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*Orginal Article*

# Diversity and abundance of microbes, pH and organic matter in soils of different forest types in tropical humid lowland forest ecosystem, Nigeria

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**Abstract**

This study examined the diversity and abundance of microbes, pH and organic matter of soils cultivated with three different plantation species and an adjacent natural forest in tropical humid lowland forest ecosystem, Nigeria. The plantations were unthinned stands of Nauclea didderrichi, Gmelina arborea and Tectona grandis established in 1979 in Akure Forest Reserve, Ondo State, Nigeria. Soil samples were collected (at a depth of 0 -15 cm) from four randomly located plots of 20 x 20 m in each forest type with soil auger. In general, there were 33 and 23 species of bacteria and fungi respectively in the soil samples. The population of bacteria ranged between 26.14 x 106 and 36 x 106 MPN g-1 dried soil while that of fungi ranged between 2.50 x 106 and 23.34 x 106 MPN g-1 dried soil. Highest species diversity and population of the microbes were isolated in soil samples from the natural forest and the least from Tectona grandis stand. Microbial diversity and abundance were influenced by soil pH and organic matter. There was no significant difference in organic matter and pH of soils from the four forest ecosystems ($p < 0.05$) but significant difference was discovered to exist in the bacteria and fungi population ($p > 0.05$). The number and diversity of bacteria was significantly more than what was obtained for fungi in all the soil samples. However, there was close association in the abundance of the microbes. Microbial abundance and diversity are affected when a natural forest is converted to plantation of fast growing species, so plantation development should be limited to degraded and marginal lands and such places where soil reclamation is required.

**Keywords:** *Forest reserve, detoxification, soil fertility, nitrogen fixation, aboveground biomass*



## INTRODUCTION

The many ecological, economical and environmental roles of the tropical rainforest ecosystem cannot be overemphasized. These roles include purification of air and water, regulation of water flow, detoxification and decomposition of wastes, generation and renewal of soil and soil fertility, carbon sequestration, biodiversity conservation, climate stabilization, moderation of temperature extremes, windbreaks, support for diverse culture and aesthetic beauty and landscape enrichment (Daily, 1997). Other socioeconomic function of the tropical rainforest ecosystem is the supply of many products for rural livelihood. These products include timber, fruits, herbs, wildlife e.t.c. In view of this, people are now becoming aware of the dangers and cost of allowing the forest ecosystem to be degraded or lost (Scherr at al., 2004).

Microbes (bacteria, archaea, fungi, and protozoans) are very important in all processes related to soil function. Some of these processes include soil formation, soil structure, cycling of carbon, nitrogen, phosphorous, and sulfur. In addition, the microbial constituents of soil are entirely responsible for the breakdown of organic matter and the degradation of toxic molecules (Forsyth, 2009). Zak et al (2003) and Nannipieri et al. (2003) reported that plant diversity usually

affects microbial process, which controls the rate of ecosystem N cycling. Moreover, soil microbial biomass is suitable and commonly used as potential indicator of soil organic matter levels. Microorganisms are also responsible for the mineralization process in forest ecosystem. They act on the humus to release CO2, water and nutrients, which could be absorbed directly by plants. The roles of microbes were summarized by Hoff et al. (2004) to include degradation of complex nutrient sources extra-cellularly, transportation of simple nutrients across cell membranes for metabolic processes and tolerating or deactivation of compounds that could inhibit fungal growth. It was also reported that bacteria allow phosphorus, zinc, potassium and other minerals to be redeposited back into the nutritional bank (Statmets, 2005). According to Rigbelis and Nahas (2004), the most important soil nutrient supply to the forest soil environment is the one derived from litter decomposition by actions of organism under conditions of high air temperature and soil moisture content. These organisms mobilized the chemical elements in the litter and make them re-absorbable by plant roots. They are able to perform these roles because of their ability to obtain nutrients through absorption. The investigations of below ground biological interactions, microorganism's population and diversity with the roles they play in forest ecosystem and their influence on carbon dynamics and ecosystem stability remain poorly understood. Copely (2002) reported that ecologists have just begun to study the contribution of biota to the dynamic interactions occurring among plant roots, animals and microbes in the forest ecosystem. Small animals usually convert dead plants and animals, animal droppings and leaves on forest floor into fine organic matter (OM) when fed upon. These fine organic matters are further broken down into humus by microorganisms. Humus is a form of organic matter that cannot be further decomposed easily. It contains the most essential nutrients (N, P and S) for plant growth and improves soil structure. Organic mater and humus have very high water and nutrient retention capacity and make them available for plant use readily as reported by Inckel et al. (1990). While soil bacterial diversity is influenced by several biotic and abiotic factors (Schmidt, 2006), it remains unclear whether there are general pattern of bacterial diversity (Liebner et al., 2008).

The rate of humus formation and mineralization depend so much on microbial population and diversity in the ecosystem. Other factors are favourable weather condition (e.g. temperature and humidity), soil acidity, quality and quantity of litters and the physical and chemical environment. All these major factors are very adequate in tropical forest ecosystem. For instance, a study by Taylor and Parkinson (1988) reported that some environmental factors affecting OM decomposition are usually higher in tropical than in temperate regions. Therefore, the study of microbial population and diversity as it affects humus formation and soil fertility is highly imperative. The objective of this study was to evaluate and compare the population and diversity of microbes, the main agents of humus formation and mineralization, obtained from soils cultivated with fast growing species and the natural forest ecosystem. This will help to determine the interrelationship among organisms and their roles in soil fertility maintenance. The study was limited to fungi and bacteria analysis because they present the highest values of biomass and respiratory metabolism and they have greater participation in OM decomposition process (Person, et al. (1980).

## MATERIAL & METHODS

**The study area:**

This study was carried out in Akure forest reserve, Ondo State, Nigeria. It lies approximately on longitude 40E and latitude 4.50N. It is located within the rainforest ecological zone, southwest Nigeria (Onyekwelu et al, 2005). This reserve was selected for this study because of the presence of a permanent sample plot demarcated in 1935 by Forestry Research Institute of Nigeria (representing an undisturbed natural forest ecosystem) and well-managed plantations of Gmelina arborea, Nauclea didderrichii and Tectona grandis. These constituted the different forest ecosystems where soil samples were collected. The plantations were established and managed by the State Forestry and Wildlife Department.

**Soil sample collection:**

Soil samples were collected at surface (surface soil 0-15 cm soil layer) using 3.5 mm diameter soil auger from four points in four randomly located sample plots (25 x 25m) in each of the forest types. In all, sixteen soil samples were collected, grouped and homogenized resulting in one composite soil sample per forest type. Litters, roots and leaves were removed from the samples and they were taken to the laboratory for analysis.

**Soil analysis:**
Soil biological properties assessment of the samples was limited to fungi and bacteria. The standard procedures for determining the total number of soil microbes were adopted for bacteria and fungi culturing (Alexander, 1982). Suspension of the soil samples was prepared with sterile water and a serial dilution of five factors was made for accurate counting. Then 1 ml of the appropriate dilution was carefully transferred to sterilized Petri dishes containing sterile molten nutrient agar at about 37oC. This was mixed and allowed to solidify. It was then incubated for 24 hours. The bacteria that grew into colonies were sub-cultured to obtain pure culture for easy identification. Identification was done according to Bergey's manual of determinative bacteriology. For fungi culturing, serial dilution of the suspension was also transferred into Petri dishes containing sterile, molten malt extract agar. This was kept in an incubator at 30oC for 5 days. Fungi that grew were sub-cultured to obtain pure culture for easy identification. Microscopic characterization was done for identification.

**Soil pH and Organic Matter determination:**
The soil pH was determined with the aid of glass electrode pH meter in soil solution of 0.01 mol L-1 calcium chloride while OM was determined after the soil sample furnace incineration at 55oC for 24 hours (Walkley and Black, 1934). All the soil analyses were done at the laboratory of the Department of Food and Industrial Microbiology, the Federal University of Technology, Akure, Nigeria.

**Method of data analysis:**
Population values for bacteria and fungi (Most Probable Number-MPN) were logarithmically transformed-Ln (x + 1) where, x = MPN g-1 dried soil x 106. All the data were subjected to one-way analysis of variance (ANOVA), means were separated where significant differences occurred by Fisher's protected Least Significant Difference (LSD) of Steel et al. (1997). Correlation between microbial populations and soil pH and soil pH and OM for each of the forest types was carried out to assess the relationship between these variables. Regression analysis of the form $Y = b0 + b1X$ was also generated between microbial population (Y) and soil pH (X1) and OM (X2). The regression equation used for the bacteria and fungi population is of the form $LnY = b0 + b1LnX$ (where, Y is the bacteria population -dependable variables. X is the fungi population - independent variable, b0 and b1 are regression constants to be estimated and Ln is natural logarithm). All the equations were assessed to be able to determine their fitness for further use and prediction. The assessment criteria used are: (i) correlation coefficient (r) which must be greater than 0.5, (ii) coefficient of determination (R2) which must be more than 50%, (iii) Standard Error of estimate (SE) must be very small and (iv) F-ratio which must be significant ($p \leq 0.05$) for the equation to have good fit (Adekunle et al., 2004).

## RESULTS & DISCUSSION

The relative abundance and diversity of the microbes encountered in the different forest ecosystems are indication that soils under forest cover are very rich in microorganisms that are very important for humus formation. This is responsible for the usual fertile land under forest cover. The different species of bacteria and fungi identified in the different forest soils are presented in Tables 1 and 2 respectively. From table 1, highest number of species of bacteria (19 species) was obtained from the natural forest. This is followed by Nauclea plantation with 16 species while the least (11 species) was from the teak stand. It was discovered that only three of the 33 species of bacteria were present in the soil samples from the four forest stands. These species (Actinomyces sp, Azotobacter agilis and Bacillus subtilis) could be referred to as habitat generalist.

Further more, the species of bacteria that were isolated in all the forest types are the aerobic spore formers. These bacteria, especially the Bacillus species are able to survive adverse environmental conditions by producing extremely drought resistant endospores (Bigelow et al., 2004). They could also thrive under any type of vegetation. The members of the genus Rhizobium, which normally form symbiotic relationship with roots of leguminous plants, are very common in natural forest area. This colonization by rhizobia results in the formation of root nodules where atmospheric nitrogen that is then made available to plants is fixed. It has been reported that Cyanobacteria, Actinomycetes and other Rhizobacteria (Azotobacter) have the ability to fix atmospheric nitrogen, thereby increasing soil fertility and cell materials (Wolters et al., 2000). In addition, excretions from soil microorganisms affect water and air movement within the soil. Ford et al. (2004) reported that some bacteria could produce antibiotics that are very useful while some fungi function largely in the breakdown of complex organic molecules like lignin (a compound that is resistant to bacteria degradation). Bacteria are also very beneficial to

trees by regulating inputs and outputs of nitrogen as noted by Sundareshwar et al. (2003).

On the whole, a total of twenty-three species of fungi were isolated from all the soil samples. The diversity and abundance of fungi followed the same trend as bacterial. The highest diversity and abundance of fungi was isolated from the natural forest. This was followed by soil samples from Nauclea didderrichii stand and the least number and diversity in soil samples from the Tectona grandis plantation.

Table 3 revealed the total number of microbes, pH and organic matter content of the forest types. While the population of bacterial is between 26.14 x 106 MPNg-1 and 360 x 106 MPNg-1, that of fungi is between 2.50 MPNg-1 and 23.34 MPNg-1. Highest population is from the Natural forest and the least is from the teak stand. Also from this table, the highest pH (6.26±0.05) was obtained in soil samples from the Nauclea didderrichii stand while the least (6.15±0.02) was obtained from the Tectona grandis stand and the pH ranged between 6.15 and 6.26. This pH range (slightly acidic) is very favourable for microbial activities and humus formation. For the organic matter content, the highest value (14.37±1.41) was present in the natural forest. This is followed by the Nauclea stand (12.68±1.42).

In the natural forest and Nauclea plantation, there was accumulation of biomass on the forest floor, there were no allelochemical compounds that could inhibit decomposition and humus formation in the ecosystem and leaves could decompose easily and quickly. This is also responsible for the high number and diversity of bacteria and fungi species obtained in these two forest types. The least amount of OM was in the stand of Tectona grandis stand (9.77±0.86). This could be attributed to the frequent fire outbreak, lack of undergrowths on the forest floor, toxic impact of harmful allelochemical compounds and coarseness of teak leaves. These could create resistance to bio-degradation and slow down the rate of leaf decomposition. Mahakur and Behera (1999) and Behera and Sahani (2003) also reported poor microbial population and diversity in Eucalyptus plantation due to low microbial growth, poor microbial activity, toxic impact of harmful allelochemical compounds released from Eucalyptus leaf and the slow rate of decomposition of Eucalyptus leaf. This corroborates the findings of (Rigobelis and Nahas (2004) that the diversity and population of microorganisms depend on the rate of OM decomposition in the forest ecosystem. In addition, a decrease in pH, reflecting in maximum acidification at the soil surface, has been observed to result from afforestation with conifers, Eucalyptus and Albizia due to the greater acidity of the litter relative to the native vegetation (Lips and Hofstede, 1998; Jobba´gy and Jackson, 2003 and Farley and Kelly, 2003).

The result of the one-way analysis of variance for assessing the presence of significant difference in relative abundance of the microbes (MPN), organic matter content and soil pH of the different forest soils types is shown in table 4. While there is no significant difference ($p \geq 0.05$) in soil pH and organic matter contents of the samples, a significant difference ($p \leq 0.05$) was discovered to exist in the number of bacteria and fungi isolated from the different forest soil environments. The LSD procedure for mean separation revealed that there is significant difference in the population of bacteria from the various forest stands. For Fungi, there is no significant difference ($p \leq 0.05$) between Gmelina arborea and Tectona grandis stands.

The highest population and diversity of microbes found in the natural forest could be attributed to the availability of different types of litters that arise from the various plant species in the tropical natural forest ecosystem. These could support the survival of many species of micro and macro-organisms. The processes of humus formation are usually rapid and occur throughout the year in the tropical rainforest ecosystem due to favourable weather condition. There is therefore a fertile soil, rich in organic matter, under natural forest cover. This has led to the increase in the rate of forest degradation and encroachment by farmers and land hungers mainly for agricultural purposes. Other variations such as litter quality, soil temperature, moisture content, pH and the nutrient status could also be responsible for the variation in microbial abundance and distribution. Below and above ground communities have been inextricably linked through complex interactions. Ford et al (2004) reported that any disturbance or change in the environment that affects above ground vegetation could also affect soil biota.

The monoculture nature of plantation ecosystem, in Nigeria affected the number and diversity of the soil microbes. Only the microbes that could thrive with the available litters from the few plant species in the plantation were therefore present. Microbial diversity and abundance is less where there are few plant species, frequent fire outbreak and coarse leaves that make decomposition very difficult. Also, litters with high content of more complex and slowly

degradable phenolic compound and lignin often decompose very slowly (Nwoboshi, 2000). The quality of plant residues is dependent on their relative contents of sugars, hemicelluloses, lignin and polyphenol and these determine the proportional content of nutrients in the litters. Based on this, plant residues were categorized into high quality and low quality residues by Young (1990). Subsequently, the population, diversity and the proportional amount of nutrients to be released into the soil by the microbes during decomposition are direct function of litter quality.

The conversion of the tropical humid lowland forest to plantations of fast growing species affected the distribution, abundance and diversity of soil microbes in the study area. The risks and the changes in sites associated with plantation forestry practices were reported by Evan (1999). Apart from the negative impacts of plantation development on flora and fauna diversity, the physical and chemical properties of the soil could also be adversely affected as discovered by Chijioke (1980) in his study. Resource availability for soil microbial communities is constrained by organic compounds in dead leaves and roots (i.e. detritus) that can be used to generate cellular energy (Smith and Paul 1990). Since plant species differ in their biochemical composition, changes in plant diversity could alter the production, as well as the range of organic compounds in debris. This could limit and control the composition and function of heterotrophic microbial communities. Also plant diversity increased the biomass and modified the composition of soil microbial communities as reported by Zak et al (2003).

The results of this study show that the population and diversity of the bacteria were more than fungi in all the sites. This supports the claim of Alexander (1977) that bacteria are by far the most abundant group of soil microbes in term of number. Generally, soil microbes possess vast phylogenetic and functional diversity and are key drivers of energy flow and nutrient cycling (Wertz et al 2006). Rigobelis and Nahas (2004) reported that bacteria represent the major group responsible for 25-30% of the total soil microbial biomass.

As shown in table 5, positive correlation was obtained between the microbes and soil pH and organic matter in each of the forest types. High and positive correlation coefficient (r) and coefficient of variation (r2) values were obtained between bacteria and OM and also between fungi and OM for all the soil samples analyzed. The r-values for fungi and OM ranged between 0.87 and 0.99 while the r2 were between 74 and 99% for bacteria and OM. The r-values for fungi and OM ranged between 0.74 and 0.99 while the r2 was between 55 and 99%. All the equations were significant ($p \leq 0.05$) with small standard error of estimate. They were therefore appropriate for predicting the bacteria and fungi population in these forest types and those in similar locations.

The results of the logarithm transformed regression equations between bacteria (dependent variable) and fungi (independent variable) revealed that there is positive and significant correlation between the two microorganisms in the four sites selected for this study. The correlation coefficient ranged between 0.75 and 0.99 while the coefficient of determination ranged between 56 and 98%. This shows that microbial load in the soils, diversity and their metabolic activities is fully supported by the site conditions especially the soil pH and there is therefore an adequate production of OM. The study corroborates the findings of Fierer and Jackson (2006). They discovered that bacterial diversity is related to pH only, and not to temperature or latitude. In contrast, Lozupone and Knight (2008) found a strong correlation between bacterial diversity and salinity, but no correlation with pH. It is also reported that slightly acidic and alkaline soils, like the ones obtained in this work, promote biodegradation activity of bacteria in soils (Obire and Nwaubeta, 2002). Baath and Arnebrant, (1994) and Oseni et al (2009) reported that higher pH could increase the percentage of culturable microbes in soils.

## CONCLUSION

The result of this study revealed that there is variation in the population and diversity of fungi and bacteria in the soil samples from the different forest ecosystem. The pH values obtained from all the soil samples favoured microbial activities as a result; organic matter decomposition and humus formation was enhanced. The highest number of microbes and species discovered existed in the natural forest when compared with the plantations. This was attributed to the quality of plant residues, favourable environmental condition and the relative abundance and richness of plant species in the natural forest ecosystem. Microbial diversity and abundance and their metabolic activities contributed to the fertility of soil under forest cover. Therefore, it is recommended that degraded lands and abandon farmlands should always be left

under fallow for them to regain their vegetation and fertility and the conversion of the natural forest ecosystem to monoculture should be discouraged. The equations with good fit in this study are recommended for further use in this kind of forest environment and similar ones.

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**Table 1.** Bacteria species diversity encountered in the different forest ecosystem

| S/N | Bacterial spp | Natural forest | Nauclea | Gmelina | Teak |
|---|---|---|---|---|---|
| 1 | *Acinetobacter parapertusis* | + | | | + |
| 2 | *Acinetobacter iwoffii* | + | | + | |
| 3 | *Actinomyces sp.* | + | + | + | + |
| 4 | *Agrobacterium sp* | + | + | | |
| 5 | *Alcaligenes feacalis* | | + | | + |
| 6 | *Bacillus cereus* | +. | + | + | + |
| 7 | *Azomonas sp* | + | | | |
| 8 | *Azotobacter agilis* | + | + | + | + |
| 9 | *Azotobacter paspali* | + | + | | |
| 10 | *Bacillus megatarium* | | + | | |
| 11 | *Bacillus polymysa* | + | + | | |
| 12 | *Bacillus subtilis* | + | + | | |
| 13 | *Citrobacter freundii* | | | + | |
| 14 | *Clostridium sporogenes* | + | | | + |
| 15 | *Coryneabacterium sp.* | | | + | |
| 16 | *Escherichia coli* | + | | | |
| 17 | *Erwinia amylovora* | + | + | | |
| 18 | *Erwinia herbicola* | + | | + | + |
| 19 | *Klebisiella sp* | | | + | |
| 20 | *Kurthia sp.* | | + | | |
| 21 | *Methylococcus sp* | | + | | + |
| 22 | *Nitrobacter winogradkyi* | | | + | |
| 23 | *Planococcus sp* | + | - | - | + |
| 24 | *Proteus vulgaris* | + | | + | |
| 25 | *Pseudomonas aeruginosa* | | | + | |
| 26 | *Rhizobium leguminosarium* | + | | + | |
| 27 | *Sarcina flora* | | | | + |
| 28 | *Serratia maccescens* | + | | | |
| 29 | *Shigella dysenteriae* | | + | | |
| 30 | *Staphylococcus aureus* | + | | | |
| 31 | *Streptococcus faecalis* | | + | + | |
| 32 | *Streptomyces sp.* | | + | | |
| 33 | *Thermobacterium lactobacillus* | | + | | |
| | **Total** | 19 | 16 | 13 | 11 |

**Table 2.** Fungi species diversity encountered in the different forest ecosystem

| S/N | Fungi spp | Natural forest | Nauclea | Gmelina | Teak |
|---|---|---|---|---|---|
| 1 | *Aspergillus flavus* | + | + | + | + |
| 2 | *Aspergillus fumigatus* | | + | | |
| 3 | *Aspergillus niger* | | | + | |
| 4 | *Aspergilus raperis* | | + | + | |
| 5 | *Boytrytis cinerea* | + | | | +. |
| 6 | *Candian sp.* | | + | | |
| 7 | *Choamehora* | + | | | |
| 8 | *Cucurbitarum* | +. | | | |
| 9 | *Fusarium sp.* | + | | | + |
| 10 | *Gonatobotrys simplex* | + | + | + | + |
| 11 | *Mucor mucedo* | + | + | + | + |
| 12 | *Neurospora crassa* | | + | | |
| 13 | *Oidiodendrum griseum* | + | | + | |
| 14 | *Passalora sp* | + | | | |
| 15 | *Penicillium italicum* | + | + | + | + |
| 16 | *Penicillium notatum* | + | | | |
| 17 | *Rhizopus sp.* | + | + | + | |
| 18 | *Sepedonium ampullosporum* | + | | | + |
| 19 | *Stachbotrys sp.* | + | | | |
| 20 | *Streptomyces sp.* | | + | | |
| 21 | *Trichoderma vivide* | | + | | |
| 22 | *Varicosporium elode* | + | | + | |
| 23 | *Verticillcium albo-atrum* | | + | + | + |
| 24 | *Wardomyces sp.* | + | + | | |
| | **Total** | 16 | 13 | 10 | 8 |



**Table 3.** The relative abundance of the microbes, organic matter content and soil pH from the different forest soil environments

| Soil parameters | Natural forest | *Nauclea didderrichii* | *Gmelina arborea* | *Tectona grandis* |
|---|---|---|---|---|
| pH | 6.19±0.3 | 6.26±0.05 | 6.20±70.2 | 6.15±0.02 |
| organic matter | 14.77±1.42 | 12.68±0.78 | 12.37±1.41 | 9.77±0.86 |
| bacteria (MPN $g^{-1}$ Dried soil) $x10^6$ | 360±12.77a | 118.44±7.24 b | 138.67±19.73 c | 26.14±1.63 d |
| fungi (MPN $g^{-1}$ Dried soil) $x10^6$ | 23.34±0.77a | 8.50±0.11 b | 2.89±0.40 c | 2.50±0.10 c |

***Means follow with the same alphabets in a row are not significantly different (p≤0.05)***

**Table 4.** ANOVA for soil parameter obtained from the different forest ecosystems

| Soil Properties | Source of variation | Sum of Square | Degree of freedom | Meansquare | Fcalculated | Sig |
|---|---|---|---|---|---|---|
| pH | Forest types | 0.016 | 3 | 0.0053 | 1.368 | 0.320 |
| | Error | 0.031 | 8 | 0.0038 | | |
| | **Total** | 0.047 | 11 | | | |
| Organic Matter | Forest types | 33.039 | 3 | 11.013 | 2.754 | 0.112 |
| | Error | 31.995 | 8 | 3.999 | | |
| | **Total** | 65.034 | 11 | | | |
| Bacterial (LnX+1) MPN $g^{-1}$dried soil | Forest types | 10.306 | 3 | 3.435 | 150.133 | 0.000 |
| | Error | 0.183 | 8 | 0.023 | | |
| | **Total** | 10.489 | 11 | | | |
| Fungi (LnX+1) MPN $g^{-1}$dried soil | Forest types | 9.877 | 3 | 3.292 | 209.919 | 0.000 |
| | Error | 0.125 | 8 | 0.015 | | |
| | **Total** | 10.002 | 11 | | | |

**Table 5.** Regression equations with their assessment criteria for microbial population and soil properties in the different forest ecosystems.

| Forest types | Soil microbes | Equation | R | $R^2$ | SE | F-ratio |
|---|---|---|---|---|---|---|
| Natural forest | Bacterial | $B = 8.30 - 0.40x_1$ | 0.42 | 17% | 3.70 | 8.13 |
| | | $B = 5.53 + 0.02x_2$ | 0.96 | 93% | 0.008 | 31.52 |
| | Fungi | $F = 0.67-0.99x_1$ | 0.78 | 61% | 0.003 | 11.23 |
| | | $F = 3.37-0.028x_2$ | 0.74 | 55% | 0.007 | 25.64 |
| | Fungi/bacterial | $LnB = 8.96 - 0.99Lnx_3$ | 0.90 | 80% | 0.04 | 51.61 |
| Nauclea stand | Bacterial | $B = 0.40 - 21.85x_1$ | 0.74 | 55% | 0.06 | 15.84 |
| | | $B = 3.46 + 0.10x_2$ | 0.97 | 94% | 0.007 | 41.45 |
| | Fungi | $F = 4.76 - 0.60x_1$ | 0.11 | 1% | 11.0 | 5.57 |
| | | $F = 2.26 - 0.08x_2$ | 0.89 | 79% | 0.02 | 20.36 |
| | Fungi/bacterial | $LnB = 8.96 - 0.99Lnx_3$ | 0.75 | 56% | 0.06 | 21.03 |
| Gmelina stand | Bacterial | $B = 0.99-1.42x_1$ | 0.82 | 68% | 0.01 | 9.35 |
| | | $B = 5.66-0.08x_2$ | 0.87 | 75% | 0.01 | 78.11 |
| | Fungi | $F = 2.88-0.60x_1$ | 0.48 | 23% | 0.19 | 4.21 |
| | | $F = 1.93-0.20x_2$ | 0.99 | 99% | 0.004 | 121.14 |
| | Fungi/bacterial | $LnB = 14.24 - 4.43Lnx_3$ | 0.90 | 881% | 0.005 | 52.14 |
| Teak stand | Bacterial | $B=3.45-17.95x_1$ | 0.93 | 87% | 0.003 | 89.45 |
| | | $B = 2.56+0.07x_2$ | 0.99 | 99% | 0.001 | 185.92 |
| | Fungi | $F = 13.64-2.07x_1$ | 0.88 | 77% | 0.002 | 75.22 |
| | | $F = 1.35-0.04x_2$ | 0.98 | 96% | 0.001 | 105.14 |
| | Fungi/bacterial | Ln B = 4.67-1.55 Ln F | 0.99 | 98% | 0.005 | 116.32 |

***F/$x_3$ = Fungi, B = Bacterial, OM = $x_1$ = pH $x_2$ = Organic Matter***