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## Soil Microbial Community Composition of White Oak Mountain, Tennessee

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## Introduction

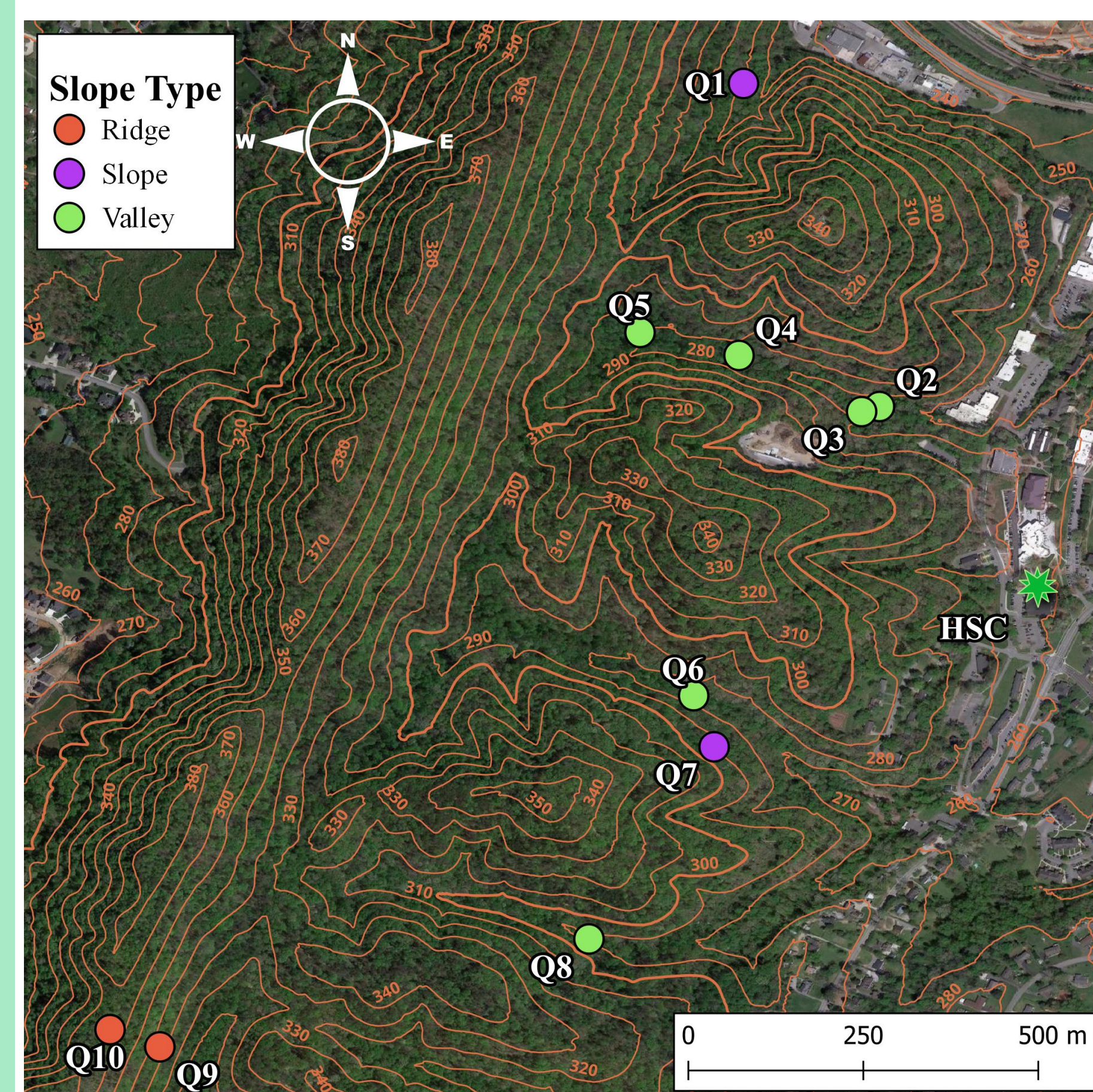
- Soil microbial communities are responsible for nutrient cycling in terrestrial ecosystems<sup>1</sup>.
- Soil microbes have important symbiotic and parasitic relationships with the plant community<sup>2</sup>.
- Soil microbial community structure can be determined by factors including plant community diversity<sup>3</sup>, seasonal variation<sup>4</sup>, and alterations in the physical environment<sup>5</sup>.

## Research Objectives

1. Characterize the soil microbial community of White Oak Mountain.
2. Determine how spring wildflowers, seasonal changes, and environments alter the soil microbial community structure.

## Site Description

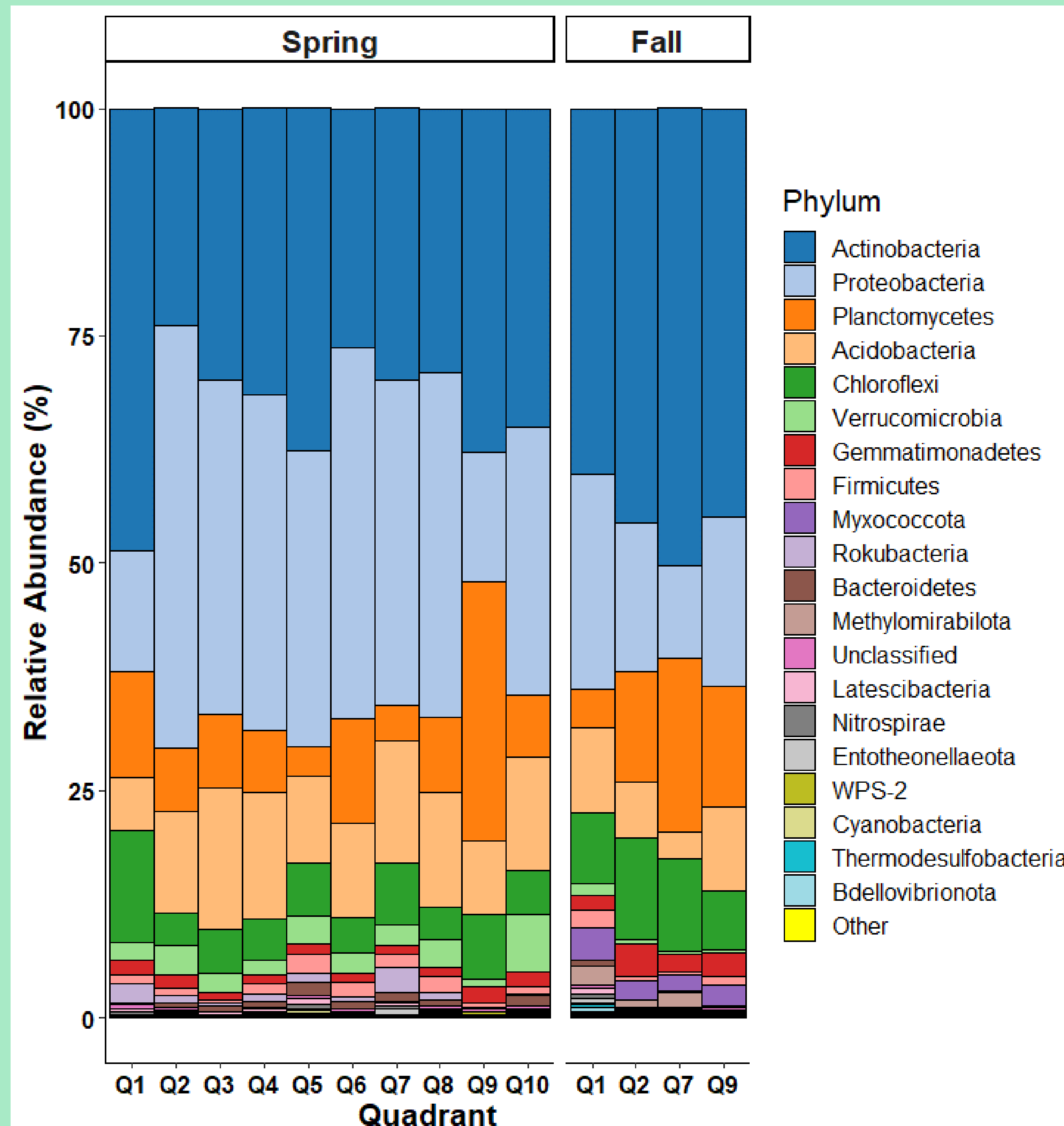
The study site is located on the eastern slope of White Oak Mountain within a second growth oak hickory forest on the campus of Southern Adventist University.



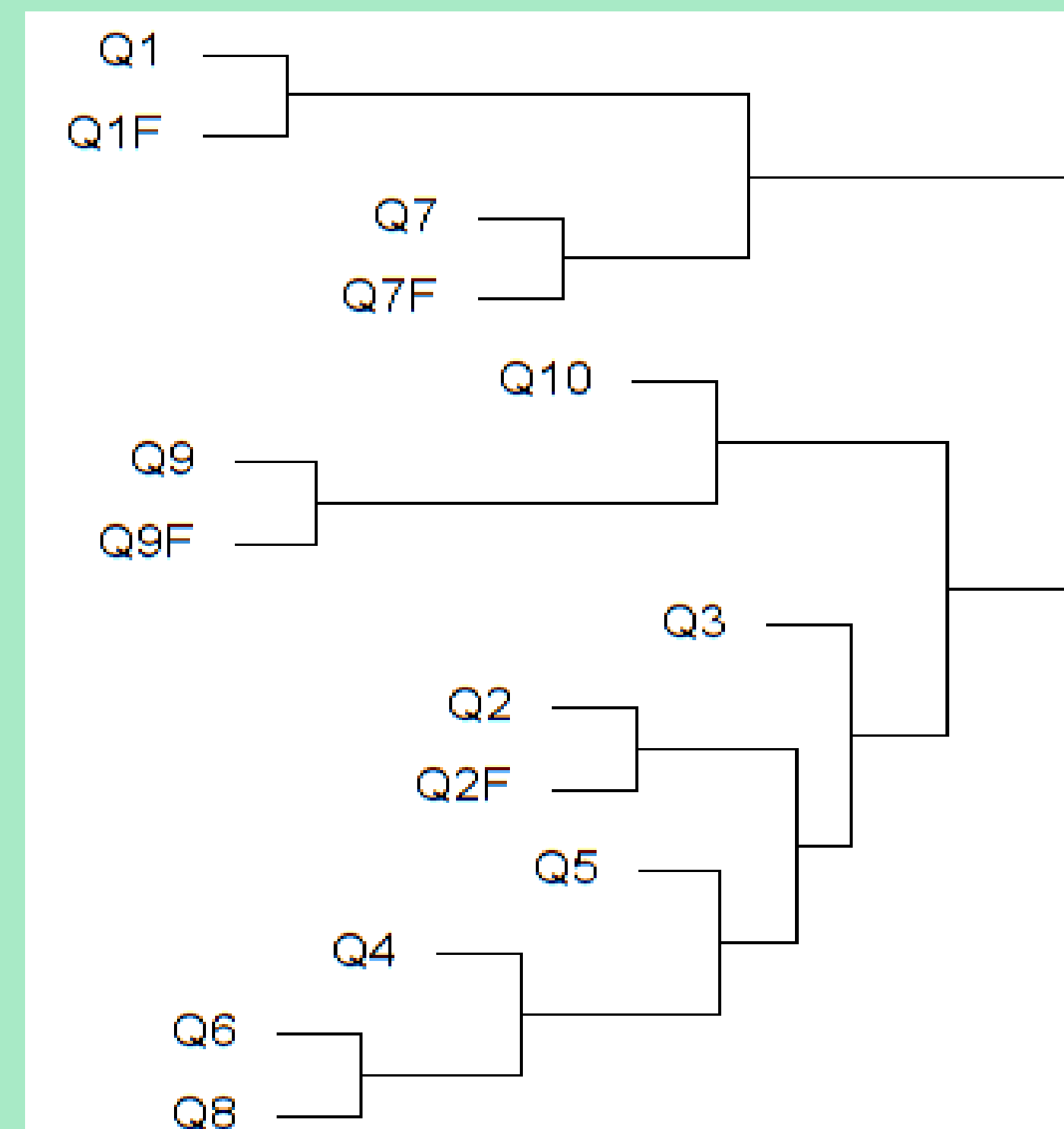
**Figure 1.** Map of the study site indicating the slope type and elevation of each quadrant located on White Oak Mountain on the campus of Southern Adventist University in Collegedale, TN. Contour lines indicate elevation in meters. HSC—Hickman Science Center.

## Methods

- Spring wildflower diversity data was collected from 1.2 X 2.4 m quadrants in April 2019.
- Soil cores were taken from each quadrant at a depth of 2 – 4 cm in April and again in October.
- Eight soil cores from each quadrant were homogenized to normalize the soil microbial community for the entire quadrant.
- Total DNA was extracted from the homogenized soil.
- Purity and quantity of extracted DNA was assessed using DNA spectrophotometry.
- Amplicon sequencing was performed by LC Sciences.
- Data analysis was performed using RStudio.



**Figure 2.** Relative abundance of the twenty most abundant bacterial phyla from 10 quadrants (Q1 – Q10) in Spring 2021 and 4 quadrants (Q1, Q2, Q7, and Q9) in Fall 2021 determined by 16S rDNA sequencing.



**Figure 4.** Cluster analysis of 16S OTUs from 10 quadrants in Spring (Q1 – Q10) and 4 quadrants in Fall (Q1F, Q2F, Q7F, and Q9F) indicating that quadrants cluster in three distinct groups and that Spring and Fall OTUs for the same quadrant always cluster together.

## Conclusions

- Actinobacteria and Proteobacteria are the most prevalent phyla of bacteria with a relative abundance greater than 50% regardless of season (Fig. 2).
- Bacterial diversity and spring wildflower diversity are significantly correlated (Fig. 3a) demonstrating that diverse floral communities are indicators of diverse bacterial communities.
- Total eukaryotic and fungal diversity have no relationship with spring wildflower diversity (Fig. 3b,c) suggesting that spring wildflower diversity does not contribute to the structure of these communities.
- Regardless of season the 16S OTUs from the same quadrant cluster together (Fig. 4) indicating that the environment is a more important factor in the structure of the soil bacterial community than seasonal changes.
- Cluster analysis of 16S OTUs revealed three distinct clusters of quadrants (Fig. 4) which seem to be determined by whether the quadrant was in the valley, on a slope, or ridge top (Fig. 1).

## Acknowledgements

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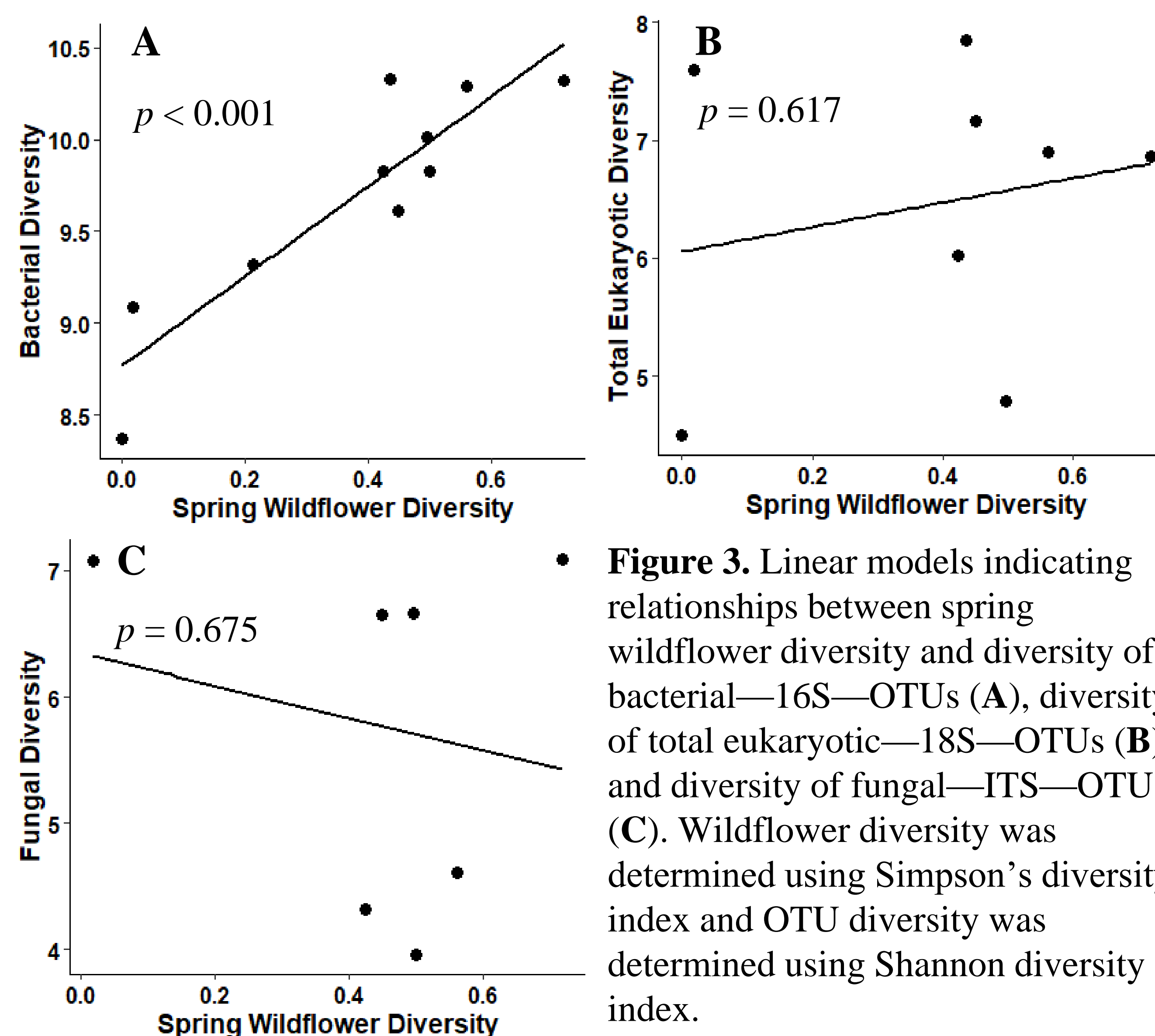
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**Figure 3.** Linear models indicating relationships between spring wildflower diversity and diversity of bacterial—16S—OTUs (A), diversity of total eukaryotic—18S—OTUs (B), and diversity of fungal—ITS—OTUs (C). Wildflower diversity was determined using Simpson's diversity index and OTU diversity was determined using Shannon diversity index.