

Organic amendments drive bacterial and fungal soil microbiomes over time in a subtropical banana agroecosystem

Background

Organic amendments are key tools for improving soil health in intensive banana agroecosystems. However, their effects on soil bacterial and fungal communities, particularly under subtropical conditions, remain poorly understood. In this study, we evaluated how commonly used organic amendments reshape the banana soil microbiome over time.

Soil properties shape microbial communities

Microbial community structure was strongly shaped by amendment type and soil properties (Fig. 3).

- Chicken manure formed a distinct cluster linked to high EC and low pH
- Cow manure and compost-based amendments were associated with organic matter and nutrients
- Bacterial communities showed stronger responses to soil gradients, while fungal communities presented moderate patterns.

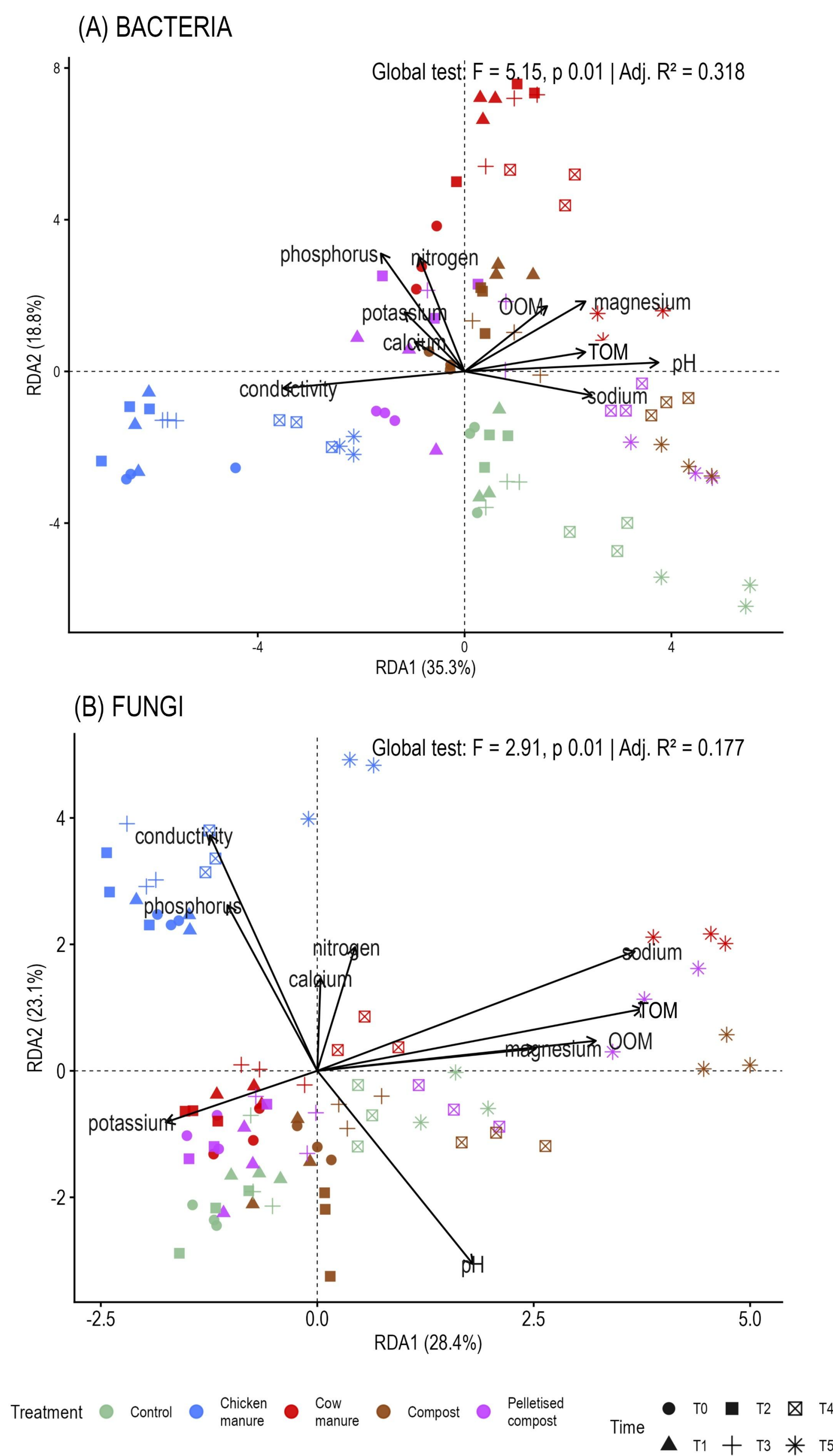


Fig 3. RDA of bacterial (A) and fungal (B) communities constrained by soil properties. Points represent samples; colours indicate treatments and shapes indicate sampling time.

Method

Soil samples were collected from a long-term greenhouse banana experiment (Correa-Delgado et al. 2026), including four organic amendments: chicken manure, cow manure, compost, and pelletised compost. Sampling was conducted at six time points across the crop cycle (Fig. 1). Bacterial (16S rRNA gene) and fungal (ITS region) communities were analysed using long-read amplicon sequencing (PacBio SMRT).

Amendment effects on microbial diversity

Organic amendments significantly influenced microbial diversity patterns (Fig. 2).

- Bacterial richness increased in amended soils (especially cow manure and compost). Diversity showed clear temporal dynamics
- Fungal richness was highest in the control and lowest under chicken manure. The diversity was mainly driven by amendment type, with limited temporal variation

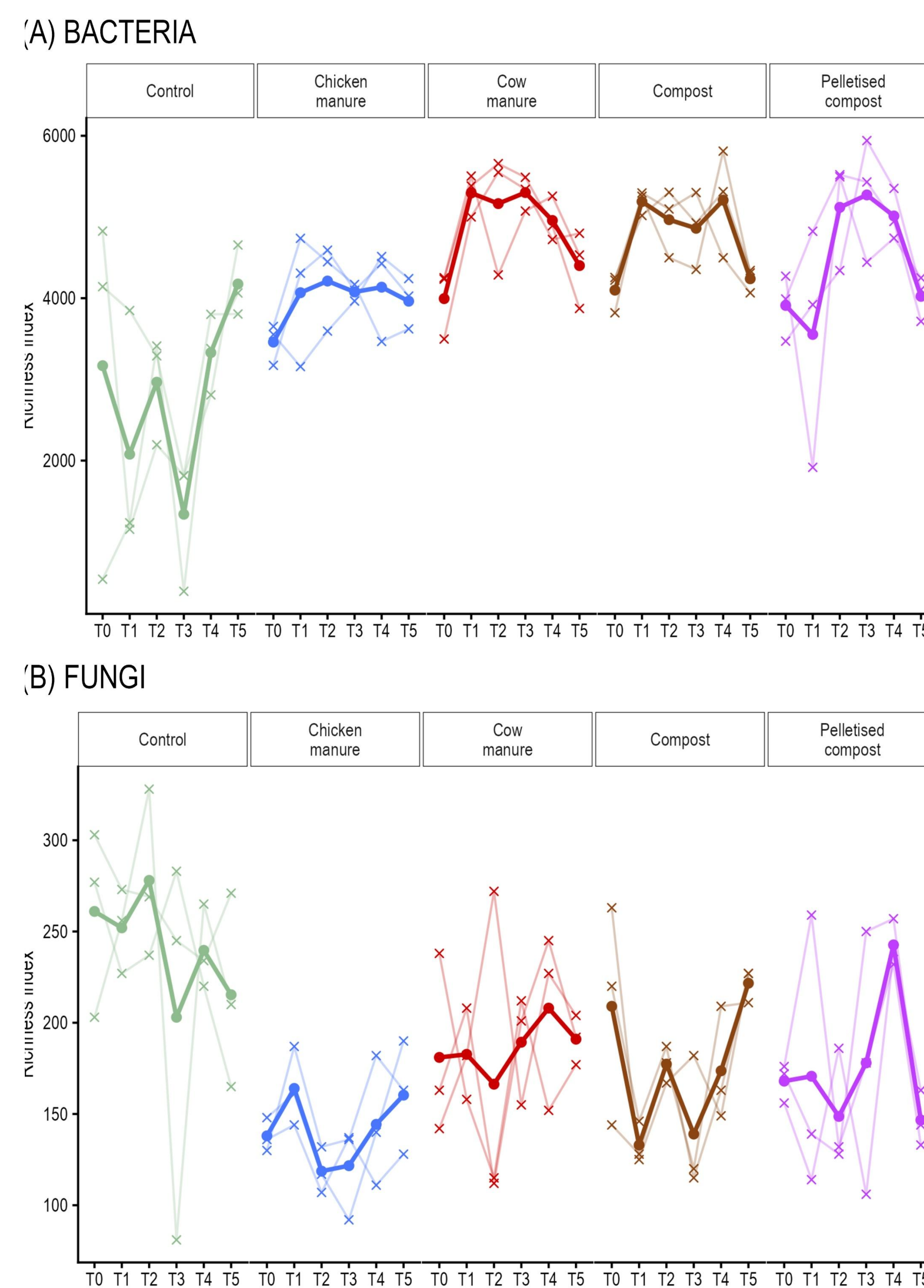


Fig 2. Temporal dynamics of bacterial (A) and fungal (B) richness across treatments. Points represent samples; lines show linear mixed-effects models

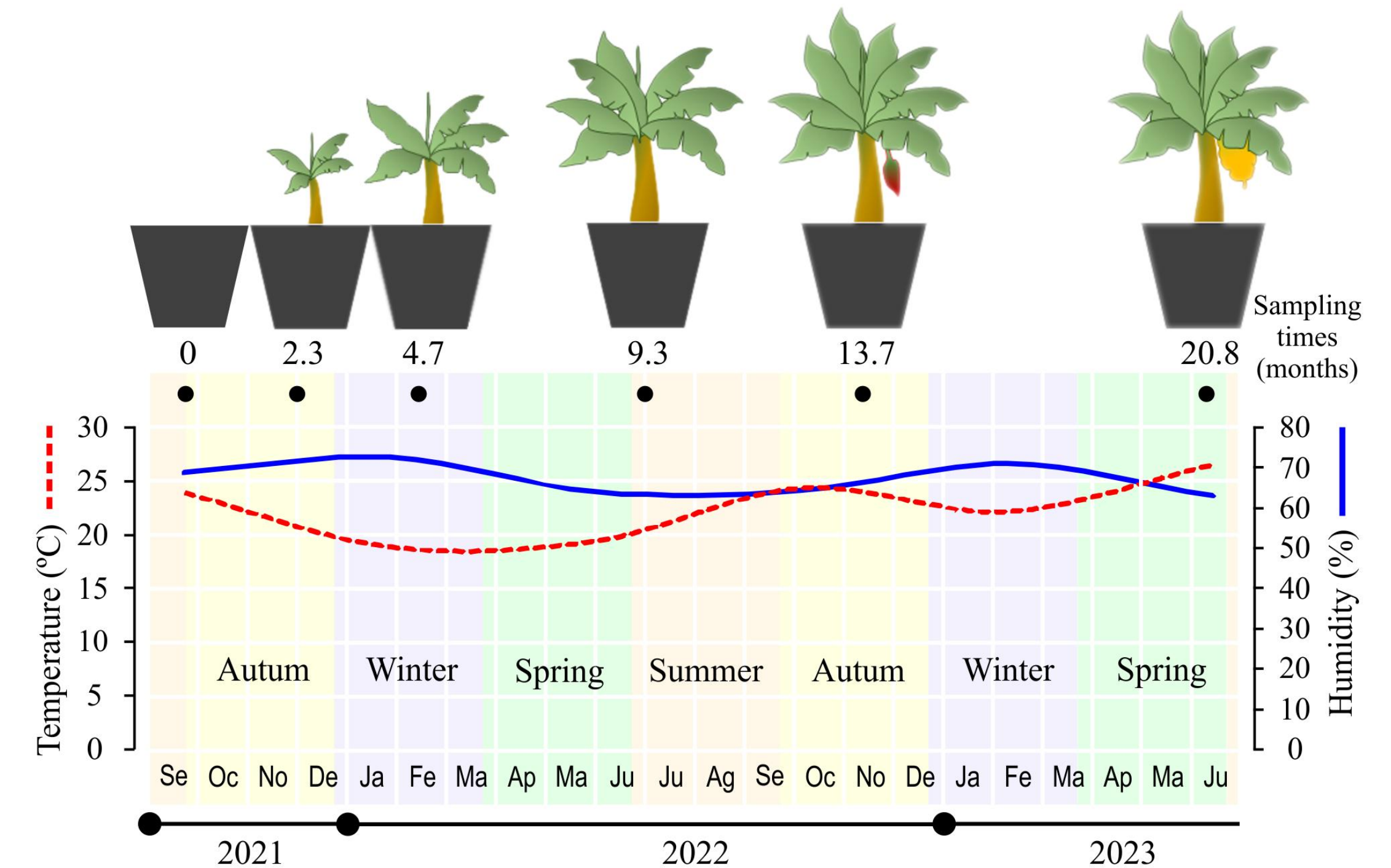


Fig. 1. Temporal sampling scheme and experimental setup.

Amendment-specific microbial shifts

Differential abundance analysis revealed amendment-specific microbial responses (Fig. 4).

- Chicken manure showed the strongest effect, with many reduced taxa
- Cow manure and compost-based amendments promoted enrichment of specific groups
- Amendment type selectively promotes or suppresses microbial taxa

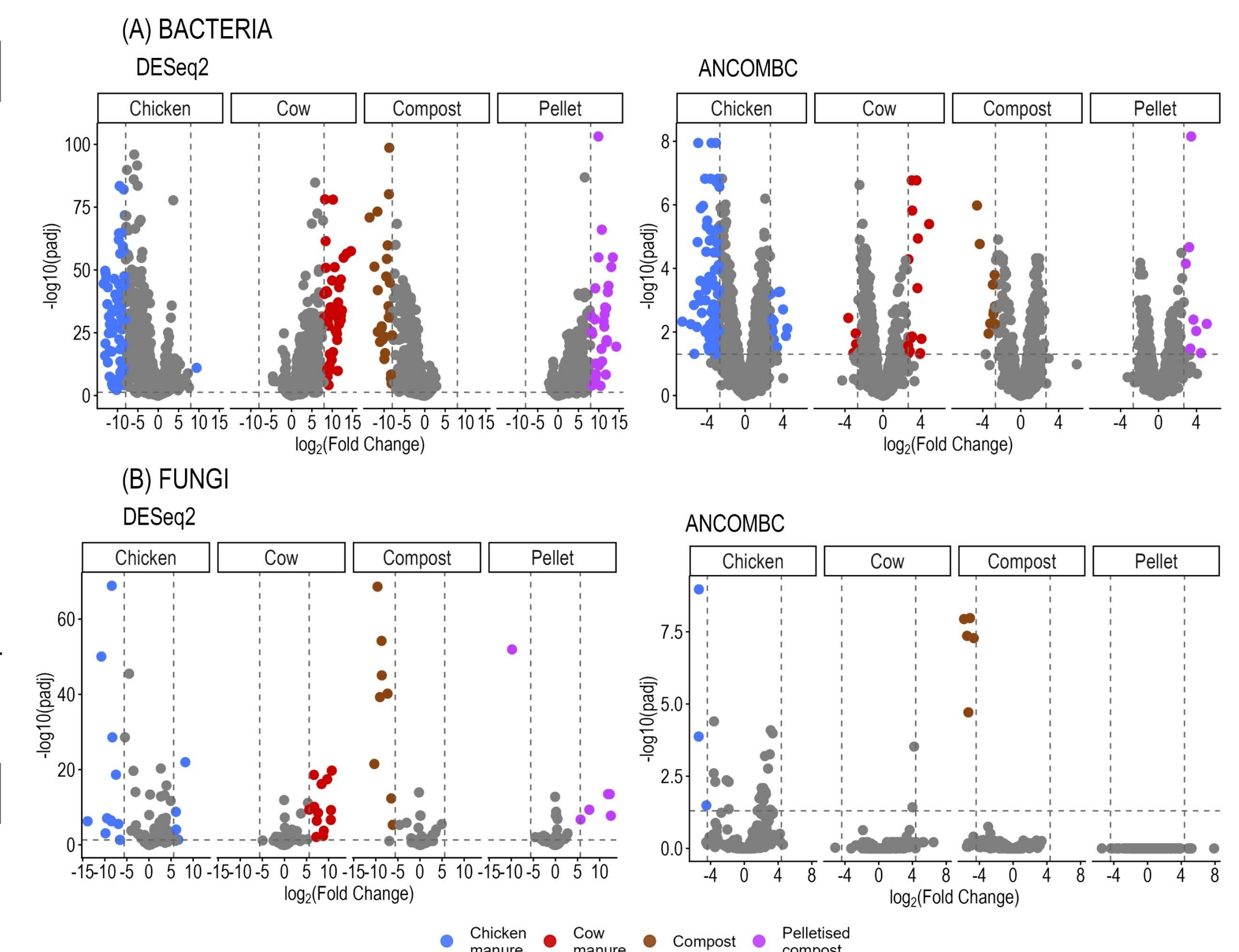


Fig 4. Differential responses of bacterial (A) and fungal (B) taxa to organic amendments. Volcano plots display changes in taxon abundance relative to the control.

Conclusion

Amendment identity is a key driver of soil microbiome restructuring in banana systems, with nutrient-rich inputs inducing strong shifts, while more stabilised amendments promote gradual and potentially more sustainable community dynamics.

