

Metagenomic Insights into Microbial Resilience in Monsoon-Driven Arid Ecosystems

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Introduction

- Dryland ecosystems, covering approximately 41.5% of the Earth's terrestrial surface [1], are characterized by extreme conditions including high temperatures, intense UV exposure, and limited water and nutrient availability [2,3]
- Microbial adaptations to fluctuating resource availability in arid soils remain underexplored, with existing studies presenting contradictory findings on microbial responses [4, 5, 6].
- To address these knowledge gaps, our study applies a comprehensive multi-omics approach, integrating amplicon sequencing, metagenomics, metatranscriptomics, and high-resolution organic matter profiling. This approach provides a holistic view of microbial community dynamics that was previously unattainable in natural settings.

Materials and Methods

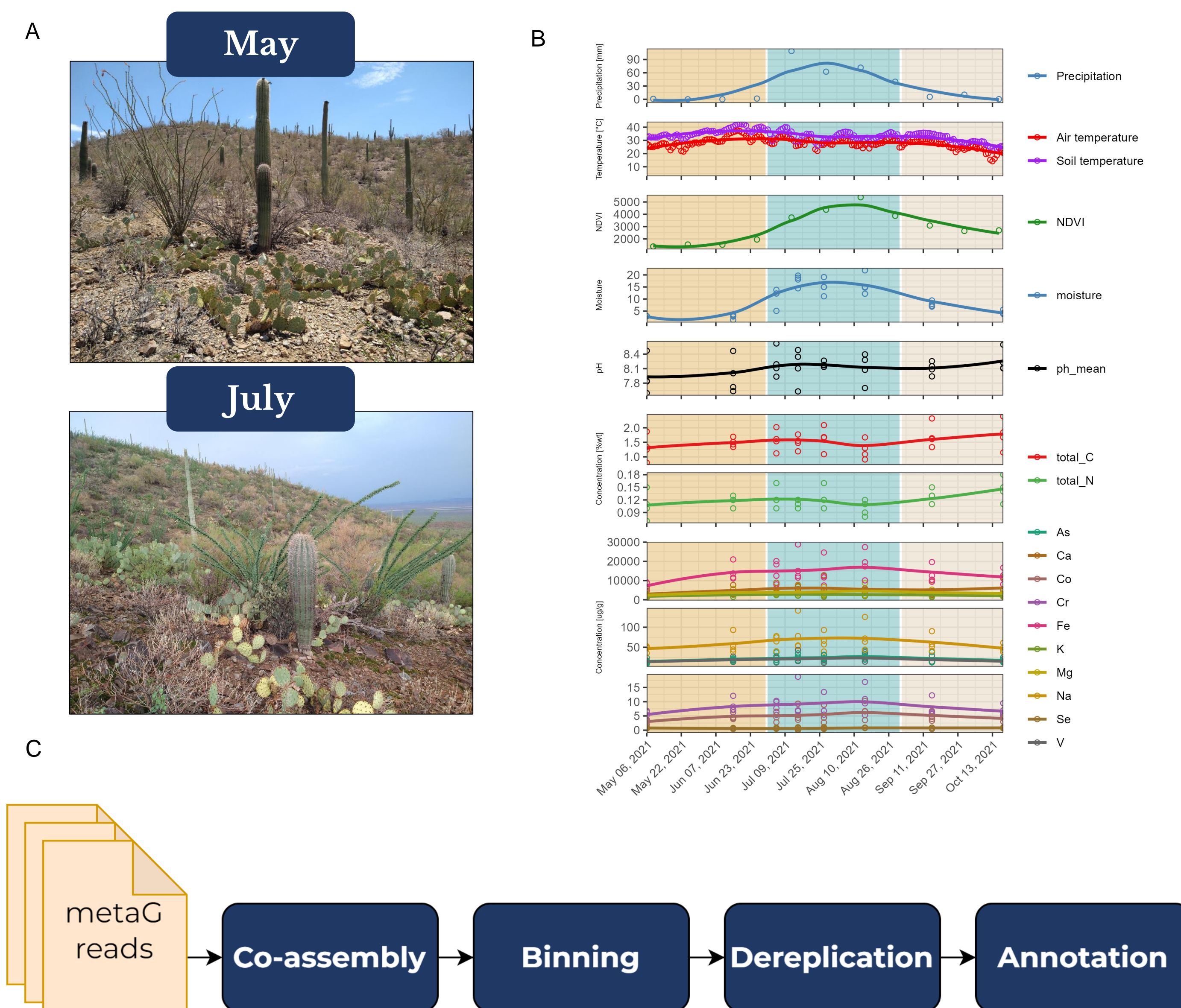


Figure 1. Soil samples were collected from Saguaro National Park at multiple time points during the 2021 North American monsoon season. (A) Photographs contrasting changes in vegetation due to monsoon rains. (B) Temporal dynamics of environmental and physicochemical factors throughout the 2021 monsoon season. (C) Simplified metagenomics workflow.

Results

- Despite subtle changes in microbial and organic matter composition during precipitation events, microbial communities remained relatively stable before and after the monsoon season. However, a decrease in diversity was observed in response to increased water availability and vegetation.

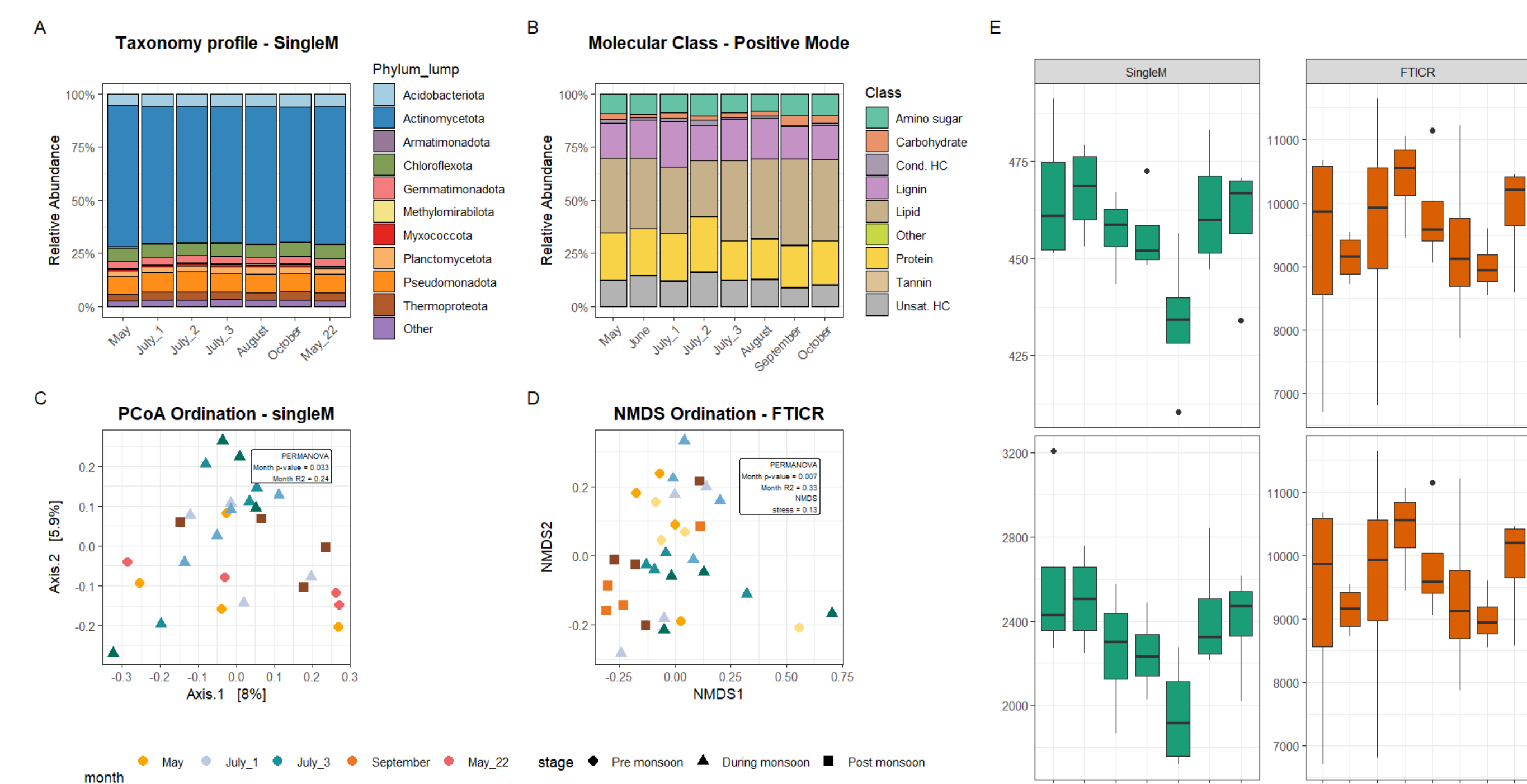


Figure 2. (A) Taxonomic profiling based on shotgun metagenomic data. (B) Organic matter profile based on FTICR-MS data. (C) Principal coordinate analysis (PCoA) of Bray-Curtis distances of SingleM inferred OUT. (D) Non-metric multidimensional scaling (NMDS) ordination of Bray-Curtis distances from FTICR-MS data. (E) Observed richness and Chao1 richness index from both datasets

- Analysis of the recovered MAGs implied that high GC content and oligotrophic strategies may be a common survival strategy in arid soils. Other widely distributed mechanisms included the production of chaperones to protect against denaturation and degradation of proteins as well as the production or transport of osmolytes.

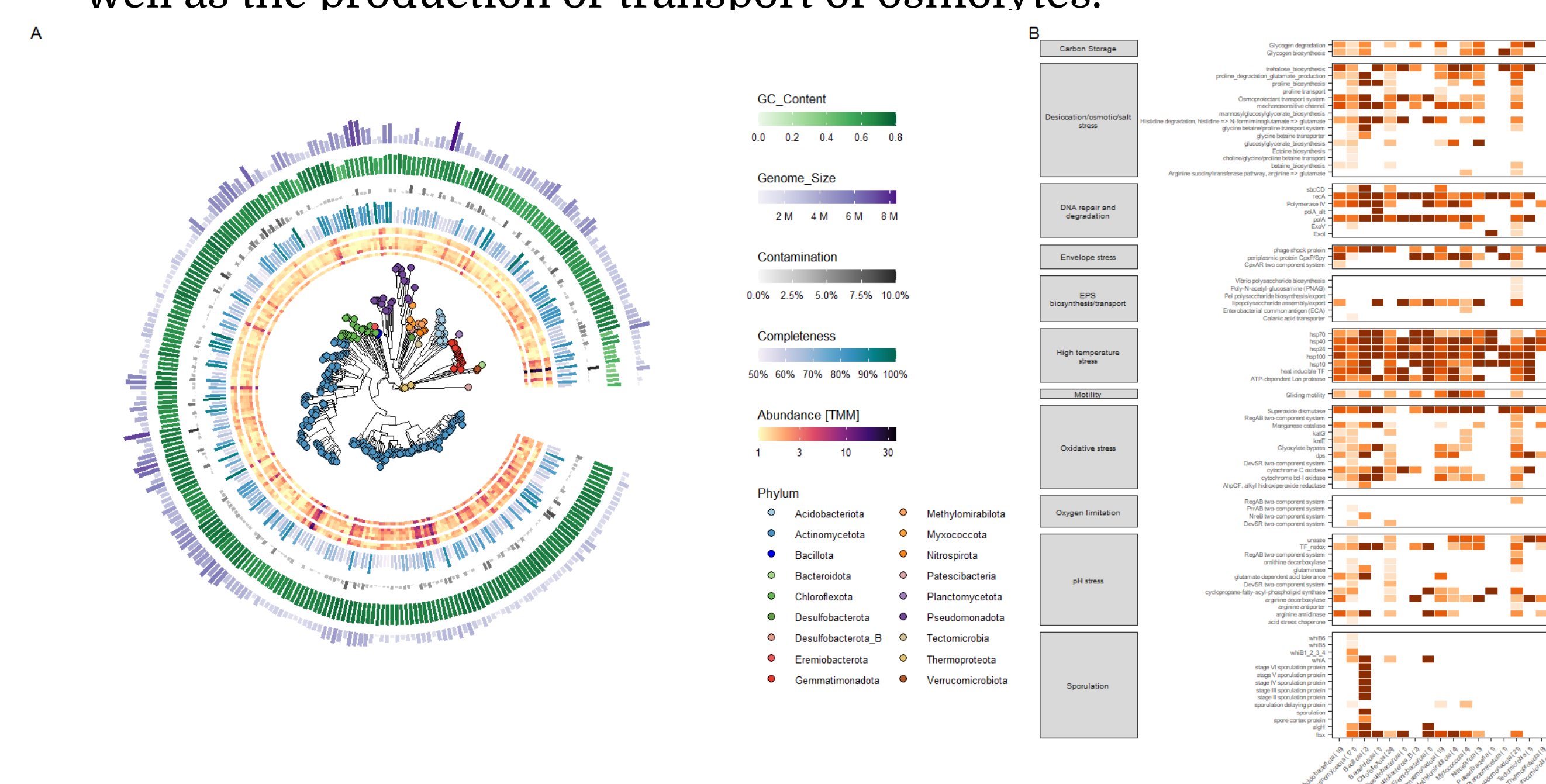


Figure 3. (A) Phylogenetic tree of the 282 recovered metagenome-assembled genomes (MAGs) showing their GC content, genome size, completeness and contamination inferred by CheckM2 as well as their changes in abundance throughout the sampling campaign. (B) Heatmap showing the presence of stress resistance traits among the different taxa of the recovered MAGs.

Results (Cont.)

- The increase in water availability appears to create a more tightly packed network, where fewer microbial organisms interact with one another (Figure 5A). These reduced interacting communities may consist of microbial species better adapted to sudden changes in water and nutrient availability caused by monsoon storms

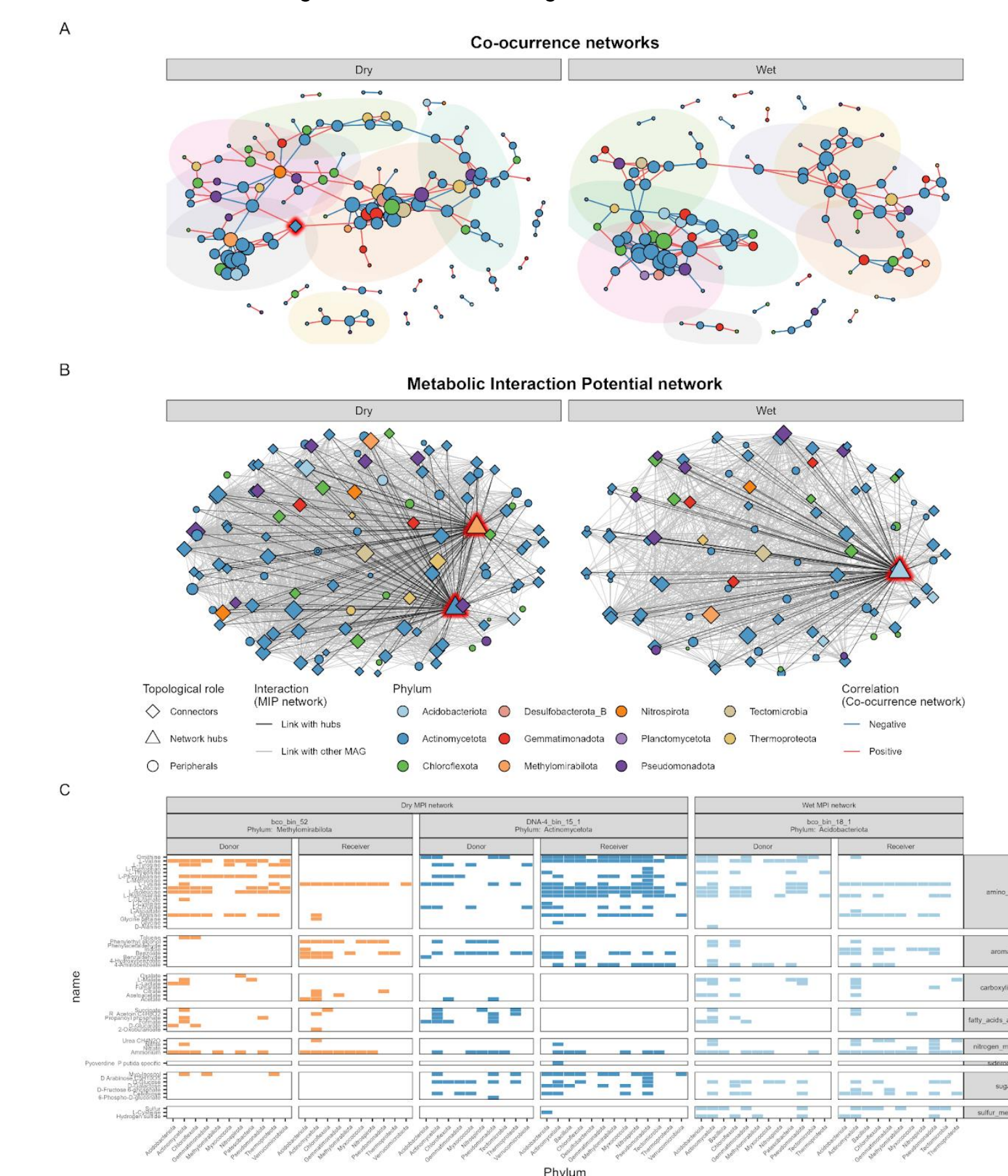


Figure 4. (A) Co-occurrence network based on MAGs abundances for the dry (May and October) and wet (July and August) months. Nodes represent MAGs and are colored based on their Phylum. Node size indicates the Degree (number of connections) of each node. (B) Social network based on the metabolic interaction potential (MIP) score calculated with SMETANA. Only genome pairs with MIP >= 5 were considered for the network.

- Among the recovered MAGs, Thermoproteota were found to encode genes for aerobic ammonia oxidation, a crucial step in the nitrogen cycle of arid lands. These genes were expressed consistently throughout the season, peaking during the dry months, which suggests that these microorganisms play a vital role in the survival of microbial communities during periods of low water availability

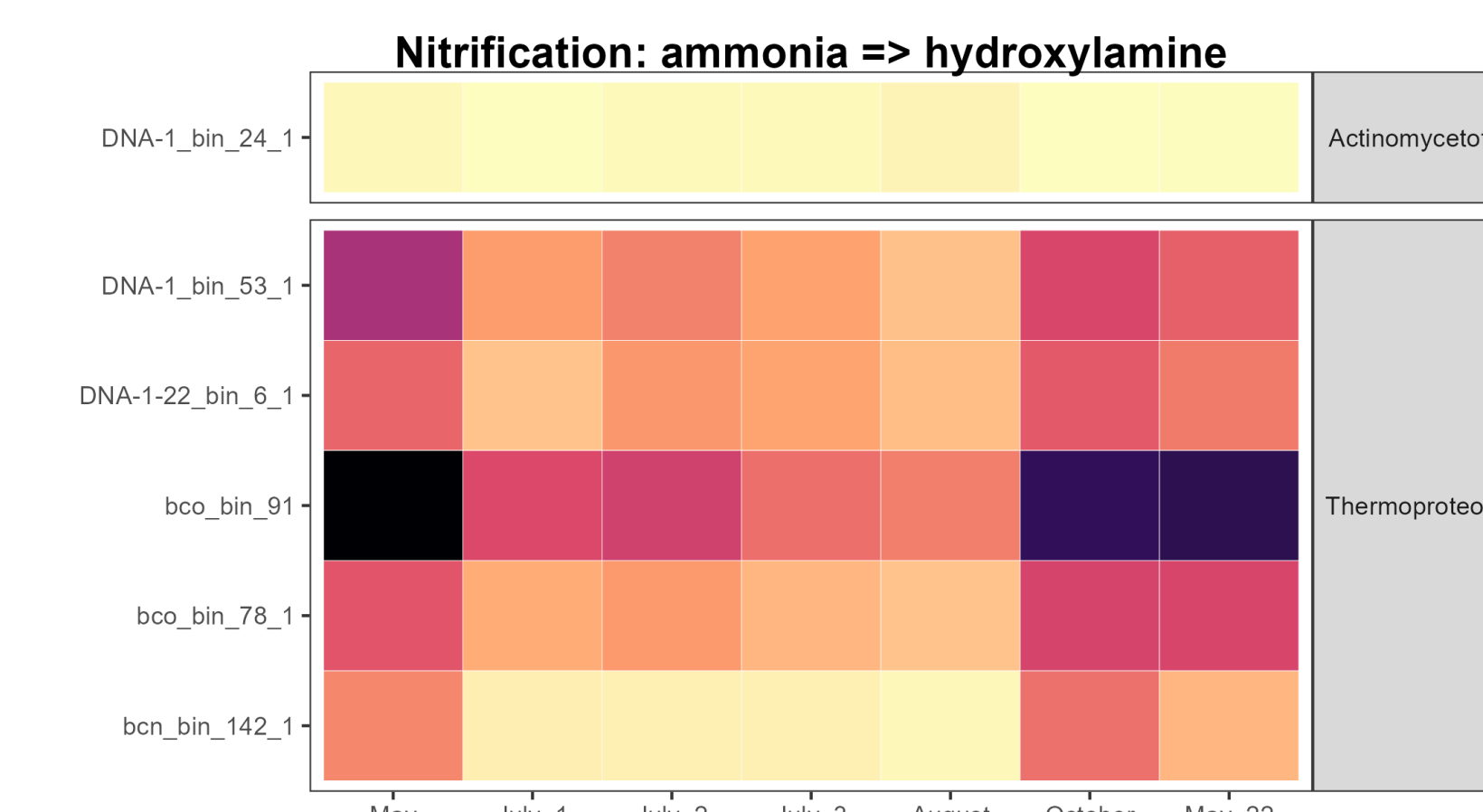


Figure 5. Normalized expression of genes involved in ammonia oxidation

Future Work

- Use metatranscriptomics to identify differentially expressed metabolic pathways and classify recovered MAGs based on their activity throughout the monsoon season.
- Long term monitoring of arid soil microbial communities to determine if there is a threshold beyond which adaptation is not possible leading to loss of diversity



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