

# Metagenomic for a better understanding of cultivated soil health

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## 1- Intro

- Soil's ability to support the growth of plants, animals, and humans is highly dependent on the microorganisms living in it, due to their role in biochemical cycles involved in the recycling and availability of nutrients such as carbon (C), nitrogen (N), and phosphorus (P). Here, we present the impact of using mulch and reduced tillage on the composition of the soil microbiome.

## 2- Methods

### Sampling:

- May and August;
- 3 samples at 0-12 cm using a Dutch auger;

- 1 composite sample/plot.

### Sequencing and Annotation:

- Metagenomic shotgun (AVITI);
- Kraken2 (taxprofiler).

### Cultures:

- 2023: Green beans Messi;
- 2024: Broccoli.

### Treatments (4 repetitions):

- SN : Naked soil (till);
- PPE: Switchgrass mulch (no-till);
- PF: Willow forest mulch (no-till);
- PS: Rye mulch (no-till);
- PV: Living mulch of festulolium and white clover (no-till).

## 3- Results

- Willow mulch negatively impacted the Mycobiome's alpha diversity in 2024 compared to all other treatments.

### Fungi Alpha Diversity Shannon by Sampling Date

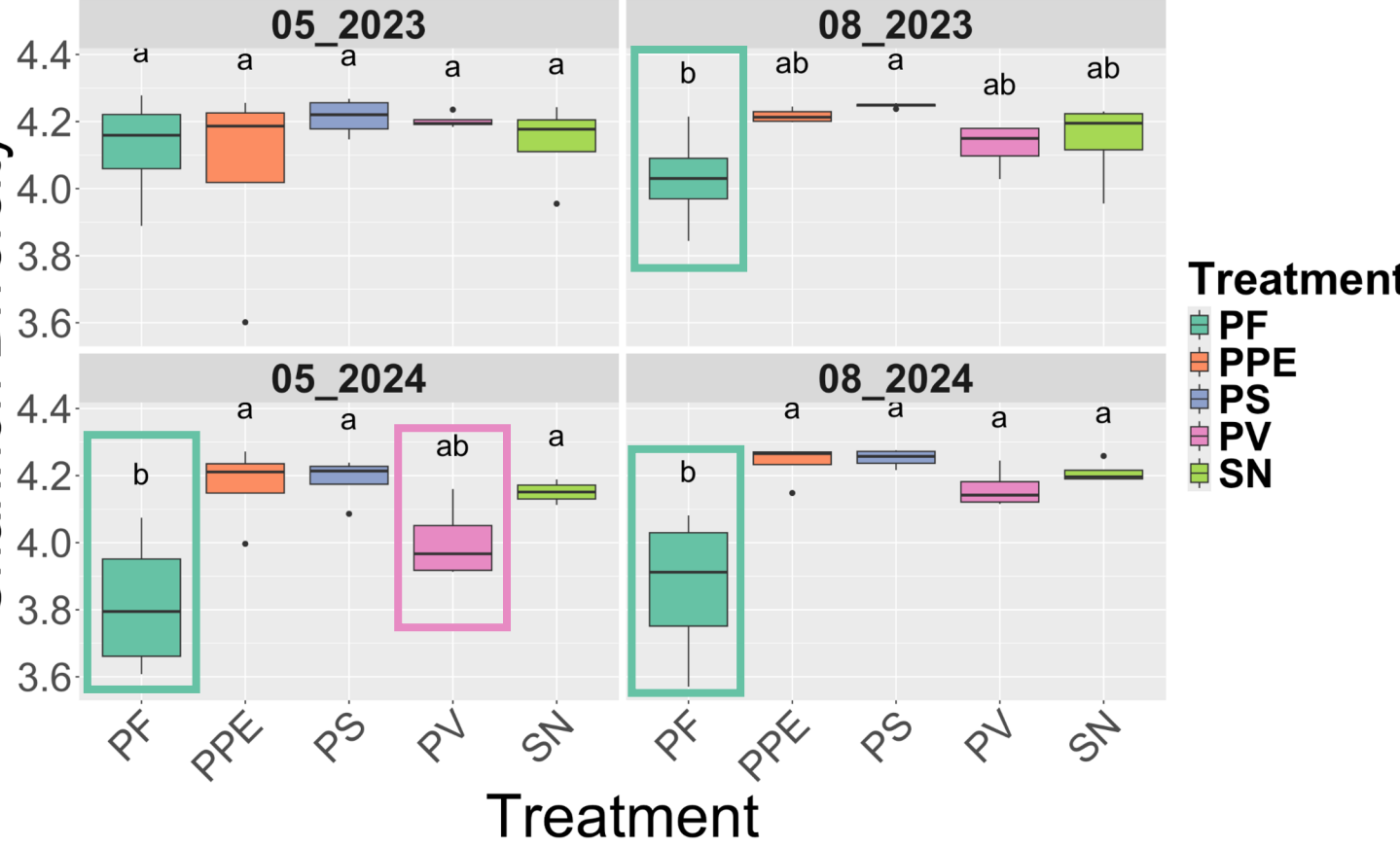


Figure 2: Fungi alpha diversity value by sampling date.



# The use of Mulch affects the Composition of cultivated soil's Mycobiome.

## Spatial and Temporal Impact of Mulch on Soil's Microbiome

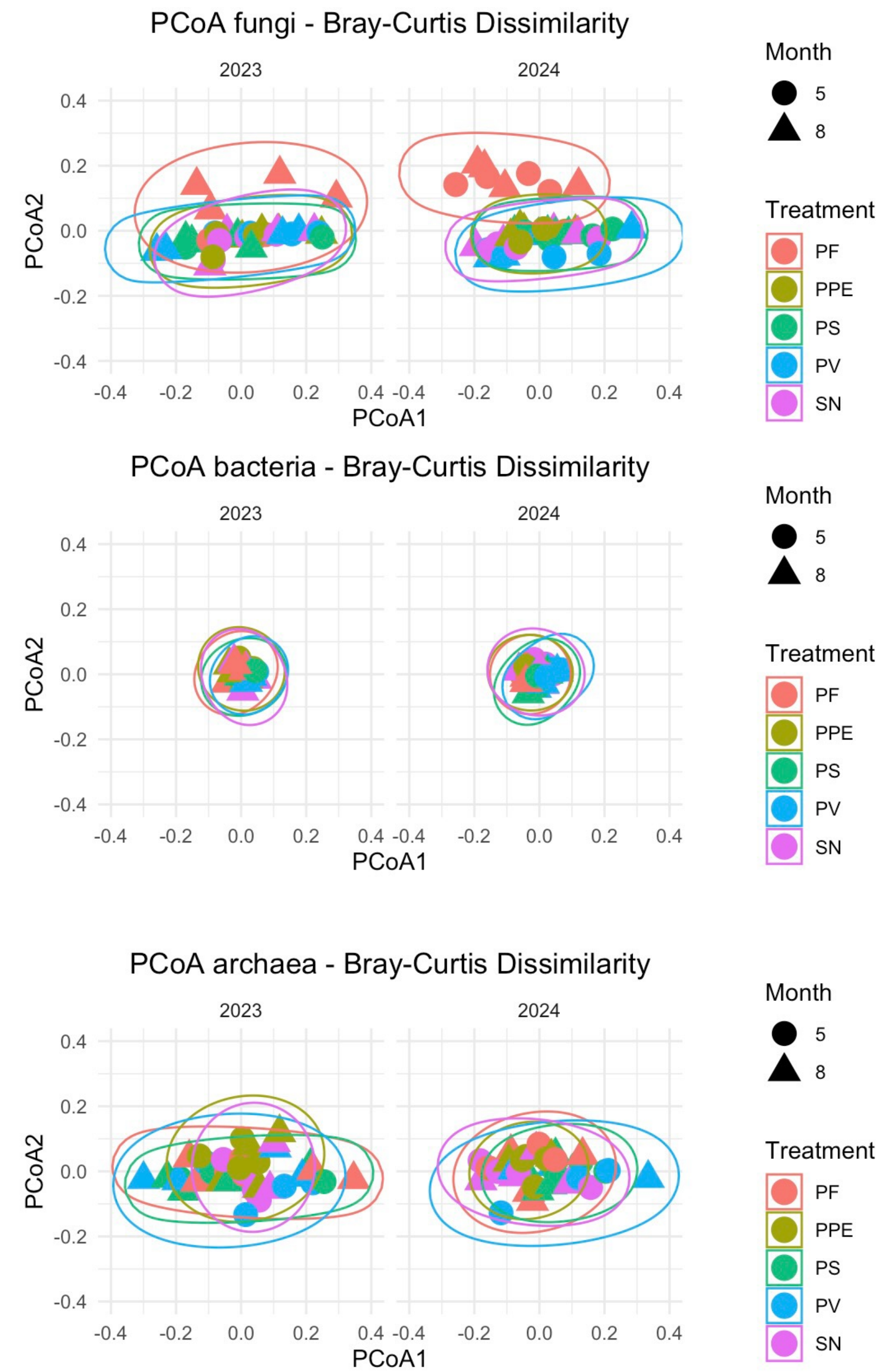


Figure 1: Spatial and Temporal Impact of Mulch on Soil's Microbiome. Treatment: SN : Naked soil (till); PPE: Switchgrass mulch (no-till); PF: Willow forest mulch (no-till); PS: Rye mulch (no-till); PV: Living mulch of festulolium and white clover (no-till). Month: 5: May; 8: August.

The Mycobiome composition seems to be particularly sensible to the use of Willow mulch. We started to observed a shift from the other treatment starting in august of 2023 (Fig. 1)

The Bacteriome spatial and temporal variation aren't affected by mulch (Fig. 1).

The spatial and temporal variation of the Archaeome composition show a pattern indicating a possible effect of mulch without being significant (Fig. 1).



Abstract

## 4- Results (cont...)

- Bacteriome compositions is not significantly affected by mulch in term of beta diversity (Fig. 1), but we observed a significant variation in the alpha diversity in 2024 when comparing per years (Fig. 3) but not by sampling date.

### Bacteria Alpha Diversity Shannon by Sampling Date

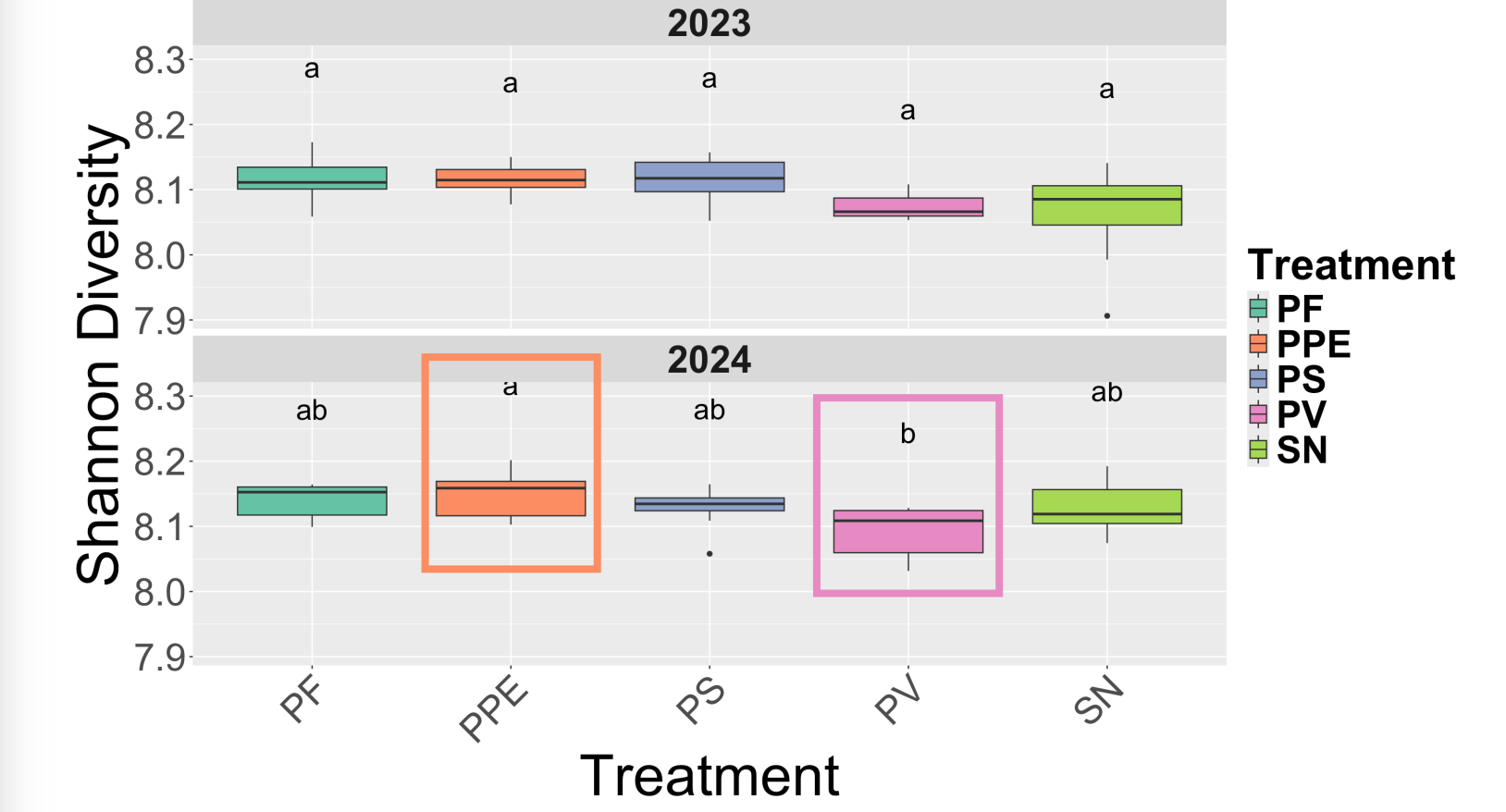


Figure 3: Bacteria alpha diversity value by years.

- The pattern observed with the spatial and temporal variation of archaeome species can be observe with the alpha diversity measurement without being significant (Fig. 4).

### Archaea Alpha Diversity Shannon by Sampling Date

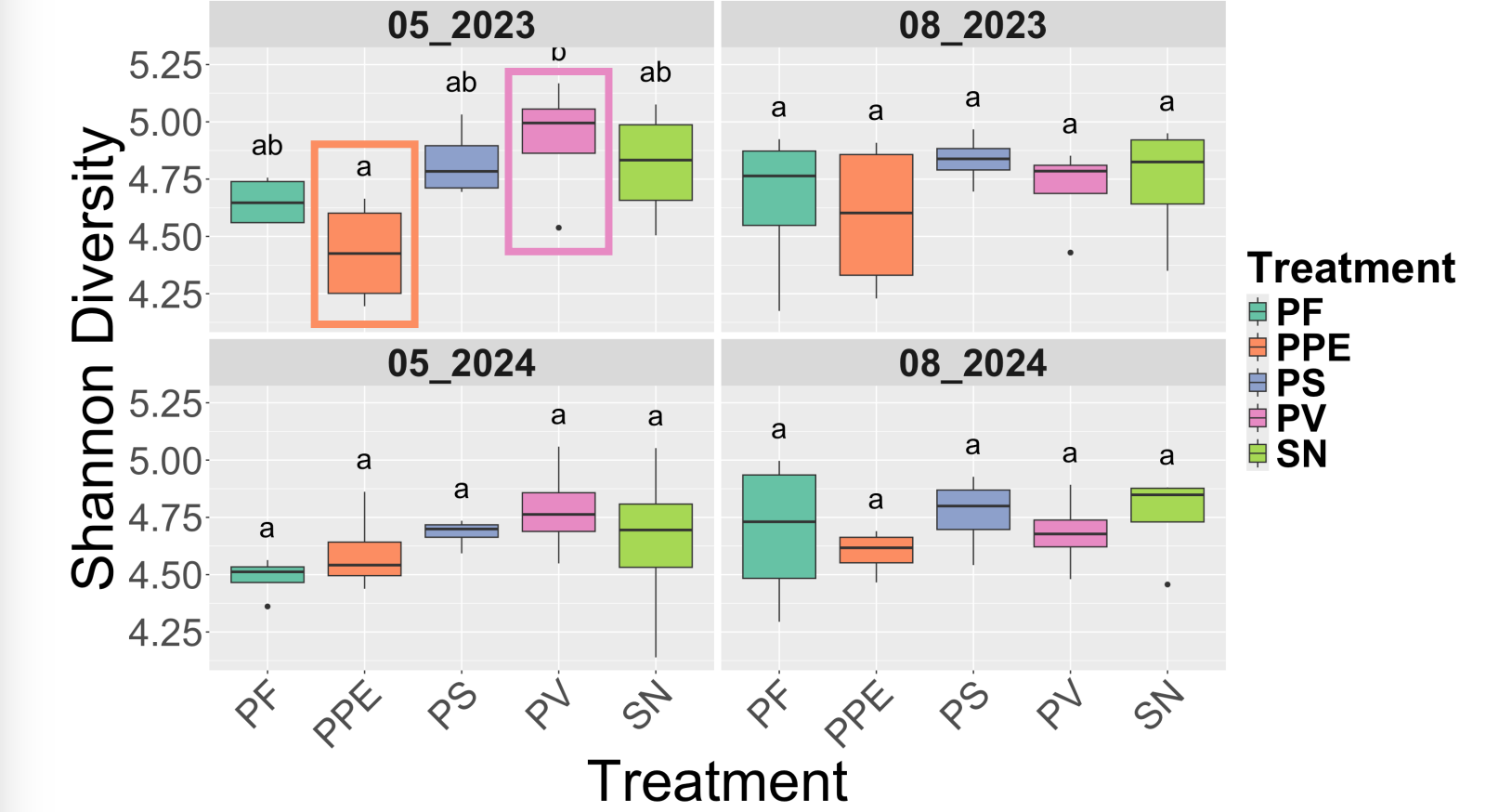


Figure 4: Archaea alpha diversity value by sampling date.

## 5- Discussion

- Initially, mulching did not appear to alter bacteriome composition; however, emerging differences in alpha-diversity observed in 2024 (Fig. 3) suggest that a longer monitoring period may be needed to capture a more substantial shift in community structure.

- We will also perform functional annotation of genes governing key steps in the nitrogen, phosphorus, and carbon biogeochemical cycles to clarify how mulching shapes soil-microbiome functions and strengthens soil resilience.

- The impact of the Willow mulch on the composition of the mycobiome could be due to the increase in hemicellulose and lignin. This question will be answered with the functional annotation.



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