Supporting Information:

Effect of Activated Carbon Amendment on Bacterial Community Structure and Functions in a PAH Impacted Urban Soil

PAOLA MEYNET[1], SARAH E. HALE[2], RUSSELL J. DAVENPORT[1], GERARD CORNELISSEN[2], GIJS D. BREEDVELD[2] AND DAVID WERNER[1,§]

[1]*School of Civil Engineering and Geosciences, Newcastle University, Newcastle upon Tyne, NE1 7RU, England, United Kingdom*

[2] *Department of Environmental Engineering, Norwegian Geotechnical Institute NGI, P.O. Box 3930 Ullevål Stadion, N-0806, Oslo, Norway*

[§]corresponding author: Phone 0044 191 222 5099, Fax 0044 191 222 6502, e-mail: david.werner@ncl.ac.uk

Supporting information is provided as a compilation of closest relatives and their similarities with the sequence of dominant bands excised from the DGGE gels and the PAH compound specific uptake by PE in soil slurries without compared to with sodium azide addition.

Table S1 Summary of the similarities for the dominant excised bands.

Isolate	Closest relative (accession no.)	Similarity %	Source	Affiliation	Class
N1	Uncultured bacterium (HQ204336)	89%	Fungal and actinobacterial communities	*Micrococcineae*	*Actinobacteria*
N2	Uncultured bacterium (DQ460791)	86 %	DGGE gel band from environmental sample	*Bacteroidetes*	*Bacteroidetes*
N3	*Chryseobacterium* sp. (FN555401)	93%	Soil	*Flavobacteriaceae*	*Bacteroidetes*
N4	*Knoellia* sp. (EF216369)	86%	Shallow water sediment	*Actinobacteria*	*Actinobacteria*
N5	*Stenotrophomonas* sp. (EU374962)	85%	Zloty Stok gold mine rock biofilms	*Gammaproteobacteria*	*Proteobacteria*
N6	*Curtobacterium* sp (GQ915093)	99%	Diverticula (unpublished)	*Microbacteriaceae*	*Actinobacteria*
N7	*Mycobacterium* sp. (FJ544446)[1]	96%	Raw surface water	*Actinomycetales*	*Actinobacteria*
	Mycobacterium vanbaalenii (JN590245)	92%	Oil-containing sewage soil		
N8	*Rhodococcus jostii* RHA1(JF915360.1)	95%	Genomic DNA	*Actinobacteria*	*Actinobacteria*
N10	*Arthrobacter nitroguajacolicus*	88%	Lespedeza root nodules	*Micrococcineae*	*Actinobacteria*
N11	Uncultured bacterium (HQ015227)	92%	Landfill leachate-contaminated soil	*Proteobacteria*	*Proteobacteria*
N12	Uncultured bacterium (GQ289453.1)	81%	Soil for onsite wastewater treatment system	*Proteobacteria*	*Proteobacteria*
N13	Uncultured *actinobacterium* clone (HM106303)	87%	Haloalkaline lake shore sediment	*Actinobacteria*	*Actinobacteria*
N14	Uncultured Actinobacteria bacterium (CU918885)	95%	Mesophilic anaerobic digester for municipal wastewater sludge	*Actinobacteria*	*Actinobacteria*
N15	Uncultured soil bacterium clone	89%	Uncultured soil bacterium	*Proteobacteria*	*Proteobacteria*
N16	Uncultured *Sphingomonas* sp (HQ711916)	95%	Drinking water	*Alphaproteobacteria*	*Proteobacteria*
N17	Uncultured *Microbacterium* sp (GQ365756)	94%	Aeration tank for waste water treatment	*Micrococcineae*	*Actinobacteria*
N19	Uncultured soil bacterium (JF399957)	90%	Uncultured soil bacterium	*Proteobacteria*	*Proteobacteria*
N20	Uncultured bacterium clone (JF295464)	91%	Soil	*Nitrospiraceae*	*Nitrospiraceae*
N21	Uncultured bacterium(FN567236)	85%	Environmental sample	*Proteobacteria*	*Proteobacteria*
N22	Uncultured bacterium clone (GQ397072)	94%	Soil	*Bacteria*	*Bacteria*
N23	*Rhodococcus erythropolis* (FN386745)	99%	Volcanic ash	*Lentzea**	*Actinobacteria*
N24	Uncultured bacterium isolate DGGE band (AY894960)	97%	Environmental sample	*Proteobacteria*	*Proteobacteria*
N26	Streptosporangium yunnanense(AF191733)	87%	Soil	*Actinobacteria*	*Actinobacteria*

*Ribosomal Database Project (RDP10) shows equal similarity to *Rhodococcus* family.

Table S2 Compound specific percent reduction in PAH uptake by PE samplers embedded in soil slurries without compared to with sodium azide addition, average ± standard deviation.[a]

	Unamended (% Reduction)	GAC (% Reduction)	PAC (% Reduction)
Acenaphthylene	96±7	n.d.	n.d.
Acenaphthene	100	100	n.d.
Fluorene	100	100	51±121
Phenanthrene	97±2	91±8	70±30
Anthracene	100	95±10	49±124
Fluoranthene	65±8	58±10	80±24
Pyrene	47±14	37±13	67±35
Benz(a)anthracene	61±31	50±39	68±34
Chrysene	41±16	28±16	68±32
Indeno(123c,d)pyrene	25±30	-2±24	21±56
Benzo(ghi)perylene	33±27	14±18	22±56

[a]n.d. means compound not detectable in both measurements, 100 means compound not detected for soil slurries without sodium azide.