# **Soil Microbiome Beta, Taxonomic and Functional Diversity in British Columbian Logged Douglas-fir Stands Differs Across the A and O Horizon**

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**ABSTRACT**

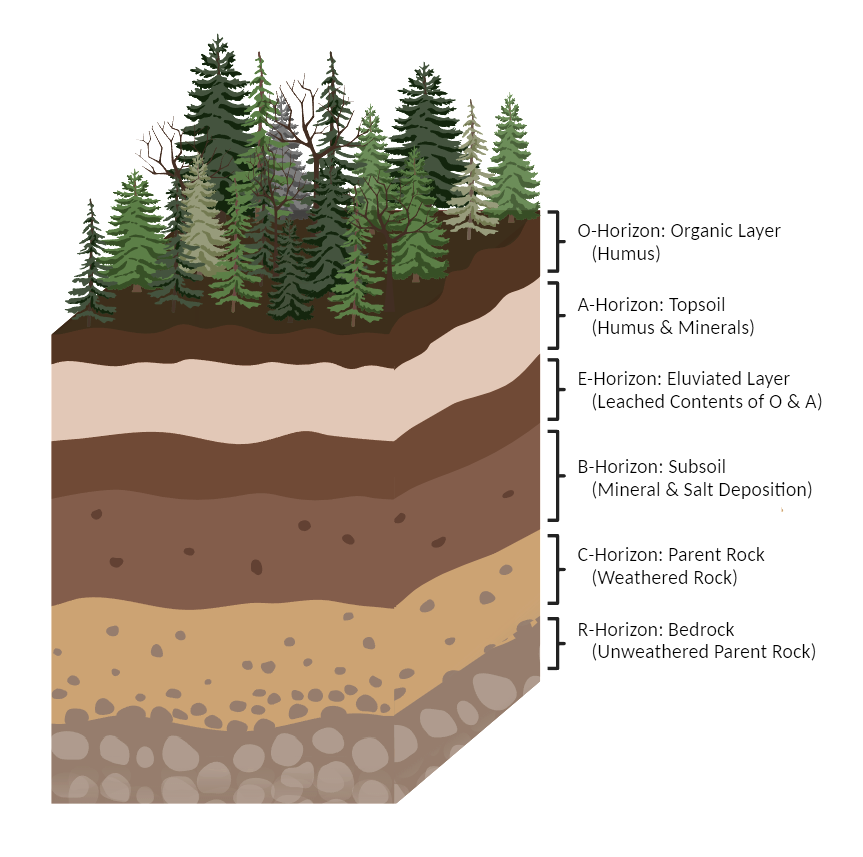
Soil bacterial composition varies based on a wide variety of factors and is responsible for much of soil nutrient cycling. To date, the correlations between these communities and different soil layers or horizons are not well studied. We investigated sites of logged British Columbian Douglas-fir trees and their correlations with microbial diversity. Specifically, we based our study on soil samples obtained from the top two organic soil layers, the A horizon and O horizon. We investigated microbial diversity through alpha, beta and core microbiome analyses. In addition to this, we aimed to determine the possible environmental quality of the Douglas-fir soil, and the corresponding ecological microbiota surrounding these regions, through indicator taxa analysis and PICRUSt2 analysis. Alpha diversity analyses indicated no significant differentiations across the A and O horizons, whereas, beta diversity analyses indicated significant clustering within each respective horizon. Furthermore, core microbiome investigations revealed some overlap at the genus level along with significantly greater diversity in the O horizon. Results from Indicator Species Analysis also reveal significant differences in the top indicator taxa for each horizon, which was further supported by the functional pathway analysis performed downstream. 407 functional pathways, including the ‘incomplete reductive TCA cycle’ pathway involved in nutrient cycling, were also significantly differentially abundant between horizons, indicating distinct functional niches. These results affirm the clear differences between the microbial diversity and community composition in the A and O horizons, indicating the need for more microbial diversity research regarding horizon depth and logged soil. This will hence improve our understanding of microbial community formation and its potential connections to environmental and human-made impacts.

**INTRODUCTION**

Initiated in 1989, the Long-term Soil Productivity (LTSP) Study has aimed to quantify site productivity, measured by the growth capacity in volume for a given species, on timber harvesting land based on soil profiles (1, 2). Soil composition sustains forest productivity and, in turn, affects climate stability, biodiversity, and economic development (3, 4) Industrial harvesting of coniferous forests alters the local soil communities and the intensity of organic matter removal (1, 3, 4). To better understand the changes in soil microbiomes post timber harvest, and provide a baseline for future LTSP studies, Wilhelm et al. collected 724 16S bacterial samples between 2008 and 2014 (1). A total of 18 sites were sampled to determine the LTSP in six predetermined coniferous ecozones of North America based on dominant tree type (1). One of these tree types is Douglas-fir, which is a large evergreen conifer native to Western North America and one of the most important timber trees of this region (5).

The data collected during the LSTP studies has since been applied as a baseline in further investigations done by the original authors, now addressing the specific effects and changes within soil microbial communities in timber harvesting regions (3, 4, 6, 7, 8). Additionally, the dataset has been implemented in downstream studies to further examine the physical, chemical, and biological measures collected from the original study (9, 10, 11, 12, 13). These studies expand on some of the main categories which play a role in soil biodiversity, which could in turn be used to better reforestation strategies in timber harvesting areas. There is a lack of focus on soil horizon data, which is a key factor in distinguishing microbial composition between the layered soil niches.

A vertical cross-section of soil reveals layers, otherwise known as soil horizons (14). Of the six master horizons (Fig. 1), Wilhelm et al. collected samples from the O horizon via trowel, along the atmospheric exposed soil, and A horizon via Stoney auger, 20 cm into the topsoil (1). As shown in Fig. 1, the O horizon is the top organic layer and forms continuously over 6-12 months (16). The humus, otherwise known as the A horizon, lies just beneath this top layer and can take anywhere from a mere 25 years, to thousands of years to regenerate (17). Due to the differences in formation rates, the O horizon soil composition will have changed dramatically post-logging, whereas the A horizon soil would not have had time to change. Therefore, the elemental composition of the A horizon soil may bear more similarity to the pre-logging or pre-timber harvesting conditions.



**FIG. 1** **Soil profile**. Distinct layers (horizons) of coniferous soil.

Different soil horizons exhibit varying physical and chemical properties, such as pH and nutrient content, creating distinct niches that influence microbial communities (13). The microorganisms in forest soil impact nutrient cycling within that system and could play an essential role in the conservation and restoration of logged environments (18). With this information, environmental scientists can assess the health of forest ecosystems and farmers may utilize it as a predictor for crop selection and planting practices (17). While significant differences in taxonomy and function have been observed in the microbiomes of various soil horizons in a tundra environment (14), there has been a scarcity of investigations pertaining to the microbiota inhabiting soil horizons in temperate regions like the Douglas-fir ecozones of BC. Furthermore, these parameters have also not been thoroughly studied in sites where there has been previous clear-cutting for timber harvesting. Organic matter removal at these sites has significant impacts on the composition and depth of the soil horizons (6) and therefore the lack of studies on the microbial communities of these environments post-logging represents a significant knowledge gap.

Yarwood et al. (18) also suggest that the microbial content of the soil in Douglas-fir stands may exhibit correlations with tree growth rates. Therefore, it is crucial to understand how logging practices impact these populations and how they could lead to improvements in forest management and more effective reforestation initiatives following timber harvesting. Due to the necessity of specific soil conditions for microbial growth, and the different compositions of the O and A horizons, we hypothesize that there will be significant variability in the taxonomic and functional profiles of the respective soil ecosystems. Our objective is to utilize the dataset provided by Wilhelm et al. (1) to investigate these potential differences in previously logged Douglas-fir stands. By doing so, we aim to provide an analysis of microbial profiles at different soil depths which can then pose as a baseline for further investigations into the role of the soil microbiome as reforestation continues.

**METHODS**

**Forest Soil Microbiome Data.** The dataset contained a collection of samples from eighteen reforested sites from six North American ecozones from the LTSP Study. Of these sites, we focused on the IDFBC , which predominantly housed the native interior Douglas-firs. While the dataset consisted of several factors, our study primarily considered horizons. For many of the 16s rRNA gene amplicon and whole shotgun sequencing libraries in Skulow Lake, samples were collected from five soil horizons and then distinguished using the Canadian Systems of Soil Classification. Further sample collection details can be found in the paper published by Wilhelm et al. Amplicon libraries were prepared for the 16s rRNA gene (V1-V3 regions). A total of 697 samples were downloaded to be used in our study. (1).

**Preliminary QIIME2 Processing.** The QIIME2 DADA2 software package was used to denoise our dataset to correct Illumina-sequenced amplicon errors (19, 20). The sequences were then truncated to 410 base pairs (bp) and a feature table containing the amplicon sequence variants (ASVs) for the BC Douglas-firs was generated. A rarefaction depth of 4092 sequence reads per sample was chosen which retained 216 samples as well as 50.19% of the total ASVs.

**Alpha and Beta Diversity Metrics based on Horizons.** Alpha and beta diversity metrics were conducted through RStudio 2023.09.0 to determine species richness and diversity. Data wrangling was performed in R using the ‘tidyverse’, ‘vegan’, ‘phyloseq’, ‘ggplot2’, and ‘ggpubr’ packages (21, 22, 23, 24, 25). Then rarefy data to the selected sample size which in this case was 4092 as explained above. To determine species richness, the Shannon's diversity index was employed specifically looking at Horizon type as the factor (26). To determine the significance of this alpha diversity test, a Wilcoxon test was conducted (27). Beta diversity was evaluated using the weighted Unifrac and unweighted Unifrac metrics to find phylogenetic distance (28). Principal Coordinate Analysis (PCoA) plots were then generated based on these analyses. PERMANOVA significance of these beta diversity plots was then determined (29).

**Indicator Species Analysis.** Indicator species analysis (ISA) was done to determine the relative abundance of each genus in the O and A horizons. Load packages ‘tidyverse’, ‘dplyr’, ‘phyloseq’, ‘vegan’, ‘ape’, and ‘indicspecies’ into RStudio 2023.09.0 for completion of analysis (21, 30, 23, 22, 31, 32). Tidyverse and dplyr packages were used for basic data manipulation while phyloseq was used to create a phyloseq object consisting of a phylogenetic tree, using the ape package, and a taxonomy table, using the vegan package. The indicspecies package was used to perform an indicator species analysis to calculate the relative abundance of the samples and find the most abundant and significant genera in the soil horizons. The ‘soil\_metadata.tsv’, ‘filtered-feature-table.txt’, ‘taxonomy.tsv’, and ‘tree.nwk’ files generated in earlier Qiime2 processing were appropriately adjusted and read into the phyloseq object (20). Grouping of the phyloseq object was done by genus to give insight into the lowest taxonomic level. Reads were then converted to relative abundance, using filtration measures of 0.001 abundance and 10% prevalence. Thus, the ASV’s would be present and in the designated horizon, and found in at least 10% of the samples. Once everything was in place, the indicator species analysis proceeded following the execution of the ‘multipatt’ command piped as per the permutation test with ‘nperm’ = 999 (33, 34). For both indicator species analysis stats and relative abundance values, data frames were merged prior to visualization as a bubble grid chart with ‘ggplot’ (24). For added accessibility, visualizations were interpreted with both size and colour for each horizon.

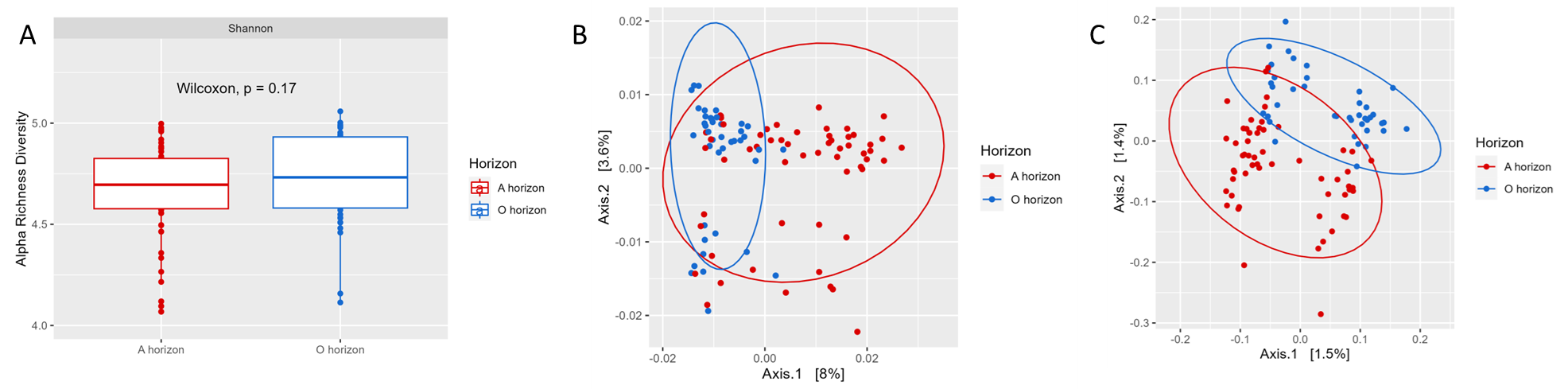
**Determine Taxon Abundance using Core Microbiome.** Core Microbiome was conducted through RStudio and utilized the phyloseq object generated from ISA (35). Load packages ‘tidyverse’, ‘phyloseq’, ‘microbiome’, and ‘ggVennDiagram’ into RStudio 2023.09.0 for completion of analysis (21, 23, 36, 37). The microbiome package was used to facilitate the analysis of taxonomic profiling data, which was visualized using the ggVennDiagram package. To enhance taxonomic resolution, the phyloseq object was transformed to the genus level using tax\_glom(). Subsequently, the dataset was filtered to include two predictor variables, denoted as the A horizon and O horizon, representing the different soil layers. The core microbiome analysis was executed with the core\_members() function, specifying a detection threshold of 0.0001 and a prevalence threshold of 0.1 to identify robust and prevalent microbial taxa across the groups. Finally, the results of the core microbiome analysis were visually represented using a Venn diagram generated by ggVennDiagram() from the VennDiagram package in R. This visualization aids in elucidating the shared and unique taxonomic components within the A horizon and O horizon groups, providing a comprehensive insight into the common members across the specified habitat.

**Functional Analysis using PICRUSt2.** The picrust2\_pipeline.py command from the PICRUSt2 QIIME2 plugin was employed to understand the metabolic pathways utilized by microorganisms in different horizons. Differential abundance was performed on the MetaCyc data using the ggpicrust2 package, pathway\_daa() with daa\_method = DESeq2. Pathways were annotated using pathway\_annotation() and filtered for only significant results with adjusted p-value ≥ 0.05. The PCA plot was generated using the ggpicrust2 package pathway\_pca(). The bar plot was generated with a modified version of the pathway\_errorbar() function which implemented an adjusted p-value cut off of ≥ 0.05 and an absolute log 2 fold change cut off of 0.58 which represents a 50% increase or decrease in abundance.

All scripts and visualizations can be viewed at <https://github.com/allyhoward/micb475.git>

**RESULTS**

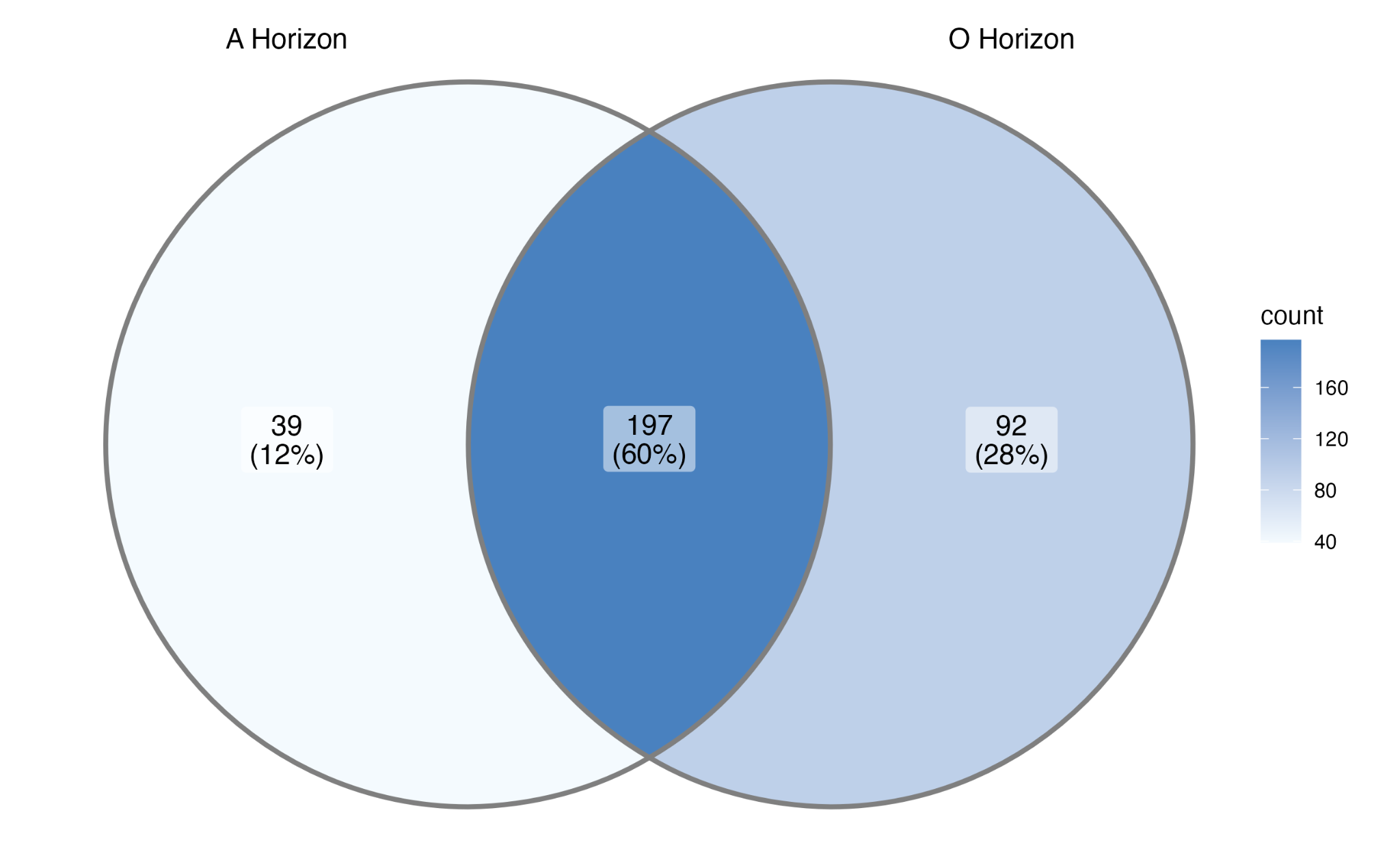
**Species richness is not significantly different between A and O horizons.** After the microbiome species present in each horizon were identified, the biodiversity of the niche at each horizon was evaluated. The alpha diversity Shannon box plot illustrates no significant differences between the species richness of the A and O horizons (Fig. 2A). The Wilcoxin T test confirms this absence of significance with a p-value of 0.17.



**FIG. 2 Alpha and Beta Diversity Analysis at A and O Horizons.** (A) No significant alpha diversity patterns across the two horizons. Y axis denotes Shannon’s Diversity Index. Wilcoxon test was conducted to test significance, p-value = 0.17. (B) Weighted Unifrac and (C) Unweighted Unifrac PCoA plots. The red ellipses encompass A horizon samples that cluster together, and the blue ellipses show the O horizon sample clustering. PERMANOVA significance was evaluated at p-value <0.001.

**A and O Horizon microbial samples are more similar to themselves than they are to the opposing horizon.** Two beta diversity PCoA plots, Weighted (Fig. 2B) and Unweighted (Fig. 2C) Unifrac analysis show that the samples cluster moderately strongly within their respective horizons and therefore suggest that these are distinct from one another. These differences are also demonstrated to be significant as seen through the PERMANOVA test run which returned a p-value > 0.001. Furthermore, comparing the two PCoA plots, the weighted Unifrac analysis reveals that when relative abundance is considered sample clustering is weaker than when only absence and presence are considered as seen in the unweighted analysis.

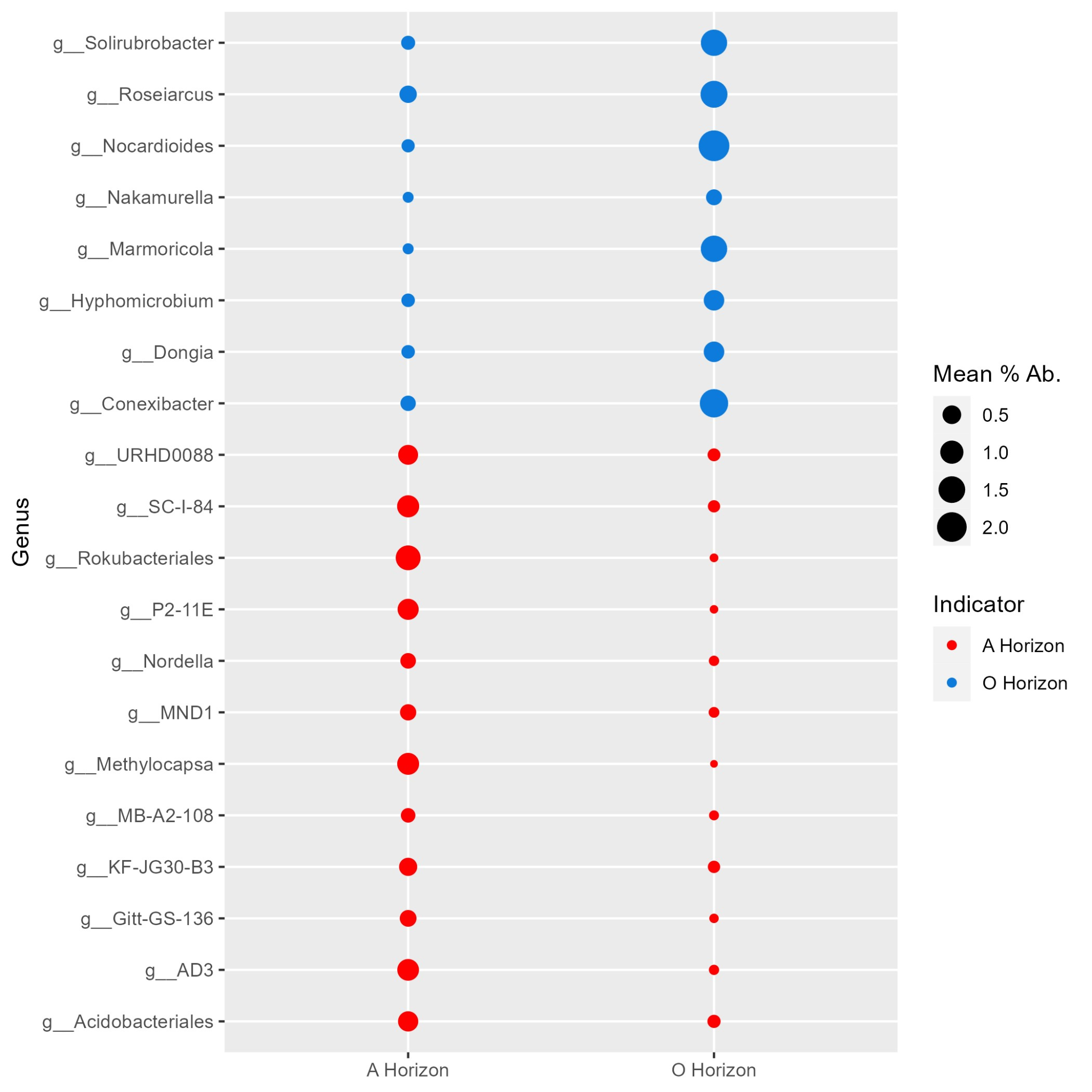
**The O Horizon exhibits a greater proportion of microbiome diversity.** In the Venn diagram (Fig. 3) illustrating the microbial composition of the A and O horizons, an overlap was observed between the two horizons. This indicates substantial similarity in the microbial composition at the genus level, showcasing a degree of continuity or shared ecological niches within the soil layers of the Douglas-fir stand environment. The higher proportion shown in the O horizon also highlights that this soil layer harbours a significantly greater number of unique microorganisms than the A horizon.

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**FIG. 3 Core microbiome at A and O horizons at the genus level.** The graph was generated using RStudio with a detection threshold of 0.0001 and a prevalence threshold of 0.1. The A horizon constitutes 12%, while the O horizon makes a more substantial contribution at 28%, indicating a more unique makeup of the microbiome in this soil layer. The overlap accounts for 60% of the core taxonomic group in common, signifying notable microbial communities shared between these two horizons.

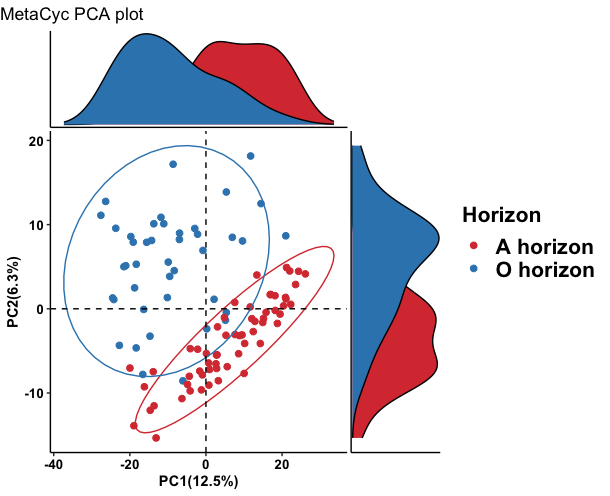
**A large number of indicator taxa are significantly different between the A and O horizons**

An indicator taxa analysis at the genus level showed a significant difference in the microbial composition of each horizon. The data was filtered to visualize results surpassing an indicator value of 0.8 to select genera with a high relative abundance and frequency that suggests the ASV’s are likely to be indicator species for the respective horizons. 8 genera were produced that were indicative of the O horizon and 12 genera that were indicative of the A horizon. The large number of indicator taxa that are significantly different between the two horizons, suggests the horizons act as separate ecological niches. While the A horizon had a greater number of readouts for the conditions set (*IV > 0.8*), only 4 of the 12 genera were classified whereas the rest were unknown or uncultured. Contrastingly, all genera from the O horizon were classified as bacteria, suggesting that microorganisms collected from deeper horizon depths are not well studied.

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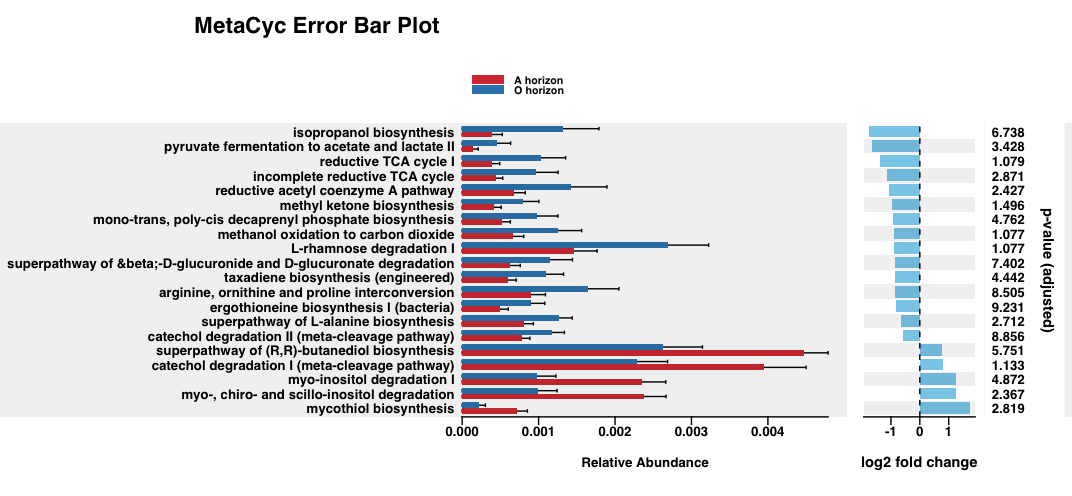
**FIG. 4 A large number of indicator taxa are significantly different between the A and O horizons.** Indicator taxa analysis shows the mean percent abundance (illustrated by dot size) of genera in the A and O horizons with an indicator value of at least 0.8 and a p-value of 0.001 for samples in each respective horizon.

**Functional profiles between the A and O horizons were significantly different.** Principal Component Analysis (PCA) of the functional profiles for each horizon showed clear clustering within the A horizon and the O horizon, but little overlap between the two horizons. This indicates greater similarity in functionality among samples in the same horizon than between horizons (Fig. 5).



**FIG. 5 Functional pathways cluster within A and O horizons but are significantly different between horizons.** PCA analysis of MetaCyc pathways generated with PICRUSt2.

The differences in these functional profiles were further explored using MetaCyc data and visualized in Fig. 6. There were 407 significant (adjusted p-value< 0.05) differentially expressed pathways among our 103 samples. Of these, 20 pathways had log2 fold changes of ≥ 0.58. Five of these pathways were more abundantly expressed in the A horizon and 15 were more abundantly expressed in the O horizon. These results show that the microbiomes of the A and O horizons act with functional profiles that are very different from each other.



**FIG. 6 Functional pathways with log2 fold change abundances of ± 0.58 are significantly different between A and O horizons.** Bar plot showing significant (adjusted p-value < 0.05) differentially abundant pathways based on MetaCyc analysis.

**DISCUSSION**

The microbial richness within the A and O horizons are similar to one another, however, the taxonomic diversity across these horizons is quite different. The Beta Diversity suggests that each horizon is a specific niche, and although these niches have around the same number of taxa, the actual overlap of species is quite small. Strong niche differentiation and little overlap suggest that the roles these bacteria may play in community composition are unique to each horizon. Conversely, the core microbiome illustrates a major overlap between the two horizons. The O horizon also resides in more unique genera, which aligns with the notion that the layer contains the newest organic material and implies a diverse microbial community within that soil layer. Bacteria from the O horizon would most likely, therefore, not fit in well in the A horizon community. Such niche differentiation is supported by previous findings (38). Both horizons are very rich, which is expected of a soil microbiome, but they differ greatly in which microorganisms they attract (39). Because of the heterogeneity of soil, it has the variety necessary for many forms of life, but differing conditions between the layers seem to exclude different taxa. However, it is noteworthy that previous research in microbial diversity across horizons has found results that are in contrast to our findings. Luo et al. (2023) showed a significant increase in species richness in the O horizon and no significant differences in beta diversity (40), however, data was collected on unlogged forests. These differing results could suggest that logging is a significant factor in horizon research and greatly alters microbial diversity, and thus community structure and composition but further investigation is required.

The A and O horizons in British Columbia Douglas Fir stands exhibit distinct ecological niches that attract specific bacteria which are more suited to the conditions. The functional profiles of the microbiomes at different horizons exhibit differences in nutrient cycling and soil pH which may impact Douglas-fir growth rates (41). We sought to determine the composition of the A and O soil horizons of BC Douglas-fir trees with respect to indicator taxa generated, while also correlating results to the functional differences exhibited by these niches. To investigate this, we evaluated the top indicator species from each horizon. Of the classified genera in the A horizon, the functional properties were linked to general metabolic activity, such as the substrate oxidations and dissimilation reactions required by the bacteria for survival, while (most) of the bacteria in the O horizon had functional roles associated with environmental interactions in addition to their metabolic roles. The top 2 bacterial taxa indicative of the A horizon are the genera *Rokubacteriales*, which is functionally associated with alcohol cycling in wetlands, and *Methylocapsa*, which acts as a methane-oxidizing bacteria (42, 43). Each of these two bacteria thus has unique metabolic roles. On the other hand, the 3 most abundant genera in the O horizon were *Nocardioides*, which has been shown to play a role in ecological nutrient cycling and chitin degradation (44, 45, 46), *Conexibacter*, which engages in the nitrification process in oxygen-limiting states (47), and *Marmoricola*, which is shown to improve the antifungal activity of soil (48, 49).

Furthermore, a large number of functional pathways were differentially abundant between the A and O horizons in these Douglas Fir stands. In the O horizon, the relative abundance of the ‘incomplete reductive TCA cycle’ and ‘reductive acetyl coenzyme A’ pathways are significantly greater than in the A horizon. These pathways are important to autotrophic organisms such as *Chlorobium* and can contribute to carbon and nitrogen cycling in the soil, which is essential to plant growth (50). The increased abundance of these pathways in the O horizon is likely due to the organic matter layer having greater access to sunlight allowing for the colonization by these autotrophic bacteria. Similarly, the O horizon had a higher abundance of organisms with the ‘L-rhamnose degradation I’ and ‘superpathway’ beta-D-glucuronide and D-glucuronate degradation’ metabolic pathways which are characteristic of plant matter degradation (51). Again, the organic layer is more likely to contain new plant matter and therefore would provide another source of nutrient cycling. This plant matter could be acting to attract taxa such as the indicator *Nocardioides* which uses L-rhamnose as a carbon source.

In the A horizon, one pathway of note is the ‘Superpathway of (R, R)-butanediol biosynthesis’ which is indicative of acid production by lactic acid bacteria (LABs) and could be a component of alcohol cycling by the indicator *Rokubacteriales*. Past studies have shown that more acidic conditions can be beneficial to the growth of Douglas firs (52), and other studies have shown the benefit of LAB in association with other plants (53). It is possible that these pathways are creating soil conditions of lower pH that can improve the growth rate of Douglas-firs in this area. Additionally, the ‘myo-inositol degradation I’ pathway, which is essential to nitrogen-fixing bacteria, especially in association with the rhizosphere of plants (54), is also more abundant in the A horizon. The significant differences between the functional profiles of these horizons could simply be a factor of natural variation in environmental conditions, but since timber logging occurred between the formations of the O horizon and A horizon, they may also be an indicator that logging drastically impacts the soil microbiome. One piece of evidence that supports the second theory is that ‘catechol degradation’ pathways are increased in both the A and O horizons (‘catechol degradation I’ in the A horizon and ‘catechol degradation II’ in the O horizon). Catechol is an environmental pollutant and is present in polycyclic aromatic hydrocarbons (PAHs) which are one of the primary components of diesel (55, 56). Aside from CO2 emissions, diesel spills are one of the primary sources of pollution in timber harvesting camps (57) and could account for this increase in catechol degradation.

**LIMITATIONS**.

One limitation of this study was the possibility of soil mixing between the A and O horizon caused by the movement of timber harvesting equipment in this area (58). This could mean that the soil horizons are not as clearly defined as in an environment with little disturbance. Additionally, our focus on the British Columbian Douglas fir ecozone limits the extrapolation of our results, which cannot be applied to similar timber harvesting sites in locations outside of British Columbia, nor to timber harvesting sites for different tree species.

**CONCLUSIONS AND FUTURE DIRECTIONS**

The microbiomes of the A and O horizons are significantly different from one another, both taxonomically and functionally. This is evidenced by distinct horizon clustering in weighted and unweighted Unifrac analysis, with the O horizon possessing a greater proportion of the core microbiome in regards to the genus level and both horizons exhibiting large numbers of significantly distinct indicator taxa. Additionally, a number of differentially expressed pathways between the two horizons have roles in nutrient cycling which may have impacts on Douglas fir growth. Our findings suggest a strong correlation between microbiomes in relation to horizons. Future research should thus aim to incorporate horizon depth and classification when investigating soil microbial communities. Furthermore, currently, our results are limited to British Columbian Douglas-firs and with microbial data present only post-logging. Future research should consider different tree covers across different sites to investigate a possible significant effect based on the horizon. Additionally, collecting samples from the same site pre and post-logging could help to establish a stronger causal relationship across patterns observed with microbial diversity and differing horizons. Similarly, we suggest collecting samples at varying intervals of depth and across multiple horizons. Investigating the differences in diversity with these metrics would determine if similar results are found and once more increase the possibilities of determining causal relationships with horizon type. Such research would help to gain insights into the role of soil microbiomes as reforestation continues.

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**CONTRIBUTIONS**

Ally contributed to all methods, results and discussion relating to PICRUSt2 analysis and helped with the introduction. Anu contributed to the introduction, and all methods and discussion relating to Indicator Species Analysis. Fatima contributed to all methods, results and discussions relating to alpha and beta diversity analysis. Jas contributed to all results and discussion relating to Indicator Species Analysis, and references. Vera contributed to all methods, results and discussion relating to Core Microbiome, and acknowledgements. Everyone proofread and edited one another’s works.

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