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RESEARCH ARTICLE

Metagenomic of soil microbiota from a tea plantation in Malaysia

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Abstract

Soil microbiota plays an important role in maintaining soil health and supporting functional ecosystems including tea plantation. In this study, a soil sample from a tea plantation in Malaysia was subjected to 16S rDNA metagenomic sequencing followed by bioinformatic analysis in order to gain insights into the diversity and composition of highland tea plantation soil microbial communities. The microbial composition at the phylum level was dominated by *Proteobacteria* (50.64%), followed by *Acidobacteriota* (12.11%), and *Bacteroidota* (8.97%) whereas at class level, *Gammaproteobacteria* (31.56%), *Alphaproteobacteria* (19.08%), and *Bacteroidia* (8.35%) were predominant in the soil sample. This study reveals a highly diverse bacterial community in the tea soil which plays an important functional role for sustainable tea cultivation. The presence of various low-abundance and unclassified genera also reflects the complex ecological interactions within the tea plantation soil and suggests the potential for discovering novel microbial functions. Overall, our findings highlight the ecological importance of soil microbial communities in highland tea plantation and posit the need to integrate microbial management into sustainable agriculture practices. Continuous efforts are required to profile and understand these microbial ecosystems in the tea plantation in order to enhance the soil fertility, improve crop productivity, and mitigate the long-term environmental impacts in tea-growing regions.

Keywords: 16S, bacteria, metagenomic, microbiota, soil, tea

INTRODUCTION

Soil microorganisms are vital for maintaining soil health and play major ecological roles in both natural and agricultural ecosystems as they drive essential processes such as nutrient cycling and organic matter decomposition (Yi et al., 2022). In an agricultural ecosystem, such as tea plantations, the microbial communities are shaped by a multitude of interacting factors such as agricultural management, plant species, and soil characteristics. As such, different tea plantation soils may harbour unique distributions of bacterial communities and their dynamic interactions with soil chemical properties influence metabolic pathways in tea plants that ultimately shape key quality attributes of tea such morphology, flavour and aroma (Li et al., 2025). In Malaysia, the Cameron Highlands is recognized as the country's premier tea-producing region and the BOH Tea Plantation (BOH Plantations Sdn. Bhd., 2025) is one of the leading estates in Cameron Highlands. Established in 1929 by British entrepreneur J.A. Russell, the BOH Tea Plantation is Malaysia's largest black tea manufacturer and a pioneer of the national tea industry (L. Kui et al., 2021).

BOH has become synonymous with highland tea production and with an annual production of approximately 4 million kilograms of tea, BOH Tea is one of Malaysia's major commercial crops (Ng et al., 2022). BOH, which stands for "Best of Highlands", reflects not only the brand's heritage but also its connection to the unique agroclimatic conditions which are characterized by high altitude, cool temperatures, abundant rainfall, and acidic soil. These factors not only contribute to the distinctive quality of BOH teas but also support about 70% of Malaysia's tea production (Remco Verwoerd & Facenda, 2013). Despite these environmental

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advantages, the long-term sustainability and productivity of tea plantations in the highlands are closely linked to the health of the underlying soil ecosystem, which plays a vital role in supporting crop growth and maintaining environmental balance. Profiling the BOH plantation soil is particularly significant because tea is a major cash crop in Malaysia, and the highland ecosystem presents unique environmental conditions that influence microbial diversity compared to lowland soils.

Several studies have investigated the soil microbial diversity of tea plantations using 16S metagenomic sequencing. For instance, a study that analyzed bacterial communities in ancient tea plantation soils in China, using high throughput 16S and ITS sequencing, has found that soil pH, altitude, and latitude strongly influenced microbial diversity, with bacterial communities being more sensitive to environmental factors (Ling Kui et al., 2021). Another study examined the rhizospheric bacterial communities of ancient wild tea plants along an elevation gradient in the Ailao Mountains, China, using 16S rRNA sequencing (Wang et al., 2017). However, such studies in Malaysia remained scarce and no comprehensive microbial profiling has been conducted on the BOH Tea Plantation which serves a major contributor to the national tea industry. Hence, this study aims to explore the microbial diversity in the unique highland agricultural ecosystem of BOH Tea Plantation soil by using 16S metagenomic sequencing. By characterizing both microbial community composition and functional potential, this study not only provides insights into the ecological roles of soil bacteria in nutrient cycling but also addresses a current knowledge gap in Malaysian highland agriculture. These findings contribute to a better understanding of how soil microbiota shape tea plantation ecosystems and offer valuable information for advancing sustainable agricultural practices and environmental management.

MATERIALS AND METHODS

Sample collection

A 10 g of soil sample was collected using random grab sampling from the BOH Tea Plantation in Brinchang, Cameron Highlands (4°31'01.3"N 101°24'42.7"E) at a depth of 5-10 cm using hand trowel. The soil sample was preserved at -20°C to preserve microbial diversity for subsequent DNA extraction.

DNA extraction

The DNA for metagenomic sequencing was extracted from 0.25 g of soil sample by using the DNeasy PowerSoil Kit (Qiagen, USA). The concentration and purity of the extracted DNA were assessed by using Biospectrometer (Eppendorf, Germany) and NanoDrop spectrophotometer (Thermo Fisher Scientific, USA).

16S metagenomic sequencing

The sequencing library was constructed by using the MetaVX 16S rDNA Library Preparation Kit (Genewiz, USA) to amplify the V3-V4 hypervariable regions of the bacterial 16S rDNA gene via a two-round PCR protocol. The 16S rDNA metagenomic sequencing was performed on the Illumina MiSeq platform (USA).

Bioinformatics analysis

Data processing

The raw data were analysed by using the Illumina utility Bcl2fastq (v2.20) for base calling and pre-processing steps.

Operational Taxonomic Unit (OTU) analysis and species annotation

OTU clustering was performed by using QIIME (v1.9.1) (Caporaso et al., 2010) and VSEARCH (v1.9.6) (Rognes et al., 2016) to group similar sequences based on a 97% sequence similarity threshold (Edgar, 2018b), facilitating microbial community analysis. To assign taxonomic classification, a representative sequence from each OTU was selected and annotated by using the Ribosomal Database Project (RDP) classifier, enabling the characterisation of microbial communities within sample (Edgar, 2018a; Kõljalg et al., 2005; Quast et al., 2013; Wang et al., 2007; Yilmaz et al., 2013).

Functional analysis

The functional profile of the microbial community was predicted by using PICRUSt2 (Douglas et al., 2020) and abundance table was generated based on metabolic pathways and enzymes from all domains of life in MetaCyc database (Caspi et al., 2020).

Alpha diversity analysis

Alpha diversity was assessed to evaluate species richness and diversity within sample by using QIIME (v1.9.1) (Caporaso et al., 2010). Species richness was estimated using the ACE and Chao1 indices, both of which infer the total number of OTUs present in the

sample. Community diversity was evaluated using the Shannon and Simpson indices, which reflect both the abundance and evenness of species. Sequencing depth and coverage were assessed using Good's coverage index and rarefaction curve analysis to determine the completeness of sampling. All indices were calculated based on representative OTUs to provide a comprehensive view of the microbial diversity within the sample.

Phylogenetic analysis

A phylogenetic tree was constructed based on inference of approximately-maximum-likelihood using multiple sequence alignments of the top 30 OTU representative sequences. The analysis was performed to infer the evolutionary relationships among OTUs. Branches in the phylogenetic tree were color-coded according to their corresponding phyla, with each colour representing a distinct phylum, enabling clear visualization of taxonomic composition at the phylum level.

RESULTS AND DISCUSSION

Microbial diversity analysis

After quality control, a total of 200,916 reads with 250 bp in length were retained and used for subsequent analysis. A total of 585 bacterial OTUs belonging to 29 phyla, 63 classes, 127 orders, 161 families, 183 genera, and 55 species were obtained based on a 97% sequence similarity threshold. The microbial composition at the phylum level (Figure 1) in the soil sample was dominated by *Proteobacteria* (50.64%), followed by *Acidobacteriota* (12.11%), and *Bacteroidota* (8.97%). Subdominant phyla included, *Nitrospirota* (5.61%), *Actinobacteriota* (4.47%), and *Chloroflexi* (3.48%), showing a composition similar to previous studies on tea plantation soils, particularly associated with a tea plant, Camellia sinensis (Lynn et al., 2017; Zheng et al., 2023; Zi et al., 2020). In addition, *Gemmatimonadota* (2.48%), *Myxococcota* (2.16%), *Latescibacterota* (2.04%), and an uncultured phylum, *RCP2-54* (1.45%) were detected in smaller proportions.

The dominance of *Proteobacteria* and *Bacteroidota* was further reflected at the class level (Figure 1), particularly within *Gammaproteobacteria*, *Alphaproteobacteria*, and *Bacteroidia* with the relative abundance of 31.56%, 19.08%, and 8.35%, respectively. Similar findings have been reported in tea orchard soils (Chen et al., 2021; Li et al., 2016), highlighting the prevalence of these bacterial groups in tea plantation ecosystems. At genus level (Figure 2), the most dominant category is labelled as "Others", indicating a high proportion of low-abundance genera collectively contributing to the microbial community. This suggests a diverse community where no single genus significantly dominates. Among the identified genera, *Nitrospira*, *TRA-3-20*, *Terrimionas*, *MND1, Vicinamibacteraceae* were among the most abundant. Additionally, the presence of several unclassified taxa suggests that a significant portion of the microbial community consists of less well-characterized bacteria.

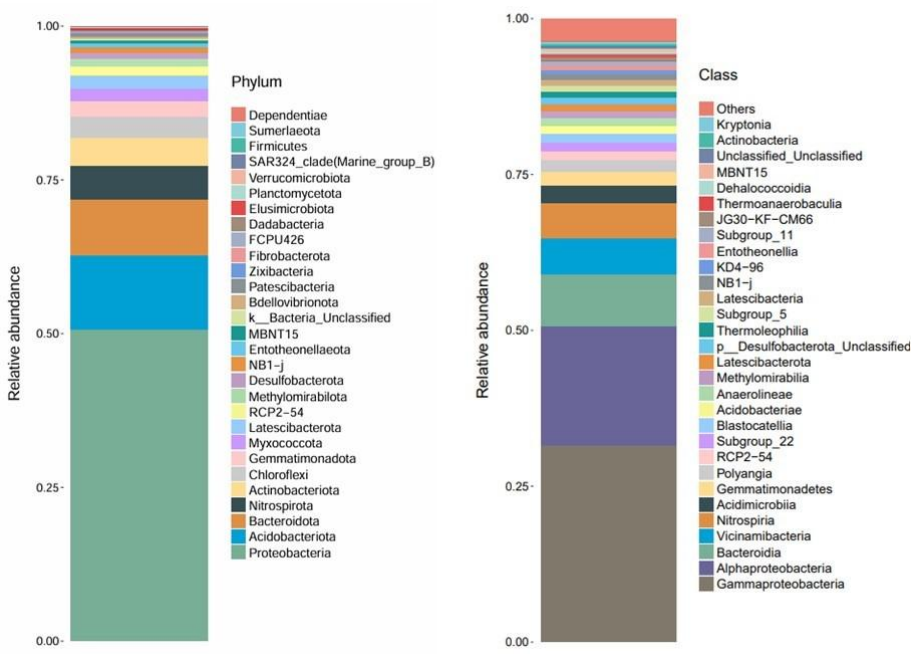

Figure 1. The top 30 species distribution at phylum level (left) and class level (right).

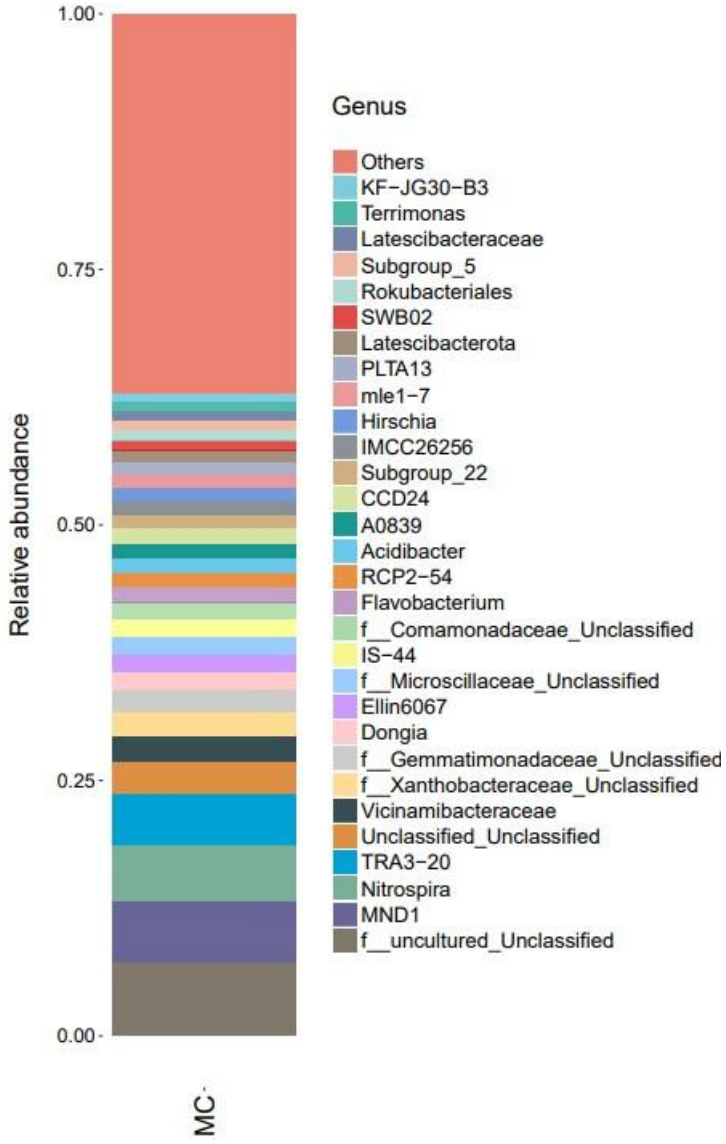

Figure 2. The top 30 species distribution at genus level.

Potential microbial functional variations influenced by tea soil

Soil microorganisms are essential for decomposing organic matter, regulating carbon storage, and nutrient cycling. They contribute significantly to ecosystem functions, including enhancing plant nutrient uptake (Delgado-Baquerizo et al., 2020). Consequently, they are widely used as key indicators for evaluating soil quality. *Proteobacteria*, now known as *Pseudomonadota* (Oren & Garrity, 2021), emerged as the most dominant bacterial phylum in this study, aligning with findings from various agricultural ecosystem studies (Borneman et al., 1996; Janssen, 2006; Lynn et al., 2017; Smit et al., 2001). The prevalence of this Gram-negative bacterial group in soil environments may be linked to long-term nitrogen fertilization, as members of this group are central to nitrogen transformation processes, including ammonia oxidation and nitrification (Jibola-Shittu et al., 2024; Kersters et al., 2006; Wang et al., 2023; Zhang et al., 2022)

Among the different classes of *Proteobacteria*, *Gammaproteobacteria* and *Alphaproteobacteria* were the most abundant observed in this study, a pattern consistent with previous findings. These classes are positively correlated with soil nitrogen availability, particularly soil organic carbon (SOC), total nitrogen (TN), and available nitrogen (AN) (Li et al., 2016). *Gammaproteobacteria* are typically associated with nutrient-rich conditions and contribute to disease suppression by producing bioactive compounds via non-ribosomal peptide synthase. In contrast, *Alphaproteobacteria* are oligotrophic organisms, capable of thriving in nutrient-poor environments, and play a key role in nitrogen fixation, often in association with plants (Ling Kui et al., 2021; Li et al., 2016). An

ecologically important group within *Alphaproteobacteria* is the order *Rhizobiales* (Beeckmans, 2009; Choma et al., 2017), which forms a symbiotic relationship with plants, converting atmospheric nitrogen into a bioavailable form through nitrogen fixation. This is especially relevant for tea cultivation, where maintaining soil fertility is crucial. The prevalence of *Proteobacteria*, especially nitrogen-fixing *Alphaproteobacteria* and nutrient-responsive *Gammaproteobacteria*, suggests that these microbial communities contribute to nutrient cycling, soil health, and potentially enhancing the resilience of tea plants under intensive agricultural management.

The *Acidobacteriota* phylum is highly abundant in the soil sample, thriving in acidic conditions with an optimal growth pH of tea plants (4.5 to 5.5), reflecting their acidophilic nature (Tang et al., 2025). *Acidobacteriota* widespread across diverse ecosystems but remain difficult to culture due to their oligotrophic nature or ecological K-strategy (Eichorst et al., 2018; Kielak et al., 2016). In tea plantation soils, their dominance increases with the age of tea plants, potentially linked to long-term fertilizer and pesticide use which contribute to soil acidification (Wang et al., 2019). Genomic evidence shows that *Acidobacteriota* possess genes for carbon, nitrogen, and sulfur cycling, as well as cellulose synthesis, exopolysaccharide (EPS) synthesis, hopanoids synthesis, siderophore synthesis, and transporter systems (Kalam et al., 2020; Yadav et al., 2021) , supporting their role in soil stability and microbial interactions (Crits-Christoph et al., 2018; Kielak et al., 2016; Ward et al., 2009). Their abundance in tea plantation soilsthus indicates functional contributions to soil health and tea quality.

The phylum *Bacteroidota* represents a highly versatile group of bacteria with unique molecular mechanisms that enable them to occupy distinct ecological niches (Lidbury et al., 2021). These bacteria are key players in carbohydrate degradation across two vastly different environments - the soil and the human gut (Gibiino et al., 2018; Larsbrink & McKee, 2020). While *Bacteroidota* are well-studied as key members of the human gut microbiome, their functional roles in soil microbiomes remain largely unexplored (Pan et al., 2023). As a dominant phylum in soil microbial communities, *Bacteroidota* thrive due to their ability to secrete a diverse array of carbohydrate-active enzymes (CAZymes), facilitating the breakdown of complex glycans (Larsbrink & McKee, 2020). Additionally, they possess genes associated with denitrification, indicating their role in nitrogen cycling (Chaparro et al., 2014; Yousuf et al., 2012), along with a potential role in phosphorus cycling (Wang et al., 2018).

Beyond the dominant phyla, several subdominant phyla also contributing to soil functionality. One key process in the terrestrial nitrogen cycle is nitrification, which involves the biological oxidation of ammonia to nitrate via nitrite (Chisholm et al., 2023; Palomo et al., 2022). However, excessive nitrification can lead to several environmental issues, including the loss of nitrogen fertilizers (Lassaletta et al., 2014), nitrate pollution in groundwater (Saâdi & Maslouhi, 2003), increased emissions of nitrous oxide, a potent greenhouse gas (Wrage et al., 2001), and soil acidification (Vitousek et al., 1997). Traditionally, nitrification was thought to occur in two sequential step process, mediated by distinct groups of microorganisms: ammonia-oxidizing archaea (AOA) and bacteria (AOB), followed by nitrite-oxidizing bacteria (NOB) (Daims et al., 2015; Séneca et al., 2020). However, recent discoveries have challenged this perception. Certain species within the phylum *Nitrospirota* and genus *Nitrospira* are capable of oxidizing ammonia to nitrate within a single cell, a new group of aerobic ammonia-oxidizing prokaryotes now known as complete ammonia oxidizers, or comammox (Daims et al., 2015; van Kessel et al., 2015). Studies have revealed that comammox *Nitrospira* can thrive under acidic conditions commonly found in heavily fertilized tea plantation soils, playing a crucial role in nitrogen cycling. Researchers successfully enriched multiple comammox *Nitrospira* phylotypes, demonstrating that their growth is influenced by ammonium availability and pH regulation (Takahashi et al., 2020).

Another bacterial phylum in soil ecosystems is *Actinobacteriota*, a group of Gram-positive bacteria characterized by a high guanine (G) and cytosine (C) content in their DNA. They are one of the largest and ubiquitously distributed bacterial phyla in both aquatic and terrestrial ecosystems. In soil, most of the *Actinobacteriota* are soil-dwelling organisms that exist as semidormant spores, particularly under nutrient-limited conditions (Mayfield et al., 1972). They can be found at varying depths, from the soil surface to more than two meters underground (Goodfellow & Williams, 1983). *Actinobacteriota* are key players in soil microbial communities, thriving due to their antagonistic and competitive nature (Bulgarelli et al., 2013). Their biocontrol properties help suppress soil-borne pathogens by producing antibiotics and other secondary metabolites that prevent pathogen colonization. Additionally, they promote plant growth through nitrogen fixation and siderophore production, which enhances iron availability. These bacteria also synthesize phytohormones that stimulate root and shoot development while facilitating the solubilization of essential minerals, improving nutrient bioavailability for plant uptake (Barka et al., 2015).

Chloroflexi are one of the main bacterial species participating in the nitrification and denitrification process in the soil (Calderoli et al., 2018; Fernández et al., 2009), contributing to nitrogen cycling within the ecosystem. Similarly, bacteria from the phylum *Gemmatimonadota* are frequently detected in environmental 16S rDNA gene libraries and have been identified as one of the top nine phyla found in soils, making up approximately 2% of soil bacterial communities (DeBruyn et al., 2011; Janssen, 2006). They are particularly abundant in arid soils, indicating an adaptation to low-moisture environments (DeBruyn et al., 2011). Within this phylum, *Gemmatimonas* are known to promote nitrogen transformation and fixation (Park et al., 2017), further contributing to soil fertility. Meanwhile, *Myxococcota*, another key bacterial group in soil ecosystems, play essential roles in microbial predation and are generally regarded as a minor component of soil bacterial communities (Zhou et al., 2014). As facultative predators, they can utilize macromolecules such as organic matter and dead cells, as well as prey on living microorganisms for sustenance. Consequently, both abiotic and biotic factors play a crucial role in shaping myxobacterial communities (Zhou et al., 2020). Additionally, an increase in the relative abundance of *Latescibacterota* has been associated with enhanced soil aggregate stability (Lan et al., 2022), potentially improving soil structure and resilience.

Nitrogen plays a crucial role in soil carbon storage and tea production within the tea plantation ecosystem (Ma et al., 2021; Yang et al., 2023). Genes for carbon degradation, such as chitinase and beta-glucosidase, are enriched under nitrogen fertilization, predominantly carried by the bacterial phyla *Acidobacteria*, *Proteobacteria*, *Actinobacteriota*, *Chloroflexi*, and *Bacteroidota* (Mondal et al., 2025). It is typically recycled by nitrogen-metabolizing microbiomes present in the rhizosphere, which enhance nitrogen absorption of plant usable forms, ultimately influencing tea growth and yield (X. Liu et al., 2022). Within the tea root system, nitrogen-metabolizing soil microbiomes, particularly *Proteobacteria*, *Actinobacteriota*, and *Chloroflexi*, have been reported in facilitating ammonia uptake and subsequent conversion into theanine, which is a key determinant of distinct tea flavour (Cheng et al., 2017; Dong et al., 2020; Xin et al., 2024).

Highly fertile soils tend to support greater bacterial diversity, with a higher prevalence of *Proteobacteria*, *Nitrospirota*, *Chloroflexi*, and *Bacteroidota* and enhanced microbial processes, including nitrate reduction, ammonia oxidation and aromatic compound degradation, as they harbour species enriched with genes associated with these processes. In contrast, low fertile soils show lower bacterial diversity and favoured cellulolytic activity (Paes da Costa et al., 2024). Additionally, the enrichment of *Nitrospirota*, *Proteobacteria*, *Chloroflexi*, and *Bacteroidota* has been associated with improved soil health. Increased nutrient availability in soil has been found to create conditions similar to those observed in the rhizosphere, where nitrogen and total organic carbon concentrations are elevated (S. Liu et al., 2022). While *Acidobacteria*, *Chloroflexi*, *Gemmatimonadota*, and *Nitrospirota* are commonly enriched in bulk soil, exhibiting oligotrophic (k-strategist) behaviour, *Bacteroidota*, *Proteobacteria*, and *Actinobacteriota* are predominantly copiotrophic (r-strategist) groups (Kalam et al., 2020; Ling et al., 2022) that thrive in resource-rich conditions such as the rhizosphere. Copiotrophic bacteria are adapted to carbon-rich conditions, supporting high metabolic activity, rapid growth, and propagation, which are the characteristics align with the dynamic nature of the rhizosphere (Kuzyakov & Razavi, 2019; Pausch et al., 2013).

The dominance of copiotrophic *Proteobacteria* and *Bacteroidota* alongside oligotrophic *Acidobacteriota* also suggests a dynamic balance between nutrient-enriched and nutrient-limited niches shaped by intensive tea cultivation. Together, these findings extend beyond confirming known phylum-level patterns by pointing to hidden microbial diversity and site-specific ecological interactions in Malaysian tea agroecosystems. Beyond these well-established patterns, our dataset revealed a high proportion of unclassified genera which is labelled as 'Others' (Figure 2) and the presence of poorly resolved groups such as *RCP2-54*, *Subgroup_22*, *TRA3-20*, and KF-JG30-B3, for example. This suggests that tea plantation soils harbour novel or underexplored microbial taxa with potential functional importance. Such findings highlight the need for deeper taxonomic and functional resolution in tea agroecosystem microbiomes, which could uncover previously overlooked contributors to soil fertility and tea quality.

In the Figure 3, *Proteobacteria* (red) emerges as a dominant and diverse group, with multiple genera clustering together. Other notable phyla include *Nitrospirota* (green), *Acidobacteria* (orange), and *Bacteroidota* (blue), each forming distinct clusters. Additionally, *RCP2-54* (light green) appears as a separate group within the tree, suggesting it represents a distinct taxonomic group with an unresolved classification. This phylum remains unclassified in taxonomic databases, suggesting it is either newly discovered or poorly studied. The placement of *RCP2-54* near *Rokubacteriales* and *Vicinamibacteraceae* suggests possible evolutionary relationships with these groups. The presence of

unclassified taxa highlights the potential existence of novel bacterial taxa that require further investigations.

In order to gain a deeper insight into the functional composition of the sampled bacterial community, PICRUSt2 was used to predict the community's functional potential based on the 16S rDNA gene sequencing profiles. PICRUSt2 predicted a total of 492 metabolic pathways that were enriched in this soil sample and the top ten enriched pathways are peptidoglycan maturation, phytol degradation, fatty acid salvage or β-oxidation degradation, L-valine biosynthesis, cis-vaccenate biosynthesis, gondoate biosynthesis (anaerobic), fatty acid β-oxidation II (plant peroxisome), L-isoleucine biosynthesis I (from threonine), pentose phosphate pathway (non-oxidative branch) I and TCA cycle V (2-oxoglutarate synthase). These pathways can be further grouped into four functional categories: cell wall biosynthesis, lipid metabolism, amino acid biosynthesis and central carbon metabolism. Peptidoglycan is the main component of bacterial cell wall and this enriched pathway indicates active bacterial growth in the soil sample. The lipid metabolism pathway (phytol degradation, fatty acid salvage, cis-vaccenate biosynthesis, gondoate biosynthesis and fatty acid β-oxidation II) is potentially linked to the presence of plant-derived lipids and phytol in the soil sample which are broken down by the microbial community (Gutbrod et al., 2019; Lu et al., 2025). The amino acid biosynthesis (L-valine biosynthesis and L-isoleucine biosynthesis I) supports microbial protein synthesis and nitrogen cycling (Li et al., 2023). Lastly, the central carbon metabolism (pentose phosphate pathway I and TCA cycle V) reflects robust microbial energy production and biosynthetic capacity in the microbial community (Lu et al., 2025).

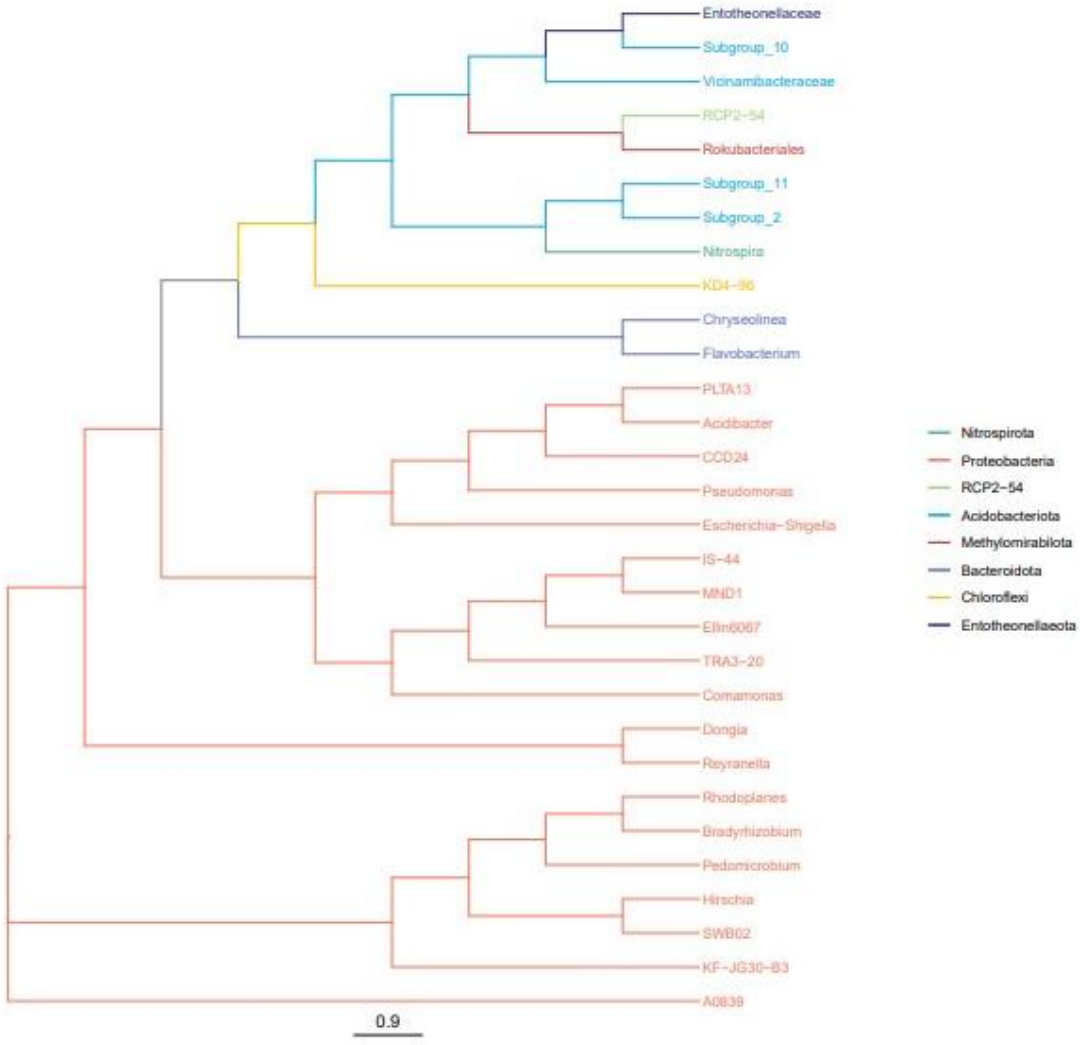

Figure 3. Maximum likelihood tree from alignments of the top 30 OTU sequences. The branches are color-coded according to bacterial phyla.

Alpha diversity index

The alpha diversity indices (Table 1) provide insights into the richness and evenness of the microbial community in this sample. The ACE and Chao1 indices, both at 585, suggest high species richness and indicate that most species have been detected, with few rare species remaining undiscovered. The Shannon index of 8.212 reflects high microbial diversity and an even species distribution, while the Simpson index of 0.994 confirms that no single species dominates the community. Additionally, Good's coverage of 1 agrees with the rarefaction analysis that overall microbial diversity was encompassed by the sequencing effort. Overall, the sample exhibits a diverse and well-balanced microbial diversity that has been effectively captured by sequencing.

Rarefaction curve

According to rarefaction analysis (Figure 4), the number of OTUs plateaued after 30,000 sequences. This suggests that the sequencing depth was sufficient to relatively and accurately capture the richness of the microbial diversity in this sample.

Table 1. Alpha diversity indices of the soil sample.

Index	Value
ACE*	585
Chao1	585
Shannon	8.212
Simpson	0.994
Good's coverage	1

*ACE (Abundance-based Coverage Estimator)

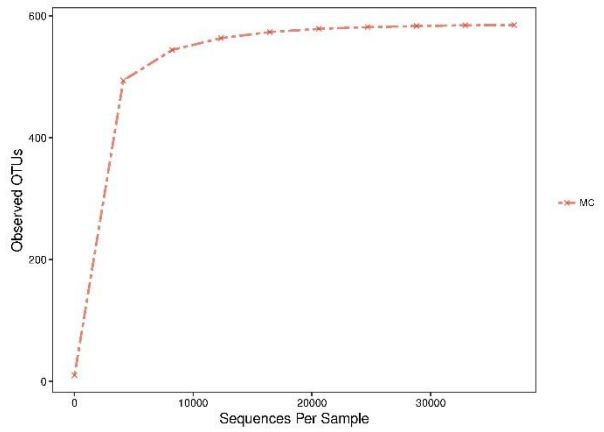

Figure 4. Rarefaction curve. X-axis represents the number of sequences per sample, showing how sequencing depth affects the number of observed OTUs, while Y-axis represents the number of observed OTUs, which measures species richness.

CONCLUSION

In this study, we provide insights into the soil microbial community structure of the BOH Tea Plantation in Cameron Highlands, Malaysia. A comprehensive assessment via 16S rDNA metagenomic sequencing revealed a highly diverse bacterial community, predominantly composed of *Proteobacteria*, *Acidobacteriota*, *Bacteroidota*, *Nitrospirota*, *Actinobacteriota*, and *Chloroflexi* in the soil sample. These phyla are known to play crucial roles in functions essential for sustainable tea cultivation. The high microbial diversity observed, including various low-abundance and unclassified genera, reflects the complex ecological interactions within the tea plantation soil and suggests the potential for discovering novel microbial functions. Although the microbial community structure may be region-specific in the vast plantation estate, the soil microbiota characterized highlight the ecological importance of soil microbial communities in highland tea plantation and underscore the need to integrate microbial management into sustainable agriculture practices as prior studies in tea plantations have shown how organic management enhanced microbial diversity and enriched beneficial taxa (Tan et al., 2019) as well as improved tea quality (Lei et al., 2024). Continuous efforts to profile and understand these microbial ecosystems will aid in enhancing soil fertility, improving crop productivity, and mitigating long-term environmental impacts in tea-growing regions. Considering that no generalizable conclusion can be drawn from the current study due to the microbial-centric analysis of a single soil sample, future work should expand upon these findings by incorporating multiple biological replicates, sampling across different sites, soil depths, and seasonal intervals, while also correlating the microbial diversity with the physicochemical properties of the soil to provide a more robust and comprehensive picture of microbial community dynamics in tea plantation ecosystems. In addition, the effects of environmental and anthropogenic stress factor such as pesticide use, fertilizer application, and land-use changes on diversity and function of microbial communities would further enhance ecological inferences and their potential applications in environmental management and sustainable agriculture. Moreover, including actual measurements or correlations with plant yield or other tea quality metrics could provide valuable insights into how soil microbial diversity and functionality contribute to plant health and overall tea production.

CONFLICT OF INTEREST

The authors have declared that no conflict of interest exists.

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