

Supplement of

Characteristics of bacterial community in fog water at Mt. Tai: similarity and disparity under polluted and non-polluted fog episodes

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Supplementary Information

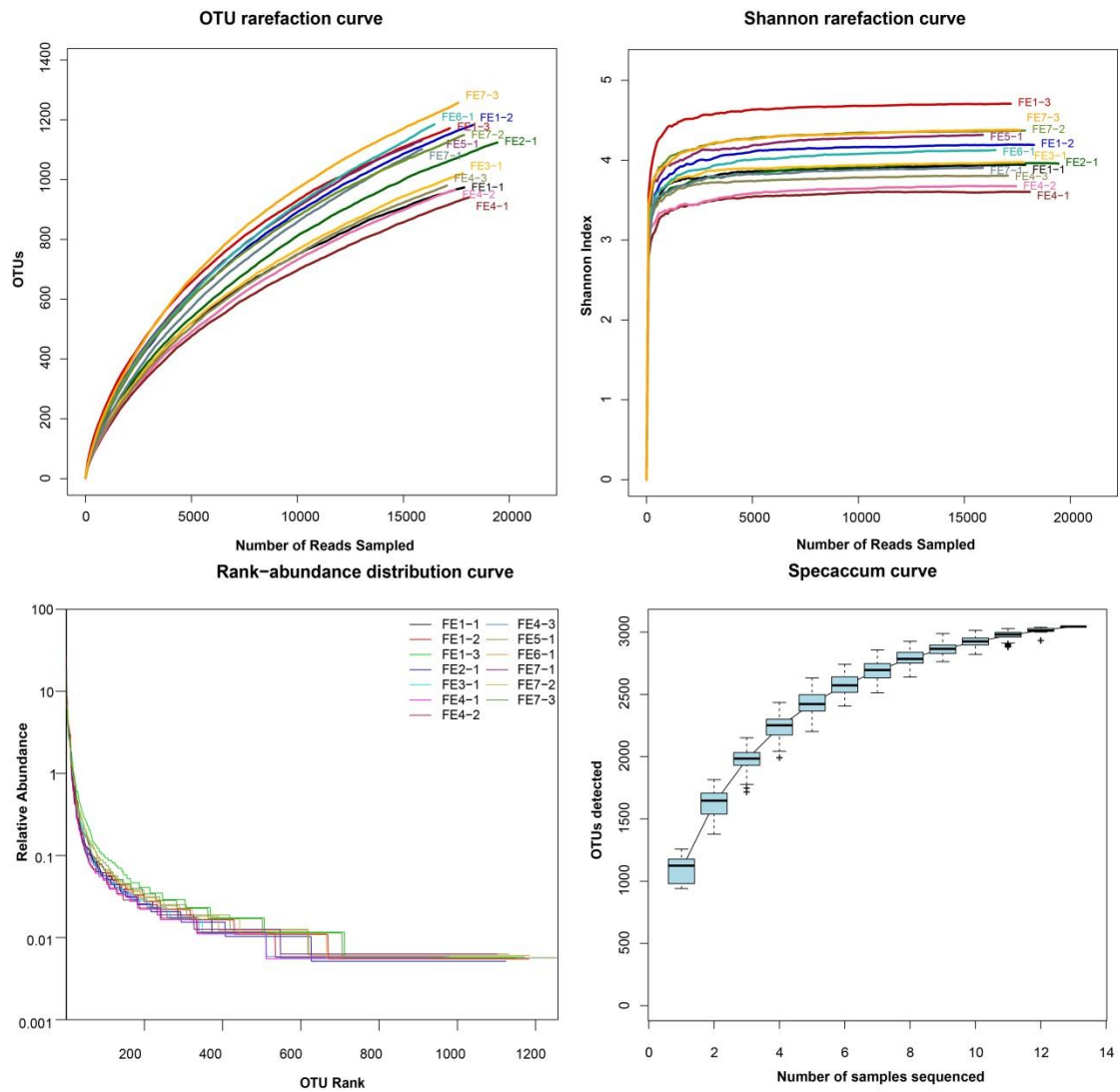


Fig S1 Summary of diversity curves calculated at 97% sequence similarity.

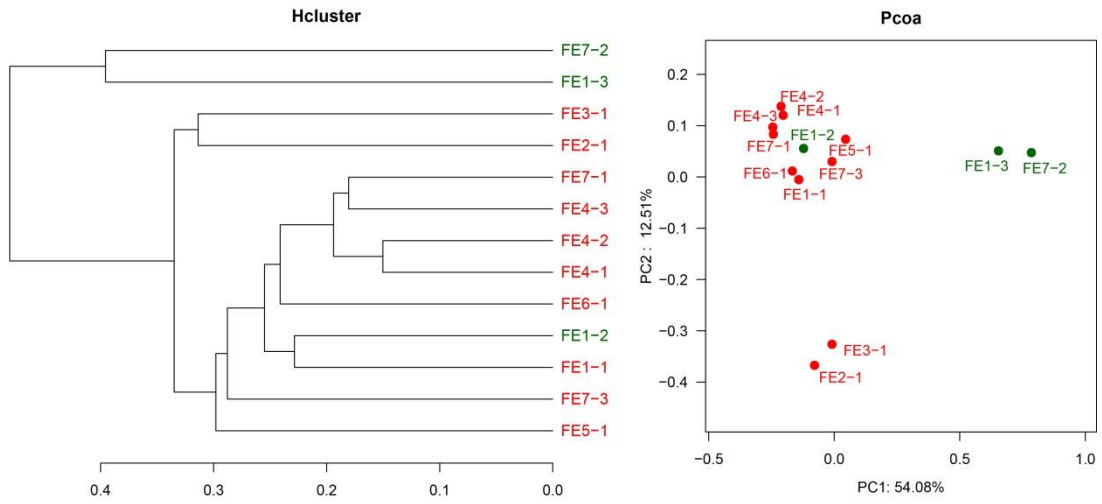


Fig S2 Hierarchical cluster (Hcluster) and principal coordinate analysis (PCoA) based on the OTUs categories

Table S1 CorE: Inter set correlations of environmental variables with axes

N	NAME	AX1	AX2	AX3	AX4
	FR EXTRACTED	0.0403	0.0642	0.0609	0.1820
1	PM2.5	-0.3277	-0.0868	-0.2748	-0.5938
2	T	-0.0661	0.368	0.0961	0.1104
3	RH	0.2810	0.3299	0.3764	-0.4929
4	WS	-0.1168	0.2657	-0.1152	0.6883
5	pH	0.0432	0.240	0.2709	-0.0574
6	EC	-0.1891	-0.0706	0.2291	-0.0854

Table S2 CFit: Cumulative fit per species as fraction of variance of species

N	NAME	AX1	AX2	AX3	AX4	VAR(y)	EXPL %
	FR FITTED	0.2726	0.0733	0.048	0.0405		
1	<i>Limnobacter</i>	0.0135	0.0408	0.081	0.1180	0.02	31.26
2	<i>Bosea</i>	0.2604	0.2734	0.2838	0.3026	0.10	32.05
3	<i>Aeromonas</i>	0.4232	0.4324	0.4885	0.6241	0.11	62.77
4	<i>Burkholderia</i>	0.2866	0.2914	0.2958	0.3212	0.13	32.79
5	<i>Nitrospira</i>	0.2166	0.3189	0.3191	0.3569	0.01	54.16
6	<i>Nevskia</i>	0.3167	0.3219	0.3254	0.3500	0.12	35.68
7	<i>Enhydrobacter</i>	0.2055	0.2100	0.2448	0.3680	0.09	38.69
8	<i>Prevotella</i>	0.4013	0.4202	0.4203	0.4437	0.08	44.77
9	<i>Bradyrhizobium</i>	0.0996	0.1356	0.3104	0.3211	0.03	46.45
10	<i>Pedobacter</i>	0.3062	0.3158	0.3172	0.3304	0.13	33.43
11	<i>Sorangium</i>	0.3331	0.3338	0.3355	0.3488	0.09	35.37
12	<i>Vibrio</i>	0.0009	0.0037	0.1581	0.3368	0.02	43.22
13	<i>Sphingobium</i>	0.3263	0.3275	0.3276	0.3322	0.10	33.28
14	<i>Mycobacterium</i>	0.3164	0.3265	0.3295	0.3512	0.13	35.29
15	<i>Streptococcus</i>	0.2220	0.4217	0.4345	0.4474	0.08	53.91
16	<i>Flavobacterium</i>	0.1801	0.1918	0.2234	0.2894	0.05	30.35
17	<i>Rhizobium</i>	0.1712	0.2014	0.226	0.2943	0.05	35.22
18	<i>Anaerococcus</i>	0.3224	0.3322	0.3368	0.3602	0.13	36.04
19	<i>Rhodopseudomonas</i>	0.3032	0.3148	0.3192	0.3483	0.13	34.93
20	<i>Kocuria</i>	0.2996	0.3101	0.3168	0.3315	0.12	33.26
21	<i>Haliscomenobacter</i>	0.3091	0.3228	0.3263	0.3573	0.13	36.05
22	<i>Paracoccus</i>	0	0.0322	0.2291	0.3799	0.58	41.41
23	<i>Aquabacterium</i>	0.0123	0.0515	0.0598	0.0606	0.03	56.01
24	<i>Novosphingobium</i>	0.2645	0.3293	0.3494	0.3593	0.06	41.38
25	<i>Bdellovibrio</i>	0.0380	0.0990	0.1471	0.1509	0.02	31.71
26	<i>Psychrobacter</i>	0.2538	0.2648	0.2792	0.3426	0.12	34.4
27	<i>Pseudoalteromonas</i>	0.3414	0.3452	0.3905	0.3905	0.06	44.14
28	<i>Deinococcus</i>	0.0377	0.2887	0.3264	0.3673	3.01	45.09
29	<i>Rhodococcus</i>	0.2281	0.2307	0.2716	0.2795	0.05	34.66
30	<i>Dietzia</i>	0.2733	0.2901	0.2975	0.3411	0.13	34.88
31	<i>Corynebacterium</i>	0.3196	0.3196	0.3911	0.3931	0.12	40.07
32	<i>Staphylococcus</i>	0.1168	0.1254	0.3055	0.8594	2.08	87.02
33	<i>Microcoleus</i>	0.2974	0.3191	0.3207	0.3370	0.15	34.99
34	<i>Mesorhizobium</i>	0.2639	0.2827	0.2851	0.3249	0.15	34.06
35	<i>Enterobacter</i>	0.1224	0.226	0.2357	0.2564	0.08	26.03
36	<i>Methylobacterium</i>	0.0228	0.0245	0.3485	0.3490	0.55	42.31
37	<i>Caulobacter</i>	0.0615	0.0618	0.3822	0.3892	0.18	56.46
38	<i>Brevundimonas</i>	0.0685	0.4890	0.5445	0.5448	0.94	58.52
39	<i>Hydrothalea</i>	0.1986	0.2280	0.2361	0.3054	0.18	34.85
40	<i>Massilia</i>	0.2202	0.2606	0.3231	0.3377	3.77	35.41

41	<i>Chryseobacterium</i>	0.3155	0.3159	0.3866	0.3885	0.27	44.25
42	<i>Bacillus</i>	0.2756	0.3282	0.3358	0.3366	1.21	36.31
43	<i>Pelomonas</i>	0.0873	0.1368	0.1466	0.2401	0.31	36.58
44	<i>Delftia</i>	0.1038	0.2707	0.3073	0.3123	0.45	40.4
45	<i>Phyllobacterium</i>	0.4274	0.4319	0.4481	0.4572	2.91	46.91
46	<i>Empedobacter</i>	0.4141	0.4144	0.4530	0.4532	11.96	45.39
47	<i>Sphingomonas</i>	0.2599	0.2855	0.3267	0.3270	5.05	33.94
48	<i>Pseudomonas</i>	0.0224	0.2861	0.4163	0.5185	2.89	52.91
49	<i>Stenotrophomonas</i>	0.1387	0.4362	0.4454	0.4796	3.24	52.45
50	<i>Acinetobacter</i>	0.3972	0.4282	0.4351	0.4388	7.59	43.99
