Table S1. Betweenness centrality score of associations for bacterial taxa in the inter-genera networks (Fig. 7a, c). The degraders for P-DOM were observed based on the genera-environment networks (Fig. 7b, d). Degraders highlighted in bold were common in all experiments, while those marked with asterisks were considered keystone taxa that acted as bottlenecks within communities. LL: low concentration + low molecular weight; HL: high concentration + low molecular weight; HH: high concentration + high molecular weight; LL+HL: the data of LL and HL experiments were combined since they showed similar bacterial dynamics

Experiments	Taxa (Genera)	Betweenness centrality	Degraders or not
LL+HL	**_Vibrio_**	0.0030	Yes
	Bacillus	0.0008	Yes
	Exiguobacterium	0	Yes
	Brevundimonas	0.0144	Yes
	Pseudomonas*	**0.1472**	Yes
	Comamonas	0	Yes
	Aeromonas*	**0.0566**	Yes
	Sphingobacterium*	**0.0760**	Yes
	Shewanella	0.0033	Yes
	_hgcI_clade_	0.0034	No
	_CL500-29_marine_group_	0.0034	No
	_norank_f_Clade_III_	0.0247	No
	_norank_f_MWH-_ _UniP1_aquatic_group_	0.0247	No
	_Cyanobium_PCC-6307_	0.0247	No
	_CL500-3_	0.0034	No
	Acidibacter	0.0093	No
	_norank_o_Chloroplast_	0.0247	No
	_Candidatus_Methylopumilus_	0.0198	No
	Polynucleobacter	0.0247	No
	_norank_f_norank_o_norank_	0.0093	No
HH		0	Yes
	Vibrio	0	Yes
	Exiguobacterium	0.0043	Yes
	Acinetobacter	0	Yes
	Bacillus	0.0043	Yes
	Elizabethkingia	0.0068	Yes
	Flavobacterium	0.0008	Yes
	Vogesella	0.0038	Yes
	Aeromonas	0.0097	Yes
	Algoriphagus	**0.0965**	Yes
	Chryseobacterium*	0.0032	Yes
	Comamonas	**0.0760**	Yes
	Pseudomonas*	0.0038	Yes
	Rheinheimera	**0.0573**	Yes
	Shewanella*	0.0929	No

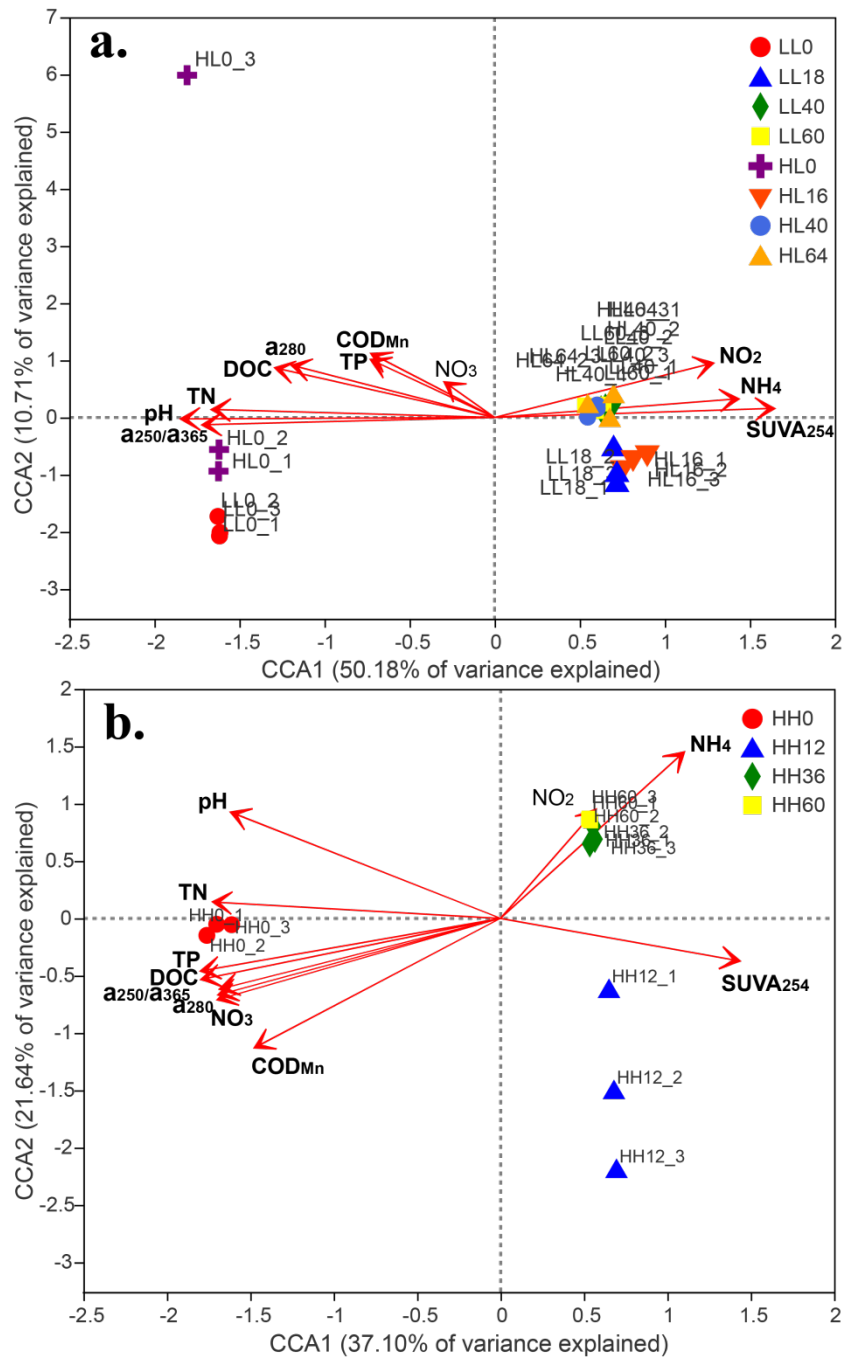|		
hgcI_clade	0.0719	No
norank_f_A0839	0.0719	No
Nodosilinea_PCC-7104	0.0719	No
norank_f_norank_o_Chloroplast	0.0410	No
CL500-29_marine_group	0.0155	No
CL500-3		

Fig. S1. Canonical correspondence analysis (CCA) for the correlation between bacterial community compositions and environmental variables (red arrows) in experiments of LL+HL (a) and HH (b), indicating significant factors (p < 0.05, in bold) influencing the dynamics of bacterial communities. LL: low concentration + low molecular weight; HL: high concentration + low molecular weight; HH: high concentration + high molecular weight; LL+HL: the data of LL and HL experiments were combined as they had similar bacterial dynamics. CCA was carried out using the online Majorbio Cloud Platform (www.majorbio.com), and the significance of the correlation with each factor was tested through Monte Carlo 999 permutations. Generally, CCA revealed that almost all water factors exhibited strong associations with bacterial communities (except nitrate in LL+HL or nitrite in HH)