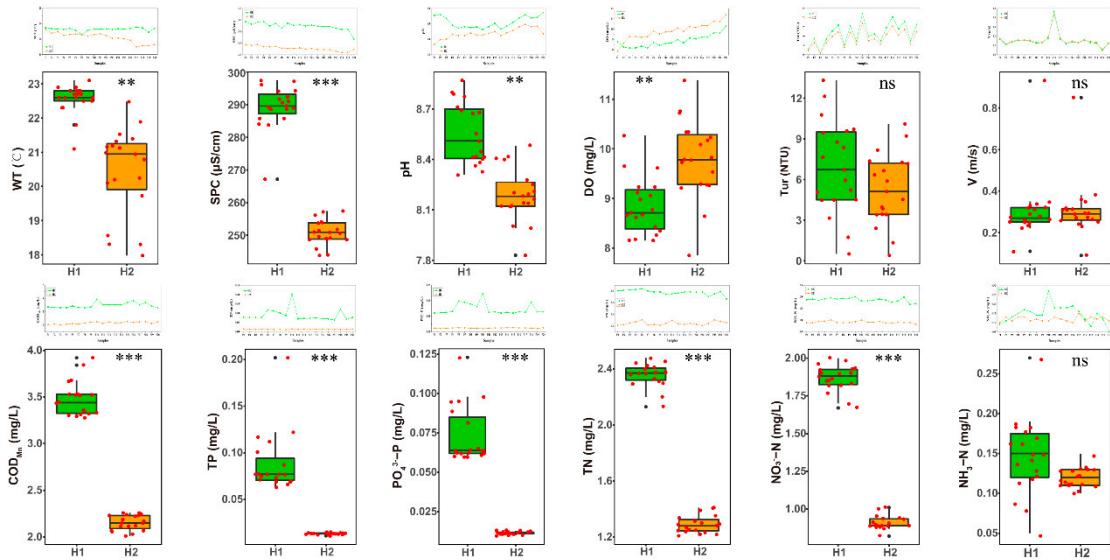
**Table S4.** Result of PERMDISP test and PERMANOVA test

**Table S5.** Alpha diversity index of periphytic algal communities

**Table S6.** Mean-nearest-taxon-distance and nearest-taxon-index



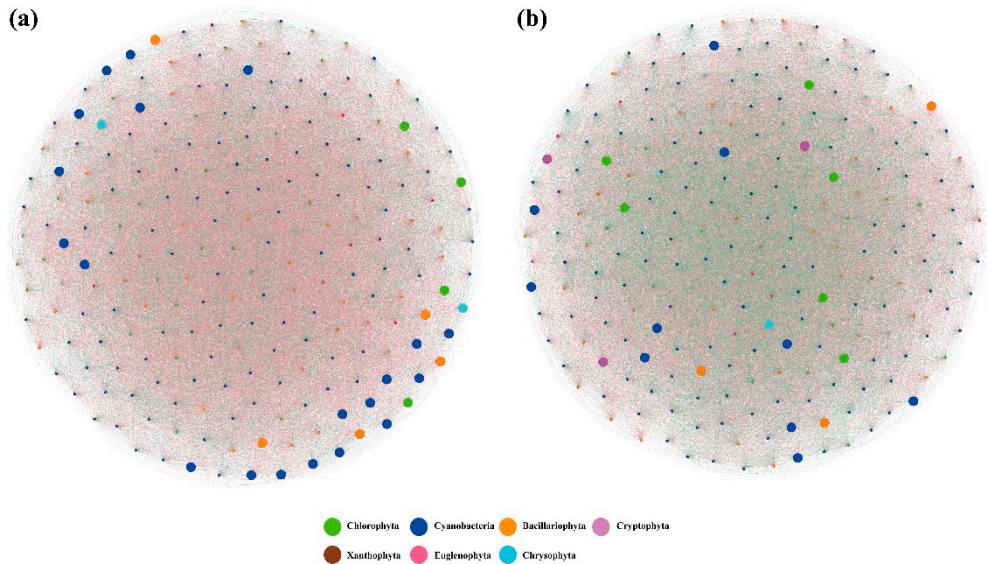
**Figure S1.** Principal coordinate analysis (PCoA) according to the similarity in periphytic algal community structure (a) based on all species; (b) based on cyanobacteria; (c) based on eukaryotic algae.



**Figure S2.** The values and trend of environmental parameters (Asterisks indicate a significant

difference between H1 and H2 (Wilcoxon test); \*  $P<0.05$ ; \*\*  $P<0.01$ ; \*\*\*  $P<0.001$ , ns: not

significant.)



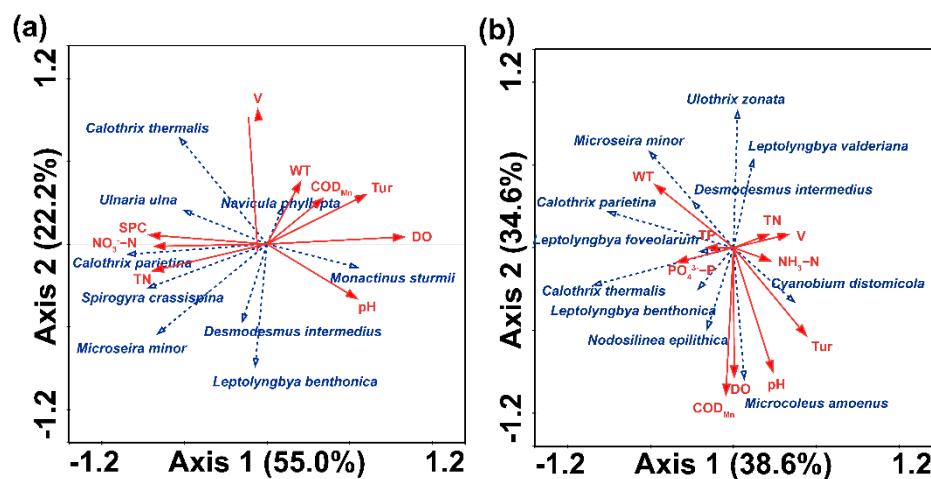
**Figure S3.** Co-occurrence network of the periphytic algal communities (a) H1 (b) H2. Each node

represents an individual species, and the species belonging to the same phylum are displayed in the

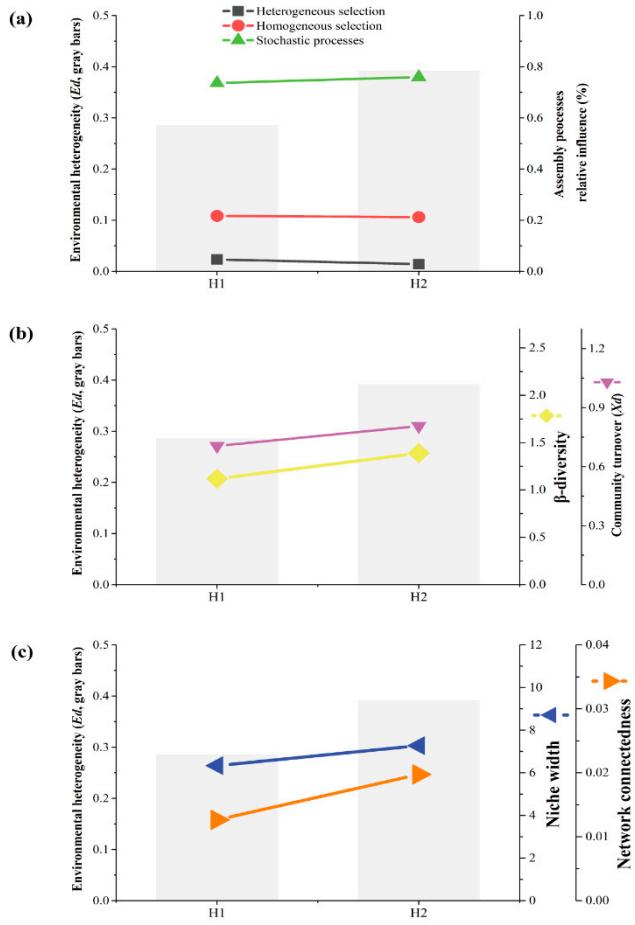
same color. The sizes of nodes reflected their connecting degrees. The higher the degree, the more

connections there were between this species and other neighboring species. Green lines and red lines

represent positive and negative correlation, respectively. Each edge between two nodes represents positive or negative interactions between the two species (b. positive correlation network; c. negative correlation network). A connection stands for a significant ( $|r| > 0.7$ ,  $P < 0.05$ )



**Figure S4.** Redundancy analysis (RDA) ordination plot for the first two principal dimensions: (a) H1; (b) H2



**Figure S5.** Environmental heterogeneity determines the action of the ecological processes assembling the periphytic algal community.

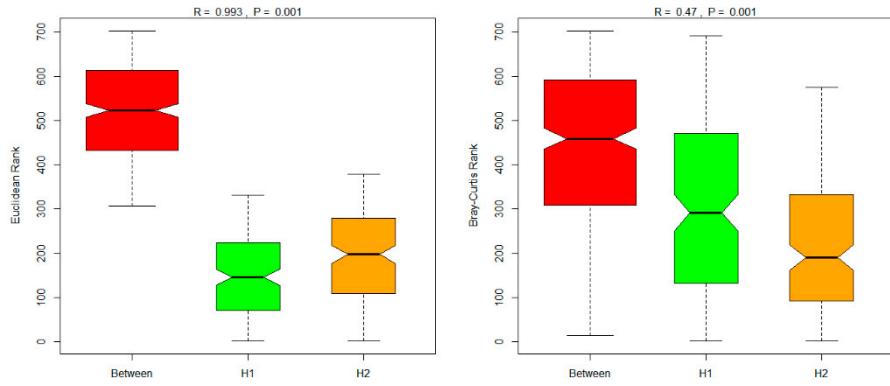
**Table S1.** Latitude and longitude of sampling sites

Site	Latitude	Longitude
P1	32.68°N	111.72°E
P2	33.01°N	112.47°E
P3	33.34°N	113.24°E
P4	33.69°N	112.95°E
P5	33.70°N	112.94°E
P7	33.82°N	113.04°E
P8	34.26°N	113.64°E
P9	34.74°N	113.57°E
P10	34.87°N	113.23°E
P11	34.90°N	113.19°E
P12	34.92°N	113.17°E
P13	35.05°N	113.10°E
P14	36.25°N	114.32°E
P15	37.44°N	114.55°E
P16	38.11°N	114.42°E
P17	39.08°N	115.39°E
P18	39.51°N	115.79°E
P19	39.14°N	117.09°E
P20	39.99°N	116.26°E

**Table S2.** Environmental heterogeneity and community structure heterogeneity

	Environmental	Community structure
<b>Heterogeneity</b>		
	Mean Ed	Mean Xd
H1 and H2	0.4391	0.9053
H1	0.2855	0.7052
H2	0.3915	0.8063

**ANOSIM**



**Table S3.** Coefficient of variation (CV%) of each environmental parameter

Parameter	H1	H2
WT (°C)	0.0199	0.0640
SPC (µS/cm)	0.0232	0.0157
pH	0.0215	0.0197
DO (mg/L)	0.0653	0.0821
Tur (NTU)	0.5019	0.5005
V(m/s)	0.5227	0.4614
COD <sub>Mn</sub> (mg/L)	0.0539	0.0379
TP (mg/L)	0.3687	0.0788
PO <sub>4</sub> <sup>3-</sup> -P (mg/L)	0.2480	0.0879
TN (mg/L)	0.0357	0.0494
NO <sub>3</sub> <sup>-</sup> -N (mg/L)	0.0465	0.0491
NH <sub>3</sub> -N (mg/L)	0.3292	0.1082

**Table S4.** Result of PERMDISP test and PERMANOVA test

Environmental	Community structure
<b>PERMDISP</b>	
Sum of squares	534.46      0.8312

Mean squares	14.846	0.0231
<i>F</i>	1.3076	1.6
<i>P</i>	0.2886	0.2195

### PERMANOVA

Sum of squares	1487.7	8.1346
Mean squares	41.3	0.226
<i>F</i>	341.95	5.5657
<i>P</i>	0.001	0.001

**Table S5.** Alpha diversity index of periphytic algal communities

Time	Site	Chao1	Coverage	Pielou	Shannon
<b>H1</b>	P1	14.640	0.998	0.602	4.138
	P2	11.892	0.997	0.697	4.681
	P3	8.679	0.999	0.586	3.966
	P4	12.465	0.997	0.515	3.398
	P5	14.640	0.996	0.688	4.780
	P7	12.200	0.998	0.576	3.699
	P8	12.465	0.998	0.557	3.711
	P9	8.679	0.998	0.527	3.528
	P10	20.599	0.997	0.540	3.669
	P11	15.533	0.999	0.269	1.700
<b>H2</b>	P12	8.146	0.999	0.403	2.718
	P13	7.298	0.999	0.547	3.596
	P14	9.295	0.999	0.472	3.011
	P15	10.016	0.990	0.664	4.149
	P16	15.118	0.999	0.230	1.421
	P17	23.459	0.999	0.414	2.742
	P18	2.977	0.999	0.530	3.695
	P19	9.897	0.999	0.542	3.891
	P20	20.827	0.997	0.533	3.619
	P1	7.270	0.991	0.622	4.122
	P2	17.965	0.992	0.726	4.812
	P3	12.606	0.995	0.770	5.146
	P4	8.920	0.996	0.592	4.074

P5	6.165	0.997	0.632	4.152
P7	8.849	0.998	0.604	3.975
P8	10.562	0.995	0.686	4.706
P9	10.733	0.988	0.713	4.493
P10	17.218	0.990	0.645	4.177
P11	7.993	0.994	0.643	4.246
P12	4.535	0.999	0.406	2.682
P13	10.991	0.998	0.298	1.846
P14	5.600	0.995	0.713	4.681
P15	9.296	0.998	0.476	3.177
P16	18.547	0.990	0.656	4.227
P17	28.518	0.993	0.689	4.485
P18	4.121	0.996	0.789	4.406
P19	7.434	0.995	0.675	4.416
P20	11.654	0.991	0.712	4.513

**Table S6.** Mean-nearest-taxon-distance and nearest-taxon-index

Time	Site	MNTD <sub>obs</sub>	MNTD <sub>rand.mean</sub>	MNTD <sub>obs,p</sub>	NTI
<b>H1</b>	P1	0.019	0.056	0.001	2.77
	P2	0.012	0.060	0.003	1.72
	P3	0.035	0.056	0.026	1.64
	P4	0.015	0.055	0.002	2.15
	P5	0.016	0.053	0.001	2.71
	P7	0.020	0.061	0.001	2.58
	P8	0.019	0.058	0.001	2.66
	P9	0.012	0.057	0.001	3.03
	P10	0.010	0.056	0.001	3.01
	P11	0.011	0.062	0.012	1.53
<b>H2</b>	P12	0.014	0.065	0.001	1.80
	P13	0.013	0.060	0.001	2.55
	P14	0.036	0.064	0.043	1.51
	P15	0.022	0.060	0.001	2.77
	P16	0.022	0.064	0.001	2.15
	P17	0.022	0.060	0.001	2.26
	P18	0.039	0.061	0.031	1.54
	P19	0.023	0.052	0.001	2.82
	P20	0.019	0.063	0.001	3.27
	P1	0.027	0.060	0.002	2.17
	P2	0.023	0.060	0.001	3.57

P3	0.033	0.059	0.001	2.63
P4	0.022	0.057	0.001	2.27
P5	0.026	0.061	0.002	2.50
P7	0.036	0.060	0.026	1.69
P8	0.025	0.056	0.001	2.75
P9	0.027	0.065	0.001	3.25
P10	0.020	0.062	0.001	3.15
P11	0.023	0.067	0.001	2.84
P12	0.035	0.056	0.218	0.83
P13	0.011	0.064	0.005	1.60
P14	0.032	0.064	0.001	2.51
P15	0.032	0.067	0.001	3.11
P16	0.028	0.064	0.001	2.90
P17	0.031	0.060	0.001	2.81
P18	0.048	0.079	0.004	2.07
P19	0.018	0.056	0.001	2.41
P20	0.036	0.061	0.002	2.39

\*MNTD<sub>obs</sub>: Observed MNTD in community. MNTD<sub>rand.mean</sub>: Mean MNTD in null communities.

MNTD<sub>obs,p</sub>: P-value (quantile) of observed MNTD vs. null communities. NTI: nearest-taxon-index.