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Abstract

- This study presents a comparison of taxonomical and functional profiles in degraded grassland and its converted mango plantation based on metagenomic sequencing, and quantified changes in soil properties like pH, organic carbon, total nitrogen and phosphorus, available phosphorus as well as CO₂ efflux during LUC.
- a diversity of soil bacterial community decreased after LUC, and the OTUs belonging to Actinobacteria, Bacteroidetes and Proteobacteria showed clear enrichment after LUC, yet the OTUs with wide range of low-abundance phyla generally depleted. soil water content was the best predictor of change in bacterial community composition, explaining 47.6% and 30.3% of the variation before and after LUC, respectively. Regarding adaptation to the environment post-LUC, dominant microbial species were enriched in large numbers, but communities that belonging to lower-abundance phyla were depleted. Clusters of orthologous group categories that involved in translation, ribosomal structure, nucleotide transport, coenzyme transport, cell motility, cell cycle control as well as cell division and chromosome partitioning were significantly higher after LUC in both dry and wet seasons. Proportion of key functional genes in tricarboxylic acid cycle increased significantly (especially for major CO₂ production process).
- Our study suggested that LUC in the dry-hot valley reshaped the bacteria community, altered the proportion of COG functional categories of soil microbes and accelerated microbial respiratory metabolism and CO₂ efflux. These effects largely resulted from changes in the soil microenvironment (especially water content).

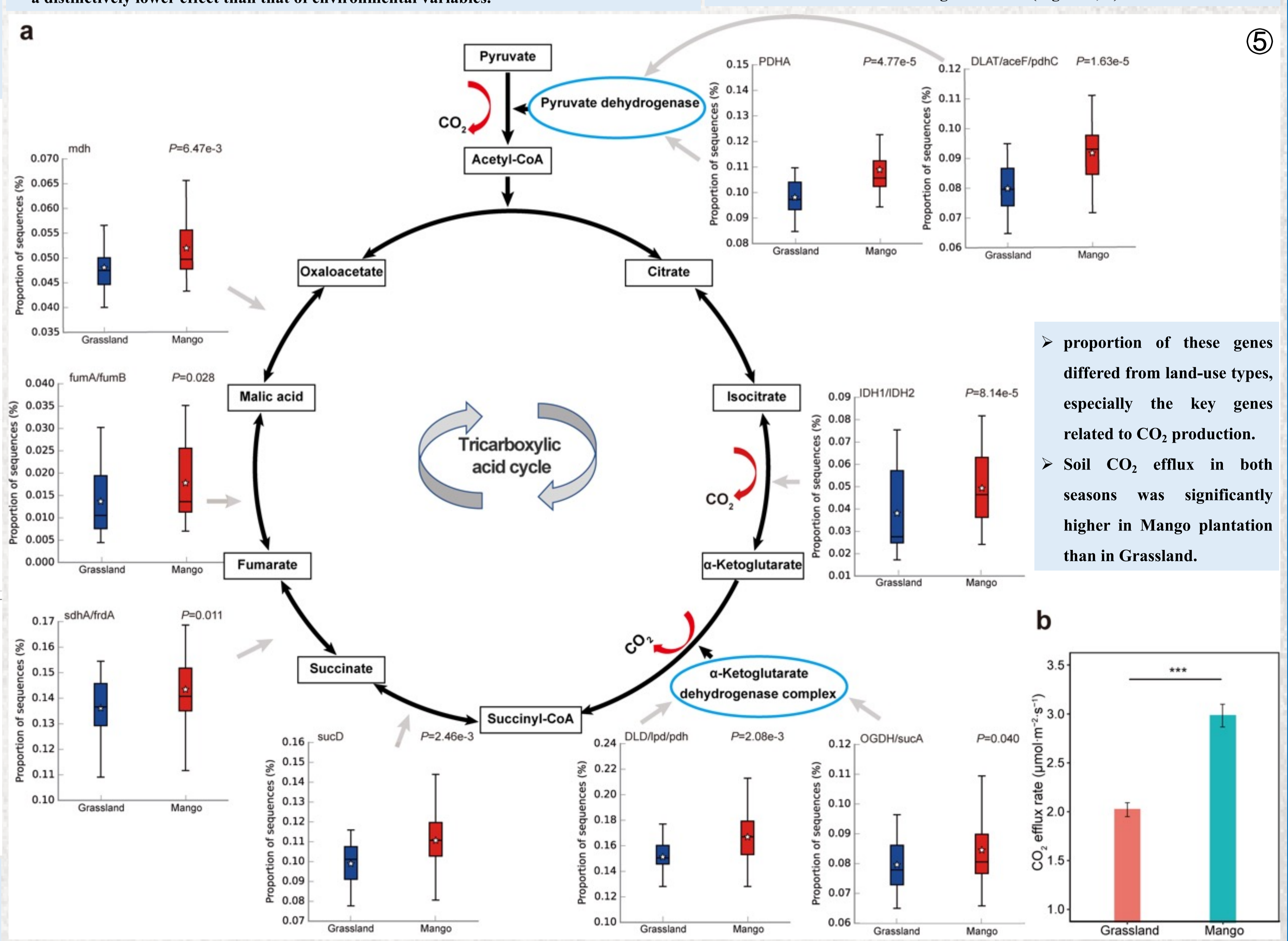
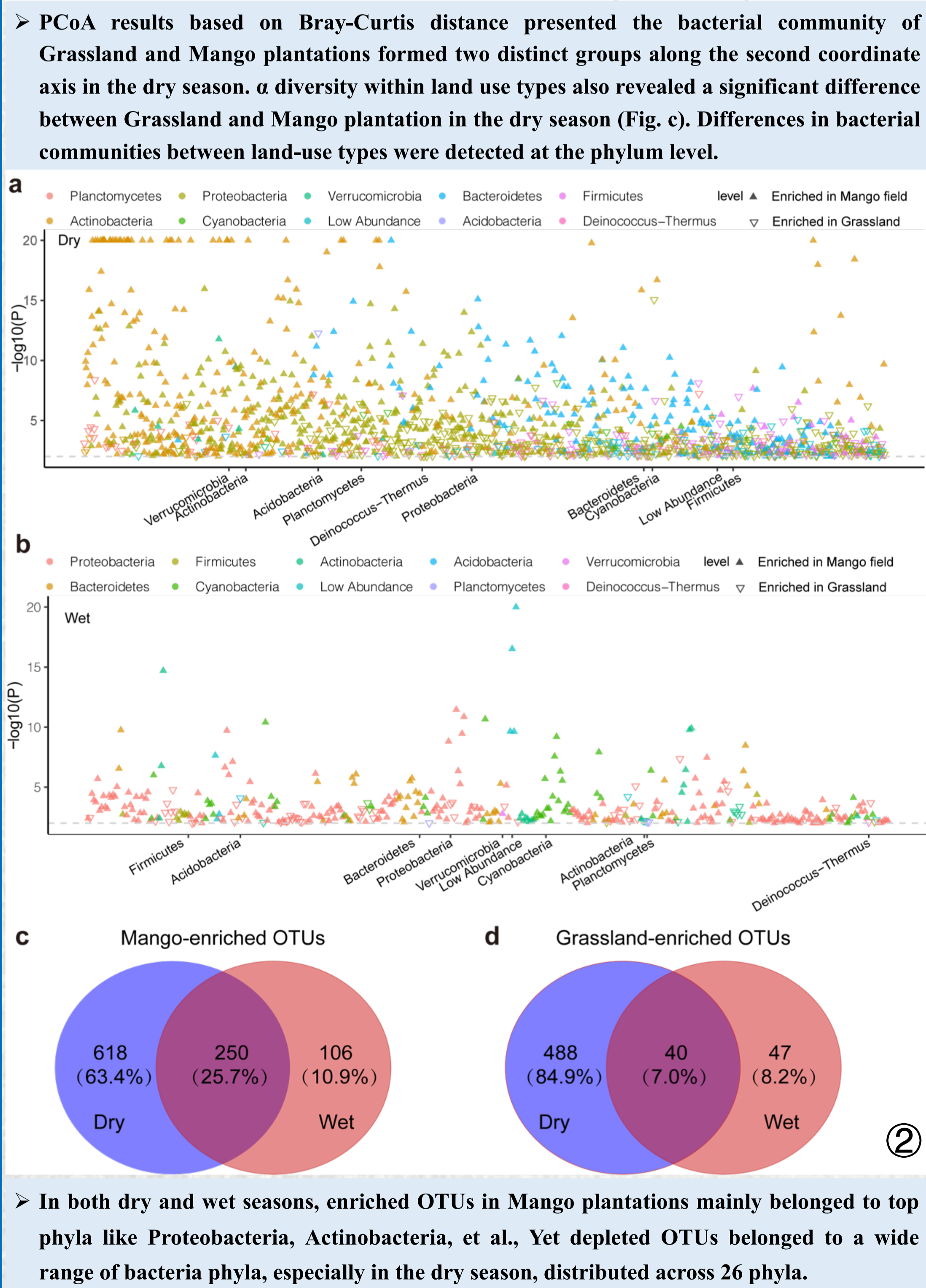
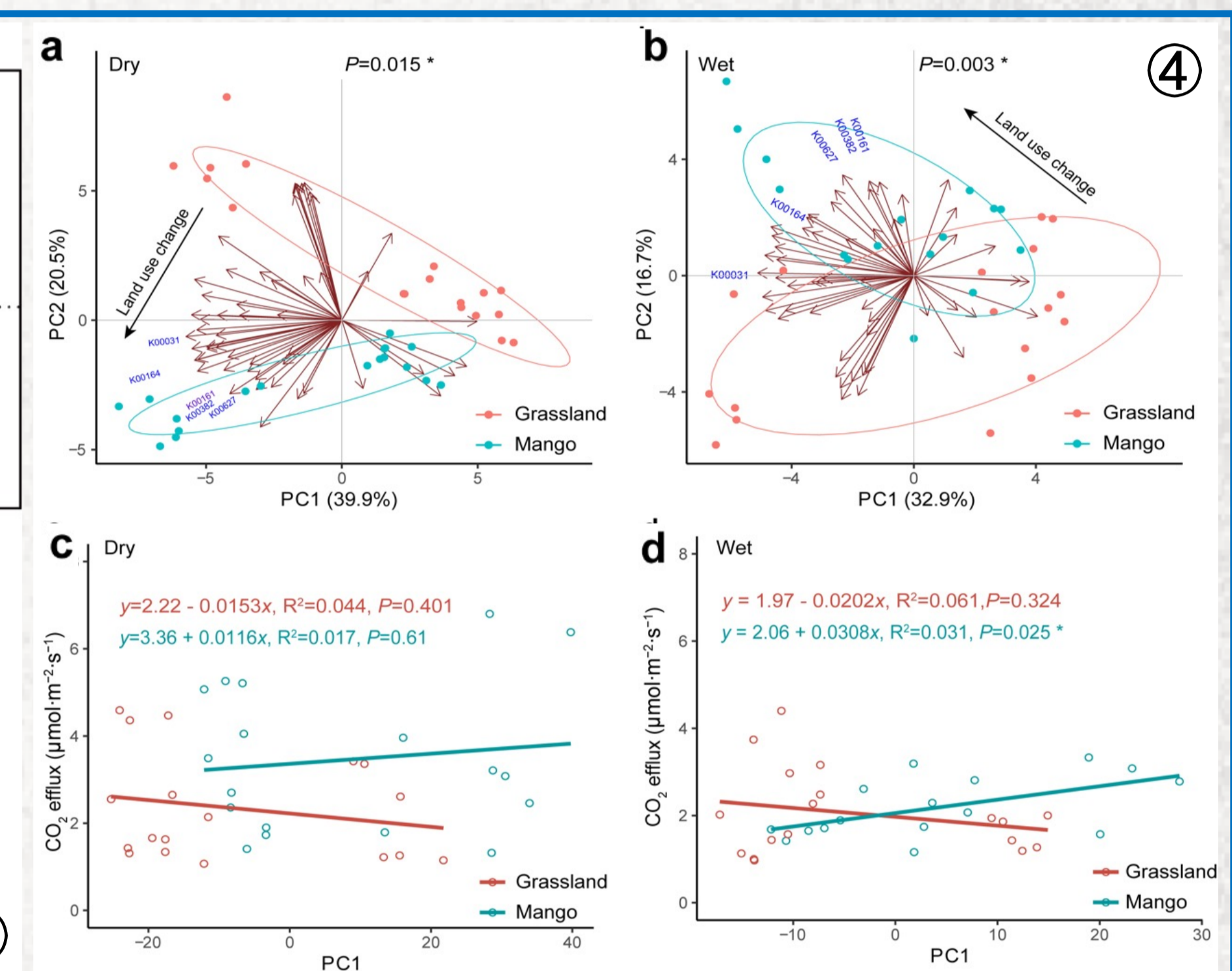
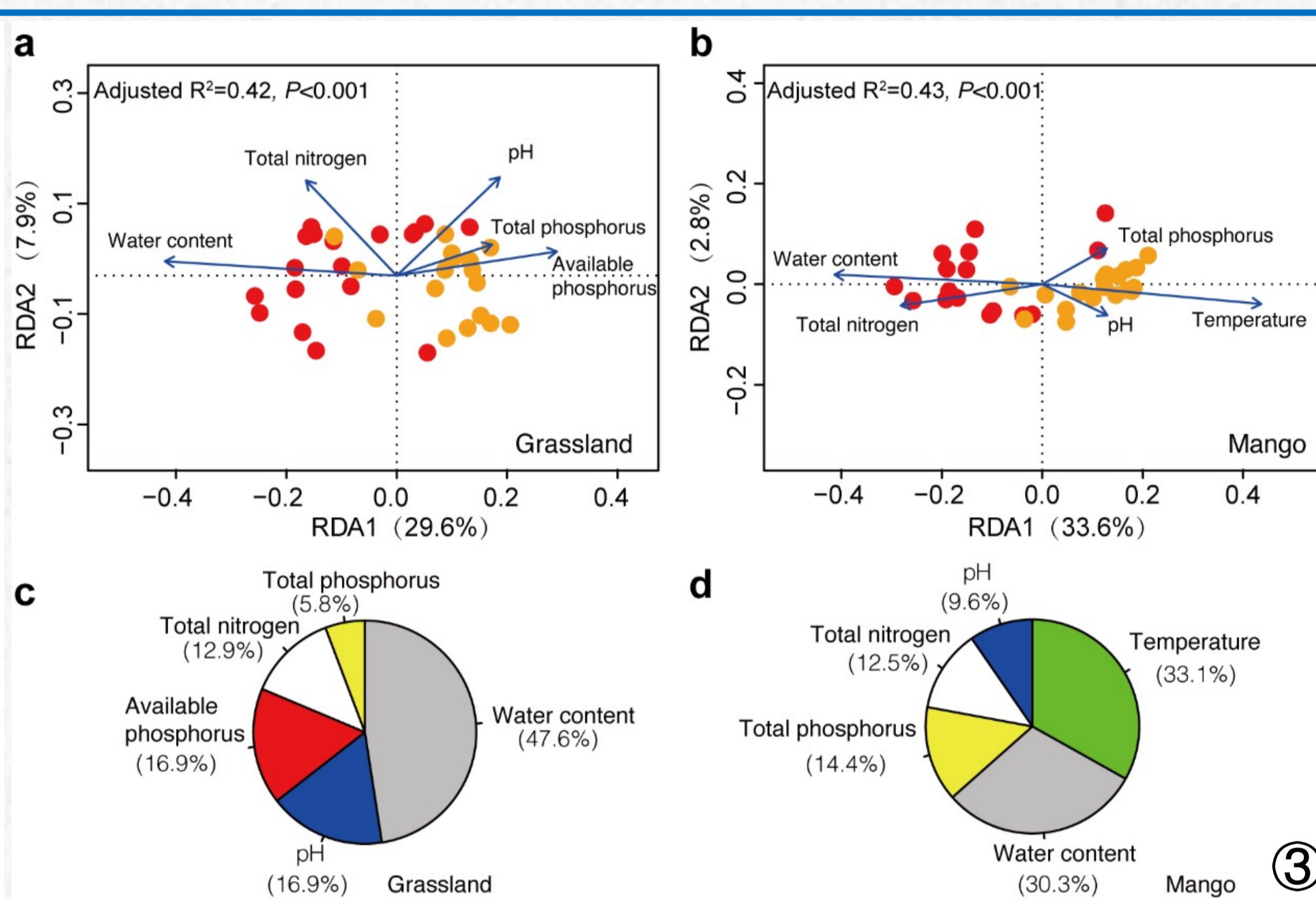
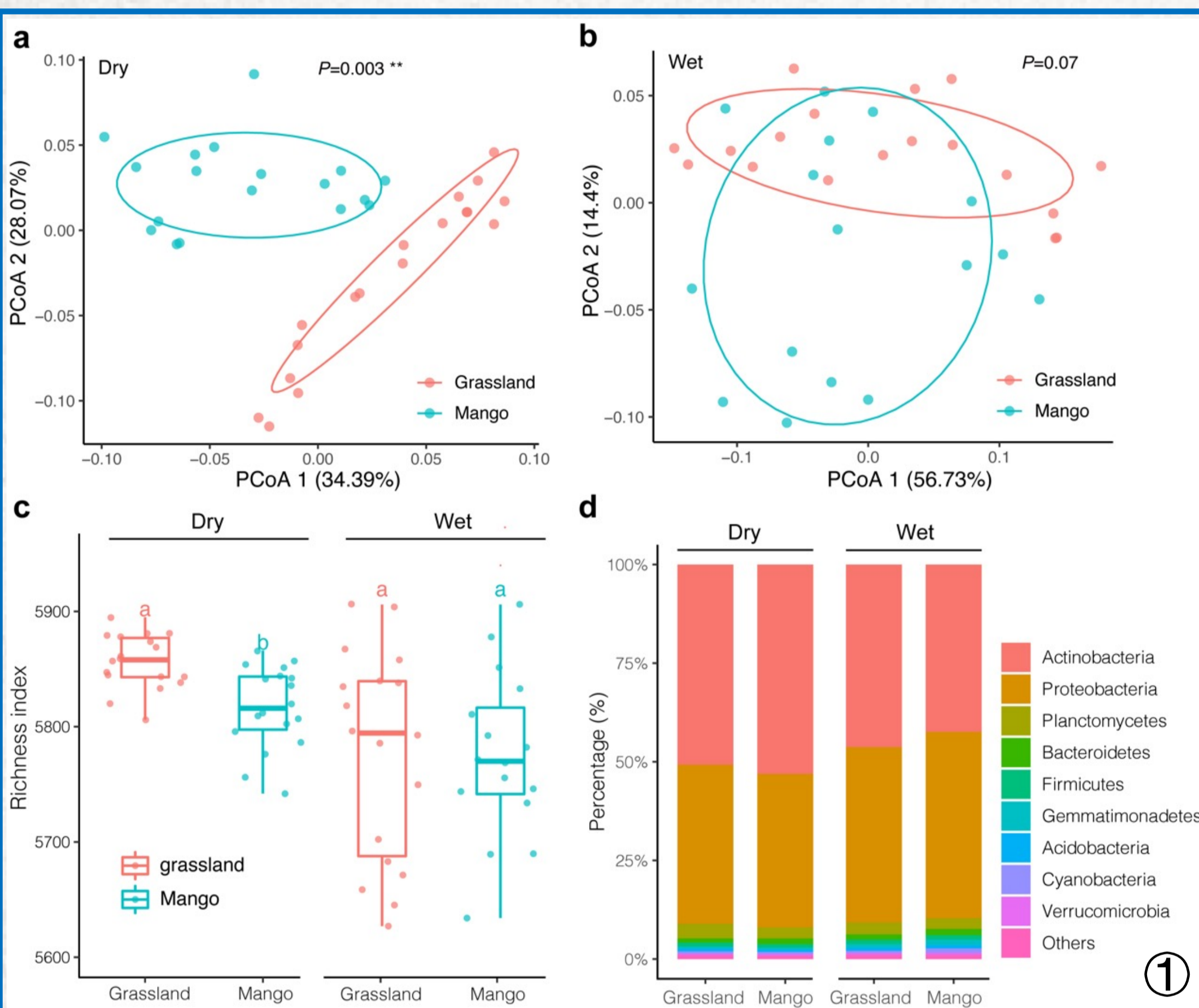
Introduction

- land-use change (LUC) has become the second-largest source of anthropogenic greenhouse gases (GHG), second only to fossil fuel combustion.
- CO₂ emissions during LUC are difficult to assess because of differences in spatial, temporal, and regional land management measures as well as differences in soil properties between ecosystems. There is now growing recognition of the vital links between microbial and global C cycle fluxes and the stabilization of soil organic carbon.
- In view of soil heterogeneity in terrestrial ecosystems, like physicochemical properties and microclimate, the ways in which these specific conditions change during LUC in dry-hot valleys and corresponding effects on soil bacteria communities and CO₂ efflux remain unclear.

Methods

- Degraded grassland and new mango plantation transformed from degraded grassland in 2017 were chose to conduct a comparative study of LUC in the dry-hot valley.
- For each land use type, three 20 m × 20 m plots were respectively selected. Five polyvinylchloride collars were installed in each plot. Soil sampling at a depth of 0 – 10cm was conducted twice during the wet season and twice during dry season from each plot.
- CO₂ efflux rate was measured using LI-COR 8100, as well as the soil temperature and volumetric water content at a depth of 10 cm.

Results



Conclusion

- Large number of microbial species in dominant phyla were enriched and wide-ranging and low-abundance phyla were depleted after LUC.
- Effects of LUC on the composition of bacterial communities were realized mainly through changing the soil water content rather than soil chemical properties. Partial bias in the metabolic functional categories of microbial communities, which may be cause by the growth/death and regeneration of large microbial communities.
- Distinct intensification of respiration characteristics of microbes after LUC is the evidence for the significant increase in CO₂ efflux.
- Informed land management practices are necessary to promote microbial carbon assimilation and increase carbon sequestration for the mitigation of carbon emissions resulting from LUC.

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