National Conference on Sustainable Developments in Engineering, Science, Humanities and Management (NCSDESHM – 2025)
28th December, 2025, Raipur, Chhattisgarh, India.

CERTIFICATE NO: NCSDESHM /2025/ C1225979

A Study to Evaluate Microbial Activity and Soil Properties in Tea Garden Soils

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ABSTRACT

Soil in tea plantations is essential for the growth of robust tea plants since it supplies water, nutrients, and a conducive environment for helpful microorganisms. The objective of this study was to investigate the soil microbiology and particular soil attributes of tea garden soils. We assessed the pH, organic content, moisture levels, available nutrients, and microbial activity of soil specimens collected from different sections of the tea garden. Soil microorganisms play an essential role in decomposition, nutrient reclamation, and the enhancement of soil fertility. Soil properties and microbial activity are mutually influential, and this study elucidates the interaction between these elements in maintaining the health and productivity of tea garden soils. The findings might assist in sustainable tea cultivation, the preservation of soil fertility, and the enhancement of soil management practices.

Keywords: *Soil Microbial, Tea Garden, Plant, Nutrient, Bacteria.*

I. INTRODUCTION

A wide variety of bacteria, fungi, and viruses make up the soil microbial community, an integral component of the soil ecology. Organic matter decomposition, nutrient cycling, and gaseous fluxes are all mediated by soil microbes. Soil geochemistry, including pH, trace metal and other element content, and phosphorus availability, is impacted by these microbes, which in turn affects plant nutrient availability and stress resistance. Soil cycling and transformation processes make accessible to plants the basic nutrients—carbon, nitrogen, phosphorous, sulphur, and potassium—needed for growth and development, in addition to carbon, which plants get by photosynthesis. Soil microbes play an active mediating role in these processes, and soil fertility is determined by the availability of these nutrients for plant absorption. Soils that are rich in nutrients tend to have a wider variety of bacteria living in them, especially Proteobacteria, Nitrospira, Chloroflexi, and Bacteroidetes. These soils also are better able to break down aromatic compounds, nitrate, and ammonia than soils that aren't as rich in nutrients. A good indicator of soil fertility and a correlate with crop production for many crops is the presence of bacteria from major groups engaged in nitrogen-cycling activities and soil nitrogen balance maintenance.

Also, the soil microbiome may help with heavy metal bioremediation, which is great for plant health but might have negative consequences for the tea leaves' quality and the people who ingest them. The nitrogen-metabolizing microorganisms in the rhizosphere typically recycle nitrogen, an essential element for tea plant growth and leaf quality. This allows for improved absorption of nitrogen in plant-useful forms (NO^{-}_3 and NH^{+}), which in turn can affect tea plant growth and yield. Root systems of tea plants convert ammonia to theanine, a non-protein amino acid that gives tea its distinctive rich flavour, when the roots draw nitrogen from the soil. Afterward, the theanine is transferred to the tea-harvested leaves and new shoots. According to reports, a group of soil microbes mainly from the Proteobacteria phylum, along with members of the Actinobacteria, Firmicutes, Chloroflexi, and Armatimonadetes, can improve the flavour and quality of tea by increasing ammonia uptake and theanine synthesis.

A great deal of tea "gardens" or regions of tea cultivation have persisted, i.e. been consistently farmed with C. sinensis, for long stretches of time, often generations. This makes tea farming distinctive. The long-term cultivation of tea plants in some locations has probably led to complex webs of interactions between the plants and the soil microbes, including perhaps novel co-adaptations. The variety of microorganisms, both helpful and detrimental to plants, may be affected by the substantial imports of fertiliser, pesticides, and even soil from other regions into many tea-growing regions. The myriad insect pests and microbiological illnesses that plague tea gardens are just one more thing that these plants must contend with. Some tea plantations, as said, employ large quantities of pesticides and fertilisers to produce high yields, which, over time, may lead to a decrease in soil microbial diversity and, in turn, has a detrimental effect on the ecosystem. Since most tea plantations are located on higher ground, any chemical fertilisers or pesticides used on the plants have a good chance of washing downstream and contaminating nearby bodies of water.

Soil microbial communities play an important role in improving soil health and suppressing plant diseases, and several research on tea garden soils have shown that a wide variety of microorganisms are present, which is associated with higher-quality tea. Keystone bacterial taxa including Bacillus, Burkholderia, Serratia, and Arthrobacter have been shown to exhibit a broad variety of growth-promoting properties, according to studies that used a culture-dependent technique and molecular identification of bacterial isolates using 16S rRNA gene sequencing. It has been reported that a Burkholderia pyrrocinia strain isolated from the tea rhizosphere contributes to abiotic stress tolerance and possesses plant growth-promoting activities through phosphorus solubilisation and production of phytohormones. Another example is the characterisation of the phosphorus solubilising abilities in Bacillus and Burkholderia isolated from rhizospheric soil samples of tea gardens in West Bengal, India. Furthermore, it was found that a Serratia marcescens biocontrol strain was effectively used to combat fungal root pathogens in tea. This strain produced antibiotics and hydrolytic enzymes like chitinase, protease, lipase, and cellulase. Research like this suggests that understanding the microbiome of tea soils and how it contributes to higher-quality tea should be a priority for anyone looking to improve nutrient availability in tea gardens and, by extension, plant yield and quality.

Agricultural ecosystem development and restoration efficacy testing may both benefit from investigations into soil microbial diversity. Such research may provide light on the roles of microbes and show how tea estates might use them to their advantage. Soil microbial phylogeny mapping has recently benefited substantially from culture-independent metagenomics approaches. Improvements in rDNA homology and descriptions of biosynthetic pathways have resulted from the development and refinement of molecular techniques, such as high-throughput sequencing, which have substantially boosted the study and understanding of soil microorganism diversity and interactions. As a result, metagenomic analyses are being used to characterise soil microbial diversity by directly capturing total soil microbial DNA, which provides a window into functional aspects of soil microorganisms. These analyses are also highly reliable and convenient for characterising root-associated microorganisms.

II. REVIEW OF LITERATURE

Jibola-Shittu, Motunrayo et al., (2024) The leaves of the Camellia sinensis plant are the basis for tea, a globally beloved beverage that boasts a number of healthful bioactive compounds. Sustainable tea cultivation has the potential to open up new agricultural opportunities and alleviate extreme poverty, among other far-reaching consequences, and is thus essential for economic reasons. The fact that different types of soil produce different quality leaves is well-known. Consequently, it may be possible to improve tea quality and production by making use of soil microbial communities, which may be enhanced by learning about the diversity and functions of soil microbes in tea gardens. Soils in tea gardens are rich in microbes, including bacteria and fungi, according to recent studies. Acidobacteria, Firmicutes, and Chloroflexi are the most prevalent bacterial groups, whereas Ascomycota, Basidiomycota, and Glomeromycota are the most prevalent fungal families. During their peak productivity, these microbes serve as biofertilizers, biocontrol agents, regulators of the nutrient cycle, and POC bioremediators, all of which contribute to the upkeep of healthy soil ecosystems in gardens. Soil microorganisms, including bacterial and fungal species, have been studied for their potential as biofertilizers, biological control agents, and bioremediators in tea gardens. This page summarises the research on the topic. Improving soil health will lead to higher yields and better quality tea, which is why these research are important. Recent advances in molecular technologies allow for an investigation of the many microorganisms discovered in tea gardens. about viruses, there is less information about the effectiveness of soil viruses in tea gardens. However, there have been instances when insect pathogenic viruses have been used to control pests in tea. This study delves into the potential of soil microbes and highlights current methods used to investigate microbial diversity and genetic manipulation in order to increase tea plant productivity and quality for sustainable production.

Billah, Sk et al., (2022) Soil samples were taken from tea gardens in Sylhet and Moulovibazar in northeastern Bangladesh. The pH, organic matter, C/N ratio, Na, K, Ca, Mg, S, Fe, and Al were examined. In addition, we checked the drainage and texture of the soil. Very acidic or acidic soils are possible, as are sandy loams and loamy soils. They had a low nitrogen content (0.051-0.122%), pH range of 3.75-4.90, and organic matter content (0.87-1.60%). Also, because of their loss in the acidic environment, the excretable bases (Ca, Mg, Na, and K) are very low. A very low C/N ratio is seen. Soils with greater concentrations of iron, aluminium, and sulphur were the ones that were researched. The soils in question do not have sufficient quantities of organic matter, pH, nitrogen, salt, calcium, magnesium, or potassium to support the cultivation of tea plants. We used LSD to do statistical analysis at the 5% significance level.

Gill, Ankit et al., (2022) Analysing the opportunities and limitations presented by soils via the evaluation of various soil factors should facilitate the formulation of sustainable agricultural strategies. The objective of this research was to assess the current status of several soil characteristics in surface (0-0.30 m) and subsurface (0.30-0.60 m) layers across 37 randomly chosen tea estates in the tea-producing regions of Himachal Pradesh during the years 2017 and 2018. The gathered soil specimens underwent analysis for electrical conductivity, microbial enumeration, water-stable aggregates, porosity, particle density, exchangeable calcium and magnesium, and water stability via standardised testing methods. The soil specimens collected from tea plantations exhibited varying particle densities, porosities, and water-stable aggregates ranging from 26 to 58%. The electrical conductivity ranged from 85 to 210 dS m-1, exchangeable calcium from 1.2 to 4.0 cmol (p+) kg-1, and magnesium from 0.6 to 2.3 cmol (p+) kg-1, with mean values of 134±35.8, 2.7±0.8, and 1.4±0.4, respectively. The microbiological assessment indicated bacterial counts between 49 and 71 x 10^6 CFU, fungal counts from 36 to 69 x 10^4 CFU, and actinomycete counts ranging from 31 to 58 x 10^4 CFU.

Yaling, Tian et al., (2013) Agroforestry methods are widely used by farmers worldwide as a means to maintain and even improve soil fertility. To better understand the impact of agroforestry on soil fertility, we measured organic carbon, total nitrogen, microbial biomass, basal respiration, enzyme activity, and tea Camellia sinensis (L.) O. Kuntze at three distinct soil depths (0–10, 10–20, and 20–30 cm). The study plots were located at Yushan Farm in Changshu, Jiangsu Province, China. One of them was a monoculture tea system (G0), the other two were hybrids of Ginkgo trees and tea (G1 and G2), and a third was a mix of the two. The findings showed that the amounts of carbon, nitrogen, microbial biomass, and enzyme activity were greater on the surface soil compared to the middle and deeper layers of soil. However, when the depth of the soil increased, the pH and metabolic quotient also rose. Phosphorus, microbial nitrogen and carbon biomass, basal respiration, and catalase and invertase activity in the 0-10 cm layer were all significantly reduced in G0 compared to G1 and G2. The polyphenoloxidase activity in the 0-10 cm layer was much lower in G2 when compared to G0 and G1. In the 20-30 cm layer, G0's metabolic quotient is much higher than G2's. Enzymes including catalase, dehydrogenase, urease, protease, and invertase in soil were positively and highly correlated with total nitrogen and organic carbon. The study's findings suggest that growing tea with Ginkgo might be a useful agroforestry practice. Soil organic matter accumulation, soil enzyme activity, soil sustainability, and production may all see improvements if this were to happen.

Balamurugan, A et al., (2013) In vitro cellulase activity testing and screening were conducted on isolated and characterised bacteria from tea garden soil. In terms of enzyme activity, these five strains were superior to the other twenty-five isolates. Although all three strains were cultivated on minimal salt medium, strains CDB 12, CDB 13, and CDB 21 exhibited the greatest levels of cellulase activity when exposed to blotting paper. The optimal conditions for cellulose degradation bacteria (CDB) were 30°C and 7.0 pH. Out of all the carbon sources tested, glucose supplemented mineral salts medium had the fastest growth rate, with fructose and maltose following closely after. The nitrogenation of CDB isolates with ammonium sulphate, ammonium nitrate, or potassium nitrate improved their performance. After the biomass was continuously removed from the tea field, natural and proven CDB strains were introduced to break down the harvested material. To maintain the tea field's productivity, it is necessary to refill this deterioration process.

Pansombat, Kanokpan et al., (2012) Protease activity was examined in tea soils to provide insight into the organic nitrogen breakdown process. At two depths, the hydrolysing activities of N-benzoyl l-arginine amide (BAA), N-benzyloxycarbonyl l-phenylalanyl l-Ieucine (ZPL), and N-benzyloxycarbonyl glycyl l-phenylalanine (ZGP) were investigated on soils in highland crop boils, acid tea soils, and uncultivated soils (soils with near neutral pH). Factors influencing protease activity were identified and accounted for based on the correlations with total nitrogen, total carbon, and microbial populations. Using a 0.2 M phosphate buffer (pH 8.1), the experiment demonstrated that among the three soil types tested (tea, upland crop, and uncultivated), BAA-hydrolyzing activity was the highest, followed by ZPL-hydrolyzing activity, and ZGP-hydrolyzing activity was the lowest. 2) The depth and type of soil had a bearing on the substrate specificity and amplitude of protease activity. Hydrolysing all of the utilised substrates was facilitated more rapidly by proteases in the surface layers (0-20 cm) as compared to those in the bottom layers (20-40 cm). The proteases in the lower layers hydrolysed BAA more effectively than their surface-layer cousins. Soils rich in volcanic ash may hydrolyse BAA and ZPL more effectively than soils deficient in this component. The presence or absence of upland crop cultivation and tea cultivation affected the quantity of protease activity. Soils established for growing upland crops (henceforth "upland crop soils") and those that remained uncultivated hydrolysed BAA more rapidly than soils established for growing tea (henceforth "tea soils"). The soil microbial community was shown to be closely connected to the hydrolysing activity of BAA or ZPL. Bacteria in acid tea soils are the most probable source of the hydrolysing enzymes BAA and ZPL.

Huidrom, Pratibha et al., (2011) Native bacterial isolates from tea garden soils were subjected to abiotic stresses like salt, pH, and temperature to determine their resistance. A total of 23 bacterial species were identified, including Azotabacter, Burkholderia, Enterobacter, and Rhizobium. Each bacterial isolate was cultured in a different broth with different pH levels (2.5 to 10.0), NaCl concentrations (0.1 to 4.5%), and temperatures (ranging from 15 to 70 °C) using a spectrophotometer after 48 hours of incubation at 28±2°C. Rhizobium, Azotobacter, Burkholderia, and Enterobacter were cultured in Yeast Extract Mannitol broths, Ashby's in an Azotobacter broth, and Luria in an Enterobacter broth. To further narrow down the possible bacterial isolates that might withstand various temperature shocks, we employed the thermal death point (TDP) technique. The standard for screening was the ability of fourteen distinct bacterial isolates to withstand these extreme conditions. In less than ideal conditions, these robust bacterial strains might be useful as PGPR (plant growth promoting rhizobacteria).

Han, Wenyan et al., (2007) Tea, whose scientific name is Camellia sinensis, grows best on acidic soils and even contributes to keeping them that way. There are valid worries about contamination due to the extensive use of fertiliser by tea stands to improve output and quality. Too little is known about the microbial ecology of tea soils to draw any firm conclusions about the role bacteria play in regulating nutrient availability and loss routes. The following soil processes and microorganisms were studied: respiration, net mineralisation, nitrification; pH, organic carbon, total nitrogen, total phosphorus, total aluminium; and total phosphorus, total carbon, total carbon, organic carbon, and biomass ninhydrin-N. We looked at fields in Hongjiashan village and at the Tea Research Institute, Hangzhou (TRI) that had varying stand ages (9, 50, and 90 years) and production levels (low, medium, and high). At both locations, the soils of the surrounding forests were compared to the soils used for tea. Soil pH was initially elevated by forest soil at both locations, but it depleted as the tea stands matured and production increased. Soil microorganisms' carbon and ninhydrin-N biomass are both drastically altered by tea growing. As a result of the following, HJS found a decrease in microbial biomass C: rise at age 50, descend at age 9, traverse the forest at age 90, and enter TRContrary to what you may expect, I observed a progression from low to moderate to high output and eventually forest. The following variables were found to be positively correlated with soil pH: respiration rate, specific respiration rate, ratio of microbial biomass C to organic C, ratio of microbial biomass ninhydrin-N to total N, and microbial biomass C. This suggests that soil pH profoundly affects the microbial biomass. Nitrogen was found to be net immobilized in certain samples below pH 3.5 (KCl), but net nitrified and mineralized in others. There was a notable shift in community composition as production levels and stand ages increased, according to PC-analyzed data from PLFAs. Particular respiration and the ratio of bacterial: fungal PLFA indicators in HJS soils were shown to have a linear negative relationship ($r2=0.93$, $p=0.03$). Our research shows that the microbiome's formation, development, and activity are significantly affected by the length and severity of the tea-making process. The use of fertilisers and soil acidity are likely to blame.

III. MICROBIAL ECOLOGY OF SOIL

The German scientist Ernest Haeckal is credited with being the first person to use and invent the phrase "microbial ecology" in the year 1866. When it comes to the study of microbial diversity, the primary objective is to get an understanding of how microorganisms operate in their natural environments. An increase in interest in this developing field of inquiry has recently occurred as a result of the widespread agreement that bacteria play an essential role in the health of all ecosystems. The most recent findings indicate that our planet is teeming with a diverse range of bacteria, each of which have the potential to completely revolutionise a number of different fields, including the scientific community, society, and the economy. Microorganisms and the metabolic changes that they undergo are of critical importance to the appropriate circulation of materials and energy across the ecosystems of the earth. This forward-thinking setting gave rise to the study of microorganisms.

Quantifying microbial diversity has proven to be difficult because to study boundaries between ecologists and microbiologists, as well as considerable theoretical and practical difficulties. This is despite the fact that microorganisms are so prevalent in ecosystems and play a crucial role in their functioning. The utilisation and management of soil fertility and physical attributes need to be optimised in order to create a more sustainable agricultural system. Soil biological processes and biodiversity are the foundations upon which these characteristics are built. When looking for metrics that might be indicators of soil quality and plant production, it is essential to take into account the perspectives of microbial diversity in agricultural contexts such as growing crops. Sustainable agricultural techniques, such as the optimisation of organic matter, the retention and effective utilisation of nutrients, and the general health of the soil, are significantly influenced by the microbes that are present in the soil. These microbes include bacteria, fungus, actinomycetes, and algae. Due to the fact that many of their secondary metabolites possess antibacterial or antifungal activities, actinomycetes are a crucial family of soil microorganisms at the soil level. It is an innovative method for enhancing crop yields and developing a natural defence against illnesses that are transmitted thru the soil to actively manipulate the populations of microorganisms that are present in the soil.

Soil Microbial Communities

In light of the fact that soil is a complex and multifaceted component of terrestrial ecosystems, there is a significant demand for further information on the microorganisms that live in soil. It is estimated that slightly more than one percent of the microorganisms found in soil ecosystems have been cultivated, identified, and investigated. There are many different types of bacteria, both prokaryotic and eukaryotic, that may be found in soil. Because of the interactions that they have with one another, these microorganisms are able to coexist with other species that are discovered in the soil.

In the same way that other levels of biology have a rich and rather fair distribution of genetic variation, the microbial community that lives in soil does as well. This connection is complicated and may need to be modified. A growing number of people are interested in gaining an understanding of the interrelationships that exist between the structure, function, and biodiversity of ecosystems. On the subject of the relationship between the diversity and composition of microorganisms and the functional capabilities of terrestrial ecosystems, several hypotheses have been proposed that have been put up. Certain hypotheses suggest that the functioning of ecosystems might be improved by microbial communities that are more geographically diversified. One school of thot holds that the functional capacities of certain microbial species, rather than the number of species, are the most important factors in determining the characteristics of an ecosystem.

Composition of Soil Microbial Communities

There are billions of animals in the dirt, and almost every phylum is there. The most complex and diverse group of organisms called microbial communities are the soil microorganisms, which include fungus, bacteria, actinomycetes, and lichens. They are sized between half a millimetre and five millimetres.

The bacteria that inhabit soil are prokaryotic, or single-celled, and may be anywhere from half a millimetre to five micrometres in size. More than 20,000 species per gram of soil are members of this highly adaptable and varied group of soil microorganisms. Soil microbes are infamously wasteful with their energy use; in fact, only about 20% of organic material breaks down into bacterial tissue.

In the soil, eukaryotic creatures called soil fungus may build buildings on a macroscopic scale. As a diverse community of microorganisms, soil is home to tens of thousands of species of fungus. Even while they are often present in much lower amounts than bacteria, fungus regulate the biomass and metabolic activity in many soils because to their huge size and branching. Considering that 30-50% of organic matter decomposes into bacterial tissue, the energy efficiency of soil fungus is very notable.

Although their mycelia threads are somewhat smaller, actinomycetes have similarities with fungus in that they possess filamentous cells, which are sometimes extremely branched. Formerly thot of as fungus, actinomycetes are now more accurately described as bacteria. They lack a nuclear membrane and often divide into spores that resemble bacterial cells. We will refer to them as soil microbes because of the unique roles they play in soil rather than bacteria. Actinomycetes are essential in salt-depleted soils in arid climates, despite the fact that they do best in moist, warm, and aerated soils.

Algae are composed of eukaryotic cells, the size of which may range from 2 µm to 20 µm. There are hundreds of species of algae in soil, but just a few of these species are really world-changers. Although most algae thrive in cool, moist conditions, a small number can withstand very hot or cold temperatures.

Determination of Soil Microbial Communities

Numerous techniques exist for the cultivation, identification, and characterisation of microbial populations. These methods identify how microbial communities use substrates in their native environments or in laboratory settings (e.g., in Biolog GN microplates) to provide physiological profiles of the whole community. Due to the absence of a single, all-encompassing technique for calculating the total microbial population, several approaches evolved over time. Primitive species, such as bacteria and fungus, have inspired the development of generalisable approaches to studying the composition and dynamics of microbial communities. The population may be determined in a number of ways: by direct counting, by analysing specific cell components, by extraction procedures, by DNA analysis, by chloroform fumigation, or by microwave incubation. More and more research is making use of molecular techniques, such cloning, 16S ribosomal RNA sequence analysis, and polymerase chain reaction amplification, to forecast the composition of bacterial communities.

IV. INTERACTIONS OF SOIL MICROBIAL COMMUNITIES

There is a wide range of soil ecosystems, each characterised by its own unique set of microorganisms and their recorded interactions with one another, with plant roots and other animals of the soil, and with the environment at large. The following are the most important links.

- **Antagonistic Interactions**

Parasitism and predation are bad microbial interactions that happen when one species dwells within another or when one species actively seeks out another. There is a net gain for one species at the expense of another in both scenarios. There is an abundance of bacteria-feeding microbes in soil ecosystems. Soil ecology is vital for more than just bacteria; protozoa and nematodes are also crucial. This might greatly affect the general public. The actinomycetes feed on the Pythium coloratum fungus, which brings about cavity-spot disease in carrots.

- **Competition Interactions**

The term "competition" describes the situation in which one group of organisms has slower growth than another due to factors such as the effective utilisation of a restricted resource by another group or the fact that one group's output hinders the development of another group. Carbon, hosts, minerals, and electron acceptors are all resources that might be in short supply.

When added to soil, heterotrophic bacteria compete with existing soil bacteria for organic wastes. When organic remnants include simple molecules, such as sugars, starches, and amino acids, bacteria take over owing to their rapid development and preference for these types of compounds. Metabolising these basic compounds causes soil fungus, and actinomycetes in particular, to alter their environments in order to gain an advantage in competition. Some microbes alter the pH of the surrounding environment to give their competitors a leg up. Some people create compounds with strong bonding qualities to protect the food supply.

The creation of antibiotic compounds may inhibit the growth of other microbes. When Pseudomonas fluorescens (Trevisan) Migula F113 synthesises 2,4-diacetylphloroglucinol, it inhibits the growth of Erwinia carotovora subsp. atroseptica (van Hall) Dye, the pathogen responsible for potato soft-rot. On the other hand, additional action pathways are not ruled out by antibiotic synthesis. It has been observed that non-pathogenic Agrobacterium strains may reduce disease expression rather than removing the pathogens.

- **Mutualistic Interactions**

The formation of symbiotic partnerships amongst soil bacteria is quite rare. Rhizobia collaborate with leguminous plants to fix nitrogen, the most famous of these processes. Communities of N-fixing and non-fixing bacteria, as well as rhizobium and arbuscular fungus, engage in symbiotic relationships. An important ecological and economic function of soil fungi is the symbiotic interaction between certain fungi and the roots of higher plants. This kind of relationship is known as mycorrhizae, which translates to "fungus root." Many plants in natural ecosystems depend significantly on mycorrhizal fungus, especially in damaged regions, even tho the interaction benefits both plants and mycorrhizal fungi.

Complex microbiotic crusts inhabit arid rangelands. These communities rely on each other for survival, and they include things like algae, cyanobacteria, mosses, bacteria, and liverworts. Indicators of ecological recovery or health are microbiotic crusts.

V. CONCLUSION

Researchers found that microbial activity in tea garden soils is a good measure of soil health. Soil microbes are affected by soil characteristics including pH, organic matter, moisture, and nutrient availability, which affect their development and activity. Better plant development and soil fertility are both supported by healthy microbial activity, which aids in organic matter breakdown and nutrient recycling. Soil microbes and their long-term production in tea gardens depend on careful control of organic matter, nutrients, water, and other soil variables. Sustainable and healthy tea growing requires continuous monitoring of soil characteristics and microbial activity, according to the research.

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