Supplement of

Carbon cycling at the aquatic-terrestrial interface is linked to parafluvial hyporheic zone inundation history

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Supplementary material

Table S1. OTUs identified from 16S and ITS sequencing.

	# OTUs
Total 16S sequencing	9893
Bacteria	9470
Archaea	2313
Unidentified kingdom	305
Total ITS sequencing	1856
Fungi	1818
Unidentified kingdom	722

Table S2. Bacteria, archaea, and fungi classes with 1% abundance or greater.

	0 m		2 m		4 m		6 m	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Bacteria								
Unidentified class	3.10	0.83	1.72	0.11	1.32	0.02	1.78	0.78
Proteobacteria								
Betaproteobacteria	10.24	1.54	9.40	1.24	10.69	0.85	8.66	1.64
Alphaproteobacteria	9.91	0.83	11.18	1.56	12.63	1.93	17.95	3.29
Gammaproteobacteria	8.64	1.11	5.80	1.08	7.37	2.79	6.76	1.89
Deltaproteobacteria	8.66	1.46	6.68	0.44	5.50	1.12	4.83	0.83
TA18	0.54	0.11	0.25	0.06	0.16	0.03	0.10	0.03
Bacteroidetes								
Sphingobacteriia	10.90	1.77	12.73	3.23	16.55	4.29	14.66	2.40
Flavobacteriia	2.38	0.71	1.92	0.82	2.81	2.39	1.79	1.36
Cytophagia	2.32	0.43	2.66	1.22	2.83	1.22	3.17	0.34
Acidobacteria								
Acidobacteria	8.13	1.18	9.46	1.02	9.62	2.70	9.03	0.87
Subgroup 22	1.22	0.33	0.40	0.10	0.24	0.16	0.09	0.03
Holophagae	0.62	0.17	0.62	0.03	0.66	0.28	0.78	0.11
Verrucomicrobia								
Spartobacteria	2.82	1.10	9.09	2.05	6.90	0.75	5.44	2.11
Verrucomicrobiae	1.82	0.41	1.50	0.65	1.11	0.36	1.04	0.58
OPB35 soil group	1.76	0.32	1.28	0.20	1.36	0.50	0.74	0.37
Actinobacteria								
Actinobacteria	1.59	0.34	2.39	0.32	3.12	0.90	5.46	1.17
Thermoleophilia	1.22	0.37	2.60	1.15	2.27	0.95	4.85	2.91
Acidimicrobiia	0.48	0.02	0.60	0.11	0.46	0.16	0.63	0.16
Planctomycetes								
Planctomycetacia	6.20	0.34	5.04	0.94	4.34	1.03	3.73	1.30
Phycisphaerae	0.78	0.18	0.52	0.10	0.46	0.14	0.50	0.09
Nitrospirae								
Nitrospira	3.12	0.63	1.62	0.31	0.95	0.30	0.75	0.25
Chloroflexi								

		1	2	3	4	5	6	7	8
	Anaerolineae	1.43	0.58	0.52	0.11	0.26	0.12	0.23	0.01
Firmicutes									
	Bacilli	2.98	3.89	0.72	0.69	0.48	0.05	0.78	0.19
Gemmatimonadetes									
	Gemmatimonadetes	1.18	0.48	0.78	0.06	0.87	0.56	1.90	0.49
Chlorobi									
	Chlorobia	0.61	0.11	0.56	0.07	0.34	0.10	0.13	0.03
Archaea									
Thaumarchaeota									
	Soil Crenarchaeotic Group (SCG)	1.92	1.99	6.61	3.47	4.08	1.31	1.77	1.22
Fungi									
	Unidentified class	22.14	5.30	14.48	5.25	11.89	3.51	28.29	6.66
Ascomycota									
	Dothideomycetes	16.48	9.29	19.68	5.40	28.25	5.02	26.59	7.80
	Eurotiomycetes	1.46	0.65	2.94	1.12	2.55	1.22	2.60	0.83
	Leotiomycetes	8.60	2.55	30.86	18.63	22.72	17.76	11.34	6.54
	Pezizomycetes	3.38	5.72	0.24	0.14	2.64	3.46	1.74	2.68
	Sordariomycetes	25.04	14.51	17.82	7.79	13.23	6.71	18.34	3.08
Basidiomycota									
	Agaricomycetes	14.88	15.30	4.46	2.04	4.37	1.17	1.52	1.87
	Microbotryomycetes	0.49	0.10	0.51	0.42	0.34	0.10	0.30	0.19
	Tremellomycetes	1.72	0.49	3.19	1.26	3.91	1.12	4.86	1.48
Zygomycota									
	Mortierellomycotina_cls_Incertae_sedis	4.20	2.50	4.80	1.68	9.56	11.92	3.58	2.81
	Mucoromycotina_cls_Incertae_sedis	0.09	0.07	0.20	0.23	0.08	0.07	0.40	0.56
Glomeromycota									
	Glomeromycetes	0.66	0.18	0.07	0.04	0.10	0.07	0.19	0.15
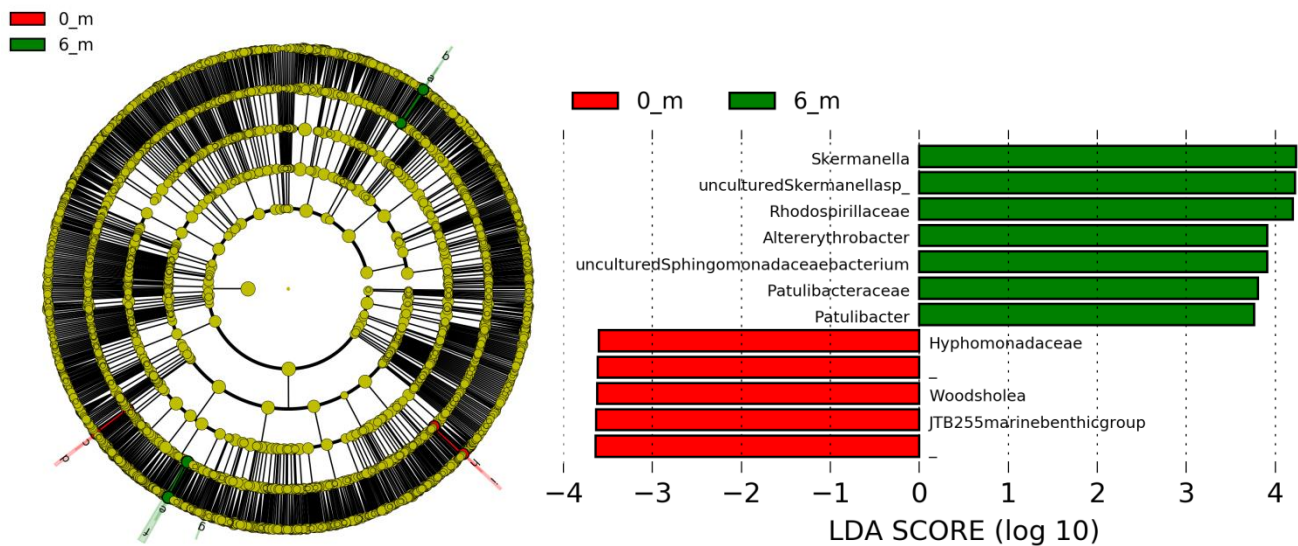
Figure S1. Linear discriminant analysis coupled with effect size (LEfSe) cladogram of bacterial taxa driving dissimilarity among elevations. Symbol diameter is proportional to relative abundance. Colors indicate elevations, and brown symbols indicate non-significant taxa. 0 m and 6 m elevations contribute 100% of taxa driving dissimilarity.

5