

Using bioinformatic predictions to identify key bacterial strains for bioremediation of wildfire affected soils

Sandra E. Rivas Morales, Gabriel Ruiz Ayma, Alina Olalla Kerstupp, José Ignacio González Rojas, Antonio Guzmán Velasco, Antonio Leija Tristan, Miguel Angel Lopez Alvarez, **Mayra A. Gómez Govea***.

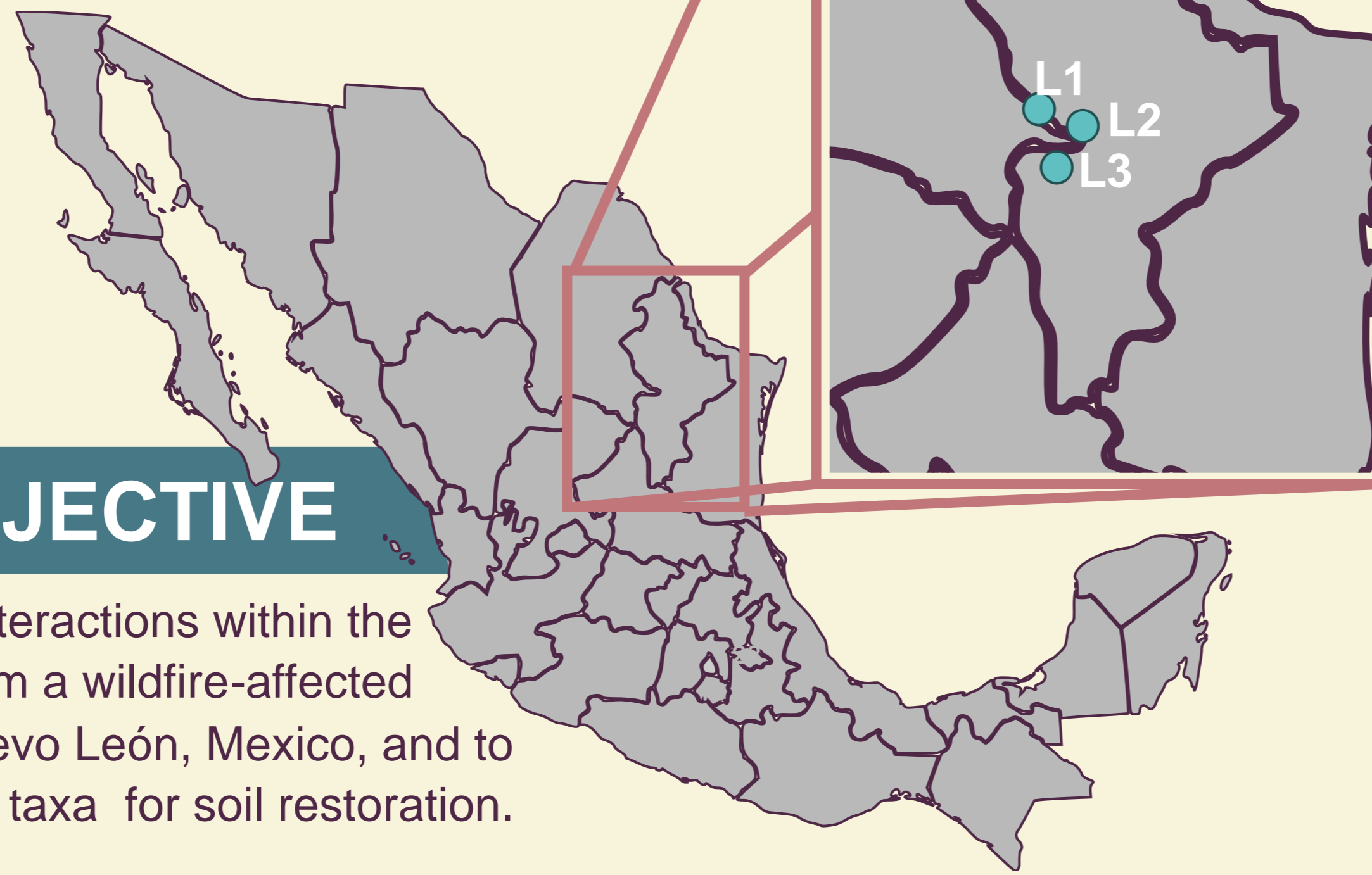
Laboratory of Conservation Biology and Sustainable Development, Faculty of Biological Sciences, Universidad Autónoma de Nuevo León.
mayra.gomezgv@uanl.edu.mx rivasel.m@gmail.com

INTRODUCTION

Current soil restoration methods are limited, and changes in soil biodiversity can have irreversible effects (2).

Therefore, integrating microbiome management into bioremediation is essential, but understanding microbiome interactions is crucial for successful applications.

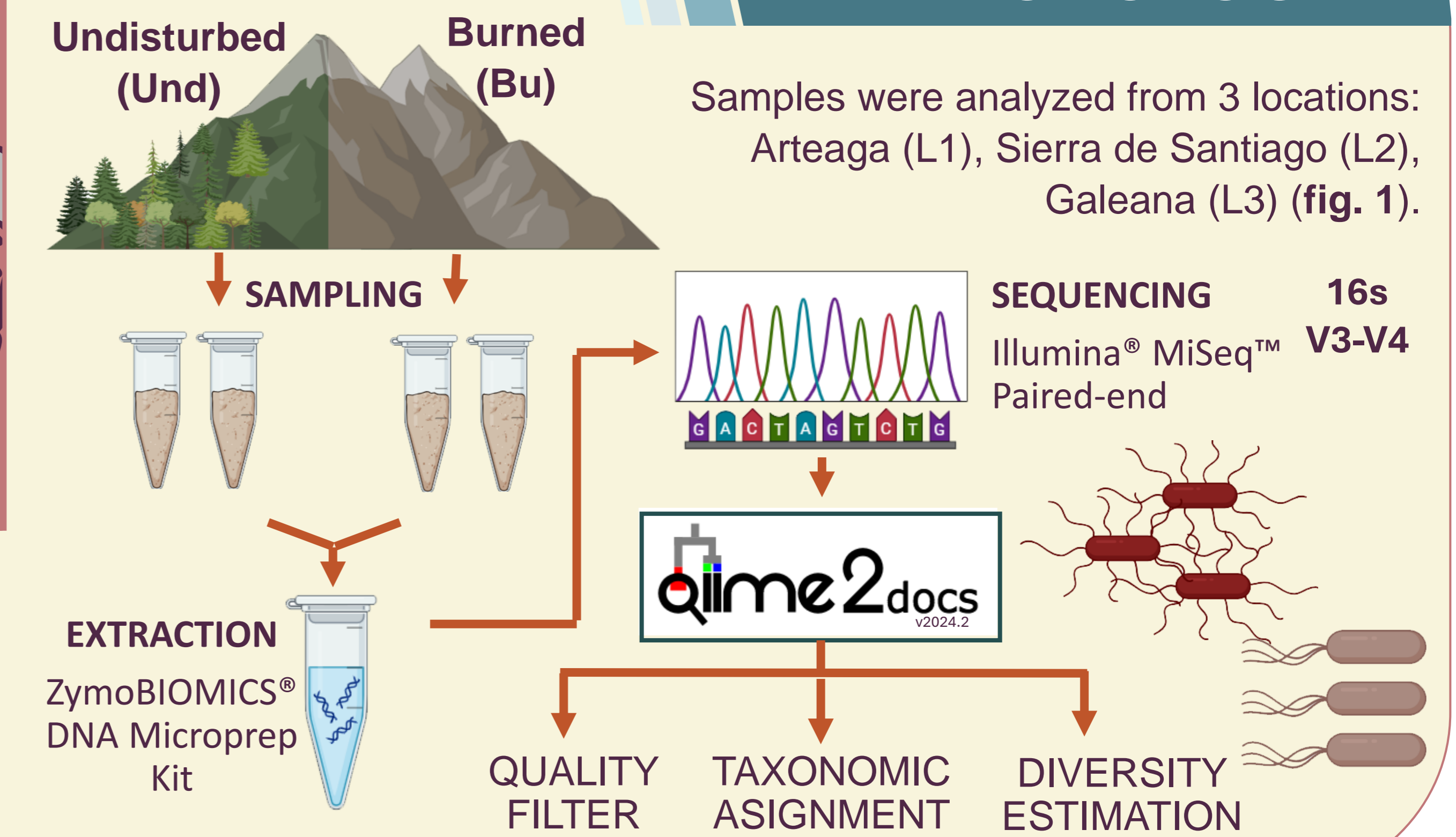
Wildfires impact ecosystem diversity, including microbial communities (1).



OBJECTIVE

The study aims to dissect interactions within the soil microbial community from a wildfire-affected forest area in southern Nuevo León, Mexico, and to select important taxa for soil restoration.

Figure 1. Selected locations for sampling



METHODOLOGY

Samples were analyzed from 3 locations: Artega (L1), Sierra de Santiago (L2), Galeana (L3) (fig. 1).

SEQUENCING 16s
Illumina® MiSeq™ V3-V4
Paired-end

QUALITY FILTER TAXONOMIC ASSIGNMENT DIVERSITY ESTIMATION

RESULTS & DISCUSSION

Physicochemical analysis showed no pattern responding to Bu or Und conditions. Most soils were classified as sandy clay loam and sandy loam, and the values of pH had little fluctuation across locations and samples (fig. 2).

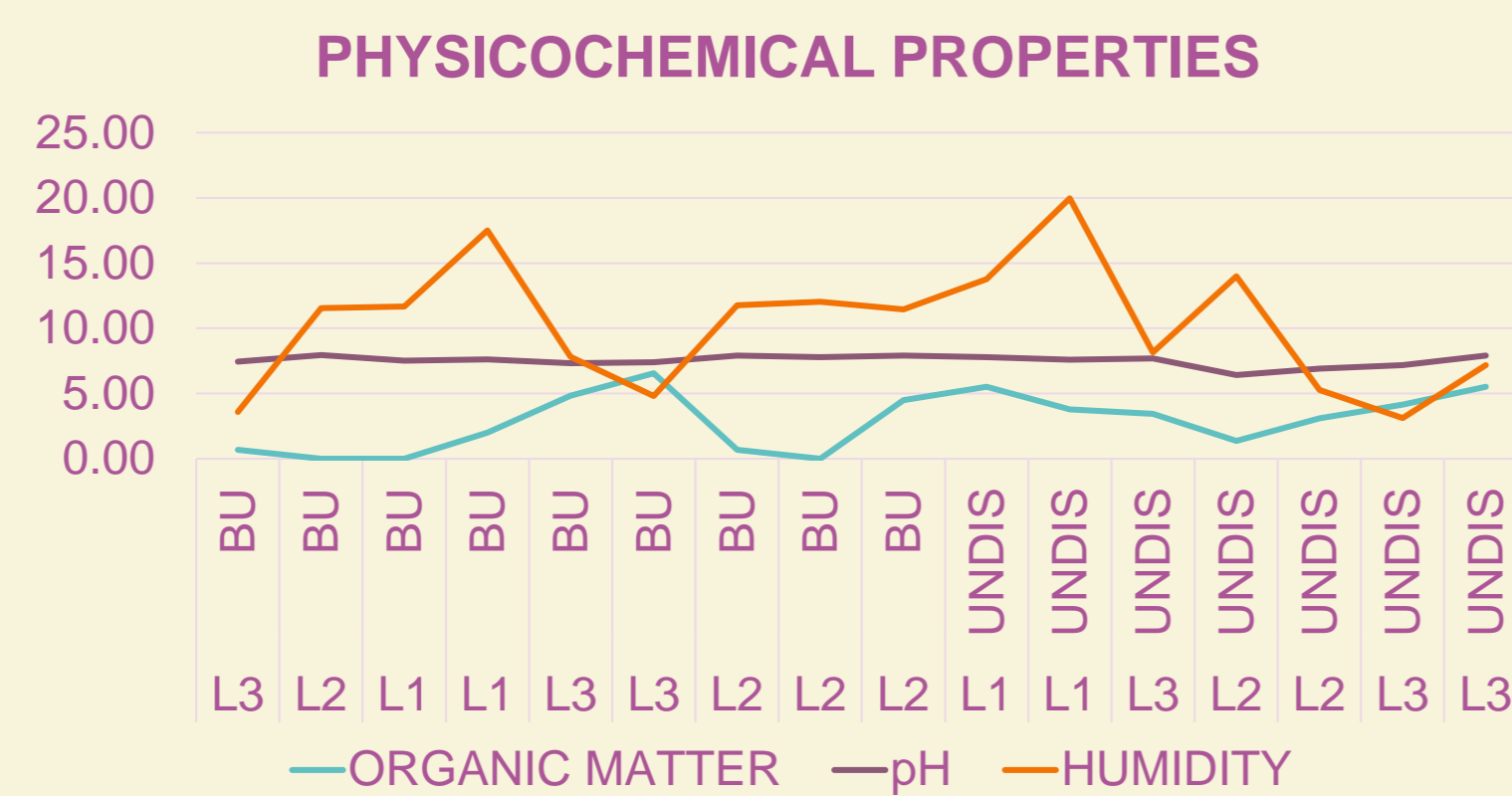


Figure 2. Visual comparison of the physicochemical parameters evaluated in each soil sample.

The similarity among physicochemical parameters or the lack of defined patterns between Burned and Undisturbed samples might be related to the intensity of the fire or the time elapsed until the sample was taken (4), as it was expected that the wildfire would change the physicochemical characteristics of the soil (3).

BIOINFORMATICS

According to the results, the absolute abundance of AVS is significantly higher in the group of soils affected by fire (fig. 3, B) except for Location 3 (fig. 3, D).

The reduction of microbial biomass is one of the best-established effects of wildfires. This reduction also implies a decrease in community richness, which in turn allows the surviving species to proliferate in an environment with less competition for resources (5), which could explain the behavior of the sampled communities.

Within the taxonomic composition of the sampled microbial communities, the predominant phyla were Proteobacteria, Actinobacteria, Acidobacteria, and Chloroflexi, varying slightly in percentage between each sample (fig. 4).

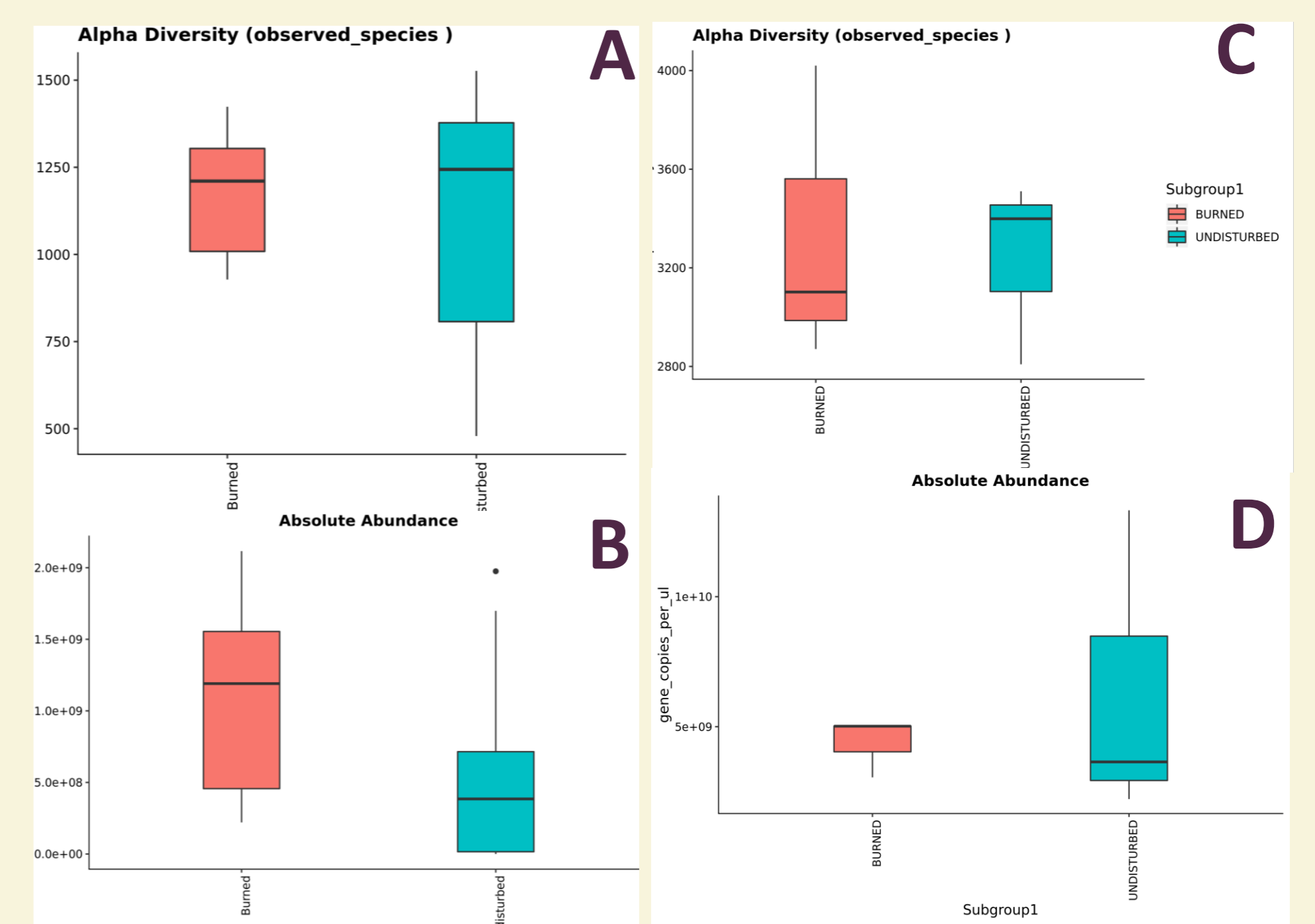


Figure 3. A) Species observed in the samples grouped by condition. B) Absolute abundance of 16s gene copies per µl in the sequenced samples grouped by condition. C) Observed species in location 3. D) Absolute abundance of 16s gene copies for location 3

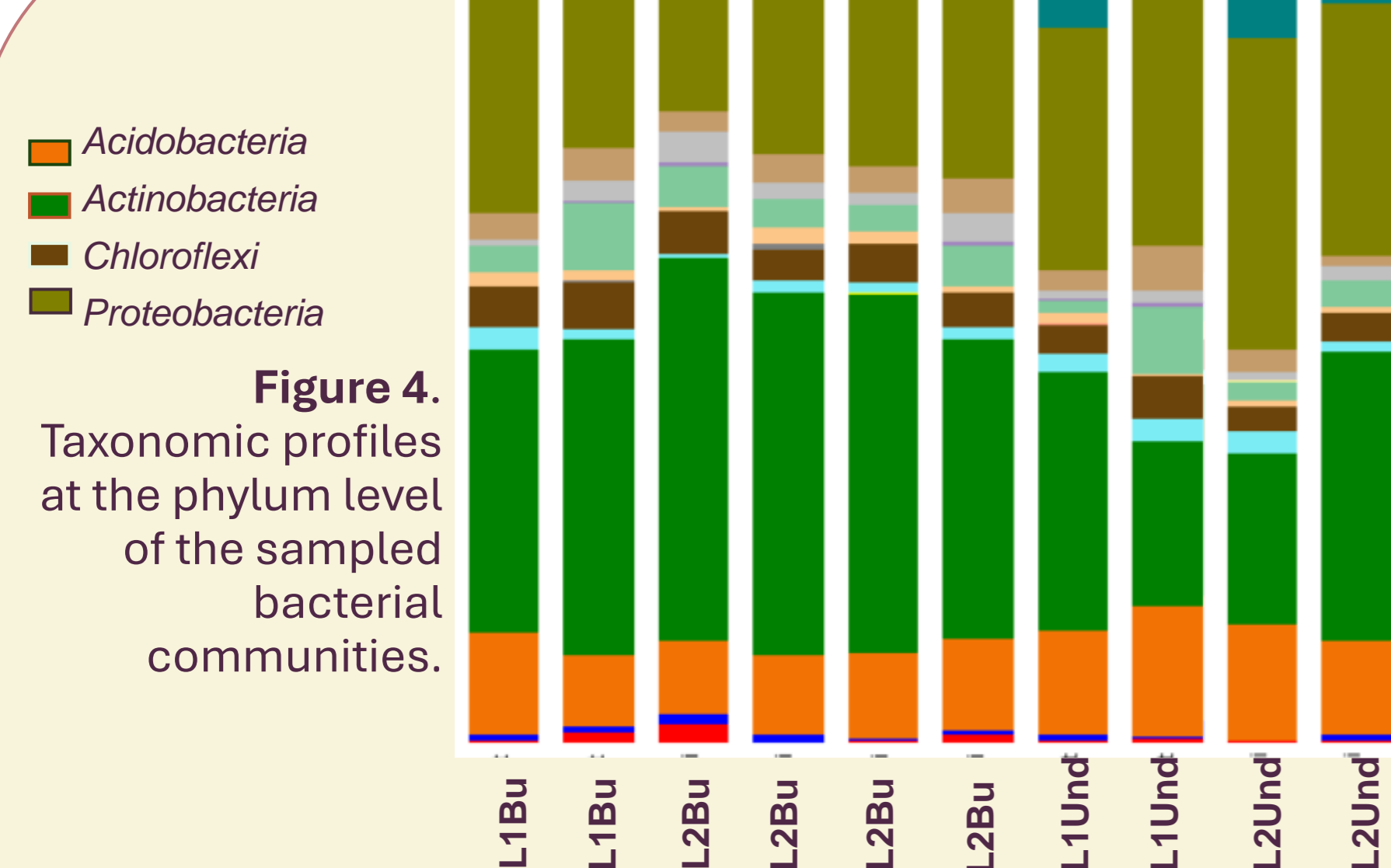


Figure 4. Taxonomic profiles at the phylum level of the sampled bacterial communities.

Additionally, the genera Streptomyces, Sphingomonas, and Afipia-Bradyrhizobium were found in greater abundance in the healthy soil samples compared to the rest of the samples.

Among these genera, it has been reported that Streptomyces can form biotrophic relationships with plants and that its abundance can increase in soil with dysbiosis (6).

Similarly, both Sphingomonas and Afipia-Bradyrhizobium are of biotechnological importance due to their nitrogen-fixing and biosynthetic capabilities (7).

One of the most interesting results was observed when comparing the similarity between communities (fig. 8), finding greater similarity among samples from sites that have been affected by fire, despite not being in the same locality, or the time elapsed after the fire.

Dove and collaborators mention that the exposure of a bacterial community to fire is a deterministic process for community assembly, where bacteria capable of withstanding high temperatures and those that can utilize pyrogenic C will prevail (8).

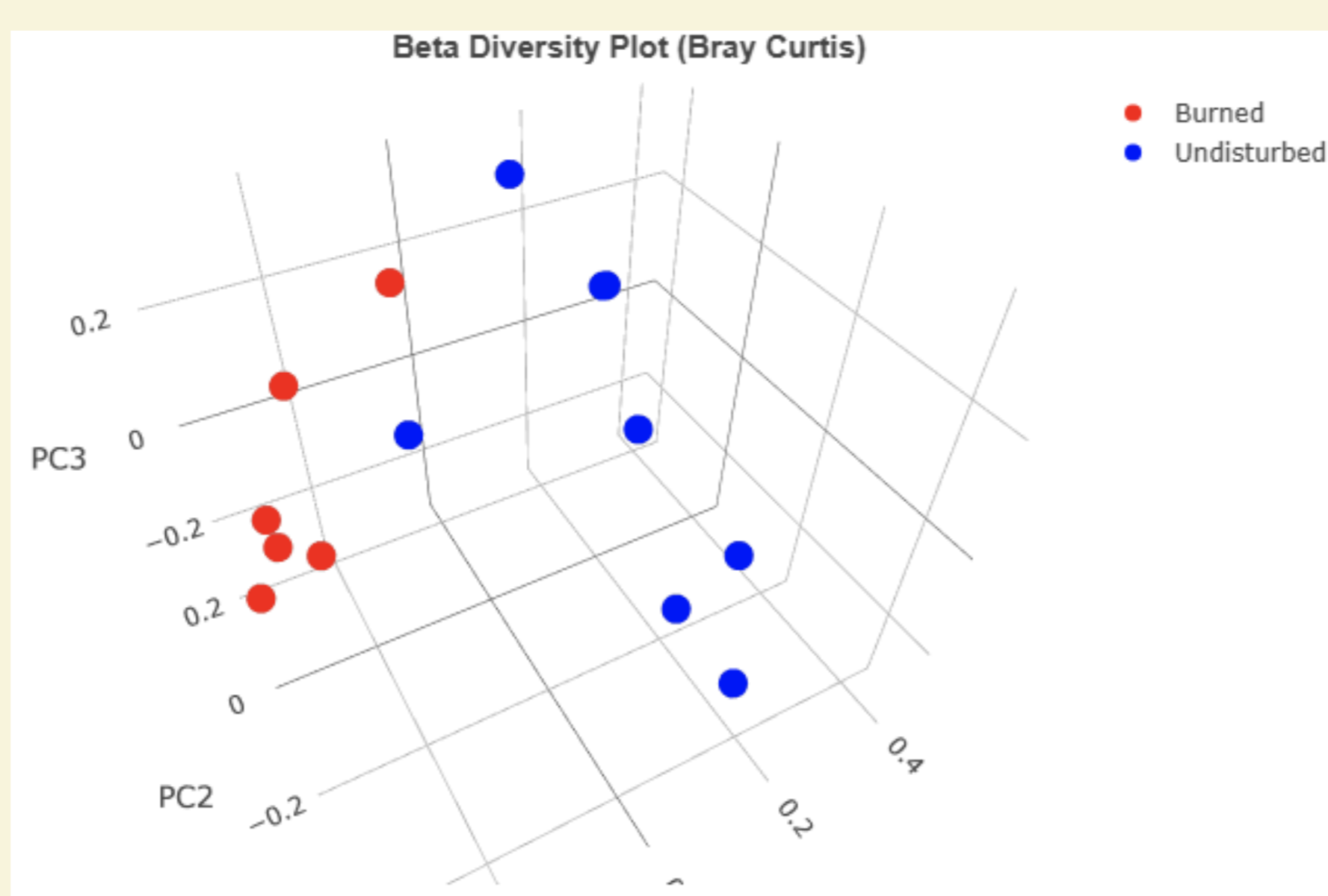
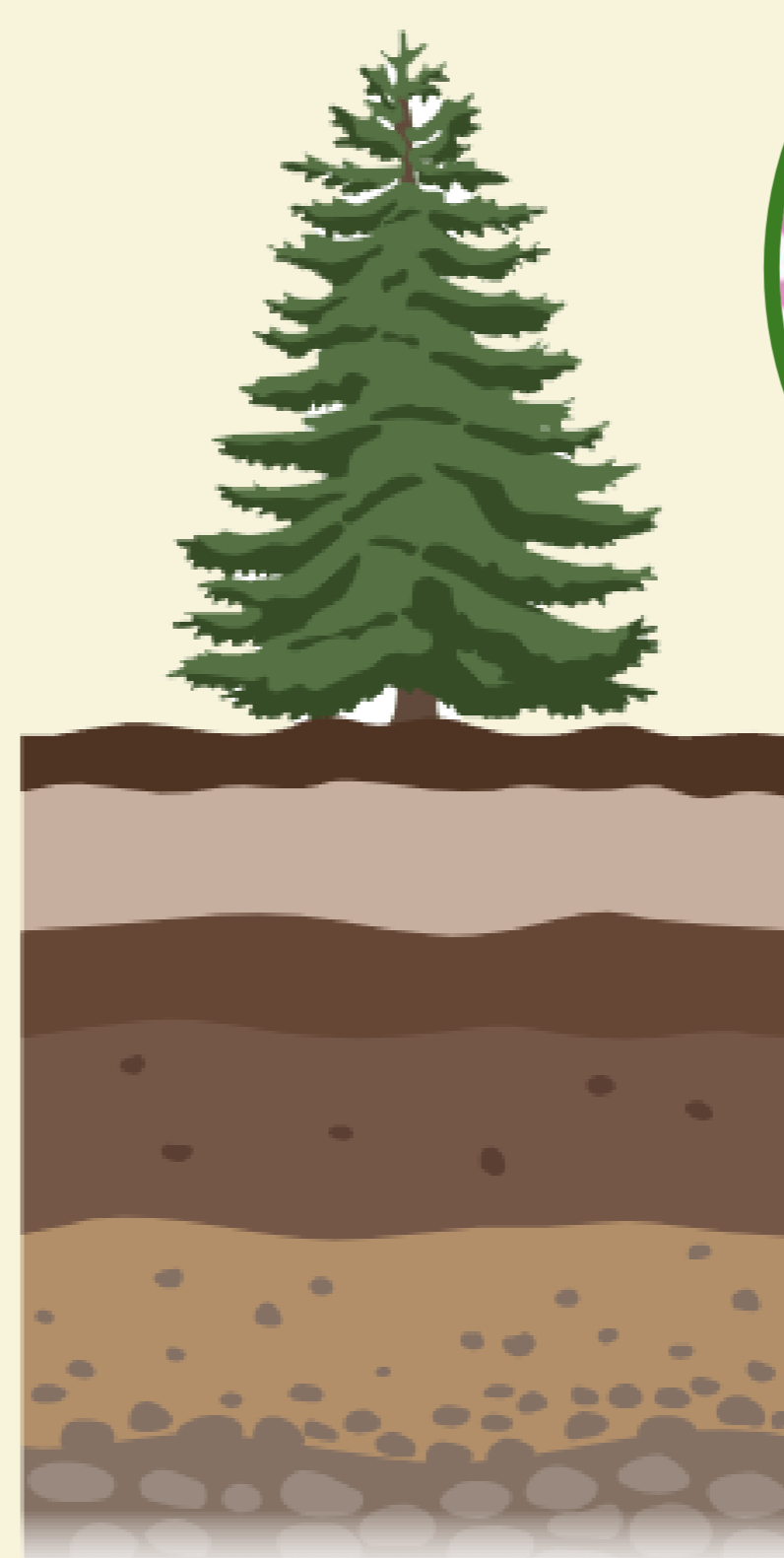


Figure 5. Three-dimensional principal coordinates graph created using the pairwise distance matrix calculated by Bray-Curtis dissimilarity.

After the fire, the change in the physicochemical conditions of the soil will continue to influence the progression of the community, reducing diversity by function selection. However, other parallel processes such as interspecific competition limit the similarity between the functions of community members (9).



CONCLUSION

Even though the physicochemical parameters did not show noticeable differences between conditions or even between locations, sequencing analyses show greater similarity among microbial communities in soils affected by fires, which could indicate that forest fire disturbance influences microbial diversity beyond other soil characteristics. Significant Taxa as Streptomyces might be participating in the regulation of the community dynamics and other taxa with promising potential for synthetic consortia design like Sphingomonas and Afipia-Bradyrhizobium. These results are a good indication of the relevance of studying bacterial communities to design forest management strategies that consider the importance of the microbiome.

LITERATURE



COLABORATIONS

