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Soil Research

Supplementary Material

Bacterial succession in an abandoned circum-neutral opencast coal mine in India

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Table S1. Notable works pertaining to physicochemical &/or microbial studies in mines of Europe, America, Africa and Asia. Studies on Indian coalmines are tabulated at the end.

Region	Location	Mine	Soil pH	Sample used: Temporal	Sample used: Spatial	Physico-chemical study	Microbial study type: Culture dependent	Microbial study type: Culture independent	Reference
EUROPE	Iberian Belt, Spain	Pyrite	**Acidic**	No	No	Yes	No	Clone library sequencing	(Gonza´lez-Toril et al., 2011)
EUROPE	Iberian Belt, Spain	Cu	**Acidic**	No	Yes	Yes	No	No	(Nieto et al., 2013)
EUROPE	Carnoules, France	Pb, Zn	**Acidic**	3 Years	Yes	Yes	No	TRFLP[#], Amplicon sequencing	(Volant et al., 2014)
EUROPE	Botswana, Germany, & Sweden	Pyrite	**Acidic**	3 Years	Yes	Yes	No	Clone library sequencing, qPCR[#]	(Korehi et al., 2014)
EUROPE	Sokolov, Czech Republic	Coal	**Neutral**	6, 12, 21 & 45 Years	No	Yes	No	PLFA[#]	(Urbanov´ et al., 2011)
EUROPE	Sokolov, Czech Republic	Coal	**Alkaline**	1 - 44 Years	No	Yes	Total Count	RFLP	(Chronˇa´kova et al., 2009)
AMERICA	California, US	Coal	**Acidic**	11 Month	No	Yes	No	FISH[#]	(Edwards et al., 1999)
AMERICA	Arizona, US	Pb, Zn	**Acidic**	No	Yes	Yes	No	Clone library sequencing	(Mendez et al., 2008)
AMERICA	Pennsylvania, US	Coal	**Acidic**	No	Yes	Yes	No	Amplicon sequencing, qPCR	(Lee et al., 2017)
AMERICA	Wisconsin, US	Pb, Zn	**Neutral**	No	No	Yes	SRB	FISH	(Labrenz and Banfield, 2004)
AMERICA	Greens Creek, Alaska	Ag	**Alkaline**	No	Yes	Yes	SRB, SOB, MPN, IOB	No	(Lindsay et al., 2009)
AMERICA	Sossego, Brazil	Cu	**Neutral**	No	Yes	Yes	No	Amplicon sequencing	(Pereira et al., 2014)
AFRICA	Mpumalanga Province, South Africa	Coal	**Acidic**	No	Yes	Yes	No	No	(Fosso-Kankeu et al., 2017)
AFRICA	Jwaneng, Botswana	Diam-ond	**Acidic**	No	Yes	Yes	No	No	(Murty and Karunakara, 2008)
AFRICA	South Africa	Coal	**Acidic**	1 - 8 years	No	Yes	Total Count	PLFA	(Claassens et al., 2008)
ASIA	Kerman–Bahabad, Iran	Coal	**Acidic**	No	Yes	Yes	No	No	(Shahabpour et al., 2005)
ASIA	Kohistan, Pakistan	Pb, Zn	**Acidic**	No	Yes	Yes	No	No	(Muhammad et al., 2011)

	Zhuji City, China	Coal	**Acidic**	No	Yes	Yes	Total Count	No	(Liao and Xie, 2007)
	Fankou, China	Pb, Zn	**Acidic**	No	Yes	Yes	No	T-RFLP	(Huang et al., 2011)
	Tongchang, Yinshan, & Yongping, China	Cu	**Acidic**	No	Yes	Yes	No	Microarray	(Xie et al., 2011)
	Southeast, China	Cu, Pb, Zn, Pyrite	**Acidic**	No	Yes	Yes	No	No	(Kuang et al., 2013)
	Southeast China	Cu, Pb, Zn, Pyrite	**Acidic**	No	Yes	Yes	No	Meta-genomics, transcriptomics	(Hua et al., 2015)
	Guangdong Province, China	Poly-metals	**Acidic**	No	Yes	No	No	Meta-genomics, transcriptomics	(Chen et al., 2015)
	Antaiba, China	Coal	**Neutral**	2 - 30 Years	No	Yes	No	PLFA, Microarray, Amplicon sequencing	(Li et al., 2016)
	Shuimuchong, China	Cu	**Neutral**	No	Yes	Yes	No	No	(Liu et al., 2014)
	Hubei, China	Coal	**Alkaline**	No	No	Yes	No	Clone library sequencing, RT-PCR	(Wei et al., 2014)
INDIA	Madhya Pradesh	Coal	**Acidic**	No	No	Yes	No	No	(Jamal et al., 1991)
	Jharkhand	Coal	**Acidic**	No	No	Yes	Total count	No	(Ghose, 2004)
	Assam	Coal	**Acidic**	No	Yes	Yes	No	No	(Saikia et al., 2014)
	Orissa	Coal	**Neutral**	2 - 10 Years	No	Yes	No	RAPD[#]	(Maharana and Patel, 2015)
	Jharkhand	Coal	**Neutral**	No	Yes	Yes	No	No	(Sinha and SlNha, 1987)
	Jharkhand	Coal	**Neutral**	No	Yes	Yes	No	No	(Masto et al., 2011)
	Jharkhand	Coal	**Neutral**	No	Yes	Yes	No	No	(Kumar and Singh, 2016)
	Jharkhand	Coal	**Neutral**	No	Yes	Yes	No	No	(Pandey et al., 2016)
	West Bengal	Coal	**Alkaline**	No	Yes	Yes	No	No	(Sadhu et al., 2012)

[#] TRFLP: Terminal restriction fragment length polymorphism, qPCR: Quantitative polymerase chain reaction , PLFA: Phospholipid fatty acid analysis, FISH: Fluorescence in situ hybridization

Table S2. Relative abundance of phyla in Tasra colliery soil samples.

Sl No	Phylum	T.13	T.14	T.15	T.16
1	Acidobacteria	0.0925315	0.0268506	0.0700743	0.0232951
2	Actinobacteria	0.2081653	0.4112589	0.2010495	0.4098296
3	AD3	0.0003803	0.0004322	0.0001558	0.0000000
4	Armatimonadetes	0.0000272	0.0000000	0.0000000	0.0000000
5	Bacteroidetes	0.0308574	0.0079857	0.0323168	0.0370104
6	BRC1	0.0000000	0.0000251	0.0000107	0.0000000
7	Chlamydiae	0.0006383	0.0000063	0.0000000	0.0000000
8	Chlorobi	0.0432438	0.0096642	0.0000000	0.0007852
9	Chloroflexi	0.0809192	0.0487157	0.1436720	0.0708426
10	Cyanobacteria	0.0016570	0.0026619	0.0101188	0.0030063
11	Elusimicrobia	0.0001087	0.0000000	0.0000000	0.0000000
12	FBP	0.0003260	0.0000626	0.0002202	0.0000000
13	Fibrobacteres	0.0000000	0.0001816	0.0003813	0.0000000
14	Firmicutes	0.0178055	0.0334960	0.0779911	0.0087198
15	Fusobacteria	0.0000000	0.0000313	0.0000000	0.0000000
16	Gemmatimonadetes	0.0757989	0.0237628	0.0269351	0.0700873
17	GN02	0.0012088	0.0002881	0.0000161	0.0001047
18	GOUTA4	0.0000272	0.0000000	0.0000000	0.0000000
19	MVP-21	0.0000000	0.0000000	0.0000000	0.0002244
20	Nitrospirae	0.0114085	0.0028373	0.0031151	0.0057359
21	OD1	0.0058265	0.0008706	0.0001128	0.0000075
22	OP11	0.0001494	0.0001942	0.0000107	0.0000374
23	OP3	0.0001901	0.0000752	0.0000000	0.0000000
24	OP8	0.0001766	0.0000063	0.0000000	0.0000000
25	Planctomycetes	0.0000679	0.0000063	0.0012514	0.0000000
26	Proteobacteria	0.3120645	0.2865759	0.2975487	0.2636948
27	Spirochaetes	0.0269595	0.0015971	0.0000000	0.0000000
28	TM6	0.0000272	0.0001816	0.0000269	0.0000075
29	TM7	0.0077551	0.0038018	0.0611694	0.0031933
30	Verrucomicrobia	0.0008013	0.0000125	0.0000752	0.0002543
31	WPS-2	0.0074291	0.0005637	0.0012353	0.0000150
32	WS2	0.0000000	0.0000063	0.0000000	0.0003814
33	WS3	0.0000815	0.0003382	0.0000000	0.0000000
34	WWE1	0.0000815	0.0000000	0.0000000	0.0000000

Figure S1. Tasra colliery as observed during the yearly soil sampling. a, b, c and d represent the view of the site during sampling in the four consecutive years, (2013-2016) and named as T.13-T.16.

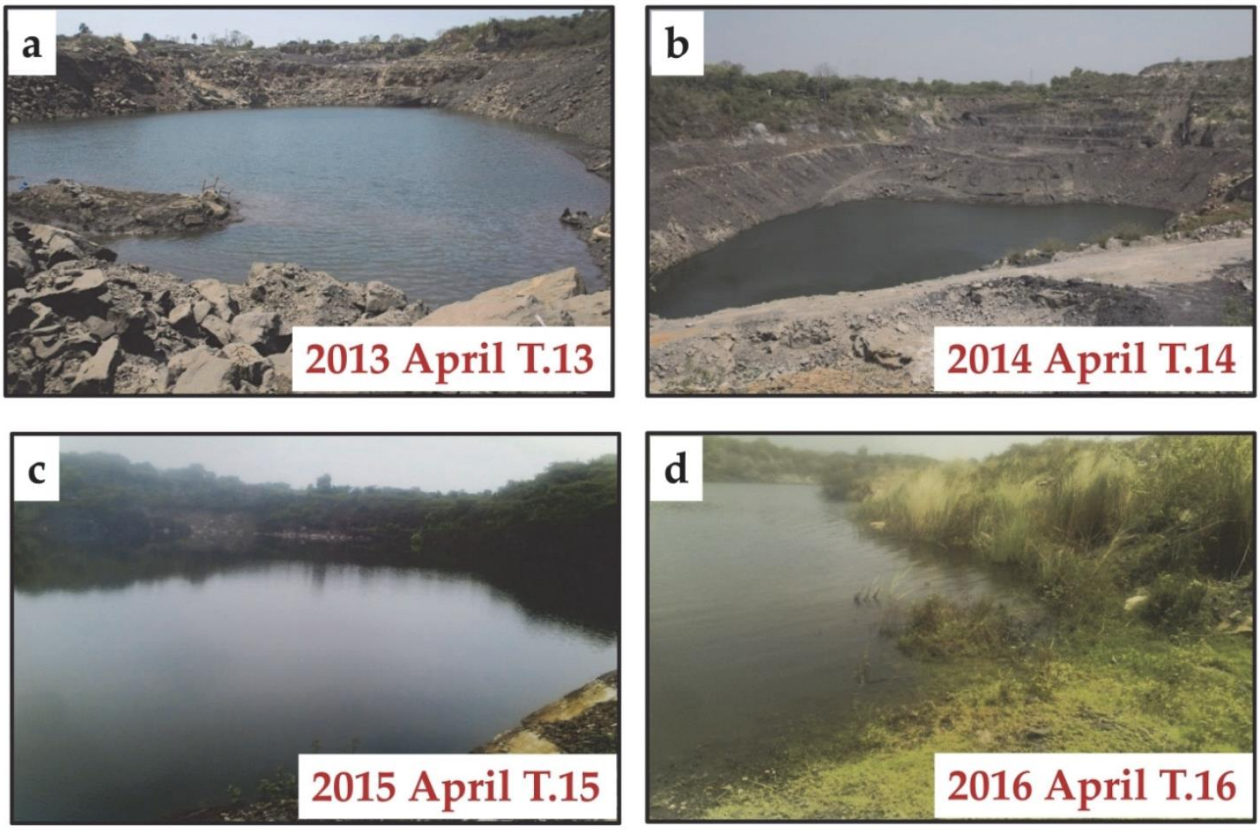


Figure S2. Box-whiskers plot representing total culturable and Cr(VI) tolerating bacterial load enumerated in Luria-Bertanni agar plates and LB supplemented with 100 mg L^{-1} $K_2Cr_2O_7$ respectively, and measured as colony forming units (CFU) per gm of soil (n= 5).

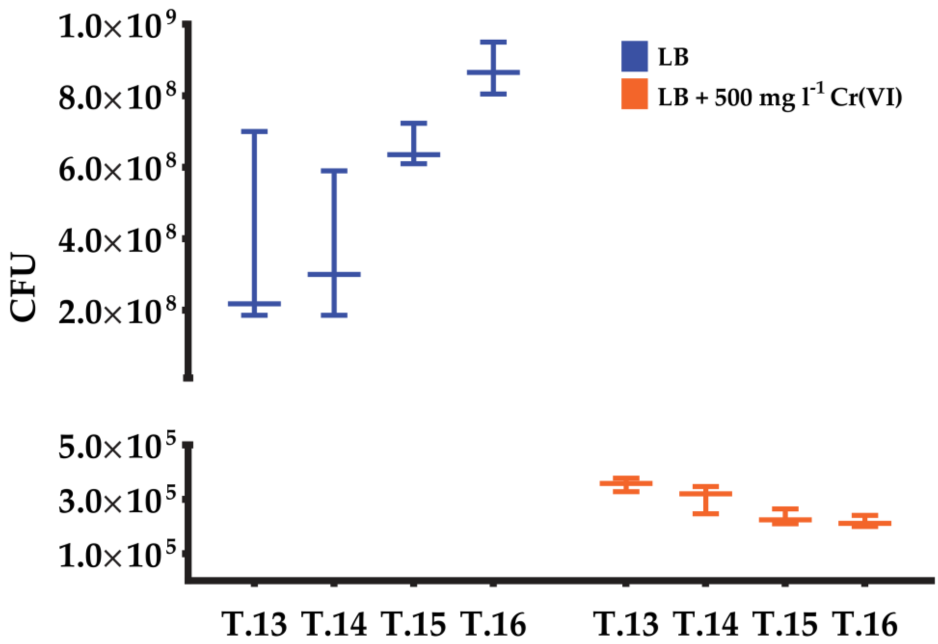


Figure S3. Bacterial phyla distribution observed for each sampling time point in Tasra colliery. For clearer resolution, only topmost abundant (0.1%) phyla are represented. Proteobacterial members are represented either as respective class (represented by pattern-filling), and those which can't be assigned to a specific class are clustered together and labeled as Proteobacteria.

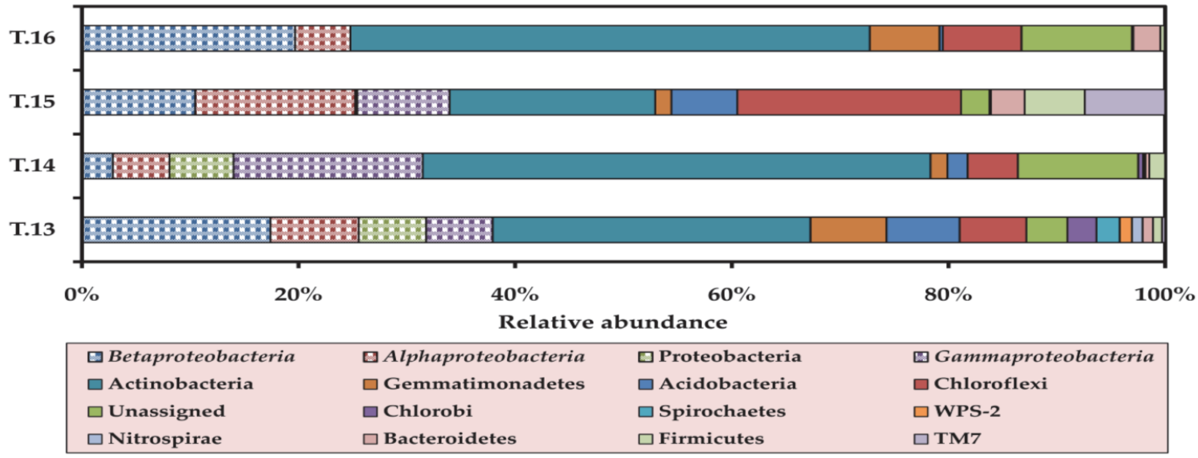
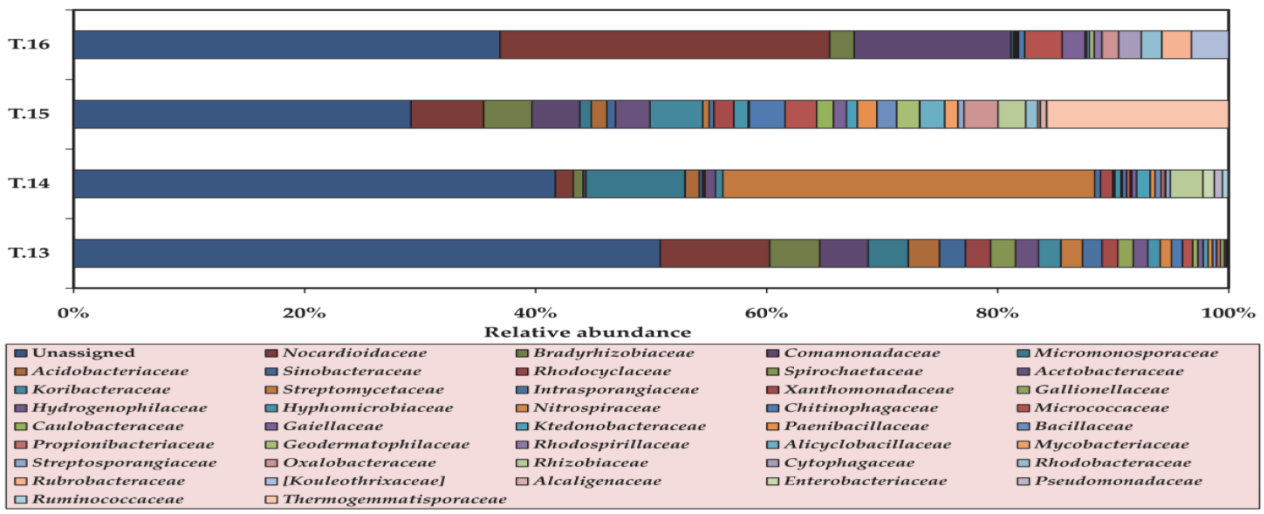


Figure S4. Relative abundance of families with OTUs with > 0.1% occurrence in Tasra Colliery.



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