



Bacterial communities established in bauxite residues with different restoration histories

Achim Schmalenberger, Orla O'Sullivan, Jacinta Gahan, Paul D. Cotter, RONAN COURTNEY

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Supporting information

Supporting Table 1

Supporting Figure S1

Supporting Figure S2

Supporting Table 1: Alpha diversity of 16S rRNA gene fragment amplicon library

Sample site	Shannon	+/-	Simpson	+/-	Chao1	+/-	PD whole tree	+/-	Observed species	+/-
M2009	6.43	0.32	0.97	0.02	446.6	100.0	37.06	4.26	294.3	52.3
M2011	6.42	0.47	0.96	0.03	491.5	102.7	39.00	5.42	310.0	52.3
J2009	8.38	0.12	0.99	0.00	1726.4	185.0	84.68	6.06	888.3	72.1
J2011	7.94	0.04	0.99	0.00	1116.0	193.1	61.57	2.66	645.0	44.5
R2009	8.46	0.18	0.99	0.00	1836.0	185.3	88.80	4.38	924.7	37.9
R2011	7.95	0.28	0.99	0.00	1359.5	420.6	70.62	11.35	720.0	150.8

Supporting Figure S1

Denaturing gradient gel electrophoresis of 16S rRNA gene fragments from bauxite residue sites M, J and R in triplicates (1-3) sampled at Aughinish Alumina, County Limerick, Ireland, in a) 2009 and b) 2011; flanked by species standards (Std).

Fig S1A

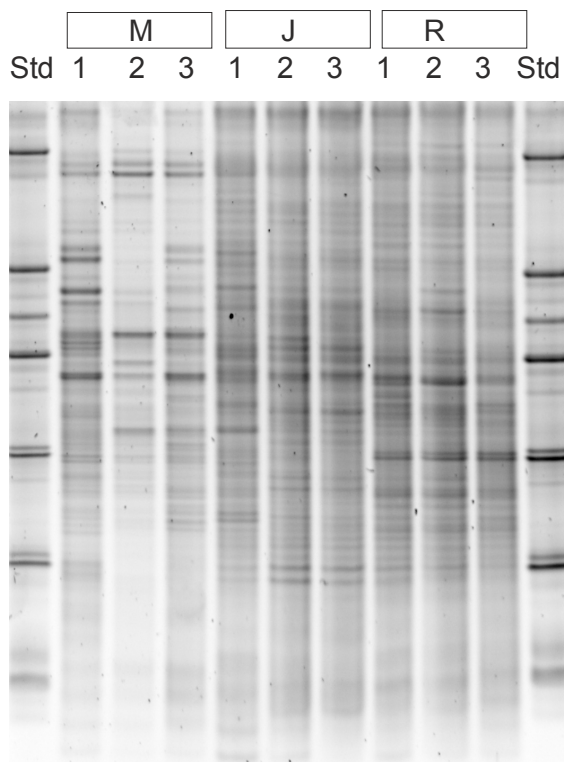
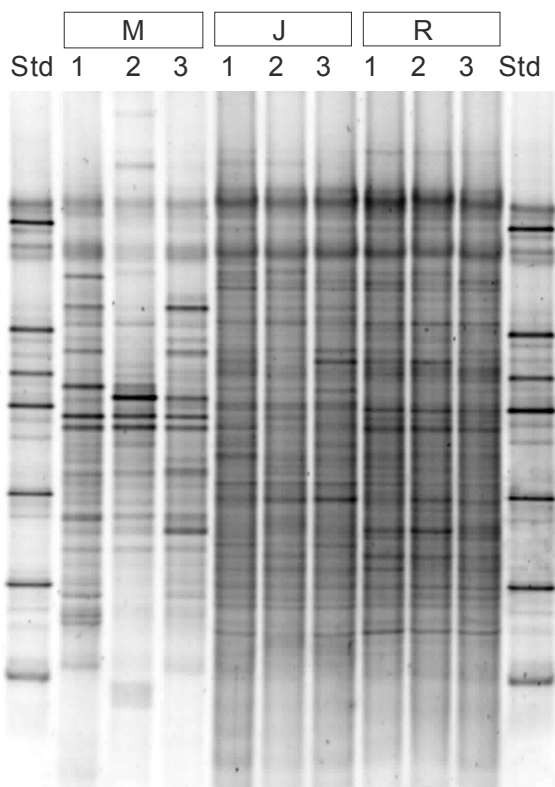


Fig S1B



Supporting Figure S2

Canonical Correspondence Analysis (CCA) of Denaturing Gradient Gel Electrophoresis (DGGE) matrices of bacterial 16S rRNA gene fragments from bauxite residue sites M, J and R (circles) sampled in triplicates (1-3) and correlation to environmental factors pH, calcium (Ca), magnesium (Mg), sodium (Na), total nitrogen (N), electro conductivity (Ec), exchangeable sodium percentage (ESP) and organic carbon (org C), sampled at Aughinish Alumina, County Limerick, Ireland in 2011.

