

Spatial and Species Variations of Bacterial Community Structure and Putative Function in Seagrass Rhizosphere Sediment

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Table S1. The sequences characteristics of the all obtained seagrass rhizosphere samples

Coral reef ecosystems	Sample ID	Raw reads	Resampling depth	Good's coverage
Daya Bay	DYH1	40,990	33,980	99.30%
	DYH2	41,929	33,980	99.32%
	DYH3	39,296	33,980	99.31%
Sanya Bay	SYT1	56,671	33,980	99.07%
	SYT2	54,384	33,980	99.12%
	SYT3	42,129	33,980	98.99%
Xisha Islands	XSC1	60,954	33,980	98.96%
	XSC2	67,941	33,980	99.06%
	XSC3	66,866	33,980	99.02%
	XST1	52,168	33,980	99.13%
	XST2	59,573	33,980	98.99%
	XST3	61,669	33,980	99.11%
	XSH1	60,647	33,980	99.01%
	XSH2	55,494	33,980	99.02%
	XSH3	63,638	33,980	99.03%
	XSC1	64,324	33,980	99.14%
	XSC2	60,165	33,980	99.06%
	XSC3	69,321	33,980	99.02%
	Nansha Islands	NSH1	68,758.	99.05%
		NSH2	69,867	99.16%
		NSH3	68,918	99.10%
		NST1	35,823	99.16%
		NST2	36,958	99.20%
		NST3	33,987	99.23%

Table S2. The significance of differences in taxonomy structure of microbial community between different seagrass species and seagrass *T. hemprichii* and *H. ovalis* from different sampling sites on the genus level

Genus	XSH-XSS	XST-XSH	XSC-XSS	XST-XSS	XSH-XSS	XST-XSC
<i>Bacillus</i>	0.0904	0.2509	0.0904	0.0117*	0.749	0.0007***
<i>Unclassified</i>						
<i>Desulfobulbaceae</i>	0.0018**	0.7373	0.0018**	0.1672	0.0022**	0.484
<i>Unclassified</i>						
<i>Rhodobacteraceae</i>	0***	0.455	0***	0.6376	0.5732	0***
<i>Unclassified Bacillaceae2</i>	0.1425	0.3012	0.1425	0.0246*	0.7447	0.0037**
<i>Lactococcus</i>	0.0934	0.2651	0.0934	0.0154*	0.589	0.0009***
<i>Unclassified</i>						
<i>Desulfobacteraceae</i>	0.0003***	0.4841	0.0003***	0.9566	0.2523	0.0069**
<i>Unclassified</i>						
<i>Gammaproteobacteria</i>	0.7368	0.2962	0.7368	0.002**	0.0119*	0.0021**
<i>Unclassified Bacillaceae1</i>	0.5845	0.3944	0.5845	0.0401*	0.3919	0.0033**
<i>Desulfopila</i>	0.7858	0.9306	0.7858	0.4427	0.4277	0.5615
<i>Unclassified Chloroflexi</i>	0.0166*	0.1042	0.0166*	0.0739	0.3986	0.0049**
<i>Unclassified Actinobacteria</i>	0.1762	0.033*	0.1762	0.0489*	0.0009***	0.2209
<i>Unclassified</i>						
<i>Flavobacteriaceae</i>	0.0124*	0.9839	0.0124*	0.0047**	0.0091**	0.0161*
<i>Unclassified</i>						
<i>Bacteroidetes</i>	0.0221*	0.1013	0.0221*	0.1726	0.3916	0.0191*
<i>Unclassified</i>						
<i>Anaerolineaceae</i>	0.4537	0.3712	0.4537	0.0899	0.7356	0.0291*
<i>Gp23</i>	0.0121*	0.0759	0.0121*	0.0284*	0.4346	0.3217
<i>Actibacter</i>	0.0001***	0.455	0.0001***	0.0363*	0.0134*	0.2008
<i>Unclassified</i>						
<i>Deltaproteobacteria</i>	0.0006***	0.0826	0.0006***	0.0516	0.0269*	0.0005***
<i>Unclassified Chromatiales</i>	0.0104*	0.7138	0.0104*	0.0011**	0.0166*	0.0004***
<i>Sulfurovum</i>	0***	0.8582	0***	0***	0.1465	0***
<i>Unclassified Myxococcales</i>	0.0913	0.0266*	0.0913	0.4293	0.0617	0.413
<i>Unclassified</i>						
<i>Ignavibacteriaceae</i>	0.0057**	0.7954	0.0057**	0.331	0.5594	0.0589
<i>Unclassified Spirochaetaceae</i>	0.0255*	0.3537	0.0255*	0.213	0.001**	0.9391
<i>Gp10</i>	0.0055**	0.9134	0.0055**	0.1297	0.0474*	0.2242
<i>Gp21</i>	0.021*	0.4181	0.021*	0.8677	0.3317	0.0062**
<i>Desulfatiglans</i>	0.0001***	0.0743	0.0001***	0.2739	0.0492*	0.0257*
<i>Caldithrix</i>	0.6846	0.2567	0.6846	0.0518	0.0848	0.0605
<i>Unclassified</i>						
<i>Thioalkalspiraceae</i>	0.7099	0.445	0.7099	0.0163*	0.0206*	0.0173*
<i>Zooshikella</i>	0.1012	0.2861	0.1012	0.0042**	0.0887	0.0048**
<i>Unclassified</i>						
<i>Planctomycetaceae</i>	0.7568	0.2933	0.7568	0.033*	0.0074**	0.0639
<i>Gp22</i>	0.0035**	0.0448*	0.0035**	0.3546	0.0175*	0.0319*
<i>Unclassified Proteobacteria</i>	0.0387*	0.2097	0.0387*	0.7704	0.0449*	0.0562
<i>Spirochaeta</i>	0.4012	0.8579	0.4012	0.3762	0.1655	0.2763
<i>Unclassified Cytophagales</i>	0.004**	0.0615	0.004**	0.0152*	0.1813	0.238
<i>Robiginitalea</i>	0.0684	0.6396	0.0684	0.0132*	0.2529	0.0002***
<i>Unclassified</i>						
<i>Bacteroidales</i>	0.6173	0.2174	0.6173	0.1695	0.9449	0.1407
<i>Aquabacterium</i>	0.7616	0.4464	0.7616	0.0439*	0.0344*	0.0467*
<i>Oceanobacillus</i>	0.1061	0.1572	0.1061	0.0135*	0.6601	0.0036**
<i>Gp9</i>	0.0005***	0.2238	0.0005***	0.0128*	0.0002***	0.0577
<i>Unclassified</i>						
<i>Helicobacteraceae</i>	1	0.1398	1	0.0485*	0.0837	0.0485*
<i>Unclassified</i>						
<i>Prolixibacteraceae</i>	0.2753	0.9885	0.2753	0.0277*	0.0499*	0.0394*
<i>Latescibacteria</i>						
<i>genera incertae sedis</i>	0.0012**	0.1555	0.0012**	0.0004***	0.814	0.1009
<i>Eudoraea</i>	1	0.0809	1	1	0.0809	1
<i>Unclassified</i>						
<i>Flammeovirgaceae</i>	0.015*	0.0553	0.015*	0.0031**	0.0348*	0.1984
<i>Unclassified</i>						
<i>Syntrophobacterales</i>	0.2508	0.0033**	0.2508	0.0025**	0.0274*	0.0009***
<i>Desulfobulbus</i>	0.1346	0.0883	0.1346	0.0057**	0.5553	0.0013**
<i>Aminicenantes genera</i>						
<i>incertae sedis</i>	0.01**	0.9808	0.01**	0***	0***	0.0015**
<i>Unclassified Euryarchaeota</i>	0.3486	0.1155	0.3486	0.2168	0.0776	0.1431

<i>Desulfosarcina</i>	0.0863	0.92	0.0863	0.0138*	0.022*	0.0298*
<i>Haliea</i>	0.1432	0.3809	0.1432	0.0114*	0.0487*	0.0068**
<i>Exiguobacterium</i>	0.0262*	0.2115	0.0262*	0.0167*	0.917	0.0009***

Note: DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands; Values in the table represent *p* values (* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$)

Table S3. The significance of differences in taxonomy structure of microbial community between seagrass *H. ovalis* from different sampling sites on the genus level.

Genus	XS-NS	NS-SY	XS-DY
<i>Bacillus</i>	0.0217*	0.0001***	0.06
<i>Unclassified Desulfobulbaceae</i>	0.0072**	0.0062**	0.0113*
<i>Unclassified Rhodobacteraceae</i>	0.0013**	0.8764	0.001***
<i>Unclassified Bacillaceae2</i>	0.0053**	0.0302*	0.2196
<i>Lactococcus</i>	0.0241*	0.01*	0.0238*
<i>Unclassified Desulfobacteraceae</i>	0.2376	0.0103*	0.0095**
<i>Unclassified Gammaproteobacteria</i>	0***	0.0001***	0.0021**
<i>Unclassified Bacillaceae1</i>	0.0076**	0.0298*	0.1974
<i>Desulfopila</i>	0.0614	0.1807	0.9682
<i>Unclassified Chloroflexi</i>	0.0401*	0.0255*	0.0222*
<i>Unclassified Actinobacteria</i>	0.0162*	0.0121*	0.0278*
<i>Unclassified Flavobacteriaceae</i>	0.0007***	0.4402	0.0174*
<i>Unclassified Bacteroidetes</i>	0.0648	0.0011**	0.001***
<i>Unclassified Anaerolineaceae</i>	0.0008***	0.0279*	0.0021**
<i>Gp23</i>	0.047*	0.0014**	0.0086**
<i>Actibacter</i>	0.0334*	0.0002***	0.0019**
<i>Unclassified Deltaproteobacteria</i>	0.0541	0.0469*	0.0112*
<i>Unclassified Chromatiales</i>	0.0071**	0.0043**	0.2486
<i>Sulfurovum</i>	0.0322*	0.0017**	0.0662
<i>Unclassified Myxococcales</i>	0.0001***	0.0886	0.0216*
<i>Unclassified Ignavibacteriaceae</i>	0.0105*	0.0011**	0.0694
<i>Unclassified Spirochaetaceae</i>	0.0034**	0.0047**	0.0973
<i>Gp10</i>	0.0021**	0.1651	0.0098**
<i>Gp21</i>	0.1402	0.0022**	0.0069**
<i>Desulfatiglans</i>	0.0267*	0.0143*	0.0107*
<i>Caldithrix</i>	0.0224*	0.0111*	0.0003***
<i>Unclassified Thioalkalspiraceae</i>	0.0029**	0.0007***	0.0742
<i>Zooshikella</i>	0.0177*	0.2157	0.0047**
<i>Unclassified Planctomycetaceae</i>	0.0029**	0.0944	0.2385
<i>Gp22</i>	0.0061**	0.0002***	0.0017**
<i>Unclassified Proteobacteria</i>	0.0279*	0.1467	0.69430
<i>Spirochaeta</i>	0.0001***	0.0002***	0.0096**
<i>Unclassified Cytophagales</i>	0.2869	0.0043**	0.0008***
<i>Robiginitalea</i>	0.0898	0.0019**	0.0132*
<i>Unclassified Bacteroidales</i>	0.0035**	0***	0.0014**
<i>Aquabacterium</i>	0.0016**	0.0015**	0.0015**
<i>Oceanobacillus</i>	0.1159	0.0935	0.3783
<i>Gp9</i>	0.0005***	0.0003***	0.1839
<i>Unclassified Helicobacteraceae</i>	0.0279*	0.03*	0.0955
<i>Unclassified Prolixibacteraceae</i>	0.0071**	0.008**	0.2985
<i>Latescibacteria genera incertae sedis</i>	0.7897	0.0501	0.0014**
<i>Eudoraea</i>	NA	NA	NA
<i>Unclassified Flammeovirgaceae</i>	0.0169*	0.4373	0.1487
<i>Unclassified Syntrophobacterales</i>	0.0847	0.087	0.8124
<i>Desulfobulbus</i>	0.5495	0.3128	0.2921
<i>Aminicenantes genera incertae sedis</i>	0.0211*	0.4574	0.0179*
<i>Unclassified Euryarchaeota</i>	0.0069**	0.0128*	0.1296
<i>Desulfosarcina</i>	0.0028**	0.3646	0.0004***
<i>Haliea</i>	0.0163*	0.2285	0***
<i>Exiguobacterium</i>	0.0028**	0.0011**	0.0636

Note: ND means not available; (DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands; Values in the table represent *p* values (* *p* < 0.05, ** *p* < 0.01, and *** *p* < 0.001)

Table S4. The significance of differences in taxonomy structure of microbial community between seagrass *T. hemprichii* from different sampling sites on the genus level.

Genus	XS-DY	NS-DY	XS-NS
<i>Bacillus</i>	0.0012**	0.0011**	0.0083**
<i>Unclassified Desulfobulbaceae</i>	0.0961	0.0148*	0.1669
<i>Unclassified Rhodobacteraceae</i>	0.0004***	0.0037**	0.0461*
<i>Unclassified Bacillaceae 2</i>	0.0012**	0.0019**	0.0006***
<i>Lactococcus</i>	0***	0.0008***	0.0013**
<i>Unclassified Desulfobacteraceae</i>	0.0037**	0.019*	0.0055**
<i>Unclassified Gammaproteobacteria</i>	0***	0.0758	0.0001***
<i>Unclassified Bacillaceae1</i>	0***	***	0.0003***
<i>Desulfopila</i>	0.0153*	0.0021**	0.0024**
<i>Unclassified Chloroflexi</i>	0.1893	0.002**	0.0059**
<i>Unclassified Actinobacteria</i>	0.0009***	0.1144	0.0033**
<i>Unclassified Flavobacteriaceae</i>	0.0044**	***	0***
<i>Unclassified Bacteroidetes</i>	0.0001***	0.0017**	0.0065**
<i>Unclassified Anaerolineaceae</i>	0***	0.0001***	0.0002***
<i>Gp23</i>	0.0004***	0.0041**	0.0015**
<i>Actibacter</i>	0.0142*	0.0062**	0.0028**
<i>Unclassified Deltaproteobacteria</i>	0.0009***	0.0602	0.0005***
<i>Unclassified Chromatiales</i>	0***	0.1776	0.0009***
<i>Sulfurovum</i>	0.0015**	0.0014**	0.0007***
<i>Unclassified Myxococcales</i>	0.0002***	0.0812	0.001***
<i>Unclassified Ignavibacteriaceae</i>	0.0309*	0.0245*	0.0627
<i>Unclassified Spirochaetaceae</i>	0.005**	0.0403*	0.0279*
<i>Gp10</i>	0.0004***	0.1867	0***
<i>Gp21</i>	0.0032**	0.0093**	0.001**
<i>Desulfatiglans</i>	0.0045**	0.0033**	0.0165*
<i>Caldithrix</i>	0.0006***	0.0007***	0.0164*
<i>Unclassified Thioalkalspiraceae</i>	0***	0.003**	0.0014**
<i>Zooshikella</i>	0.0121*	0.0122*	0.4226
<i>Unclassified Planctomycetaceae</i>	0.0041**	0.0001***	0.335
<i>Gp22</i>	0.0053**	0.2157	0.0004***
<i>Unclassified Proteobacteria</i>	0.0015**	0.0552	0.0981
<i>Spirochaeta</i>	0.0027**	0.007**	0.1369
<i>Unclassified Cytophagales</i>	0.0063**	0.0253*	0.0107*
<i>Robiginitalea</i>	0.0193*	0.0106*	0.0008***
<i>Unclassified Bacteroidales</i>	0.0003***	0.0001***	0.1061
<i>Aquabacterium</i>	0.0124*	0.011*	0.0055**
<i>Oceanobacillus</i>	0.0251*	0.0066**	0.0507
<i>Gp9</i>	0.0012**	0.0116*	0.0474*
<i>Unclassified Helicobacteraceae</i>	0.0083**	0.0083**	1
<i>Unclassified Prolixibacteraceae</i>	0.0077**	0.0113*	0.0057**
<i>Latescibacteria genera incertae sedis</i>	0.0001***	0.0002***	0.1574
<i>Eudoraea</i>	0.001***	0.001***	1
<i>Unclassified Flammeovirgaceae</i>	0.0032**	0.0664	0.011*
<i>Unclassified Syntrophobacterales</i>	0.0001***	0.261	0.0177*
<i>Desulfobulbus</i>	0.0267*	0.0246*	0.1649
<i>Aminicenantes genera incertae sedis</i>	0.4785	0.0017**	0.0029**
<i>Unclassified Euryarchaeota</i>	0.0052**	0.0058**	0.0003***
<i>Desulfosarcina</i>	0.0675	0.079	0.0509
<i>Haliaea</i>	0.009**	0.0117*	0.041*
<i>Exiguobacterium</i>	0.0145*	0.0007***	0.0399*

Note: DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T.*

hemprichii collected from the Nansha Islands; Values values in the table represent p values (* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Table S5. The significance of differences in functional groups of microbial community between different seagrass species on the genus level.

Functional groups	XST-XSC	XSH-XSC	XSS-XSC	XST-XSS	XSH-XSS	XSH-XST
Methanotrophy	0.0628	1	1	0.0628	1	0.0628
Methanogenesis by reduction of methyl compounds with H ₂	1	1	0.6856	0.6856	0.6856	1
Hydrogenotrophic methanogenesis	1	1	0.6856	0.6856	0.6856	1
Methanogenesis	1	1	0.6856	0.6856	0.6856	1
Methanol oxidation	0.6495	0.0322*	0.0106*	0.0193*	0.2524	0.0494*
methylotrophy	0.0533	0.0766	0.021*	0.0921	0.2619	0.0706
Aerobic ammonia oxidation	0.1235	0.0248*	0.0189*	0.2878	0.0048**	0.0733
Aerobic nitrite oxidation	0.0728	1	0.4226	0.0765	0.4226	0.0728
Nitrification	0.1164	0.0248*	0.0178*	0.264	0.0048**	0.071
Sulfate respiration	0.0161*	0.8032	0.0025**	0.0645	0.0005***	0.0111*
Sulfur respiration	0.0055**	0.0248*	0.3009	0.0286*	0.7024	0.0087**
Sulfite respiration	0.0514	0.3166	0.1346	0.0661	0.0641	0.0398*
Respiration of sulfur compounds	0.0161*	0.8189	0.0026**	0.064	0.0006***	0.0111*
Chitinolysis	0.0576	0.2567	0.1841	0.4204	1	0.5176
Cellulolysis	0.0453*	0.2185	0.089	0.0779	0.2619	0.0413*
Xylanolysis	0.0576	0.2567	0.1841	0.4204	1	0.5176
Dark oxidation of sulfur compounds	0.2846	0.1641	1	0.2846	0.1641	0.3235
Fermentation	0.1872	0.0032**	0.083	0.0982	0.002**	0.9741
Aerobic chemoheterotrophy	0.0009***	0.6795	0.0046**	0***	0.0221*	0.0054**
Human pathogens all	0.0168*	0.0361*	0.0325*	0.3973	0.1835	0.0559
Animal parasites or symbionts	0.0168*	0.0361*	0.0325*	0.3973	0.1835	0.0559
Aromatic compound degradation	0.3643	0.0587	0.3944	0.1687	0.4957	0.0572
Hydrocarbon degradation	0.0572	0.1835	0.1835	0.0602	1	0.0602
Iron respiration	0.1394	0.0572	0.6495	0.1021	0.2254	0.0634
Nitrate respiration	0.0836	0.1289	0.0201*	0.3089	0.0594	0.024*
Nitrate reduction	0.1349	0.1179	0.0289*	0.5014	0.0552	0.0278*
Nitrogen respiration	0.0836	0.1289	0.0201*	0.3089	0.0594	0.024*
Fumarate respiration	0.1394	0.0572	0.6495	0.1021	0.2254	0.0634
Intracellular parasites	0.0098**	0.2124	0.0997	0.0287*	0.1454	0.0039**
Predatory or exoparasitic	0.0354*	0.0311*	0.0133*	0.0124*	0.0126*	0.1042
Chloroplasts	0.1728	0.1299	0.2837	0.026*	0.0086**	0.0088**
Anoxygenic photoautotrophy S oxidizing	0.0388*	0.0022**	0.0083**	0.1605	0.0105*	0.0043**
Anoxygenic photoautotrophy	0.0388*	0.0022**	0.0083**	0.1605	0.0105*	0.0043**
Photoautotrophy	0.0388*	0.0022**	0.0083**	0.1605	0.0105*	0.0043**
Phototrophy	0.0388*	0.0022**	0.0083**	0.1605	0.0105*	0.0043**
Chemoheterotrophy	0.0179*	0.0253*	0.0016**	0.3086	0.0008***	0.0071**

Note: DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands; Values in the table represent *p* values (* *p* < 0.05, ** *p* < 0.01, and *** *p* < 0.001)

Table S6. The significance of differences in functional groups of microbial community between seagrass *T.hemprichii* from different sampling sites on the genus level

Functional groups	XS-DY	NS-DY	XS-NS
Methanotrophy	0.0064**	0.0064**	1
Methanogenesis by reduction of methyl compounds with H ₂	0.0064**	0.0064**	1
Hydrogenotrophic methanogenesis	0.0064**	0.0064**	1
Methanogenesis	0.2557	0.0056**	0.0023**
Methanol oxidation	0.0047**	0.0108*	0.0061**
methylo trophy	0.1791	0.5788	0.0511
Aerobic ammonia oxidation	1	0.4226	0.4226
Aerobic nitrite oxidation	0.1791	0.5437	0.0621
Nitrification	0.0002***	0.0002***	0.0183*
Sulfate respiration	0.0048**	0.077	0.2981
Sulfur respiration	0.0267*	0.0246*	0.1649
Sulfite respiration	0.0002***	0.0002***	0.0182*
Respiration of sulfur compounds	0.3841	0.0824	0.8194
Chitinolysis	0.0289*	0.0017**	0.4048
Cellulolysis	0.3841	0.0824	0.8194
Xylanolysis	0.0069**	0.7127	0.0231*
Dark oxidation of sulfur compounds	0***	0***	0.0369*
Fermentation	0.2719	0.0023**	0.0039**
Aerobic chemoheterotrophy	0.0057**	0.0027**	0.0622
Human pathogens all	0.0057**	0.0027**	0.0622
Animal parasites or symbionts	1	0.0702	0.0702
Aromatic compound degradation	0.0005***	0.0232*	0.1072
Hydrocarbon degradation	0.1835	0.0445*	0.0459*
Iron respiration	0.4226	0.077	0.0741
Nitrate respiration	0.0124*	0.0635	0.0113*
Nitrate reduction	0.0086**	0.0052**	0.0054**
Nitrogen respiration	0.0124*	0.0635	0.0113*
Fumarate respiration	0.4226	0.077	0.0741
Intracellular parasites	0.0515	0.1219	0.5475
Predatory or exoparasitic	0.2031	0.2031	1
Chloroplasts	0.0105*	0.0156*	0.0126*
Anoxygenic photoautotrophy S oxidizing	0.2267	0.0026**	0.0027**
Anoxygenic photoautotrophy	0.2267	0.0026**	0.0027**
Photoautotrophy	0.2267	0.0026**	0.0027**
Phototrophy	0.2267	0.0026**	0.0027**
Chemoheterotrophy	0.0026**	0.0015**	0.0467*

Note: DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands; Values in the table represent *p* values (* *p* < 0.05, ** *p* < 0.01, and *** *p* < 0.001).

Table S7. The significance of differences in functional groups of microbial community between different seagrass *H.ovalis* from different sampling sites on the genus level.

Functional group	XS vs SY	NS vs SY	XS vs NS
Methanotrophy	0.0628	0.4226	0.0642
Methanogenesis by reduction of methyl compounds with H ₂	0.4226	0.0339*	0.0271*
Hydrogenotrophic methanogenesis	0.4226	0.0339*	0.0271*
Methanogenesis	0.4226	0.0339*	0.0271*
Methanol oxidation	0.0201*	0.0248*	0.0142*
methylotrophy	0.1574	0.0024**	0.2212
Aerobic ammonia oxidation	0.005**	0.0059**	0.3134
Aerobic nitrite oxidation	0.5185	0.7415	0.3486
Nitrification	0.0055**	0.0046**	0.3047
Sulfate respiration	0.0116*	0.0445*	0.0155*
Sulfur respiration	0.0011**	0.0474*	0.0034**
Sulfite respiration	0.2921	0.3128	0.5495
Respiration of sulfur compounds	0.0116*	0.0446*	0.0154*
Chitinolysis	0.0505	0.353	0.1159
Cellulolysis	0.1982	0.0259*	0.0255*
Xylanolysis	0.0505	0.353	0.1159
Dark oxidation of sulfur compounds	0.0782	0.0009***	0.0008***
Fermentation	0.1204	0.1397	0.0646
Aerobic chemoheterotrophy	0.0021**	0.7545	0.0107*
Human pathogens all	0.0198*	0.1333	0.0095**
Animal parasites or symbionts	0.0198*	0.1333	0.0095**
Aromatic compound degradation	1	0.4226	0.4226
Hydrocarbon degradation	0.0602	0.029*	0.5421
Iron respiration	0.0584	0.3897	0.0587
Nitrate respiration	0.0634	0.0198*	0.3785
Nitrate reduction	0.0268*	0.2846	0.0277*
Nitrogen respiration	0.0327*	0.0104*	0.0095**
Fumarate respiration	0.0268*	0.2846	0.0277*
Intracellular parasites	0.0634	0.0198*	0.3785
Predatory or exoparasitic	0.005**	0.0213*	0.0073**
Chloroplasts	0.8615	0.0867	0.0766
Anoxygenic photoautotrophy S oxidizing	0.0233*	0.057	0.0229*
Anoxygenic photoautotrophy	0.0312*	0.004**	0.005**
Photoautotrophy	0.0312*	0.004**	0.005**
Phototrophy	0.0312*	0.004**	0.005**
Chemoheterotrophy	0.0312*	0.004**	0.005**

Note: DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands; Values in the table represent *p* values (* *p* < 0.05, ** *p* < 0.01, and *** *p* < 0.001).

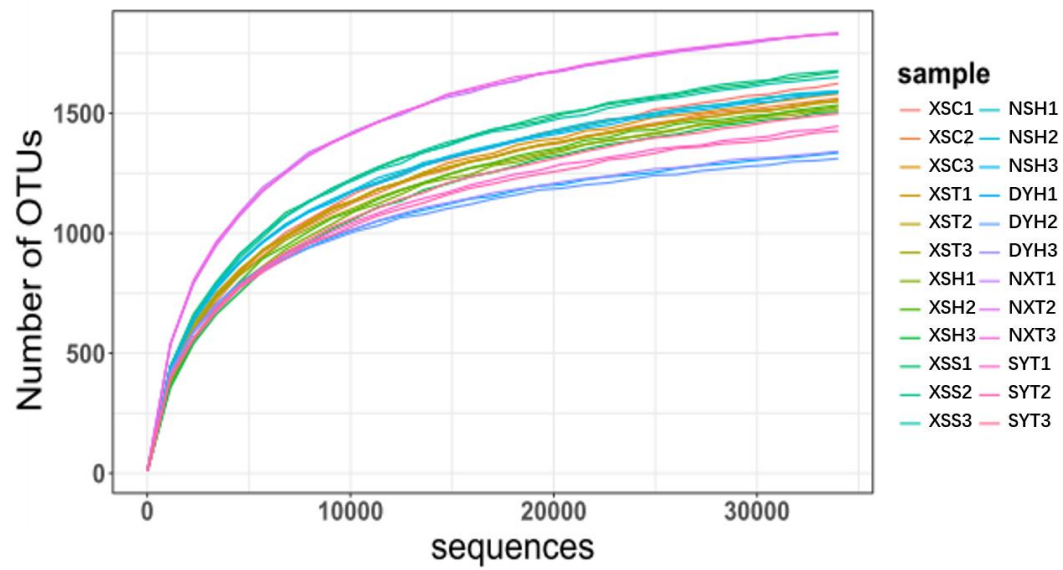


Figure S1 Rarefaction curves of OTU diversity in each sample (n=24) (DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands)

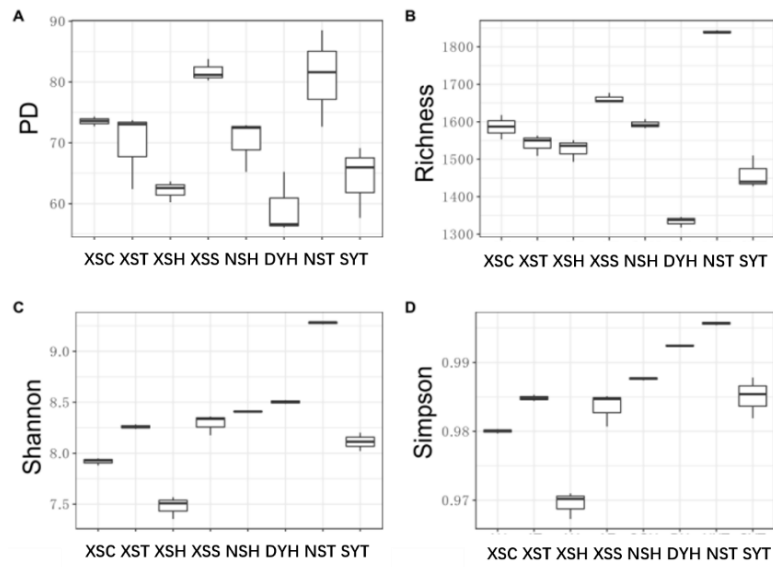


Figure S2. Phylogenetic and taxonomic alpha diversity of seagrass rhizosphere microbial communities (A: phylogenetic diversity; B: richness; C: Shannon; D: Simpson) ((DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands))

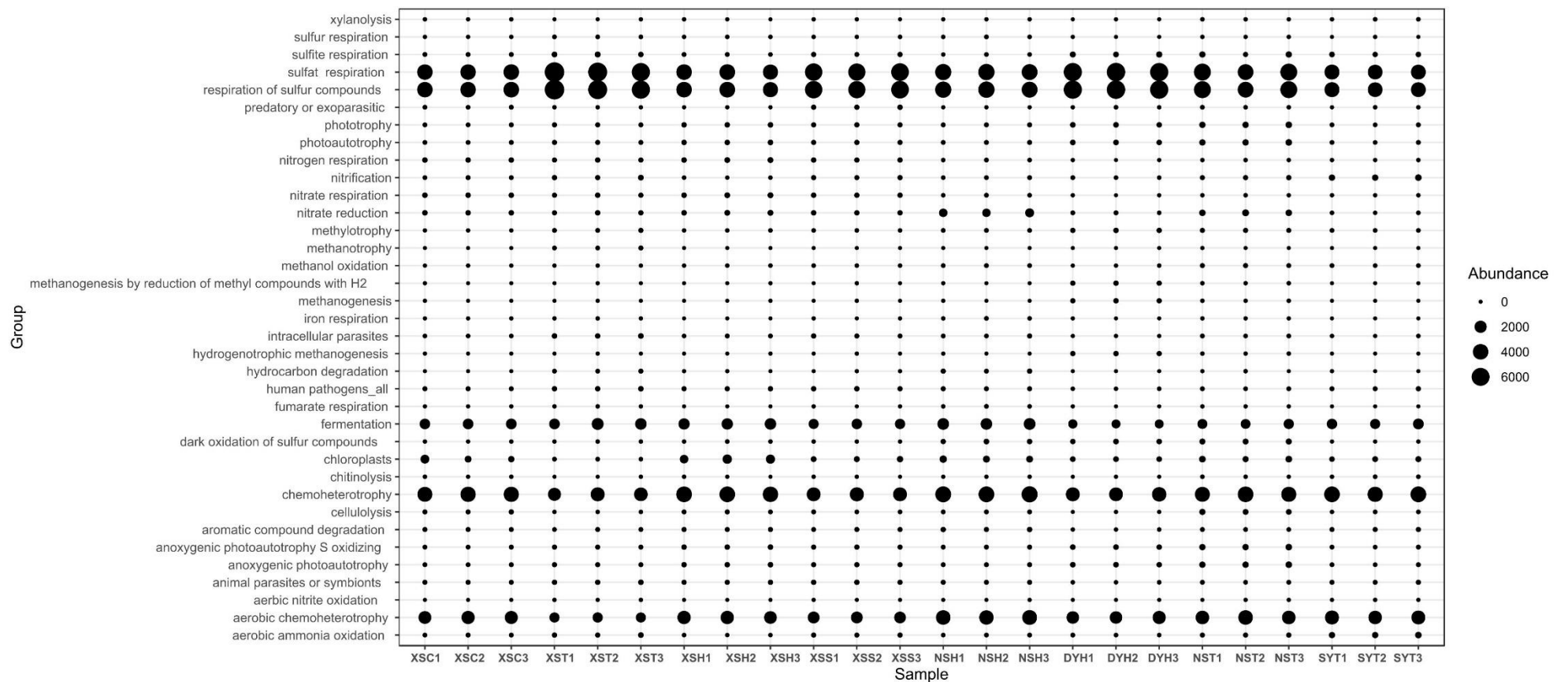


Figure S3. The bubble plot of functional groups in all rhizosphere microbial communities of seagrass (DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands)

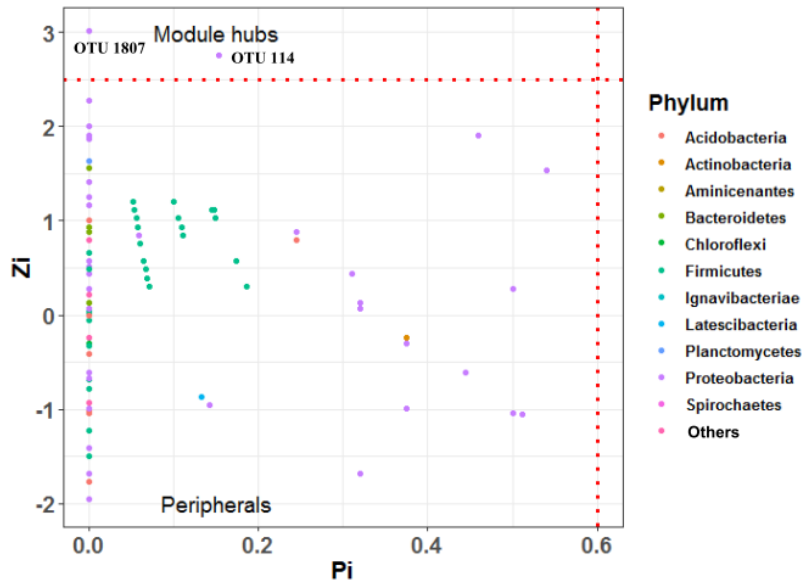


Figure S4. Zi-Pi plot of network nodes of core microbial community shared by all samples ((DYH indicates seagrass *Halophila ovalis* from Daya Bay; SYT indicates seagrass *Thalassia hemprichii* from Sanya Bay, XST, XSH, XSC, and XSS indicate *T. hemprichii*, *H. ovalis*, *Cymodocea nodos* and *Syringodium isoetifolium* collected from the Xisha Islands, and NSH and NST indicates seagrass *H. ovalis* and *T. hemprichii* collected from the Nansha Islands))