Interchanging Microbial Communities: The Effects of Soil-to-Soil Transfer

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Can Soil Microbes Create High-Performing Soils?

- Agricultural growing regions contain a multitude of edaphic conditions & soil types that foster the growth of specific microorganisms (**microbes**).
- Microbes are an important part of soil function, including the breakdown, movement, and uptake of nutrients that lead to **plant growth**.
- **Microbial functions** relate to the composition of soil microbiomes. Adding microbes to enhance soil performance is not a new concept e.g. nitrogen-fixing rhizobia in legumes.
- Meta-analysis reveals consortia of microbes colonise soil more efficiently and effectively vs single species.
- So, how does an **entire microbial community (microbiome)** from a high-performing soil respond to being transferred to an underperforming soil, and vice versa?

Methodology

- Soils were sampled from 3 locations with **varying environments, land use, and soil types** (see Figure 1).
- Sink soils were sterilised with **gamma radiation.**
- Microbiomes were transferred using a **Soil-to-Soil transfer** method with filter paper as a barrier.
- **Metagenomic and metabolomic** analysis were performed on subsamples.

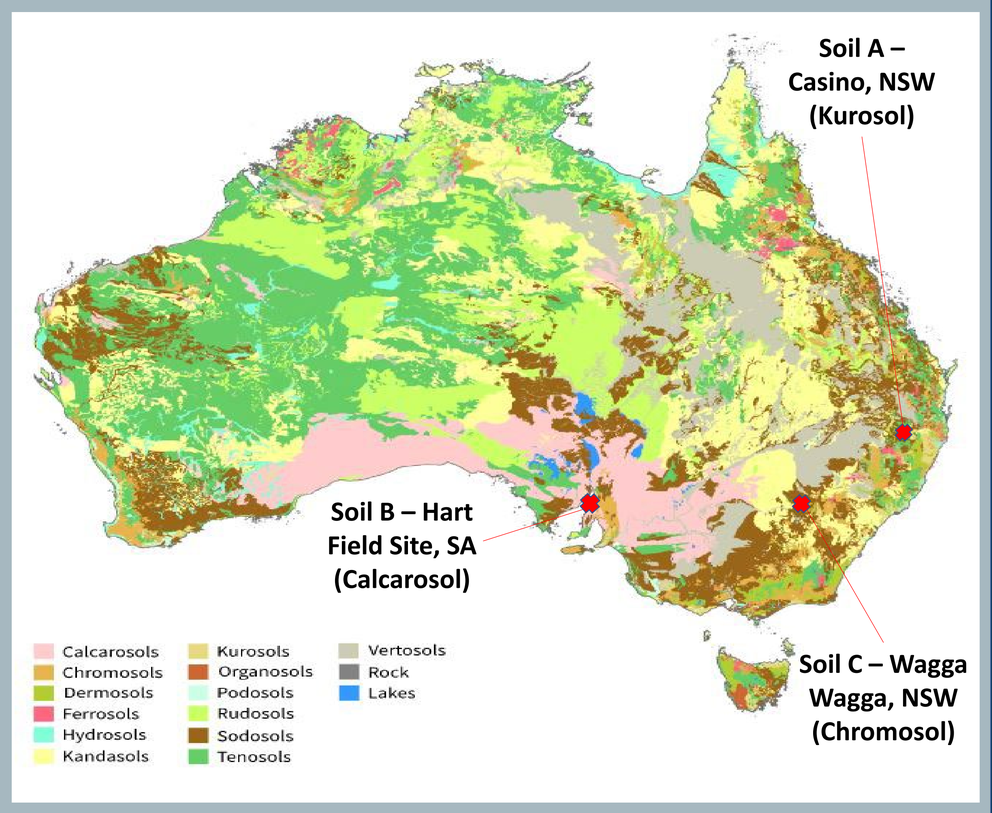

Figure 1: Map showing various soil types across Australia, in addition to sampling locations.

Findings

- **Microbial composition** of the treatments significantly shifts away from both the source and sink microbiomes (baselines) indicating a new microbiome is created (Figure 2).
- There is both a significant **source and sink effect** on the microbial composition of treatments despite the formation of a 'new' microbiome. This means the new microbiome is influenced by both the original soil and the soil in which it was transferred.
- By-products of microbes in the soil (**soil metabolites**) and how they use carbon-based materials (**function**) correspond significantly with the new microbiomes compared to the microbes in the original or the new soil.
- All comparative **fungal results** were statistically similar to bacterial results, however, were often less significant. This could be due to less taxonomic classification and identification of fungal species than bacterial species in soil.

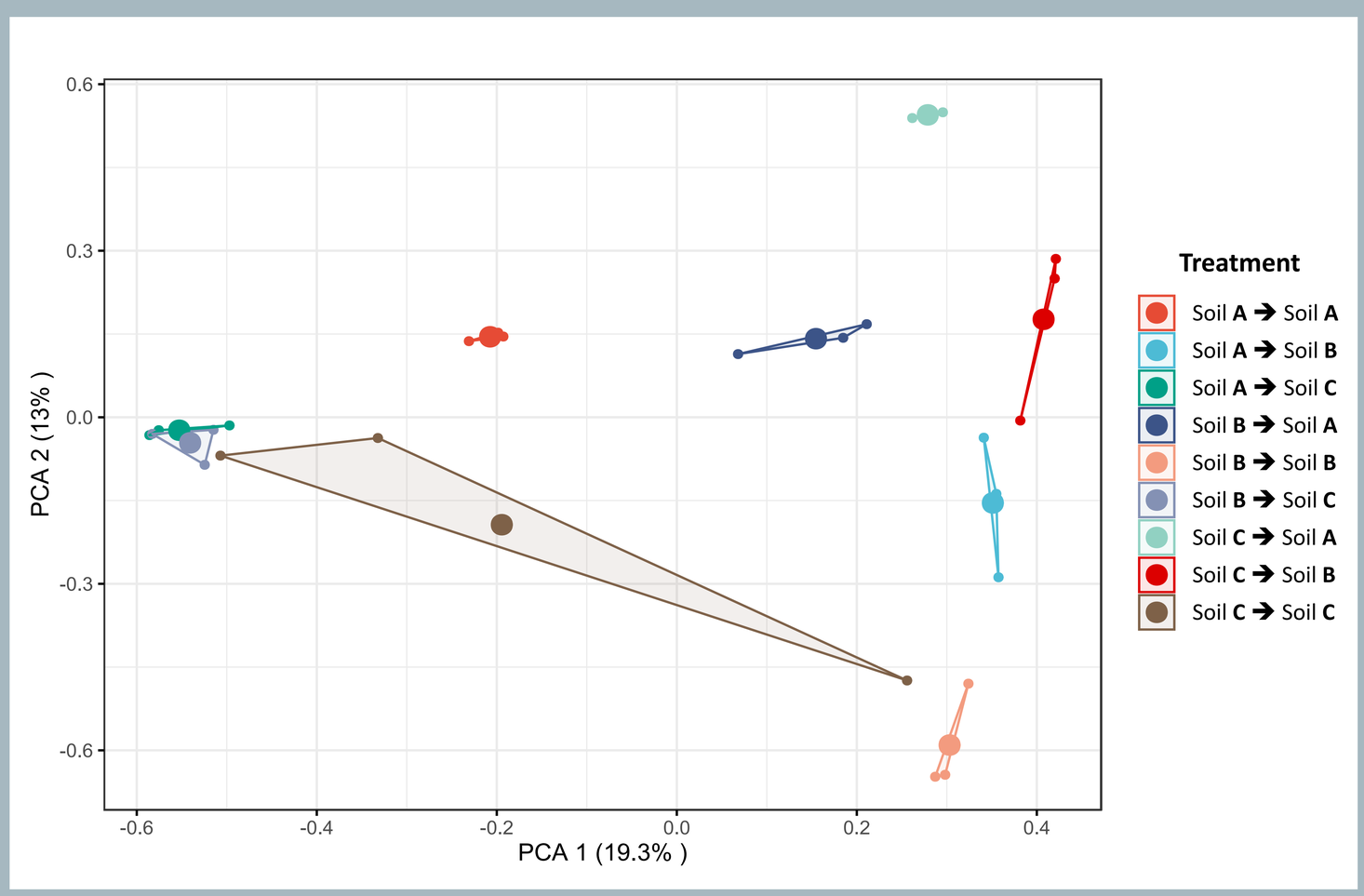

Figure 2: Principal Component Analysis (PCA) of Bacterial gene sequences, assessing similarities in microbial composition between baseline and treatment samples. A, B, and C represent the soil types (see Figure 1).

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