

Soil microbial community succession patterns over a 30-40 year chronosequence of post-mining ecosystem restoration

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eDNA assessment of soil microbiota:
 Diversity and species composition across 30-40 year rehabilitation chronosequence

Contrast to pre-disturbance reference systems

A novel measure of restoration success/completion criteria

• **Key question:**

Q1. Impact of the mining and initial rehabilitation process on soil microbial community?

Q2. Trajectory through time of the soil microbial community post-rehabilitation?

Q3. Does the soil microbial community diversity /composition return to reference state in 30 yrs

Q4. If not, can we predict time to recovery?

Q5. What are the compositional differences in the soil microbial community between rehabilitated and reference sites?

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Chronosequence Sampling Alcoa Huntly (September 2016)

36 sites: 18 rehab sites (3 reps of each of 6 ages), each with an adjacent natural reference site (18 in total), each at 2 depths

Year of rehab	1987	1991	1999	2002	2008	2014
Age (years) of rehab when sampled	29	25	17	14	8	2
	1 1 2 2 3 3	1 1 2 2 3 3	1 1 2 2 3 3	1 1 2 2 3 3	1 1 2 2 3 3	1 1 2 2 3 3

3

Sample site locations showing year/age of post-mining rehabilitation

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Sampling of soil and sequencing

Conducted as per BASE protocols:
 Biomes of Australian Soil Environments microbial diversity database

Unique identifiers (supplied by BPA)

High-throughput Sequencing
 Illumina MISEQ
 Fungal ITS region (ITS1F-ITS4)
 Bacterial 16S rRNA gene (27 F-519R)
 Archaeal 16S rRNA gene (A2F-519R)

Sequencing conducted at AGRF

Details of workflow summarised in Bissett et al (2016)

OTUs initially identified using:
 UNITE (v7.0) for fungi,
 Green Genes for bacteria and archaea

From: Bissett et al (2016) Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. Gigascience 5:21. doi:10.1186/s13742-016-0126-5

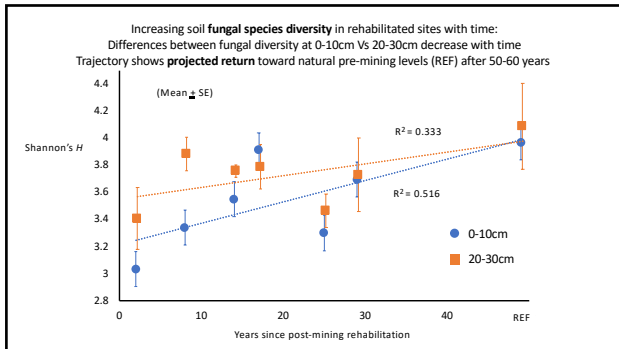
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Fungal ITS data summary - total number of sequence reads per sample
 In total: 4,944,651 sequences and 12,004 OTUs identified

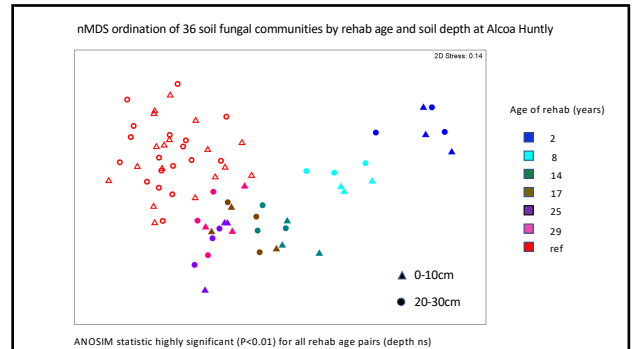
All analyses conducted on sub-sampled data standardised to 16,749 reads

36 sites (18 rehab, 18 reference sites, each site sampled at 2 depths)

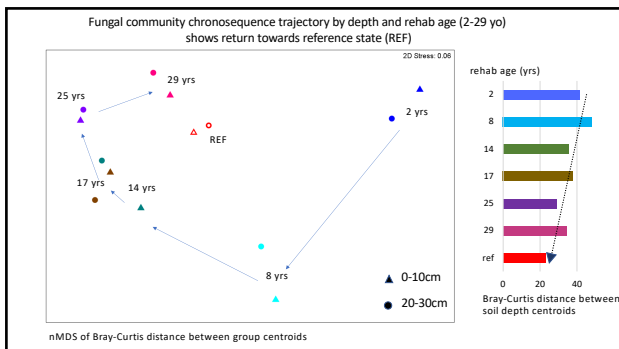
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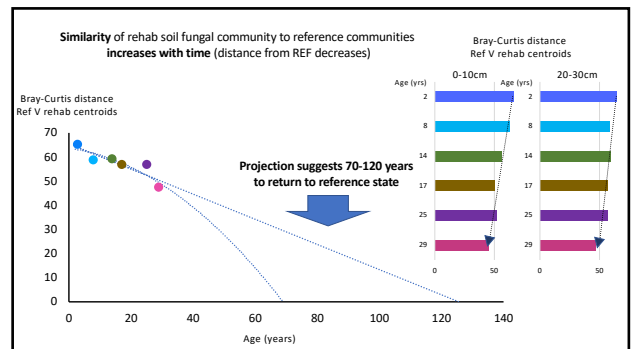
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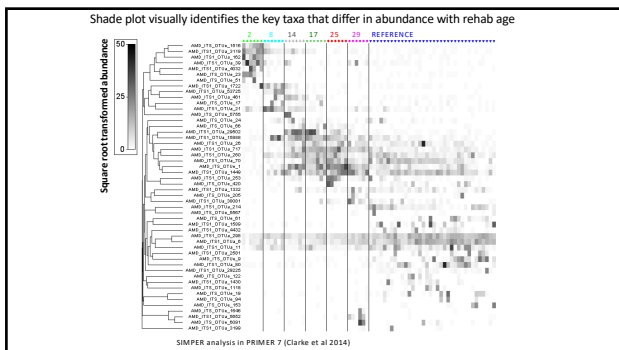
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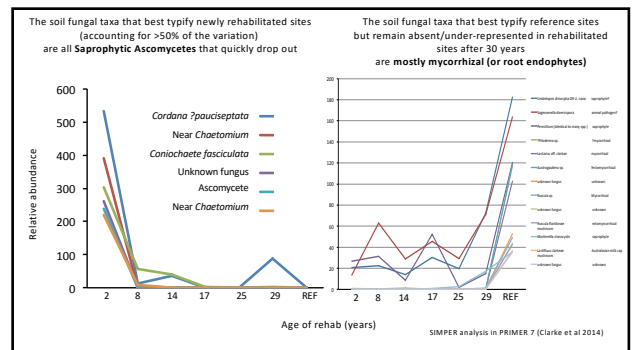
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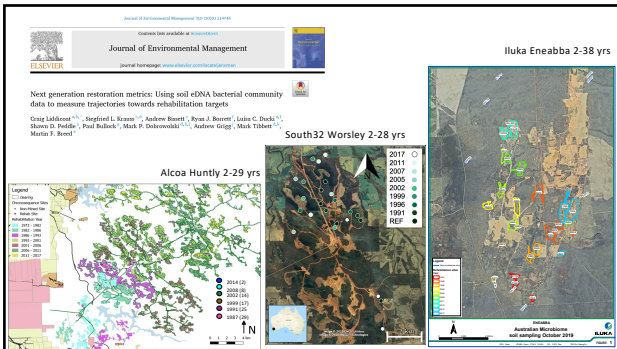
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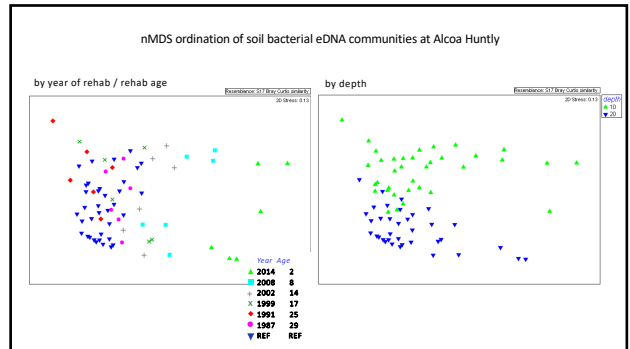
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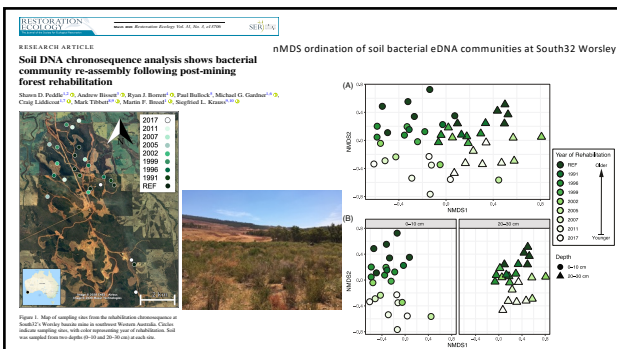
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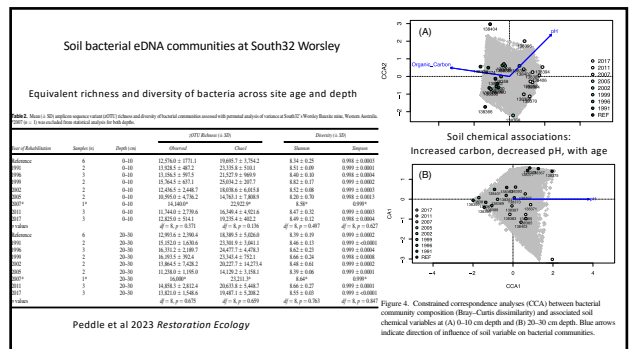
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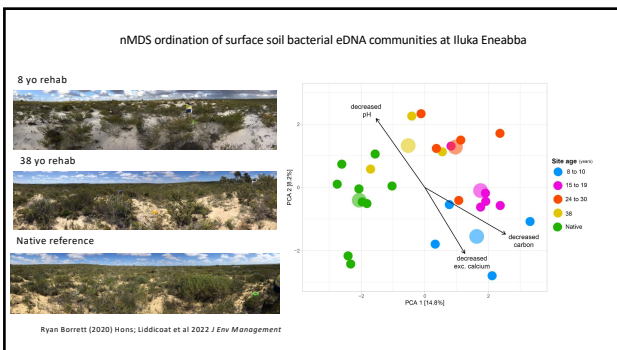
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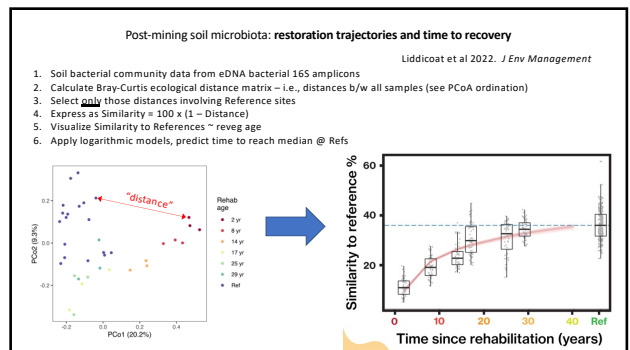
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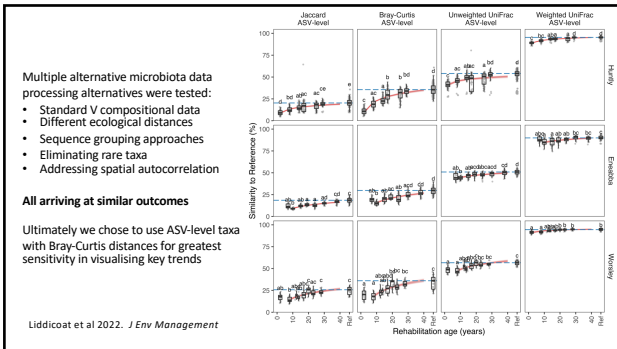
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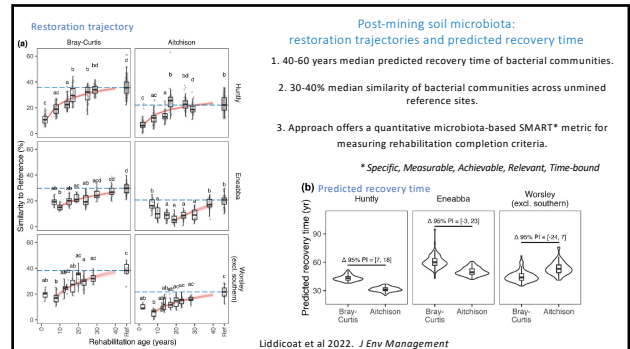
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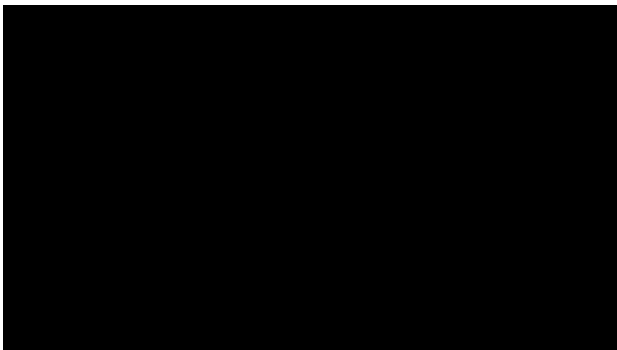
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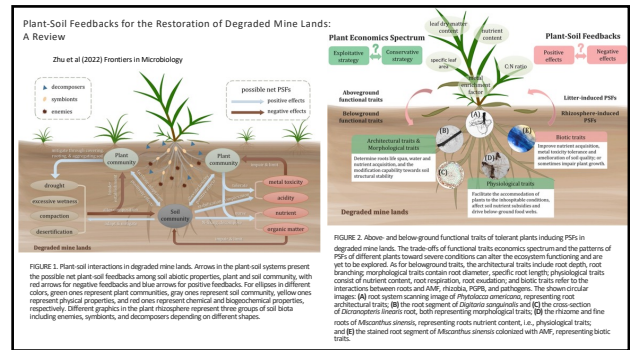
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