MICROBIAL ANALYSIS OF SOIL IN A BAMBOO GROOVE AT THE FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA, OGUN STATE, NIGERIA.

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Abstract
Microorganisms in the soil play a crucial role in plant growth, soil sustainability, the balance of the soil ecosystem, and the restoration of lost nutrients. This study was conducted to identify microbial populations at varying depths in the bamboo grove behind the University Health Centre of the Federal University of Agriculture, Abeokuta, Nigeria. Soil samples were collected at depths of 0–15 cm, 15-30 cm, and 30–45 cm for microbial analysis. The dilution spread plate method of identification of microbial population was used. The results showed that 7 bacterial species and 5 fungal strains were isolated from all the soil samples used. The probable isolated bacterial species were *E coli, Bacillus subtilis, Clostridium septicum, Bacillus, Proteus, Enterobacter, Klebsiella aerogenes,* and the isolated fungi species were *Aspergillus funmigatus, Alternaria alternate, Aspergillus niger, Penicillium spp, and A niger.* The microbial colony-forming units decreased progressively with increasing soil depth, indicating microbial activity is highest within the top 0-30 cm. This suggests that the upper soil layer should remain undisturbed as it contains vital microorganisms essential for nutrient recycling and plant productivity. The morphological characteristics of the isolated bacteria and fungi indicate that the *Bacillus spp and the Aspergillus spp* are the dominant bacteria in the soil, highlighting their importance in organic matter decomposition and soil fertility enhancement. The study underscores the ecological significance of bamboo groves as a biodiversity hotspot that supports diverse microbial communities crucial for sustainable soil health and management.

Keywords: Bamboo, Soil, Micro-organism (bacteria and fungi)

Introduction

Bamboos are evergreen perennial flowering plants belonging to the subfamily Bambusoideae of the grass family Poaceae, comprising about 1,500 species across 87 genera (Li and Kobayashi, 2004; Zhou *et al*., 2011). They are widely distributed in tropical and subtropical regions of Asia, Africa, and South America, where they play significant ecological, economic, and environmental roles. Although its exact origin is unknown, the name "bamboo" most likely comes from the Dutch or Portuguese languages, which first took it from Malay or Kannada. Bamboos are the largest members of the grass family and are distinguished by their unique rhizomatous growth system, which enables rapid regeneration and high biomass accumulation (Banik, 2015). Due to a special rhizome-dependent structure, bamboos

contain some of the fastest-growing plants on the planet. Certain bamboo species have a maximum 24-hour growth rate of 910 mm (36") or over 40 mm (1+12 in.) per hour (equivalent to 1 mm every 90 seconds). Because of this rapid growth and adaptability, bamboo has become a promising species for afforestation, carbon sequestration, erosion control, and climate change mitigation (Zhou *et al*., 2005; Nath *et al*., 2015). Bamboo forests also improve soil physical and chemical properties by enhancing organic matter, nitrogen, phosphorus, potassium, and pH levels (Kleinhenz and Midmore, 2001; Sharma *et al*., 2021). These benefits are largely attributed to soil microorganisms, which play fundamental roles in decomposition, nutrient mineralization, and maintenance of soil fertility.

Soil microorganisms, particularly bacteria and fungi, form the foundation of bamboo soil ecosystems. They facilitate organic matter breakdown, nitrogen fixation, and phosphorus solubilization, while also influencing soil structure and nutrient availability (Tripathi *et al*., 2016; Joshi *et al*., 2020). The activity of these microbial communities varies with soil depth, organic matter content, and bamboo root density, making them sensitive indicators of soil health (Chen *et al*., 2019). The soil from bamboo forests is thought to have higher soil enzymatic activity and microbial populations than the soil from bare areas. The soil, litter, and root biomasses have higher chemical compositions, enzymatic activity, and microbial counts in bamboo-dominated forests.

Despite extensive global research on bamboo ecology, there is limited information on the composition and distribution of microbial populations in bamboo grove soils in Nigeria. Most studies in the country have focused on bamboo utilization and growth performance, with little attention to its below-ground microbial ecology. Understanding microbial variation across soil depths in bamboo groves is essential for sustainable forest management, soil restoration, and ecosystem resilience. Therefore, this study was conducted to assess the diversity and distribution of microbial populations at varying soil depths within a bamboo grove located at the Federal University of Agriculture, Abeokuta, Nigeria. The findings will provide insight into the ecological functions of microorganisms in bamboo soils and contribute to sustainable soil management.

Materials and methods

Study Area

The study was carried out at the bamboo grove behind the university health center of Federal University of Agriculture, Abeokuta (FUNAAB), Ogun State. This area falls within Latitude 7° N and 7°58' and Longitude 3°20 ' E and 3°37 ' E. The area has a tropical climate with a bimodal distribution of rainfall; it lies within the humid lowland tropical rainfall with two distinct seasons (the wet season from March to October and the dry season from November to February). The mean annual rainfall is about 1113 mm, which peaks in July and September. The relative humidity of the area is 82.4, and the average monthly temperature is 35.8°C.

Experimental Design and Sampling

A completely randomized sampling design was adopted for this study. Soil samples were collected from three randomly selected plots (replicates) within the bamboo grove to capture spatial variability. Within each plot, soil samples were collected at three depths: 0–15 cm (surface layer), 15–30 cm (subsurface), and 30–45 cm (deep layer). Each depth sample was collected at three different points and pooled to form a composite for that replicate. In total, nine composite samples were analyzed (three depths × three replicates).

Materials

Soil auger, Soil bag, Secateurs, Bamboo grove soil, Microscope, Potato Dextrose Agar (PDA), Nutrient Agar, Plate count agar, Petri dishes, Spirit, Cotton wool, and Foil paper were used.

Soil Sample Collection

Soil samples were collected randomly from the bamboo grove from a depth of 0-15 cm, 15- 30 cm, and 30-45 cm using a soil auger. The samples were collected randomly and mixed to form a composite sample, poured into a sterile sample bag, and labeled appropriately. They were then taken to the laboratory for analysis. Samples were air-dried at room temperature (28 ± 2°C) for 48 hours and sieved (2 mm mesh) before microbial analysis.

Sterilization of Apparatus

All glassware (Petri dishes, test tubes, and pipettes) was washed, air-dried, and sterilized in an autoclave at 121°C for 15 minutes before use. All culture media were prepared according to the manufacturer's instructions under aseptic conditions. Sterility controls (uninoculated plates) were incubated alongside test plates to confirm the absence of contamination. Media pH and sterilization efficiency were checked before inoculation to ensure quality assurance.

Preparation of Media

Three culture media were used: Nutrient Agar (NA) and Plate Count Agar (PCA) for bacterial enumeration, and Potato Dextrose Agar (PDA) for fungal isolation. They were prepared following the manufacturer's instructions.

Laboratory Analysis: Microbial Analysis

The number of soil microorganisms was determined using the dilution spread plate technique. Total plate count agar, Nutrient agar (NA), and Potato Dextrose agar (PDA) were used for bacteria and fungi. One ml of the sample was pipetted into a sterile test tube and serially diluted in another six sets of test tubes, each containing 9ml of sterile distilled water to a dilution ratio of 10^{-6}. While 0.1 ml portion of the diluents from the fourth (10^{-5}) and fifth (10^{-6}) dilution factors were pipette separately aseptically into different sterile petri dishes and 15 ml of the cool (45ºC) sterile molten agar media was added under aseptic condition, swirled gently for even distribution of the inocula and allowed to set and incubated at 30–37 ºC for 24 hours (for bacterial), and at 25–27 ºC for 72 hours for fungi. At the end of incubation (24 hours), microbial colonies were counted and recorded appropriately for bacteria, while

after 72 hours, microbial colonies were counted and recorded.

Data Analysis

Colony counts from triplicate plates were averaged, and microbial populations were log-transformed before analysis. Differences in bacterial and fungal populations across soil depths were tested using one-way Analysis of Variance (ANOVA). Means were compared using Duncan's Multiple Range Test (DMRT) at $p < 0.05$ significance level. Statistical analysis was performed using SPSS version 25.0 (IBM Corp., USA).

Results and discussion

Microbial populations in soil are determined by various factors such as oxygen level, soil depth, and carbon dioxide concentration (Bhattarai *et al.*, 2015). The microbial population in this study was studied using the soil depth. The populations of bacteria and fungi were considerably higher at the upper depth of the soil. Result showed that the highest population of fungi and bacteria was at the 0-15 cm depth of the soil, and the lowest population was at the 30-45 cm depth of the soil, the population of the microbes decreases with depth of the soil. The result indicates that the first 30 cm of the soil habitat should not be disturbed. Although bamboo soil has nothing growing on it, but they are microbes in the soil and in the bamboo vegetation.

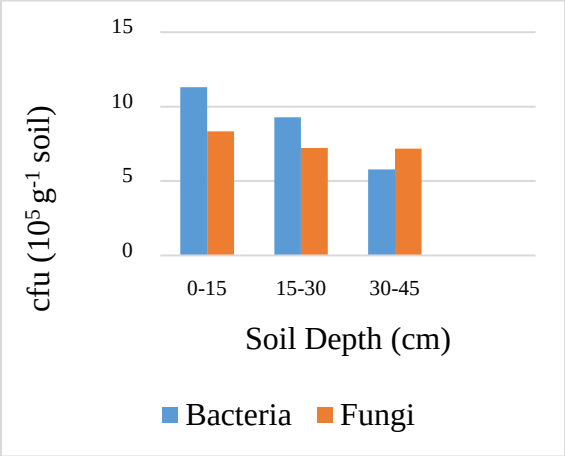

Fig 1: Microbial Population across Soil Depths

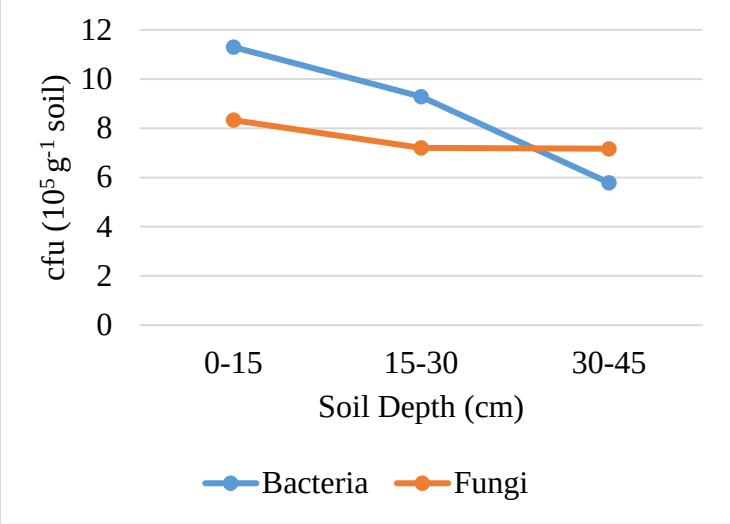

Fig 2: Variation of Microbial Count with Soil Depth

The microbial population varied significantly across soil depths in the bamboo grove ($p < 0.05$). Bacterial and fungal colony-forming units (CFU g^{-1}) were highest in the surface layer (0–15 cm) and decreased progressively with depth (Figure 1). The mean bacterial count was 11.30×10^5 CFU g^{-1} at 0–15 cm, 9.28×10^5 CFU g^{-1} at 15–30 cm, and 5.79×10^5 CFU g^{-1} at 30–45 cm. correspondingly, fungal counts were 8.33×10^5 CFU g^{-1}, 7.21×10^5 CFU g^{-1}, and 7.15×10^5 CFU g^{-1}, respectively. One-way ANOVA confirmed a significant difference ($F_{2,6} = 7.42$; $p = 0.02$) among bacterial populations but not among fungal populations ($p > 0.05$).

The bar chart and line plots (Figures 1 and 2) clearly illustrate this decreasing trend with depth. The sharp decline in microbial counts at 30–45 cm can be attributed to reduced oxygen, limited organic matter, and lower root density in deeper soil layers. These findings agree with Tripathi *et al.* (2016) and Chen *et al.* (2019), who reported that microbial biomass in bamboo soils is concentrated in the top 20 cm due to organic litter accumulation and root exudates that provide carbon sources for microbial metabolism.

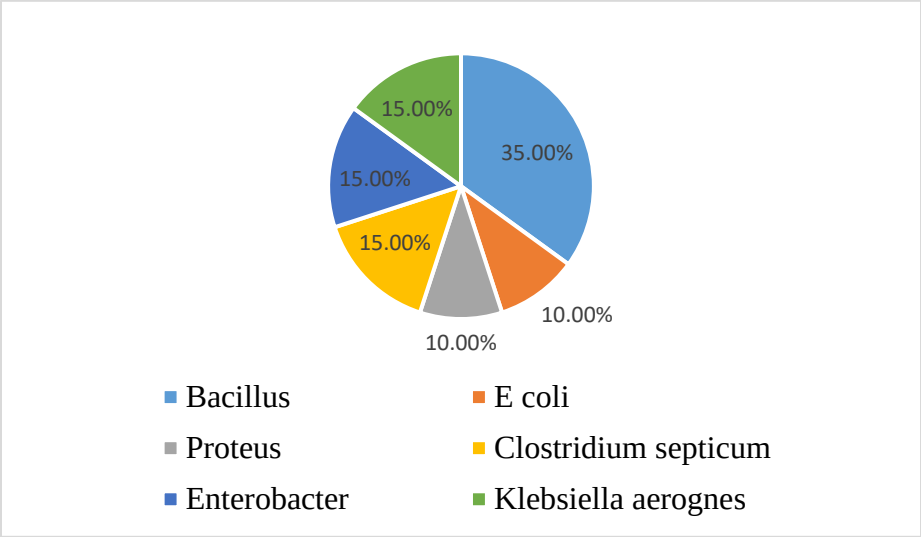

Fig 3: Relative Abundance of Bacterial Species

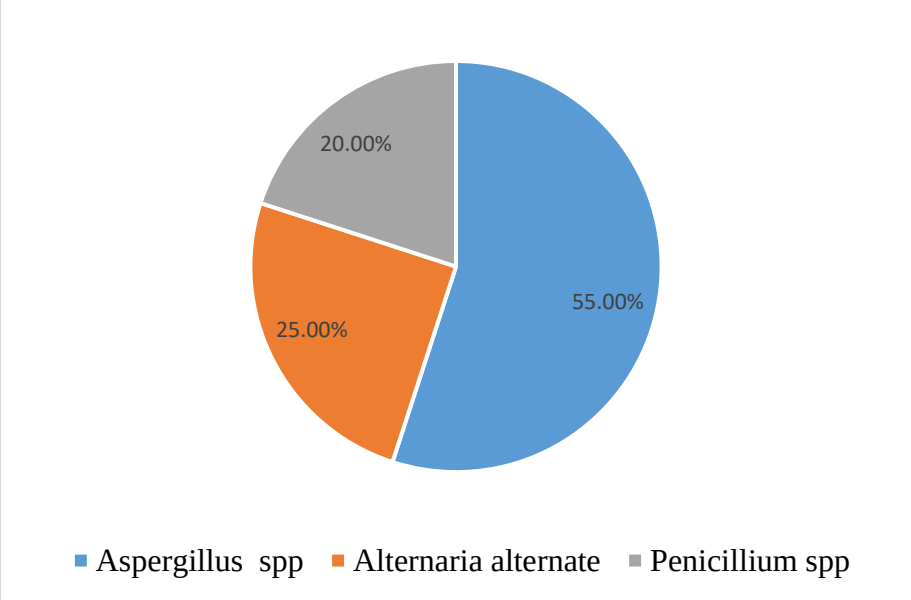

Fig 4: Relative Abundance of Fungal Species

Microbial isolates obtained from the bamboo grove soils included seven bacterial and five fungal species. The relative abundance of bacterial species is presented in Figure 3, while fungal composition is shown in Figure 4.

The bacterial community was dominated by *Bacillus spp*. (35%), followed by *Clostridium spp*. (15%), *Enterobacter spp.* (15%), *Klebsiella spp*. (15%), *Proteus spp*. (10%), and *E. coli* (10%). Among fungi, *Aspergillus spp*. Accounted for 55% of isolates, followed by *Alternaria alternata* (25%) and *Penicillium spp. (20%).*

The predominance of Bacillus and Aspergillus species across all depths indicates their ecological adaptability and functional dominance in bamboo grove soils. Bacillus spp. are aerobic, spore-forming bacteria capable of surviving harsh environmental fluctuations such as variable temperature and moisture (Tabbene *et al*., 2009). Their presence also reflects their role in decomposing cellulose-rich bamboo litter through the secretion of hydrolytic enzymes such as cellulases and proteases (Sharma *et al.,* 2021).

Similarly, *Aspergillus spp*. thrive in oxygen-rich surface soils, utilizing complex organic substrates from bamboo litter. They are known to produce extracellular enzymes like amylases and ligninases, facilitating rapid decomposition and humus formation (Joshi *et al*., 2020). The high organic carbon and aeration in the bamboo grove topsoil create favorable conditions for Aspergillus dominance (Chen *et al*., 2019). *Aspergillus fumigatus*, which is one of the isolated *Aspergillus spp*, is a saprophytic fungus that plays an essential role in recycling environmental carbon and nitrogen (Haines *et al.,* 1995). Its natural ecological niche is the soil, wherein it survives and grows on organic debris.

Conclusion

This study examined the diversity and distribution of soil microorganisms at varying depths within a bamboo grove at the Federal University of Agriculture, Abeokuta, Ogun State, Nigeria. The results revealed that microbial populations, particularly bacteria, declined significantly with increasing soil depth, reflecting the influence of organic matter and oxygen availability near the surface. *Bacillus spp.* and *Aspergillus spp*. were identified as the dominant microbial taxa across all depths. Their abundance demonstrates strong ecological adaptation to the bamboo grove environment, which is rich in organic litter, moderately aerated, and characterized by constant nutrient recycling. These microorganisms play essential roles in organic matter decomposition, nutrient mineralization, and the maintenance of soil fertility.

Overall, the bamboo grove soils in FUNAAB represent a biologically active ecosystem that supports high microbial diversity and contributes significantly to soil health and carbon cycling. The findings highlight the importance of bamboo ecosystems as

microhabitats that enhance belowground biodiversity and promote sustainable ecological balance.

Recommendations

Based on the study, the following recommendations are made:

Soil Conservation: The upper soil layer (0–15 cm), which harbors the highest microbial activity, should be protected from disturbances such as tillage, compaction, or excessive harvesting to maintain microbial integrity and nutrient recycling efficiency.

Comparative Studies: Future research should extend to other bamboo groves across different ecological zones in Nigeria to compare microbial composition, environmental drivers, and seasonal variations.

Applied Research: The dominant microbial isolates, especially Bacillus and Aspergillus species, should be further studied for their potential use as biofertilizers and biodegraders, promoting organic agriculture and sustainable soil management.

Community Awareness and Policy Integration: Environmental education programs should highlight the ecological benefits of bamboo groves in maintaining soil fertility and biodiversity. Policymakers should also recognize bamboo forests as vital components of ecosystem restoration and climate change mitigation strategies.

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