

ULRR

Bacterial communities established in bauxite residues with different restoration histories

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Figures and tables

- Figure legends
- Figure 1
- Figure 2
- Figure 3
- Table 1
- Table 2
- Table 3
- Supporting information

Figure legends

Figure 1

Detrended Correspondence Analysis (DCA) of Denaturing Gradient Gel Electrophoresis (DGGE) matrices of bacterial 16S rRNA gene fragments from bauxite residue sites M (white box), J (grey box) and R (black box) sampled at Aughinish Alumina, County Limerick, Ireland in a) 2009 and b) 2011. Error bars indicate standard deviation.

Figure 2

Principal Coordinate Analysis (PCoA) of bacterial community sequences based on 16S rRNA gene amplicons from bauxite residue sites sampled in 2009 (black) and 2011 (grey) from site M (circle), R (diamonds) and J (squares). PCoA was calculated using an unweighted Unifrac distance matrix and visualised with King.

Figure 3

Abundance of sequences allocated to major bacterial phyla after taxonomic analysis of 16S rRNA gene amplicons from bauxite residue sites M (black bars), J (dotted bars) and R (checked bars) from samples taken in a) 2009 and b) 2011.

Fig1A

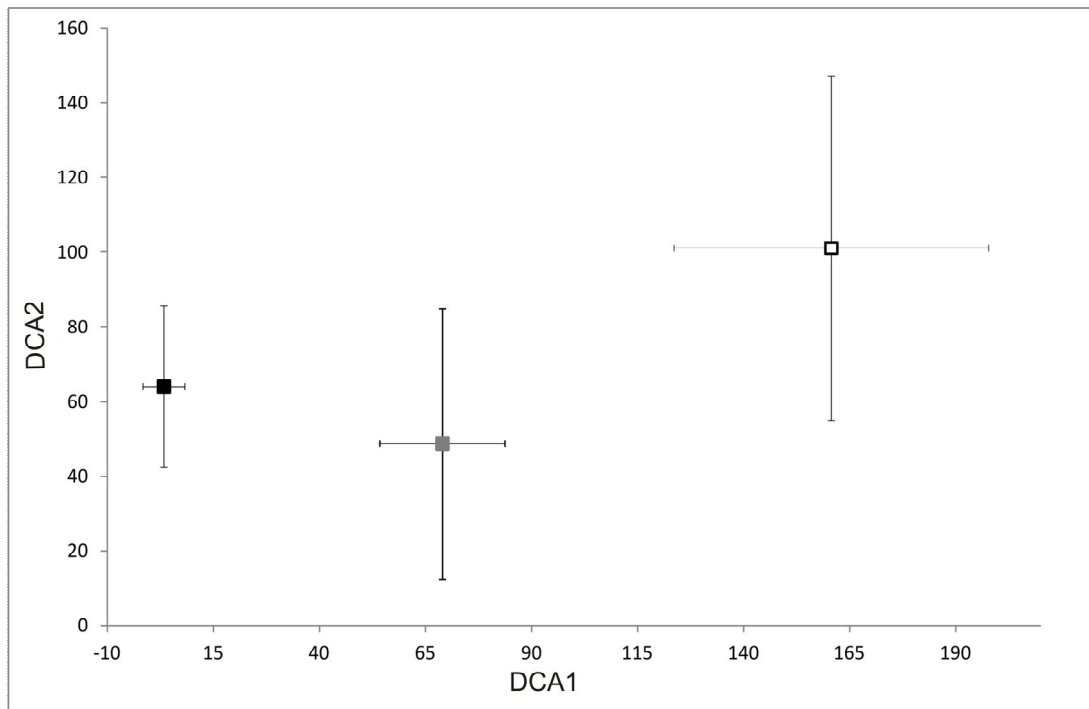


Fig1B

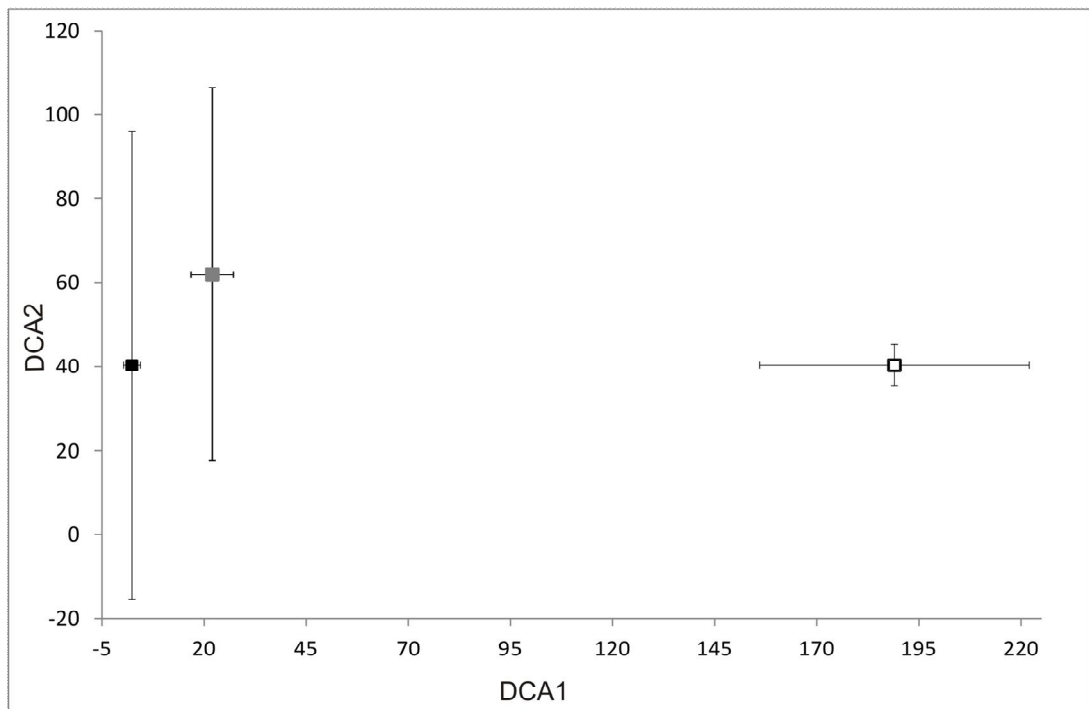


Fig. 2

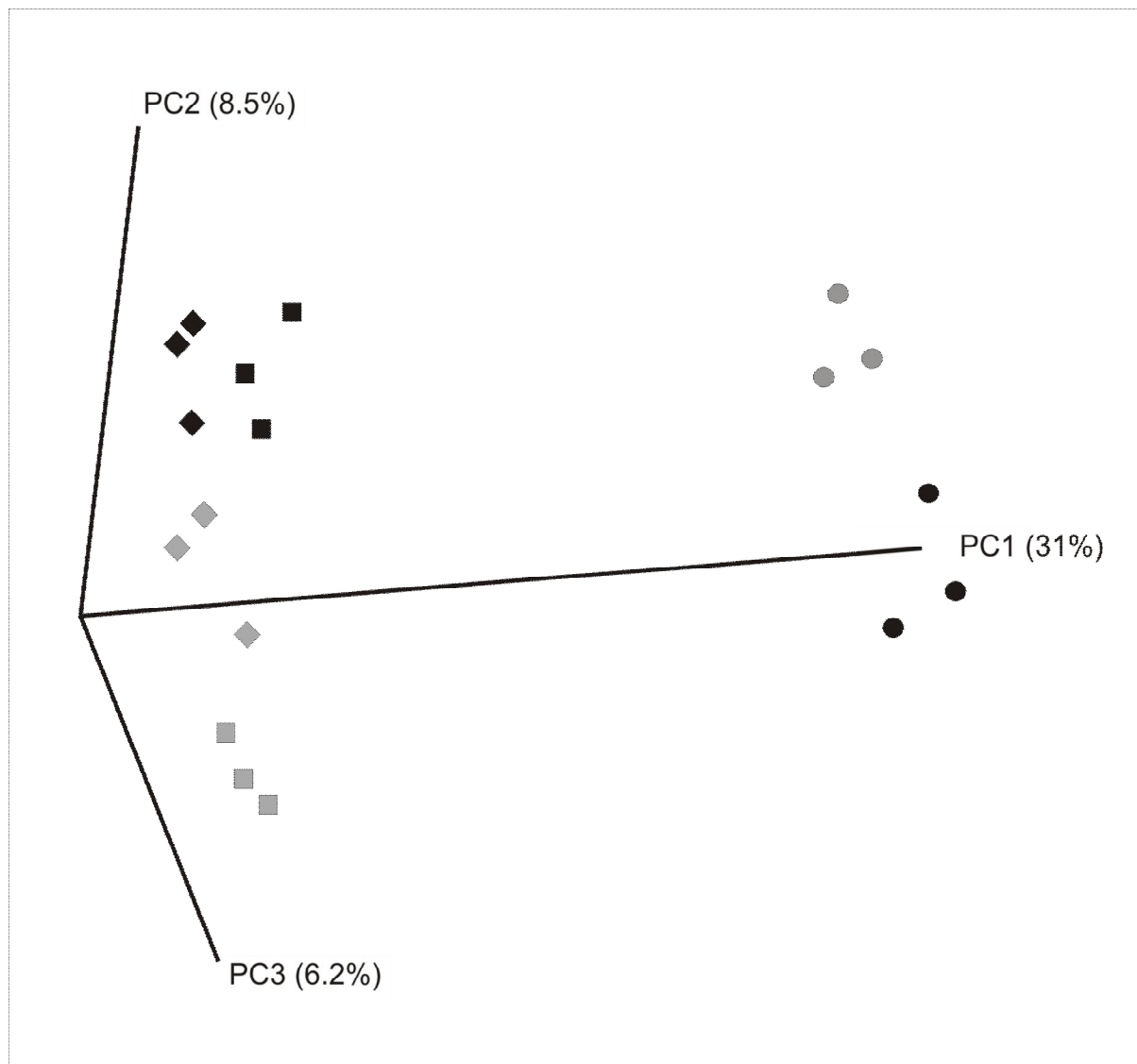


Fig 3A

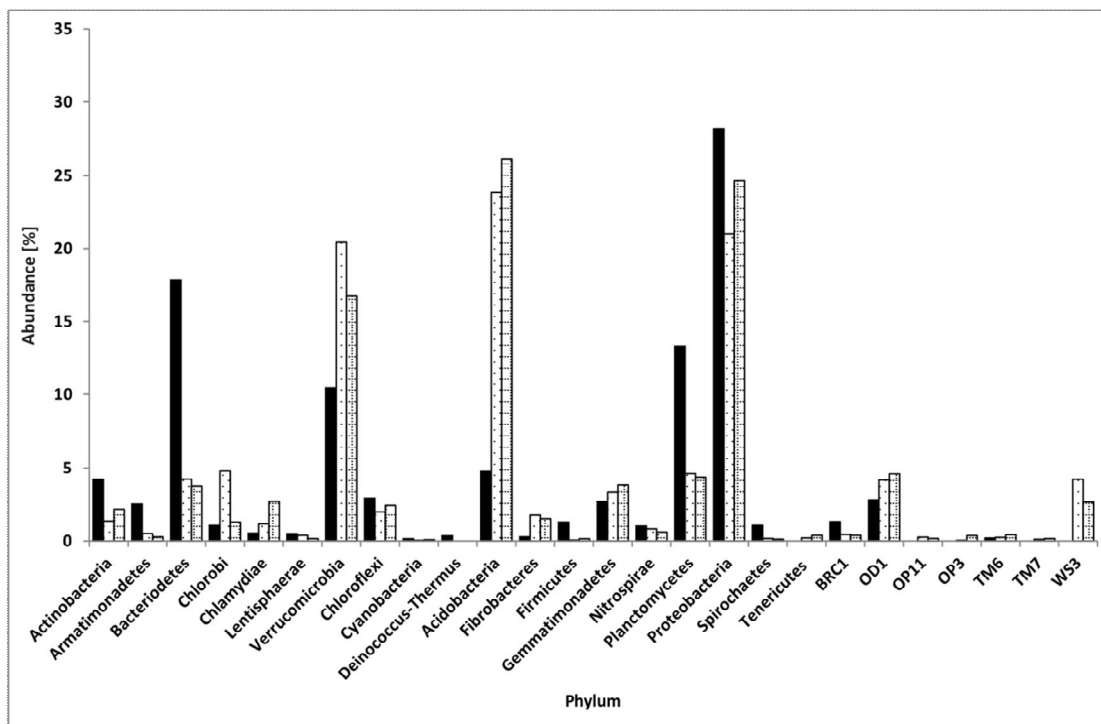


Fig 3B

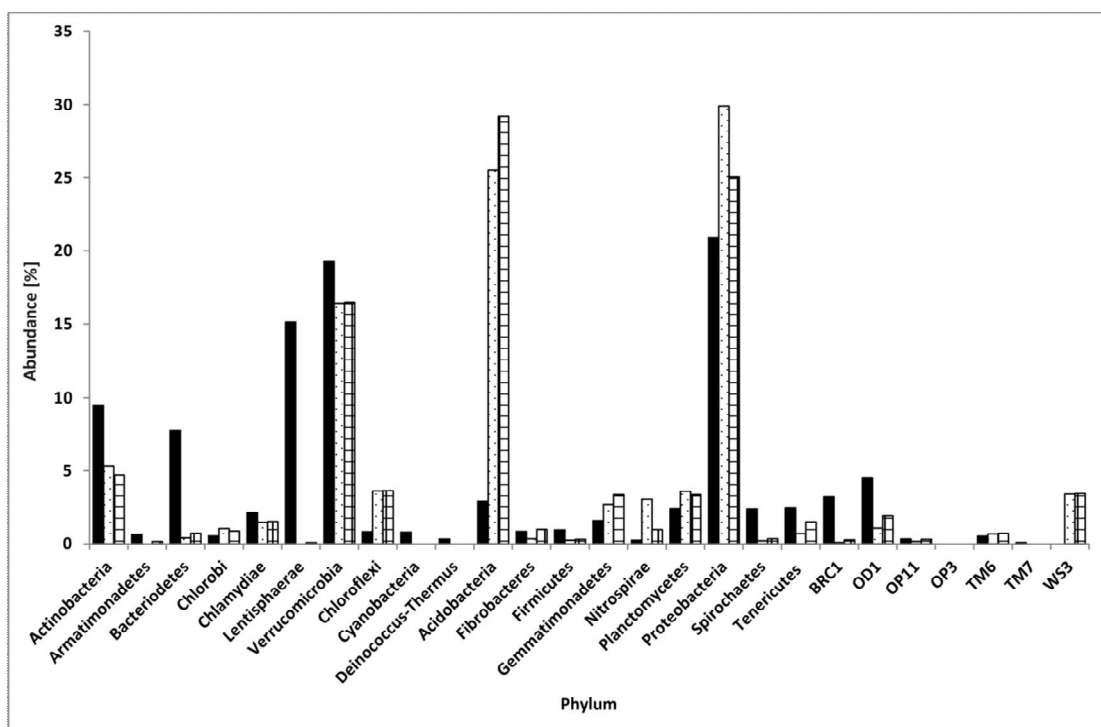


Table 1 Physico-chemical properties (0-10 cm) from restored (J, R) and bare (M) bauxite residue sites

		M	+/-	J	+/-	R	+/-
	pH	10.32 ^A	0.02	7.86 ^B	0.22	7.73 ^B	0.02
mS cm ⁻¹	Ec	2.88 ^A	0.88	0.26 ^B	0.04	0.48 ^B	0.07
	Na	20.69 ^A	5.41	1.06 ^B	0.17	1.24 ^B	0.10
	Mg	0.03 ^A	0.00	0.52 ^B	0.23	1.17 ^C	0.22
	Ca	2.97 ^A	0.18	9.34 ^B	1.09	17.41 ^C	3.23
cmol kg ⁻¹	K	0.32 ^A	0.10	0.4 ^A	0.11	0.39 ^A	0.10
	ESP	78.85 ^A	10.26	9.79 ^B	1.89	6.52 ^B	1.55
	org C	0.18 ^A	0.00	2.52 ^B	1.62	3.49 ^B	1.44
%	N	0.03 ^A	0.00	0.24 ^B	0.09	0.53 ^C	0.05
mg kg ⁻¹	Available P	2.83 ^A	0.30	8.57 ^B	0.89	9.93 ^B	0.84

Ec = electroconductivity; ESP = exchangeable sodium percentage; mS = milli Siemens;

cmol = centimole

ABC= Significantly different (P<0.05); +/- = standard deviation

Table 2: Relative abundance [%] of major bacterial phyla and families in 16S rRNA gene fragment amplicon library

Phylum	Family	M2009	M2011	J2009	J2011	R2009	R2011
Actinobacteria	<i>Propionibacteriaceae</i>	0.08	1.46	n.d.	0.06	n.d.	0.06
	<i>Nocardioideaceae</i>	n.d.	0.16	0.12	1.25	0.10	1.44
Armatimonadetes		2.32	0.55	n.d.	n.d.	0.28	0.16
Bacteroidetes	<i>Chitinophagaceae</i>	7.74	4.94	0.95	n.d.	1.04	0.13
	<i>Rhodothermaceae</i>	1.17	0.20	n.d.	n.d.	n.d.	n.d.
	<i>Cyclobacteriaceae</i>	2.26	0.76	n.d.	n.d.	n.d.	n.d.
	<i>Cytophagaceae</i>	1.41	0.13	1.19	0.19	1.27	0.29
Chlorobia	<i>Chlorobiales</i>	0.98	0.47	4.70	1.01	1.25	0.85
Lentisphaerae		0.45	13.33	0.37	n.d.	n.d.	0.09
Chlamydiae	Unclass. <i>Chlamydiales</i>	n.d.	0.16	0.51	0.16	1.28	0.27
Verrucomicrobia	<i>Opitutaceae</i>	4.60	2.20	2.54	1.29	1.86	1.05
	<i>Methylacidophilaceae</i>	n.d.	1.23	n.d.	n.d.	n.d.	0.09
	Verrucomicrobia sub div 3	0.73	2.20	1.36	0.48	1.22	0.89
	<i>Verrucomicrobiaceae</i>	0.93	1.00	1.42	0.49	0.80	0.68
	<i>Spartobacteria (class)</i>	1.19	3.75	5.29	6.65	3.82	4.22
Chloroflexi	Anaerolineae (class)	0.10	n.d.	1.09	1.47	1.59	2.38
Fibrobacteres	<i>Fibrobacteraceae</i>	0.26	0.74	1.72	0.34	1.48	0.95
Acidobacteria	<i>Acidobacteriaceae</i>	4.38	2.54	21.70	23.20	20.76	26.38
	Holophagae (class)	n.d.	n.d.	0.24	0.64	3.60	0.95
Gemmatimonadetes	<i>Gemmatimonadaceae</i>	2.04	1.24	2.96	2.27	3.35	3.14
Planctomycetes	<i>Phycisphaeraceae</i>	11.20	1.22	1.94	0.53	1.19	0.66
	<i>Planctomycetaceae</i>	1.07	0.70	1.09	2.40	1.53	2.05
Proteobacteria	<i>Beijerinckiaceae</i>	1.99	3.86	n.d.	n.d.	n.d.	n.d.
	<i>Rhodospirillaceae</i>	0.53	0.30	0.99	0.49	0.40	0.60
	<i>Caulobacteraceae</i>	n.d.	n.d.	1.28	0.86	1.25	1.26
	<i>Acetobacteraceae</i>	1.24	1.09	0.22	0.21	0.23	0.25
	<i>Nitrosomonadaceae</i>	0.61	0.45	3.07	2.63	2.95	3.19
	<i>Xanthomonadaceae</i>	4.77	2.17	0.24	0.07	n.d.	0.07
	<i>Enterobacteriaceae</i>	n.d.	0.06	n.d.	n.d.	2.28	0.17
	<i>Halomonadaceae</i>	1.35	n.d.	n.d.	0.00	n.d.	n.d.
	<i>Coxiellaceae</i>	0.61	2.40	0.86	0.80	1.68	0.72
	<i>Nitrospinaceae</i>	n.d.	n.d.	0.36	0.76	1.01	0.68
Tenericutes	<i>Acholeplasmataceae</i>	n.d.	2.15	n.d.	0.00	0.00	n.d.
	<i>Anaeroplasmataceae</i>	n.d.	n.d.	0.20	0.68	0.37	1.45
BRC1		1.22	2.84	0.43	0.09	0.37	0.27
OD1		2.58	4.00	4.05	1.03	4.50	1.85
WS3		n.d.	n.d.	4.10	3.32	2.59	3.36

n.d. = not detected

Highlighted numbers indicate significant differences (P<0.05)

Table 3: Quantitative PCR of bauxite residue sites in 2011 (M, J, R) and a reference soil (S)

Bauxite residue site	<i>Acidobacteriaceae</i> / 16S [% gene copy number]	Standard deviation [+/-]	Univariate analysis [P=0.05]
M	0.29	0.31	A
J	13.55	3.98	B
R	15.85	5.01	B
S	15.11	7.98	B