

Supplementary Text

Equipment details, detection and quantification and quality control procedures

PAHs Extraction and Analysis

All freeze-dried samples were ground and passed through a 150 micron mesh sieve. We then extracted the PAHs using an accelerated solvent extraction solution (ASE-350, Dionex Company, Sunnyvale, CA, USA). Briefly, 5 g samples were mixed with 1g diatomite and PAH standards of 20 μ L 1mg/L, and were then poured into a 34mL extraction vessel. The extraction solvent was a 20mL mixture of n-hexane and dichloromethane with a 1:1 volume ratio. The extraction pressure was 1500 psi and the temperature was 100°C. The heating and static extraction times were 8min and 10min, respectively. The flushing volume was set at 60%, and the nitrogen purging time was 60s. Three cycles were carried out. The extract was concentrated to 15mL on a RE-52A rotary evaporator (Yarong Technology Co., Ltd., Fujian, China), purified using sulfuric acid and desulfurized using copper powder, concentrated to 2mL in the rotary evaporator, and then purified with a composite silica gel purification column. The purification column was filled with 2g of deactivated silica gel, 1g acidic silica gel, 1g deactivated silica gel, 1g alkaline silica gel, 2g activated silica gel and 2g anhydrous sodium sulfate from bottom to top. PAHs were eluted with a mixture of 100mL n-hexane and dichloromethane (1:1, V/V). The eluent was collected and concentrated to 2mL in the rotary evaporator. Using a nitrogen sweeper, the eluent was slowly blown to nearly dry, with a constant volume of 300mL.

The PAHs were analyzed by gas chromatography mass spectrometry (GC-MS, Agilent 7890A/5975C, Agilent Technologies Inc., CA, USA) with a DB-5MS capillary column (0.25 mm \times 0.25 μ m \times 30 m J&K Scientific, San Jose, CA, USA). The carrier gas was high purity He (99.999%) with a 1.0 mL/min flow rate. A sample (1 μ L) was injected using an automatic sampling system. The temperatures of the inlet, ion source, and transmission lines were 25°C, 240°C, and 280°C, respectively. The oven temperature was initially set at 80°C for 2 min, then gradually increased (15°C/min) to 215°C for 1 min. The oven temperature was further increased (6°C/min)

to 280°C for 1 min, and finally reached 300°C at 10°C/min for 5 min. The GS-MS detector was operated in electron impact mode at 70 eV with an ionic source temperature of 240°C. A selected ion mode was used to identify the PAHs. The concentrations of the PAHs are given as the dry mass of the sample.

References and Reagents

Major reagents included the mixed standard solution of 16 priority PAHs: Naphthalene (Nap), Acenaphthylene (Acy), Acenaphthene (Acp), Fluorene (FLR), Phenanthrene (PHE), Anthracene (Ant), Fluoranthene (FLT), Pyrene (PYR), Chrysene (CHR), Benzo [a] anthracene (BaA), benzo[k]flfluoranthene (BkF), Benzo[a]pyrene (BaP), Benzo[b]flfluoranthene (BbF), Dibenz[a,h]anthracene (DhA), Benzo[ghi]perylene (BgP), and Indeno[1,2,3,cd]pyrene (IcP). The mixed standard solution was purchased from AccuStandard Company, New Haven, CT, USA. Chromatography-grade n-hexane and dichloromethane as an extract and eluent of PAHs were purchased from TEDIA Company, Fairfield, OH, USA. The anhydrous Na₂SO₄ was purified and activated prior to analysis in a muffle furnace at 400°C for 4h. The internal standard compound, Philppine-d₁₀, was purchased from the J & K Company (San Jose, CA, USA). The internal standard compound was a pure substance, and the contents of the measured components were determined by comparison. Copper powder and silica gel were purchased from the National Pharmaceutical Group (Beijing, China). All other chemicals were analytical grade.

Quality Control

After each triplicate sample group (n = 3) analysis, a blank sample was analyzed to monitor interference during sample processing. The analyte concentration of blank samples was less than 5% of the minimum concentration of all samples, representing the background signal due to sample extraction and measurement procedures. The limit of quantitation (LOQ) was defined as ten times that of the signal to noise ratio (10 S/N). In this study, the quantitative limit of PAHs in the samples was obtained by

adding the standard to 5 g sediment (dry weight). The LOQ of the PAH compounds ranged from 0.015 ng/g to 0.095 ng/g. The recoveries of the 16 PAH species ranged from 73.5% to 116.8% and the recovery of the internal standard compounds ranged from 86.3% to 108.4%. The calibration curves were plotted by peak area versus the concentrations of PAH compounds with R^2 values ranging from 0.990 to 0.998 for the 16 examined PAHs.

Table S1 Physicochemical parameters of sediment/soil of samples

Sample	Nitrate	Ammonia	Total	Water	pH	Conductivity	TOC	Acy (Total	FLR (ng/g	PHE	Ant (ng/	FLT (ng/	PYR		CHR		BaA (n	BkF (ng	BaP (ng/	BbF (ng/g	DhA (n	BgP (ng	IcP (ng/g
	nitrogen	nitrogen	nitrogen					Nap (n	ng/g	ng/g						(ng/g	(ng/g	BaA (n	BkF (ng	BaP (ng/	BbF (ng/g					
name	(mg/kg)	(mg/kg)	(mg/kg)	content		(μs/cm)		g/g)))	PAH (ng/g))	(ng/g)	g)	g)))	g/g)	/g)	g))	g/g)	/g))		
Dit-bh-2	3.96	42.02	1721.97	0.27	6.47	308.00	11.04	3.96	3.10	3.57	896.04	16.21	91.03	38.60	69.03	97.74	107.96	51.28	142.19	81.48	37.34	16.18	68.96	67.40		
Dit-bh-4	1.72	22.29	1876.01	0.28	6.92	256.00	13.12	58.15	4.38	5.92	1248.41	25.48	147.99	91.51	119.98	123.31	144.61	64.84	168.83	67.74	42.58	19.89	78.89	84.32		
Dit-es-1	4.79	198.64	1316.95	0.40	6.50	1833.00	5.47	32.07	1.19	3.01	633.07	11.37	86.10	55.74	54.75	46.94	51.84	39.54	85.02	42.33	28.04	15.83	36.17	43.14		
Agr-bh-2	1.11	2.17	772.53	0.21	7.05	279.00	5.40	5.68	0.67	0.43	106.21	3.67	23.74	2.28	12.69	6.82	11.52	4.27	3.70	10.06	4.06	0.55	8.11	7.96		
Agr-bh-4	2.71	25.10	772.99	0.27	6.93	160.80	10.30	16.69	0.68	0.60	75.39	2.82	13.64	8.13	6.37	3.58	5.30	2.00	2.06	3.12	1.54	0.55	3.95	4.36		
Agr-es-1	0.37	8.89	690.86	0.22	7.02	134.00	10.30	16.31	0.50	0.43	55.45	4.68	17.79	3.01	3.78	3.12	2.64	0.64	0.43	0.30	0.43	0.55	0.30	0.55		
Riv-bh-2	0.92	2.70	1373.16	0.19	6.80	259.00	25.70	74.14	0.87	0.93	496.16	11.78	62.16	95.66	37.02	21.51	37.51	15.30	16.45	22.19	15.12	8.59	41.08	35.86		
Riv-bh-4	0.76	4.19	946.35	0.23	7.15	132.90	20.10	2.80	0.52	0.45	166.63	2.84	30.09	17.29	15.46	9.25	17.53	6.45	6.47	9.26	6.74	3.85	20.14	17.50		
Riv-es-1	0.49	5.30	943.81	0.22	6.99	70.10	0.90	12.79	0.95	0.91	156.45	2.84	16.60	29.61	17.52	10.51	12.59	9.72	6.60	9.46	6.56	0.55	9.37	9.87		

Table S2 KEGG Orthology contributed by the main PAHs degrading bacteria at different sampling points

Sampling points Genus									
	Dit-bh-2	Dit-es-1	Riv-bh-4	Riv-es-1	Dit-bh-4	Agr-bh-4	Agr-bh-2	Riv-bh-2	Agr-es-1
<i>Actinoplanes</i>	K00480		K00448				K00448		
	K04102	K00480	K00480	K00448	K00480	K00480	K00480	K00480	K00480
							K04102		
	K00448				K00448			K00448	K00448
<i>Bradyrhizobium</i>	K00449		K00449	K00448	K00449	K00480		K00449	K00449
	K00480	K00480	K00480	K00449	K00480	K04100	K00448	K00480	K00480
	K04100	K04100	K04100	K00480	K04100	K04101	K00480	K04100	K04100
	K04101		K04101	K04101	K04101	K04102	K04101	K04101	K04101
	K04102		K04102		K04102			K04102	K04102
					K00449	K00449	K00449	K00449	K00449
<i>Mycobacterium</i>			K00449		K00480	K00480	K00480	K04102	K00480
	K00449		K04102	K00449	K11946	K04102	K04102	K11946	K04102
	K00480		K11948		K11948	K11946	K11946	K11948	K11946
			K18252		K18252	K11948	K11948	K18252	K11948
<i>Nocardioides</i>	K00448			K00448					
	K00449		K00449	K00449	K00449	K00449	K00449	K00449	K00449
	K04101			K04101	K04101	K04101		K04101	K04101
<i>Pseudolabrys</i>	K00448		K00448		K00448	K00448	K00449	K00448	K00448
	K00449		K00449	K00448	K00449	K00449	K00480	K00449	K00449
	K00480		K00480	K00449	K00480	K00480	K04102	K00480	K00480

Sampling points									
Genus	Dit-bh-2	Dit-es-1	Riv-bh-4	Riv-es-1	Dit-bh-4	Agr-bh-4	Agr-bh-2	Riv-bh-2	Agr-es-1
<i>Rhizobium</i>	K04100		K04100		K04100	K04102		K04102	K04102
	K04101		K04102		K04101	K18069		K18069	K18069
	K04102		K18069		K04102				
	K18069				K18069				
				K00448					
			K00448					K00449	
	K00480		K00480	K00449	K00480	K00480	K00480	K00480	K00480
	K04102		K04102	K00480	K04102	K04102	K04102	K04102	K04102
			K04102	K04102					
<i>Rhodoplanes</i>	K00480	K00480	K00480		K00480		K00480	K00480	K00480
	K04100	K04101	K04100	K00480	K04100	K04101	K04100	K04100	K04100
	K04101	K04102	K04101	K04102	K04101	K04102	K04101	K04101	K04101
	K04102		K04102		K04102		K04102	K04102	K04102
<i>Rubrobacter</i>			K00448				K00448	K00448	K00448
	K00448		K00449	K00449	K00448	K00448	K00449	K00449	K00449
	K00449		K00480		K00449	K00449	K00480	K00480	K00480
						K00448	K00448		K00448
<i>Streptomyces</i>	K00449				K00449	K00449	K00449	K00480	K00449
	K00480		K00480	K00480	K00480	K00480	K00480	K04101	K00480
	K04101		K04101	K04101	K04101	K04101	K04101	K04102	K04101
					K04102	K04102	K04102		K04102
<i>unclassified_c__Betaproteobacter</i>	K00480		K00480		K00480	K00480	K00480	K00480	K04102
<i>ia</i>	K04100		K04100		K04100	K04101	K04101	K04100	K18067

Sampling points									
Genus	Dit-bh-2	Dit-es-1	Riv-bh-4	Riv-es-1	Dit-bh-4	Agr-bh-4	Agr-bh-2	Riv-bh-2	Agr-es-1
	K04101		K04101		K04101	K04102		K04101	
	K04102		K04102		K04102	K18067		K04102	
			K14581					K18074	

