

Land use influences on soil microbiota on the South Atlantic island of St Helena

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Introduction

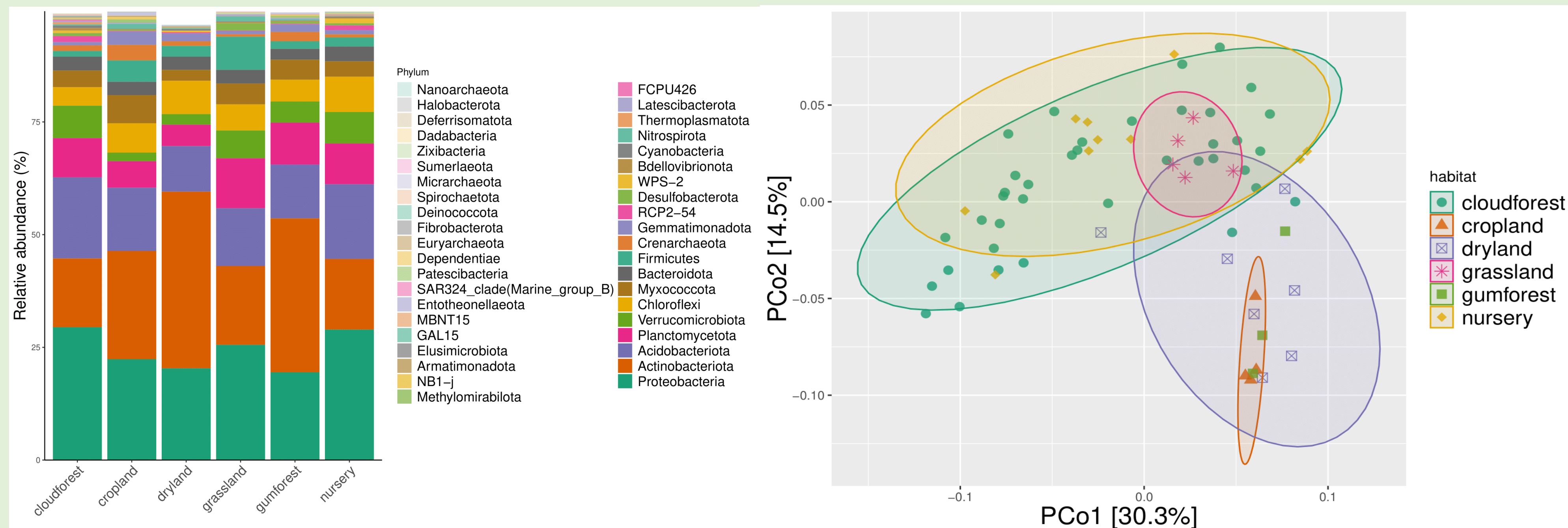
- Soil microbiota is pivotal to the functioning of terrestrial ecosystems, influencing nutrient cycling, ecosystem stability and productivity¹. Determining ecological factors that influence microbial community structure is important for habitat conservation and sustainable management.
- St Helena is a remote volcanic island in the South Atlantic, containing a third of all endemic species of the UK and its Overseas Territories. There has been one study of St Helena's microbiota so far, looking at soil fungi from mid altitude forests². The microbiome of the Peaks National Park high altitude cloud forest, containing most of the island's numerous endemic species and vital to its water security, remains unknown. Additionally, no prokaryotes or protists have been studied on the island.
- Here, we use eDNA metabarcoding to characterise for the first time prokaryotic, protist and fungal communities of Peaks National Park cloud forest soils and compare them to samples from other habitats.



Four types of St Helena habitat, from top left clockwise: Cloud forest, gumwood forest, grassland, dryland

Materials and Methods

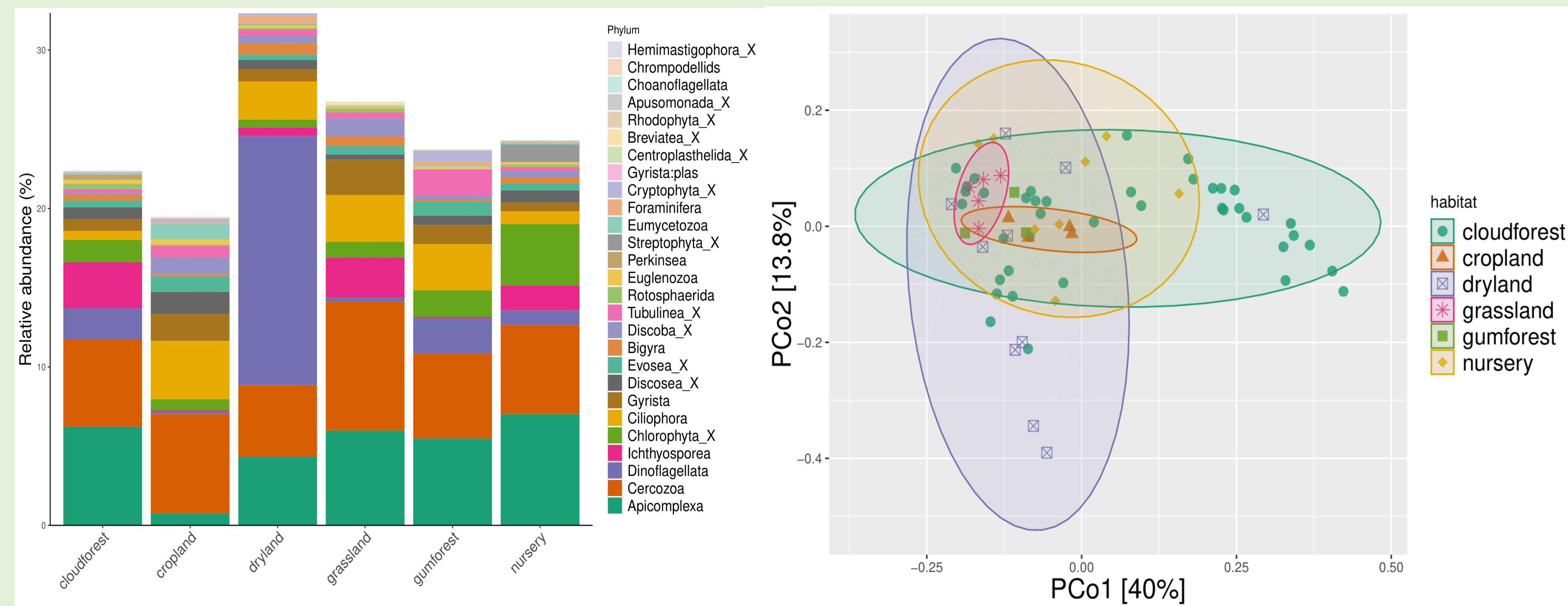
- 90 soil samples were collected from around different endemic and invasive plants in different habitats on the island.
- Marker genes used for Illumina sequencing were 16S rRNA gene V4 region for prokaryotes, 18S rRNA gene V9 region for protists and internal transcribed spacer 1 (ITS1) for fungi.
- Data were processed in QIIME 2 and R package *microeco* to determine relative abundances and α - and β -diversity.



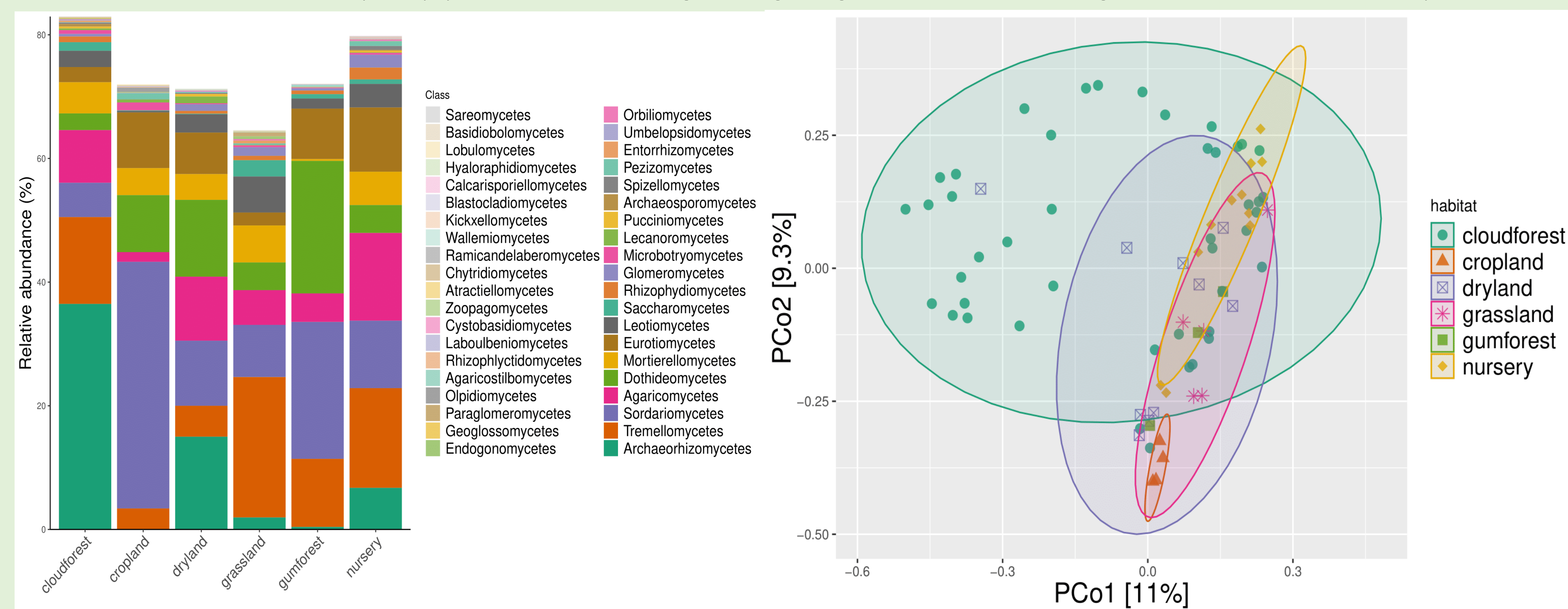
Left: Relative abundances of prokaryotic phyla detected with 16S rRNA gene V4 region. Right: First two PCoA axes of weighted UniFrac distances between samples.

Results and Discussion

- Habitat type explained community structure better than location or dominant plant species. Communities of cloud forest, plant nursery and grassland soils overlapped significantly. Cropland samples had strong overlap with dryland ones, which overlapped with the former three differently depending on microbe group.
- Dinoflagellates were present across sample types and dominated drylands. Although dinoflagellates have recently been detected in soil³, they have never been described.
- Ichthyosporean protists from a genus parasitic on anurans were detected in high abundance in areas where frogs were found, corroborating findings that soils can have significant parasitic protist load⁴.
- Cloud forest soils were very abundant in Archaeorhizomycetes, a recently described ascomycete class of unclear ecological function. This is their first detection in the Southern Hemisphere.
- Forests of St Helena gumwood were unusually rich in Dothideomycetes and poor in basidiomycetes, corroborating previous findings². This may be due to less recalcitrant organic matter in mid altitude soils.
- Croplands had a very high abundance of Sordariomycetes. Lower taxonomic resolution will be examined to determine ecological significance.



Left: Relative abundances of protist phyla detected with 18S rRNA gene V9 region. Right: First two PCoA axes of weighted UniFrac distances between samples.



Left: Relative abundances of fungal classes detected with ITS1 region. Right: First two PCoA axes of Bray-Curtis distances between samples.

Conclusions and Future Directions

- The cloud forest of the St Helena Peaks has a distinct microbiome which likely plays a significant role in the provision of ecosystem services. Functional annotation may help determine this more precisely. Abundant presence of certain taxa in particular sample groups presents questions regarding the drivers and functions of this specificity.
- Soil physicochemical data (pending) could help better disentangle the drivers of microbial community structure. Analysis at lower taxonomic level could reveal abundant taxa of particular interest.

References

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