Supplementary material

Community structure of epiphytic bacteria on *Potamogeton pectinatus* and the surrounding bacterioplankton in Hongze Lake

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Table S1. The relative abundance of the predominant phylogenetic groups at the genus level

Taxa represented occurred at >0.5% abundance in at least one sample

Taxon	EPB3	EPB5	EPB7	EPB10	PTB3	PTB5	PTB7	PTB10
Actinobacteria								
Agrococcus		1.00			1.50			1.10
Propionibacterium							1.00	
Bacteroidetes								
Fluviicola	0.50	2.00			2.50			1.90
Flavobacterium	7.80	6.90	6.40	5.40	16.60	5.90	5.80	7.90
Cyanobacteria								
Synechococcus	0.60	1.10	0.50					
Prochlorothrix						1.60	1.00	
Pseudanabaena						1.60	1.20	
Firmicutes								
Brochothrix			1.10					
Lactococcus	4.70		0.90					
Clostridium				2.20				
Faecalibacterium							1.00	
Alphaproteobacteria								
Rhodobacter	1.10	0.60	0.70	0.70	0.70	1.50	1.00	
Betaproteobacteria								
Polynucleobacter	0.80	1.20			0.90			1.10
Vogesella	1.10		1.70	1.10	0.80	1.10	0.90	0.90
Gammaproteobacteria								
Methylocaldum		1.30						
Acinetobacter	2.40	0.90	1.80	1.00	0.70	1.20	0.90	0.60
Pseudomonas	18.5	14.20	22.00	11.80	11.80	14.70	12.80	9.70

Table S2 Statistical analysis of PTB communities with physical and chemical indicators

Correlations are significant at: *, 0.05 level; **, 0.01 level

	TP	TN	NO$_3$-N	NO$_2$-N	DO	WT	pH	Depth
Actinobacteria	−0.165	−0.383	0.859*	0.682	−0.832*	−0.774	−0.683	0.853*
Bacteroidetes	−0.084	0.005	0.216	0.201	−0.640	−0.676	−0.119	0.311
Cyanobacteria	−0.436	−0.760	0.905**	0.897*	−0.334	−0.572	−0.614	0.938**
Firmicutes	0.912**	0.917**	−0.421	−0.904**	0.005	0.929**	−0.088	−0.775
Gemmatimonadetes	0.045	0.247	−0.812*	−0.568	0.896*	0.714	0.698	−0.767
Planctomycetes	0.314	0.490	−0.811*	−0.752	0.741	0.868*	0.562	−0.878*
Verrucomicrobia	−0.323	−0.396	0.624	0.634	−0.704	−0.895*	−0.380	0.741
Alphaproteobacteria	−0.087	0.058	−0.676	−0.387	0.931**	0.637	0.636	−0.607
Betaproteobacteria	−0.700	−0.876*	0.768	0.987**	−0.314	−0.894*	−0.341	0.971**
Deltaproteobacteria	−0.591	−0.391	−0.562	0.033	0.975**	0.137	0.796	−0.273
Gammaproteobacteria	0.023	0.312	−0.934**	−0.634	0.873*	0.631	0.829*	−0.841*
OTU number	0.088	−0.200	0.335	0.161	0.204	0.404	−0.385	0.162
Chao 1 estimator	−0.335	−0.543	0.269	0.408	0.446	0.141	−0.108	0.289
Shannon index	0.200	0.565	−0.986**	−0.789	0.569	0.513	0.804*	−0.916**

Table S3. Statistical analysis of EPB communities with physical and chemical indicators

Correlations are significant at: *, 0.05 level; **, 0.01 level

	TP	TN	NO_3-N	NO_2-N	DO	WT	pH	Depth
Actinobacteria	−0.447	−0.140	−0.797	−0.222	0.964**	0.224	0.945**	−0.516
Bacteroidetes	−0.077	0.280	−0.840*	−0.463	0.430	0.031	0.853*	−0.614
Cyanobacteria	−0.692	−0.479	−0.500	0.129	0.948**	0.036	0.782	−0.182
Firmicutes	0.617	0.302	0.703	0.032	−0.871*	0.055	−0.961**	0.336
Gemmatimonadetes	0.839*	0.640	0.162	−0.496	−0.329	0.726	−0.610	−0.278
Planctomycetes	0.990**	0.881*	0.006	−0.671	−0.548	0.582	−0.504	−0.407
Verrucomicrobia	−0.772	−0.509	−0.526	0.184	0.852*	−0.189	0.871*	−0.130
Alphaproteobacteria	−0.466	−0.501	0.471	0.665	−0.503	−0.958**	−0.142	0.694
Betaproteobacteria	−0.697	−0.388	−0.605	0.095	0.746	−0.257	0.925**	−0.197
Deltaproteobacteria	0.592	0.574	0.084	−0.309	−0.763	−0.131	−0.320	−0.079
Gammaproteobacteria	0.590	0.268	0.727	0.066	−0.870*	0.034	−0.970**	0.367
OTU number	0.088	−0.206	0.335	0.161	0.204	0.404	−0.384	0.162
Chao 1 estimator	−0.410	−0.548	0.269	0.408	0.445	0.141	−0.106	0.289
Shannon index	0.232	0.567	−0.986**	−0.789	0.569	0.513	0.803*	−0.916**