SOIL PRODUCTIVITY CHANGES UNDER SELECTED INDIGENOUS FOREST TREE SPECIES WITH SPECIAl REFERENCE TO BENEFICIAL MICROFLORA

By

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(2012-17-111)

THESIS

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DECLARATION

I hereby declare that this thesis entitled "**Soil productivity changes under selected indigenous forest tree species with special reference to beneficial microflora**" is a bonafide record of research done by me during the course of research and that the thesis has not previously formed the basis for the award of any degree, diploma, fellowship or other similar title, of any other University or Society.

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LAKSHMY. A

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Introduction

1. INTRODUCTION

Soil is an essential natural resource and it plays a key role for maintaining a sustainable natural ecosystems. Soil contains the most complex and dynamic microbial assembly in the biosphere (Curtis *et al.*, 2002). The structure and diversity of soil microbial communities play a critical role in the function and long term sustainability of soils. Microorganisms play a fundamental role in establishing biogeochemical cycles and are involved in forming the structure of a soil. The influence of soil microorganisms on above ground ecosystems by their contribution to plant nutrition, plant health, soil structure and soil fertility and the consequent increase in the biomass production is of greater relevance.

The chemical and physical soil parameters such as organic matter, nutrient status, run-off measurements or aggregate content have been used to measure soil quality (Parr and Papendick, 1997). However, these parameters change very slowly, and therefore many years are required to measure significant changes. A small area of soil surrounding the roots of plant is called as rhizosphere. Microbial communities in the rhizosphere of trees differ from those in bulk soil (Marschner and Rengel, 2007; Shi *et al.*, 2012), which is thought to result from release of a diverse array of exudates as well as growth regulators and inhibitory compounds. On the other hand, soil biological and biochemical properties are responsive to these small changes that occur in soil, thereby providing immediate and accurate information on changes in soil quality. This is because soil microbial activity has a direct influence in ecosystem stability and fertility (Parr and Smith, 1969). Therefore, it is important to study the microbial diversity not only for basic scientific research, but also to understand the link between diversity and their functions in relation to plant growth. Moreover, understanding the diversity and dynamics of microflora population will also throw light into various aspects of possible soil productivity and its changes over time due to long term occupancy of tree species. The raising of indigenous tree species is expected to offer added ecosystem benefits and specifically, the microsite improvement.

The wild jack tree, *Artocarpus hirsutus* is one of the endemic timber species of the south Western Ghats. It is especially popular along the Malabar Coast (Mathew *et al.*, 2006). This tree is considered as one of the 'keystone species' of the Western Ghats (Nayar, 1996). The other tree species like *Hopea parviflora* and the *Pterocarpus santalinus* have greater ecological importance and these plants are included in IUCN red data book as endangered plant species (Manoj *et al.*, 2012) and the *Pterocarpus marsupium* is being selected for planting due to multitude of its uses. The possible effects of different tree species on the microflora population will give valuable information to the overall micro site enrichment potential of these indigenous tree species. However, such information on soil productivity and soil health is scarce in the tree species in relation to the beneficial microflora

Hence, a detailed study was under taken on four important indigenous tree species such as *Artocarpus hirsutus* Lamk., *Hopea parviflora* Bedd., *Pterocarpus santalinus* L.f. and *Pterocarpus marsupium* Roxb. with the objective to monitor the soil productivity changes due to long term occupancy of these tree species with special reference to the quantity and quality of the soil microflora.

Review of literature

2. REVIEW OF LITERATURE

The literature pertaining to the study entitled "Soil productivity changes under selected indigenous forest tree species with special reference to beneficial microflora" is presented under the following headings

2.1 "Soil microorganisms"- Keeps soil living

2.2 The aboveground and belowground interactions in the ecosystem

2.3 The role of microorganisms in plant growth

2.4 Association of soil microorganisms and plants

2.5 Soil microorganisms in agroforestry and land reclamation

2.1 "SOIL MICROORGANISMS"- KEEPS SOIL LIVING

Soil is an important natural resource and it contains the most complex and dynamic microbial assembly in the biosphere. A recent estimate suggests that a ton of soil may harbor at least one million species of microorganisms (Curtis *et al.*, 2002). Soil microbial communities are extremely diverse and contribute to a wide range of ecosystem services that are essential to the sustainable functions of natural and managed ecosystems. The soil biota may exert direct and indirect impacts on land productivity. Direct impacts are those where specific organisms affect crop yield immediately and the indirect effects include those provided by soil organisms participating in carbon and nutrient cycles, soil structure modifications and food web interactions that generate ecosystem services that ultimately affect productivity (Thoms *et al.*, 2010). The microbial communities also play an important role in nutrient cycling functions such as organic matter decomposition, mineralization, nutrient immobilization and carbon sequestration (Reynolds *et al.*, 2003; Rousk, 2010).

Doran and Parkin (1994) defined soil quality as "the capacity to function within an ecosystem and sustain biological productivity, maintain environmental quality and promote plant, animal and human health". Soil quality is the outcome of interactions among physical, chemical and biological characteristics, and its proper assessment requires the determination of a large number of parameters

(Bloem *et al.*, 2006; Marzaioli *et al.*, 2010). The Soil microbial biomass carbon could be related to diverse soil processes, including decomposition of organic residues, nutrient cycling, solubilization of nutrients (particularly phosphates), degradation of xenobiotic compounds and pollutants, soil structuring, organic matter storage, and biological control and suppression of plant pathogens; and for that reason, it has often been regarded as an important index of soil quality and plant productivity (Curtis *et al,* 2002). According to Schloter *et al.* (2003), soil enzymes and microbial based processes are considered particularly important because they usually respond more rapidly than chemical and physical parameters to environmental changes and stresses.

2.2. THE ABOVEGROUND AND BELOWGROUND INTERACTIONS IN THE ECOSYSTEM

Interactions between the aboveground and belowground components of terrestrial ecosystems are receiving much research attention in light of their importance in driving ecosystem processes that govern ecosystem productivity, gas fluxes and carbon sequestration (Wardle *et al.*, 2004). The distribution and abundance of the soil microbial communities is a function of abiotic (physical and chemical) conditions and biotic factors (interactions among species/food supply) (Bloem *et al.*, 2006).

Plant cover is an important aspect that affects the soil quality factor, mainly through its contribution towards maintaining a stable biological population in soil by supplying carbon and energy sources from root exudates and plant remains (Balloni and Favilli, 1987). The vertical and horizontal distribution of soil microorganisms can differ extremely in forest soil but microbes are generally most abundant in the upper surface soil layer in particular, within the first few centimeters of the topsoil (Fierer *et al.*, 2003). The large food supply through decomposition of plant litter and plant residues supports a high microbial abundance at the top soil surface.

Furthermore, the microbial communities in the rhizosphere of trees differ from those in bulk soil (Marschner and Rengel, 2007; Shi *et al.*, 2012), which

may be resulted from release of a diverse array of exudates as well as growth regulators and inhibitory compounds. Tree exudates are comprised of carbohydrates, amino acids, low molecular weight aliphatic and aromatic acids, fatty acids, enzymes and hormones (Grayston *et al.*, 2005; Jones *et al.*, 2004). The activities of rhizosphere microorganisms are influenced by several kinds of environmental factors. These factors can be divided in to two groups according to the directness of their effects. Proximal factors that directly affect microbial community structure and activities (e.g. soil moisture, temperature, pH, organic matter content and nutrient availability) and the site factors that have indirect effects (e.g. latitude, elevation, regional climate, parent material, soil texture, depth, mineralogy, topographic positions, land use and the nature of the vegetation).

Prescott *et al.* (2013) reported that there is evidence of differences in microbial communities in litter, forest floors and soil that can be attributed to differences in the tree species occupying the site. The factors identified as underlying differences in microbial communities in litter, forest floors and soil are the pH and base cation content of the litter and whether the trees are broadleaf or coniferous (needle leaf). Differences in microbial communities have been demonstrated in the rhizosphere of different tree species, probably reflecting differences in the amount and nature of root exudates. Rhizosphere microbial community structure has been shown to vary depending on tree species. The quality and quantity of inputs, in the form of litter and rhizodeposits and soil organic matter, are likely important factors for structuring the microbial communities in different ecosystem.

Soil microbial communities are more complex under tropical rain forests, which house the majority of plant diversity on earth (Dirzo and Raven, 2003). Tropical rain forests contribute some of the highest levels of primary production on the planet (Lewis *et al.*, 2009) much of which ultimately falls as leaf litter. Leaf litter from different plant species can present dramatically different growth substrates for microorganisms (Ushio *et al.*, 2008; Strickland *et al.*, 2009), due to variation in plant species functional traits, such as leaf litter, carbon and nutrient

concentrations. As a result, soil microbial community composition often associates with the composition of the plants in the overlying vegetation (De Deyn *et al.*, 2008).

Thoms *et al.* (2010) investigated the link between aboveground and belowground diversity in temperate deciduous forest ecosystems. They determined the effects of the tree species composition on the biomass and composition of the soil microbial community using phospholipid fatty acid (PLFA) profiles in the Hainich National Park, a deciduous mixed forest on loess over limestone in Central-Germany. They investigated the effects of the leaf litter composition on the microbial community, hypothesizing that distinctive leaf litter compositions increase signature PLFAs. In addition, they studied the impact of clay content, pH and nutrient status of the soil on the microbial community in different surface soil layers. Consequently, soil was sampled from depths of 0-5 cm, 5-10 cm and 10-20 cm. Plots with highest leaf litter diversity had the largest total amounts of fatty acids, but only PLFA 16:1ω5, which is a common marker for arbuscular mycorrhizal fungi, was significantly increased. In the uppermost soil layer, the pH explained most of the variance in microbial composition. In the deeper surface soil layers, nutrients such as carbon, nitrogen and phosphorus determined the microbial abundances and composition. The results suggest that the soil microbial community is mainly indirectly influenced by aboveground diversity. Changes in soil pH or the soil nutrient status that are driven by specific plant traits like leaf litter quality drive these indirect changes. Specific direct interactions are most reasonable for mycorrhizal fungi.

Russo *et al.* (2012) conducted a study related to bacterial community structure of contrasting soils under lying bornean rain forests, Lambir Hills National Park, Sarawak, Malaysia. The Park encompasses 6800 ha of lowland mixed dipterocarp forest with the highest tree species richness recorded in the Palaeotropics (Lee *et al.*, 2002). Using pyro sequencing and microarray methods, they quantified the structure of bacterial communities in two contrasting soils (clay and sandy loam) that differ markedly in soil properties, aboveground tree flora, and leaf litter decomposition rates. They found significant soil-related

taxonomic and phylogenetic differences between communities that, due to their proximity, are independent of climate. Bacterial communities showed distinct compositional and taxon abundance distributions that were significantly correlated with the structure of the overlying tree community. Richness of bacteria was greater in the more resource rich clay soil. Phylogenetic community analyses suggested that environmental filtering may be an important mechanism of community assembly in clay, compared to niche-competition in sandy loam. The acidobacteria were the most abundant group in clay, but the proteobacteria dominated in sandy loam. Of the ten most abundant classes, the actinobacteria, betaproteobacteria, clostridia, bacilli, and gammaproteobacteria were more abundant in sandy loam than clay. In addition to the direct effects of soil properties, they noticed that the biochemical composition of carbon and nutrient resources in plant litter and soil pH and oxygen availability as important determinants of the distribution of bacterial diversity.

Koranda *et al.* (2013) stated that the plant-induced variation in resource availability in temperate forest soils leads to a seasonal variation in functional properties of soil microorganisms, resulting from seasonal changes in microbial community structure and physiological adaptations of microorganisms.

A study conducted by Silpkar *et al.* (2010) on dominance of different types of microbial communities at different monsoon seasons in rhizospheric soils of *Aegle marmelos* tree. Nutrients content of soil were also determined simultaneously to correlate with the microbial population. Results show that the rhizosphere of *Aegle marmelos* contains gram-negative bacteria, *Rhizobium*, *Azotobacter*, actinomycetes and yeast and major plant nutrients and their count as well as dominance changes with moisture content in rhizosphere. Except actinomycetes all the microorganisms were found highest during monsoon season whereas in post-monsoon season actinomycetes were dominant. Amount of water in rhizosphere soil also affects soil chemical properties. Soil pH, organic carbon, C: N ratio, available nitrogen and available phosphorus were recorded maximum in monsoon, whereas electrical conductivity and total nitrogen content were found maximum in post-monsoon.

Grayston *et al.* (2005) compared forest floor microbial communities in pure plots of four tree species. The species were *Thuja plicata* (Western red cedar), *Tsuga heterophylla* (western hemlock), *Pseudotsuga menziesii* (Douglas fir), *Picea sitchensis* (Sitka spruce) and replicated at 3 times on Vancouver island. Microbial communities were characterized through community level physiological profiles (CLPP) and profiling of phospholipid fatty acid (PLFA). Microbial communities from cedar forest floor had higher potential C utilization than other species. The F layer of the forest floor under cedar contained significantly higher bacterial biomass (PLFA) than the F layer under the other three tree species. There were differences in microbial communities among the 3 sites. Upper Klanawa had the highest bacterial biomass and potential C utilization. This site also had the highest N availability in the forest floors. Forest floor H layer under hemlock and Douglas fir contained greater biomass of gram negative bacteria and actinomycetes than F layers based on PLFA and H layer under spruce contained greater biomass of gram negative bacteria than F layers. There were no significant differences in bacterial biomass between forest floor layers under cedar. Fungal biomass displayed opposite trends to bacteria and actinomycetes, being lowest in cedar forest floors and highest in the Flayer and at the sites with lowest N availability. There were also difference in community composition among species and sites with cedar forest floor having a much lower fungi: bacteria ratio than least fertile sarita lake site had a much greater fungal: bacteria ratio than the more fertile San jun and upper Klanawa sites. Forest floor had the greatest effect on microbial community structure and potential function followed by site and tree species. The similarity in trends among measures of N availability and microbial communities is further evidence that these techniques provide information on microbial communities that is relevant to nitrogen cycling processes in the forest floor.

Shrama *et al.* (2010) can be concluded from present study that a great number of beneficial, harmful and saprophytic microflora co-exist in rhizosphere and rhizoplane habitats of healthy and diseased mulberry gardens there by balances the population in the ecosystem. The beneficial ones are important for

optimum growth of mulberry depending on the availability of organic nutrient in soil. The beneficial forms such as *Trichoderma larzianum, Azotobacter spp, Bacilllus subtills, Pseudomonas flourescence* could be exploited after isolation while formulations and Integrated Plant Disease Management (IDM) package for management of harmful forms such as *Fusarium solani, F. oxysporum, Botryodiplodia theobromae* and *Macrophomina phaseolina* which causes root rot diseases.

The exotic trees have often been recommended in the past as a management option to enhance the productivity and biodiversity of disturbed ecosystems (Cossalter, 1987). Among these fast-growing tree species, the potential economic value of Australian Acacia species has been systematically assessed (Midgley and Turnbull, 2003). Although these species are recommended to restore degraded ecosystems, it is now well established that this group of leguminous woody plants includes some of the most important plant invaders (Richardson and Rejmanek, 2011).

Boudiaf *et al.* (2013) was carried out a study on Algerian El Kala Biosphere reserve. Where, the introduction of *Acacia mearnsii* led to the invasion of natural formations to the detriment of *Quercus suber*, a native tree species. They hypothesized that shifts in soil microbial functions and ectomycorrhizal (EcM) fungal community structure triggered by this exotic Acacia species might correlate with a decrease of the early growth of *Q. suber*. Soil samples were thus collected from 3 different sites where the exotic species was at different stages of invasion in the Algerian El Kala Biosphere reserve, (i) a *Q. suber* forest free of *A mearnsii* (site S1), (ii) a *Q. suber* / *A. mearnsii* mixed forest where the Australian Acacia has been recently detected (site S2) and (iii) pure stands of *A. mearnsii* formed more than 20 years ago (site S3). Plant growth, EcM community structure associated with *Q. suber* roots and soil microbial functionalities were assessed for 6 month-old cultures of *Q. suber* in glasshouse conditions. The results clearly demonstrated a strong deleterious impact of *A. mearnsii* invasion level on soil chemical characteristics, microbial functions and EcM community structure and colonization, correlated to a decrease in the early

growth of *Q. suber* seedlings. The current study gives new insights into both the negative impact of exotic species on soil functioning and their effect on indigenous vegetation growth

Aponte *et al.* (2013) conducted integrated studies on the functioning of a mixed mediterranean oak forest to demonstrate the tree-soil interactions underpinning a positive feedback process that sustains the coexistence of two oak species. The studies focused on the foliar functional traits, plant regeneration patterns, biogeochemical cycles, soil microbial biomass and ectomycorrhizal (ECM) fungal diversity associated with the co-dominant evergreen *Quercus suber* and deciduous *Quercus canariensis* in a mediterranean forest in southern Spain. In this forest, oak species leaf-fall quality (particularly nutrient content) determined nutrient return, leaf-fall decomposition and nutrient release into soil, leading to different levels of soil fertility. In turn oak species generated changes in soil nutrient concentrations, particularly N and Ca, further affected the size and composition of the soil microbial community. Overall, the two oak species generated soil conditions that aligned with their resource use strategies and would enhance their own competitive capabilities, potentially creating a positive feedback. The two Quercus created soil spatial heterogeneity that could enable their coexistence through spatial niche partitioning. This study demonstrates the critical role of aboveground-belowground interactions underpinning forest community composition. The results reinforce the suggestion that plant-soil feedbacks influence species abundance, persistence and succession and thereby underpin species coexistence (Bonanomi *et al.*, 2005; Brandt *et al.*, 2013).

Thoms *et al.* (2013) conducted a study on seasonal differences in the tree species influence soil microbial communities. The study was carried out in Hainich national park, Germany. The selected species are *Fagus sylvatica, Fraxinus excelsior, Tilia cordata, T.platyphyllos, Carpinus betulus, Acer pseudoplatanus, A.platanoids* and *A.campestre*. The results showed that the soil microbial community differed more markedly between the tree diversity levels in early summer than in autumn. The acidifying character of the decaying beech litter strongly influenced the soil pH values and structured the soil microbial

community indirectly in early summer as it had in autumn. However, the measured differences in the microbial composition in early summer could be attributed primarily to litter quality. This direct influence of plant traits appeared to be eclipsed in autumn because of the high nutrient supply from fresh litter input. Following litter decomposition in the topsoil, however, litter-based plant traits emerged as a factor structuring the soil microbial community in early summer. The results suggest that the PLFAs i14:0 and i15:0, indicative of gram-positive bacteria, are strongly involved in decomposition processes and may be promoted by readily available nutrients. Furthermore, results indicate that a dense root network in association with arbuscular mycorrhizal fungi strongly supported microbial growth in the more diverse forest stands. High proportions of arbuscular mycorrhizal fungi (PLFA 16:1ω5), root-associated microorganisms (PLFAs 16:1ω9, 16:1ω7, 17:1ω8 and 18:1ω7) and bacterial grazers (PLFA 20:5) characterized the microbial community in early summer on these study plots. We conclude that microbial communities are strongly influenced by abiotic controls. However, seasonal differences in litter decomposition rates and root activity should be considered in the analysis of the effects of tree diversity or species on soil microbial communities.

2.3 THE ROLE OF MICROORGANISMS IN PLANT GROWTH

Sturtz and Christie (2003) conducted an experiment on beneficial microbial allelopathies in the root zone: the management of soil quality and plant disease with rhizobacteria. They proposed that by virtue of their physiological adaptability and metabolic versatility, bacteria in plant root zones are a key agent of change in soil agroecosystems. Interactions between plant root systems and rhizobacteria have a profound effect on crop health, yield, and soil quality. Through the selective release of exudates and leachates, plants activate and sustain specific rhizobacterial communities in the root zone. In turn, root zone bacteria are able to generate a wide array of secondary metabolites which can have a positive influence on plant growth; enhancing the availability of minerals and nutrients, improving nitrogen fixation ability, decreasing susceptibility to

frost damage, improving plant health through the biocontrol of phytopathogens, inducing systemic plant disease resistance and facilitating plant establishment, growth and development. The benefits from root zone bacterial biodiversity are moot in managed agroecosystems, where community complexity is minimized, and ecosystem stability is often disrupted for the purpose of disease control and yield maximization. The complexity of plant-soil-microbial interactions are so varied, that a complete understanding of all the relationships involved is unlikely to be achieved, even in a production monoculture. Nevertheless, the consequences of beneficial biological interactions that stimulate crop yields and improve plant health can be evaluated relatively simply and a number of general management strategies can be devised accordingly. Changes in the soil organic matter, soil temperature, soil moisture and pH can affect biomass and the activity of both bacteria and fungi, including ectomycorrhizal (ECM) fungi (Baath *et al.*, 1980).

YuanYuan *et al.* (2011) conducted an experiment to study the soil microbial community dynamics of larch plantation by the dilution plate method using Biolog detection techniques. Monthly changes of soil nutrients were determined. Result demonstrated that, among the three groups of soil microbes, bacterial population was dominant, followed by actinomycetes and fungi in order. The bacterial population in the surface and upper soils (0-10 cm) first increased and then decreased from May to October, while it gradually decreased in 10-20 cm depth soil. The fungal population in the surface soil showed an increasing tendency in May and October, while it changed irregularly in other soil layers. The actinomycetes population in the surface soil exhibited a decreasing tendency during May and October, while it changed irregularly in other soil layers. Available potassium had a negative correlation with bacterial population, while available potassium and effective phosphorus had a significantly positive correlation with actinomycetes population. The diversity index, richness index and evenness index of the microbial communities in the surface and upper soils (0-10 cm) as well as the diversity index and richness index in the 10-20 cm depth

soil all first increased and then decreased, but the evenness index of the microbial communities in the 10-20 cm depth soil first decreased and then increased.

Kinsbursky *et al.* (1990) carried out a study to follow root-microbial population dynamics in the soil profile under *Zygophyllum dumosum*. They reported that root area was greater in the lower soil profile (20-30 cm) during the rainy season, except when the soil was drying out after a period of minimal rainfall. Root production was enhanced in the surface layer (0-10 cm) as the soil dried in the wet season, and throughout the soil profile as the soil dried before the dry summer period. This suggests two functional root types exist for Z. dumosum, one which exploits a relatively stable water supply, and another which captures less available, and reliable sources. Soil bacteria populations were relatively stable throughout the study period, whereas fungi and actinomycetes appeared to have an inverse relationship, with fungi increasing after the early rains, while actinomycetes declined. Actinomycetes may be a more important component of the microflora during drought periods, since their numbers were relatively high following 2 years of below-normal rainfall, but never recovered after a year of normal rainfall.

The importance of fungi in the decomposition of plant remains, biogeochemical recycling in the soil/litter subsystem, and overall ecosystem functioning is well recognised (Carroll and Wicklow, 1992). Krivstov *et al.* (2007) documented the ecology and biodiversity of fungi in a unique Dawyck cryptogamic sanctuary in Britain, where data on species composition have been collected since 1994. The results of this study highlighted the complexity of factors influencing temporal dynamics and spatial variability of fungal biomass in forest soil and litter. Most of the registered interactions appeared to be transient, i.e. manifested only at certain parts of the research period. Analyses showed that the dynamics of microbial community in beech and birch plots appears to be considerably different. In particular the abundance of arbuscular mycorrhizal fungi (as indicated by levels of easily extractable glomalin) was greater in birch plots, corresponding to a more dense grass cover in this habitat. Total soil fungal biomass (as indicated by ergosterol measurements), however, was higher in beech

plots, thus suggesting a notable difference exhibited by different members of fungal community (e.g. saprotrophic and arbuscular mycorrhizal, as opposed to ectomycorrhizal fungi). On the other hand, the abundance of soil bacteria was not significantly different between beech and birch plots. In forest litter, however, the pattern was reversed: fungal levels did not appear to differ much, whilst bacterial abundance in birch plots was considerably higher. Based on the patterns observed, they reported that decomposition in beech-dominated habitats is delayed (i.e. in comparison with birch dominated) because of the differences in the extent to which these plants create and maintain a litter and humus layer (Wardle, 2004). Decomposition rates and patterns are dependent upon chemical composition of litter. As the leaf litter produced by beech trees is of lower quality compared with birch (Melillo *et al.*, 1982), the decomposition in beech-dominated habitats occurs somewhat deeper in the soil profile, and may be carried out with some considerable involvement of ectomycorrhizal fungi.

Mokrane *et al.* (2013) deals with the taxonomy, ecology and antagonist properties of actinomycetes isolated from soils of 7 Saharan palm groves. These microorganisms constitute an important part of the microflora of non-saline soils, but their density is very low in saline soils, particularly when the electrical conductivity exceeds 4 mS/cm. Salinity is the major factor governing their distribution in regularly cultivated parcels. Seven hundred and eighty nine isolates were identified for 12 genera and identified presumptively on the basis of their phenotypic characteristics to about 90 species. The genus *Streptomyces* is predominant (59.8%), Micromonospora (25.6%), *Actinomadura* (4.3%), *Nocardia* (3.0%), *Nocardiopsis* (2.5%) and *Amycolatopsis* (1.5%) also noticed. Soil salinity plays an important role in the dominance of certain species of Streptomyces from which, *Streptomyces griseoincarnatus* is the most frequently isolated. The study of antagonistic properties of isolated actinomycetes showed that *Fusarium oxysporum, F. albedinis,* pathogen of date palm, is inhibited by 15.0% of isolates belonging to the genus *Streptomyces*.

2.4 ASSOCIATION OF SOIL MICROORGANISMS AND PLANTS

2.4.1 NITROGEN FIXING BACTERIA

Nitrogen fixation can only be performed by certain strains of prokaryotic microbes (Fisher and Binkley, 2000). It is commonly found in both archea and bacteria of prokaryotes. These microbes use the nitrogen fixing enzyme, nitrogenase, to reduce atmospheric N_2 to ammonia (NH_3), which is a form that plants can utilize (Walker *et al.*, 1983). Many plants form symbiotic, mutualistic relationship with these prokaryotes, which receive carbohydrates and micro aerobic environments and supply reduced N for use in amino acids, proteins and other biochemical (Binkley and Giardina, 1997). Plants capable of forming such symbioses, such as legumes or actinorhizal plants are sometime used in agroforestry and forestry system. Legumes such as *Acacia, Falcataria, Leuceana*, *Lupinus* and *Robinia* have symbiotic, mutualistic relationships with the bacteria genera Rhizobium and *Bradyrhizobium* (Binkley and Giardina, 1997; Fisher and Binkley, 2000).

Nitrogen (N) is an important factor limiting the growth of trees in many forest ecosystems (Vitousek, 2004). Species influence on soil N cycling can be controlled by both above and below-ground activities, and it may work through multiple mechanisms. Above-ground litter fall provides an important input of C and N to forest soils. Soil microbial communities regulate key processes that control ecosystem N cycling, and they potentially represent a link between the composition of tree species and soil N cycling.

Wild legumes (herbs, shrubs or trees) play a critical role in natural ecosystems, agriculture, and agro- forestry, where their ability to fix nitrogen in symbiosis makes them excellent colonizers of low-N environments, and hence an economic and environmentally friendly species (Rejili *et al.*, 2012).

Rejili *et al.* (2012) conducted a study on symbiotic nitrogen fixation of wild legumes in Tunisia: Soil fertility dynamics, field nodulation and nodules effectiveness. Eight legume species (*Retama retaem*, *Genista saharae*, *Argyrolobium uniflorum*, *Vicia sativa*, *Trigonella maritima* and *Hedysarum*

spinosissimum) were investigated for the first time for nodulation in natural conditions. The investigation showed that bacteria originating from nodules of wild legumes in different Tunisian soils were genetically diverse and affiliated to *Rhizobium*, *Mesorhizobium* and *Sinorhizobium* genera. The root nodulating bacteria belonging to the genus *Sinorhizobium* exhibited higher tolerance to salt stress and elevated temperatures. Based on symbiotic properties, the reports indicated that the wild legume rhizobia formed effective and successful symbioses with their legume hosts. The diversity and effectiveness of the nitrogen-fixing wild legumes are of major significance to soil fertility dynamics in the arid regions. Effects on enzyme activities, microbial biomass and respiration, were evaluated in different agricultural soils and in the presence of different wild legumes such as *G. saharae* and *R. raetam*. Results showed that legumes–rhizobia symbiosis improves enzyme activities, microbial biomass and respiration of field soils and regenerate microbiological properties and the microflora activity involved in the decomposition of organic matter.

2.4.2 PHOSPHATE SOLUBILIZING MICROORGANISM

Phosphorus (P) is one of the major essential macronutrients for biological growth and development. Most of P exists in nature in a variety of organic and inorganic forms, but the concentration of available P in soil is usually very low, normally at levels of 1 mg kg^{-1} or less (10 M H_2PO_4) (Rodriguez and Fraga 1999). Mineral forms of phosphorus are represented in soil by primary minerals, such as apatite, hydroxyapatite and oxyapatite. The principal characteristic of these mineral forms is their insolubility (Behera *et al.*, 2014). The plants obtain their P requirements from the soil pool. It occurs in soil as inorganic phosphate, produced by weathering of parent rock or as organic phosphate derived from decayed plant, animal or microorganisms.

Phosphrous cycle in the biosphere can be described as 'open' or 'sedimentary', because there is no interchange with the atmosphere. Microorganisms play a central role in the natural phosphorus cycle. These are effective in releasing P from inorganic and organic pools of total soil P through

solubilization and mineralization (Hilda and Fraga, 1999). Fungi and bacteria have the ability to solubilize inorganic P compounds (Illmer, 1995). PSB (Phosphate Solubilizing Bacteria) have been used to convert insoluble rock P material into soluble forms available for plant growth (Bojinova *et al.*, 1990). *Bacillus megaterium* is known for its ability to solubilize rock P material. Inorganic-phosphate-solubilizing bacteria (IPSB) have been isolated from the rhizosphere of many terrestrial plants (Sundara-Rao and Sinha 1963). These bacteria may benefit crop plants like legumes, maize, and lettuce by increasing their phosphate content when inoculated alone (Chabot *et al.* 1996) or in combination with mycorrhizal fungi (Singh and Kappor 1998).

Both bacteria and fungi are known to solubilize phosphorus; bacteria are more effective in phosphorus solubilization than fungi (Alam *et al.*, 2002). Among the whole microbial population in soil, phosphate solubilizing bacteria (PSB) constitute 1–50%, while phosphorus solubilizing fungi (PSF) are only 0.1–0.5% in P solubilization potential (Chen *et al.*, 2006). A considerably higher concentration of phosphate solubilizing bacteria is commonly found in the rhizosphere in comparison with the non-rhizosphere soil (Katznelson *et al.*, 1962; Raghu and MacRae, 1966). High proportion of PSM found in the plant rhizosphere, are metabolically more active than other sources (Vazquez *et al.*, 2000). Population of PSB depends on different soil properties (physical and chemical properties, organic matter, and P content) and cultural activities (Kim *et al.*, 1998). The bacteria such as *Bacillus megaterium, Bacillus circulans, Bacillus subtilis, Bacillus polymyxa, Bacillus sircalmous, Pseudomonas striata*, and *Enterobacter* could be referred as the most important phosphate solubilizing strains (Subbarao, 1988; Kucey *et al.*, 1989). Several reports have been examined that the bacterial genera like *Pseudomonas, Bacillus, Rhizobium, Achromobacter, Agrobacterium, Micrococcus,* and *Flavobacterium* and fungi genera like *Pencillium, Aspergillus, Fusarium, Helminthosparium, Alternaria*, have the ability to solubilize insoluble inorganic phosphate compounds such as tri-calcium phosphate, di-calcium phosphate, hydroxyapatite and rock phosphate (Goldstein, 1986).

The mechanism of mineral phosphate solubilization by PSB strains is associated with the release of low molecular weight organic acids, gluconic and ketogluconic acids (Goldstein, 1995), which through their hydroxyl and carboxyl group chelate the cations bound to phosphate, thereby converting it into soluble form (Kpomblekou and Tabatabai, 1994). Production of organic acids results in acidification of the microbial cell and its surroundings.

Mangrove forests near the coastal ecosystem are the most productive ecosystem in the tropical and subtropical regions of the world. Mangrove soils have a strong capacity to absorb nitrates and phosphates carried by the tides (Hesse, 1962). But most of the inorganic phosphate present in the sediment is bound to calcium, iron and aluminum ions as insoluble phosphates (Alongi *et al.*, 1992). Fungi and inorganic phosphate solubilizing bacteria present in the mangrove rhizosphere, are the potential suppliers of soluble forms of phosphorus, would have a great advantage for these plants (Holguin *et al.*, 2001; Sahoo and Dhal 2009).

Vazquez *et al.* (2000) carried out an experiment on phosphate-solubilizing microorganisms (PSB) associated with the rhizosphere of mangroves in a semiarid coastal lagoon. The phosphate-solubilizing potential of the rhizosphere microbial community in mangroves was demonstrated when culture media supplemented with insoluble, tribasic calcium phosphate, and incubated with roots of black (*Avicennia germinans* L.) and white (*La- Guncularia racemosa* (L.) Gaertn) mangrove became transparent after a few days of incubation. Thirteen phosphate-solubilizing bacterial strains were isolated from the rhizosphere of both species of mangroves: *Bacillus amyloliquefaciens, Bacillus licheniformis, Bacillus atrophaeus, Paenibacillus macerans, Vibrio proteolyticus, Xanthobacter agilis, Enterobacter aerogenes, Ente- robacter taylorae, Enterobacter asburiae, Kluyvera cryocrescens, Pseudomonas stutzeri, and Chryseomonas luteola.* One bacterial isolate could not be identified.

The rhizosphere of black mangroves also yielded the fungus *Aspergillus niger.* The phosphate-solubilizing activity of the isolates was first qualitatively evaluated by the formation of halos (clear zones) around the colonies growing on

solid medium containing tribasic calcium phosphate as a sole phosphorus source. Spectrophotometric quantification of phosphate solubilization showed that all bacterial species and *A. niger* solubilized insoluble phosphate well in a liquid medium, and that *V. proteolyticus* was the most active solubilizing species among the bacteria. Gas chromatographic analyses of cell free spent culture medium from the various bacteria demonstrated the presence of 11 identified, and several unidentified, volatile and nonvolatile organic acids. Those most commonly produced by different species were lactic, succinic, isovaleric, isobutyric, and acetic acids. Most of the bacterial species produced more than one organic acid whereas *A. niger* produced only succinic acid. They also proposed that the production of organic acids by these mangrove rhizosphere microorganisms as a possible mechanism involved in the solubilization of insoluble calcium phosphate.

Muthukumar *et al.* (2001) were studied the response of neem (*Azadirachta indica* A. Juss) to indigenous arbuscular mycorrhizal fungi, phosphate-solubilizing and asymbiotic nitrogen-fixing bacteria under tropical nursery conditions. Inoculations of *G. intraradices, G. geosporum*, PSB and *Azospirillum* increased seedling growth and quality. Significantly higher mycorrhizal colonization and PSB and *Azospirillum* populations accompanied growth stimulation. The growth response produced by *G. intraradices, G. geosporum, A. brasilense* and PSB when inoculated simultaneously suggested that this combination was the best over other combinations involving these microbes. So the *G. intraradices, G. geosporum, A. brasilense* and PSB combination can thus be used for routine inoculation of neem seedlings in nurseries for production of healthy, vigorously growing seedlings. Furthermore, the results of this study clearly demonstrate that application of native microbes can be very effective in enhancing seedling growth in tree nurseries in tropical regions.

Yu *et al.* (2011) conducted a study on isolation and characterization of phosphate-solubilizing bacteria from walnut and their effect on growth and phosphorus mobilization and to evaluate the effect of inoculation with the selected PSB stains to walnut seedlings fertilized with or without insoluble phosphate. Thirty-four PSB strains were isolated and identified under the genera

Pseudomonas, Stenotrophomonas, Bacillus, Cupriavidus, Agrobacterium, Acinetobacter, Arthrobacter, Pantoea, and *Rhodococcus* through a comparison of the 16S ribosomal DNA sequences. All isolated PSB strains could solubilize tricalcium phosphate (TCP) in solid and liquid media. Phosphate-solubilizing activity of these strains was associated with a drop in the pH of medium. A significantly negative linear correlation was found between culture pH and phosphorus (P) solubilized from inorganic phosphate. Three isolates *Pseudomonas chlororaphis* (W24), *Bacillus cereus* (W9), and *Pseudomonas fluorescens* (W12) were selected for shade house assays because of their higher phosphate-solubilizing abilities. Under shade house conditions, application of W24 or W12 remarkably improved plant height, shoot and root dry weight, and P and nitrogen (N) uptake of walnut seedlings. These increases were higher on combined inoculation of PSB with TCP addition. The most pronounced beneficial effect on growth of walnut plants was observed in the co-inoculation of the three PSB strains with TCP addition. In comparison, the isolate of W9 failed to increase available soil P, nutrient levels in plants, or to promote plant growth, suggesting that more insoluble phosphate compounds than tricalcium phosphate should be used as substrates to assess the phosphate-solubilizing ability of PSB under greenhouse conditions. The present results indicated that strains *P. chlororaphis* or *P. fluorescens* could be considered for the formulation of new inoculants of walnut, even of more woody plants.

2.4.3 POTASH SOLUBILIZING BACTERIA

Potassium is a third, major essential macronutrient for plant growth and development. It plays an essential role for enzyme activation, protein synthesis and photosynthesis. Potassium in soil is present in water soluble (solution K), exchangeable, non-exchangeable, structural or mineral forms. Potassium from water soluble and exchangeable pools is directly available for plant uptake, but its presence is low level in soil pool. The bulk of total soil K is in the mineral fraction (Sparks, 1987).The main reasons for deficiency of K in soil are runoff, leaching and soil erosion (Sheng and Huang 2002). Rock K material is cheaper

sources of K; however, most of this is not readily available to a plant because the mineral is released slowly.

Han *et al.* (2006) carried out an experiments to evaluate the potential of phosphate solubilizing bacteria (PSB) *Bacillus megaterium* var. *phosphaticum* and potash solubilizing bacteria (KSB) *Bacillus mucilaginosus* inoculated in nutrient limited soil planted with pepper and cucumber. Results showed that rock P and K applied either singly or in combination did not significantly enhance soil availability of P and K, indicating their unsuitability for direct application. PSB was a more potent P-solubilizer than KSB, and co-inoculation of PSB and KSB resulted in consistently higher P and K availability than in the control without bacterial inoculum and without rock material fertilizer. Integrated rock P with PSB increased the availability of P and K in soil, the uptake of N, P and K by shoot and root, and the growth of pepper and cucumber. Similar but less pronounced results were obtained when rock K and KSB were added concomitantly. Combined together, rock materials and both bacterial strains consistently increased further mineral availability, uptake and plant growth of pepper and cucumber, suggesting its potential use as fertilizer.

Han and Lee (2005) conducted studies to evaluate the potential of phosphate solubilizing bacteria (PSB) *Bacillus megaterium* and potash solubilizing bacteria (KSB) *Bacillus mucilaginosus* inoculated in nutrient limited soil planted with egg plant. Results showed that rock P and K materials either applied singly or in combination did not significantly enhance soil availability of P and K. PSB increased higher soil P availability than KSB, which was recommended as a K solubilizer. Inoculation of these bacteria in conjunction with amendment of its respective rock P or K materials increased the availability of P and K in soil enhanced N, P and K uptake, and promoted growth of eggplant.

Sugumaran and Janarthanam (2007) were examined Potash solubilizing bacteria, isolated from soil, rock and mineral samples and their effects on solubilization from microcline, orthoclase and muscovite mica minerals and groundnut plant growth. One of the bacteria, *Bacillus mucilaginosus* MCRCpl, had particularly strong ability to form slime. The maximum potassium

solubilization (4.29 mg L-1) was found in muscovite mica. MCRCpl bacterium could colonize and develop in soil than the control. Total number of bacteria increased due to inoculation from 8.4 x 10^3 cfu g^{-1} to 9.6 x 10^6 cfu g^{-1} respectively. Results revealed that PGPR significantly improved the assimilation of potassium markedly improved through inoculation of this bacterium. The results showed that available P and K are increased from 6.24 to 9.28 mg kg-1 and 86.57 to 99.60 mg kg-1 in soil. Groundnut plant dry matter increased by 125% and the oil content 35.41% were increased through inoculation of MCRCpl bacterium.

Basak *et al.* (2010) made a greenhouse trial to study the effect of co-incubation of potassium solubilizing (*Bacillus mucilaginosus*) and nitrogen (N) fixing (*Azotobacter chroococcum*) bacteria on solubilization of waste mica and their effects on growth promotion and nutrient uptake by a forage crop of sudan grass (*Sorghum vulgare* pers.) in a Typie Haplustalf. Results revealed that significantly higher biomass accumulation and nutrient acquisition were obtained in all the pots treated with mica and/or bacterial strain as compared to control. Data indicated that co-inoculation of waste mica with *B.mucilaginosus* and *A. chroococcum* A-41 resulted in highest biomass strains maintained consistently highest amounts of available K and N in soils even at 150 days of crop growth than other treatments. *B.mucilaginosus* strain was more effective and potent K solubilizer than *A.chroococcum* A-41. Thus, co-inoculation of potassium solubilizing and nitrogen fixing bacteria to waste mica could be a promising and alternative options for utilizing this potent source as K fertilizer to crops and maintaining greater nutrients availability in soil.

Basak *et al.* (2009) studied the dynamics of K release from waste mica inoculated with potassium solubilizing microorganisms (*Bacillus mucilaginosus*) and investigated its effectiveness as potssium fertilizer using sudan grass (*Sorghum vulgare* Pres) var sudanensis as test crop grown under two alfisols. Results revealed that application of mica significantly enhanced biomass yield, uptake and percent K recoveries by sudan grass than control (no- K). Biomass yield, uptake and percent K recoveries increased further when mica was inoculated with bacterial strain in both the soils than uninoculated mica. Alfisol

from Hazaribag recorded higher yield of K and K recoveries than alfisol from Bhubaneswar. The dynamics of K in soils indicated that K was released from mica to water soluble and exchangeable pools of K due to inoculation of mica with *Bacillus mucilaginous* in both the soils. Significantly greater amounts of water soluble, exchangeable and non-exchangeable K were maintained in alfisol from Hazaribag than Bhubaneswar. Release kinetics of K showed significant release of K from mica treated with bacterial strain

2.5 SOIL MICROFLORA IN AGROFORESTRY AND LAND RECLAMATION

Understanding influences of tree species on soils also informs decision making around environmental service provisioning and environmental issues such as effects of species shifts in response to climate change, C sequestration in soil, ecosystem responses to invasive species, restoration of degraded sites, afforestation, and short rotation forestry for biomass production (Prescott and Vesterdal, 2013).

The soil organisms are directly dependent on sustainable function of natural and agricultural ecosystems and a wide range of ecosystem services. These services have been conceptually organized as those associated with the provision of goods, the regulation of ecosystem processes, and those essential to life on earth. Soil microbial biomass comprise about 1-5% of total organic carbon in soil so the biomass itself constitutes the part of soil organic matter and served its most dynamic pool.

The soil enzyme activities are greater in agroforestry alley cropping practices due to differences in litter quality and quantity and root exudates. The organic matter subjected to microbial decay in soils comes from several sources. The fast growing woody perennials in agroforestry provide an almost permanent litter cover; the decomposing organic matter in the form of litter being replenished by freshly falling material.

Sinha *et al.* (2009) investigated a topic on rhizosphere soil microbial index of tree species in a coal mining ecosystem. Microbial characterization of the tree rhizosphere provides important information relating to the screening of

tree species for revegetation of degraded land. Rhizosphere soil samples collected from a few predominant tree species growing in the coal mining ecosystem of Dhanbad, India, were analyzed for soil organic carbon (SOC), mineralizable N, microbial biomass carbon (MBC), active microbial biomass carbon (AMBC), basal soil respiration (BSR), and soil enzyme activities (dehydrogenase, urease, catalase, phenol oxidase, and peroxidase). Principal component analysis was employed to derive a rhizosphere soil microbial index (RSMI) and accordingly, dehydrogenase, BSR/MBC, MBC/SOC, EC, phenol oxidase and AMBC were found to be the most critical properties. The observed values for the above properties were converted into a unitless score (0–1.00) and the scores were integrated into RSMI. The tree species could be arranged in decreasing order of the RSMI as: *Aegle marmelos* (0.718), *A. indica* (0.715), *Bauhinia bauhinia* (0.693), *Butea monosperma* (0.611), *Eugenia jambolana* (0.601), *Moringa oleifera* (0.565), *Dalbergia sissoo* (0.498), *Tamarindus indica* (0.488), *Morus alba* (0.415), *Ficus religiosa* (0.291), *Eucalyptus sp.* (0.232) and *Tectona grandis* (0.181). It was concluded that tree species in coal mining areas had diverse effects on their respective rhizosphere microbial processes, which could directly or indirectly determine the survival and performance of the planted tree species in degraded coal mining areas. Tree species with higher RSMI values could be recommended for revegetation of degraded coal mining area. Among the tree species studied *A. marmelos, A. indica, B. bauhinia, B. monosperma, E. jambolana* and *M. oleifera* could be used for reclamation purposes.

Tian *et al.* (2012) conducted a study to characterize the effects of land use intensity on dissolved organic carbon (DOC) properties and microbial community structure by comparing greenhouse vegetable fields with contrasting management intensity and adjacent cereal fields (wheat and maize rotation) in Shouguang and Quzhou in North China. This study indicated that land use change, particularly to high intensity management, affects soil chemical and biological properties. High rates of fertilizer and manure application not only increased nutrient and carbon input, but also resulted in soil acidification and changes of DOC composition. This affected soil microbial communities, favoring

microbes that are more competitive at high substrate concentrations and adapted to lower soil pH. While the impact of high-intensity greenhouse vegetable management on soil functioning was the accumulation of aromatic compounds in the DOC may suggest a lack of microbial species capable of decomposing these compounds.

Silva *et al.* (2012) conducted a study on Soil microbial biomass and activity under natural and regenerated forests and conventional sugarcane plantations in Brazil. The objective of this study was to evaluate the changes in soil microbial biomass and activity after the regeneration of deforested and cultivated soil in Brazil. Soil sampling was carried out in June and December 2007 (wet and dry seasons, respectively), at four areas, including: a native forest (NF), a 10 years old regenerated forest (RF10), a 20 years old regenerated forest (RF20) and a conventional sugarcane plantation (CL). Microbial biomass C, substrate-induced respiration and cellulase, saccharase, hydrolysis of fluorescein diacetate and dehydrogenase activities were analyzed. The microbial variables varied significantly among different areas depending on the season. Usually, larger differences were observed in the RF10 than in others, in dry season, for soil microbial biomass C and enzyme activities. The multidimensional scaling analysis showed that the RF10 has distinct microbial and biochemical characteristics comparing with the other areas. In general form, microbial activity, as measured by enzyme activities, is higher in native forest and regenerated lands than in cropland.

Lacombe *et al.* (2009) tested the hypothesis that tree based intercropping (TBI) increases the beta-diversity and stability of soil microbial communities compared to conventional monocropping (CM) systems. Soil from TBI research plots in St-Re´mi (Que´bec) and Guelph (Ontario) were intensively sampled along 56-point grid patterns and compared to soil sampled in a similar manner in adjacent CM systems. Compared to CM systems, TBI systems present a more heterogeneous vegetation cover and, by implication, a patchier distribution of leaf litter and rooting patterns that can affect chemical and nutritional soil properties. Thevathasan and Gordon (1997) showed that soil mineral N and total C pools in a

TBI system were higher within a 2.5 m margin close to tree rows compared to the middle of the crop alley.

The study compared TBI and adjacent CM fields at two study sites. The first site is located near the Town of St-Re´mi, Que´bec, Canada. Mean annual temperature is 6^0C and mean annual precipitation is 979 mm of which 22% falls as snow. The TBI field was created in 2000 using alternating rows of hybrid poplar clones TD-3230 (*Populus trichocarpa* Torr. & A. Gray ex Hook. x *Populus deltoides* Bart. ex Marsh.), NM-3729 (*Populus nigra* L. x *Populus maximowiczii* A. Henry), DN-3308 (*P. deltoides* x *P. nigra*), and alternating rows of black walnut (*Juglans nigra* L.) and white ash (*Fraxinus americana* L.), with 8 m spacing's between rows. Soybean (*Glycine max* L. (Merr.)) was grown between tree rows since 2004. This field was paired with a CM field, situated 1.5 km northeast, with similar soil texture and drainage and planted with a soybean monoculture for the last 3 years. The second study site is located near the City of Guelph, Ontario, Canada. Mean annual temperature is 8^0C and mean annual precipitation is 793 mm of which 15% falls as snow. The TBI field was created in 1987 using 10 tree species. The section that sampled consisted of rows of black walnut (*J. nigra*) and silver maple (*Acer saccharinum* L.), with 12.5 m spacing's between rows (Thevathasan and Gordon, 2004). This field was paired with a CM field, situated 300 m southwest, which had been planted with the same crop rotation of maize, soybean, winter wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) as the TBI field.

Phospholipid fatty acids (PLFAs) were extracted from each sample, purified and methylated, and subsequently analyzed by gas chromatography. The spatial heterogeneity (i.e., microbial beta-diversity) of whole PLFA profiles from each field were analyzed using multivariate statistical procedures, and those of individual PLFAs were analyzed using Levene's and Moses' tests. Microbial beta-diversity, based on a measure of dispersion among PLFA profiles within each sampling grid, was significantly higher in the TBI than in the CM system at the St-Re´mi site only. They compared the concentrations of broad microbial groups in both cropping systems using Tukey's test and found a higher incidence of

arbuscular mycorrhizal fungi (AMF) in TBI systems at both sites, and a greater ratio of gram positive-to-gram negative bacteria in the TBI system at the St-Re´mi site only. In order to determine microbial stability, they monitored changes in microbial biomass of bulked soil samples from the sampling grids after these had been exposed to varying concentrations of a heavy metal (Cu) contaminant. Data were then fitted to decreasing exponential functions and model parameters were used to derive an index of microbial stability. Higher microbial stability was found in the TBI than in the CM system at the St-Re´mi site only.

The Acacia species, very abundant in savannas and arid regions of Australia, Africa, India and the Americas, are dependent on mycorrhizae for the absorption of nutrients (particularly P) required for their growth and on *Rhizobia* for nitrogen fixation (Colonna *et al.*, 1991).

Duponnois *et al.* (2002) conducted a research study, in a natural soil of Senegal to follow the development of four provenances of *Acacia mangium* inoculated with an ectomycorrhizal fungus *Pisolithus sp.* (strain COI024) and/or a *Bradyrhizobium sp.* isolate (Aus 13c), to evaluate the impact of these symbioses on the microbial biomass and on the indigenous rhizobial and fungal symbiotic microflora and to determine the impact of these controlled inoculations on the structure of nematode communities. The results showed that the dual inoculation significantly improved plant growth for all provenances. When the plants were transferred into 20l pots filled with a non-sterilized soil, the positive effect on the plant growth of the dual inoculation disappeared and no significant difference was recorded between the plants inoculated with the fungus alone and those inoculated with both *Bradyrhizobium* and the ectomycorrhizal fungus. However, the microbial biomass, the nitrogen contents, the number of nodules per plant and the structure of the nematode communities were significantly influenced by the *A. mangium* provenances and the microbial treatments. This positive effect could be very useful in afforestation programs in order to decrease the mortality usually observed at the first steps of forest plantations.

Zhang *et al.* (2012) carried out an experiment to study the effects of afforestation with *Eucalyptus grandis* on soil physicochemical and

microbiological properties. For this soil physicochemical and microbiological properties were measured across a range of *E. grandis* plantation ages (1–10 years) in south-western China. The results indicate that afforestation with *E. grandis* caused changes in soil properties with soil depth, and the changes were dependent on the stand age. Soil bulk density decreased significantly, but water-holding capacity increased significantly with time. Soil organic matter content, C:N ratio, and soil microbial biomass C and N concentrations showed an initial phase of decline and then increased significantly over time in the upper soil layers of *E. grandis* plantations aged from 1 to 4 or 5 years. Soil pH in *E. grandis* plantations did not change significantly with stand age or soil layer. Cation exchange capacity in the upper soil layer of *E. grandis* plantations increased significantly over time. Total exchangeable bases and base saturation in the soil decreased significantly with depth and with increasing plantation age. Furthermore, *E. grandis* afforestation of arable soils had no significant effects on total N, total P, and available P contents. The requirements of the trees, understory micro environmental conditions, and allelopathic effects might play important roles in the dynamic changes of soil physicochemical and microbiological properties. The results demonstrate the progressive development of processes that lead to the restoration of soil fertility following *E. grandis* afforestation of arable soils. However, most of the properties measured for the afforested soils resembled the properties of arable soils and did not resemble those of the soil of control forests. Thus, reversion of soil properties in the study plantations is likely to require a considerable period of time.

Siviero *et al.* (2008) conducted an experiment on interaction among N fixing bacteria and AM fungi in amazonian legume tree (*Schizolobium amazonicum*) in field conditions. The challenge is to develop new technologies for wood production in agroforestry systems. *Schizolobium amazonicum* is a legume tree, with fast growth and its wood is employed to make furniture. In the present study three arbuscular mycorrhizal fungi (*Glomus clarum*, *Glomus intraradices* and *Glomus etunicatum*) associated with three N-fixing bacteria strains (two *Rhizobium sp.* and one *Burkholderia sp*). Two methods of planting

were used: direct sowing or transplantation of seedlings after initial growth in nursery. *G. intrarradices* was more effective in plant growth when inoculated in seed, and the bacteria strains had no effect when inoculated alone or with AM fungi. However, in seedlings the dual inoculation was more effective. At 210 days Rhi1 and Rhi2 associated with *G. clarum* or *G. etunicatum* increase plant growth. At 390 days *G. clarum* associated with LEM6 or Rhi1 increased most of the parameters evaluated, including biomass and wood production. The presence of microorganisms showed significant differences when compared with non-inoculated plant. The results suggested that the growth stimulating effect of combined microbial inoculations can be much greater than individual inoculants.

Thombre *et al.* (2011) demonstrated that there was considerable variation in the microbial population in the sandy and lateritic soils of coconut rhizosphere. Maximum mean microbial population (96.57×10^3 cfu g^{-1}) was recorded in lateritic soil in comparison with that of sandy soil (64.61×10^3 cfu g^{-1}). Bacterial population was maximum in both the soil types and was 27.57×10^3 cfu g^{-1} and 75.88×10^3 cfu g^{-1} in sandy and lateritic soils respectively. It was followed by fungi. However, the actinomycetes population was comparatively very low. When fungal population was compared with the total microbial population, it was revealed that sandy soils recorded comparatively more fungi load of 47.34×103 cfu g^{-1} as compared to lateritic soils is 8.39×103 cfu g^{-1}. Most predominantly occurring bacteria were species of *Bacillus* and *Pseudomonas* while two species of *Aspergillus viz. A. niger* and *A. terreus* and *Penicillium chrysogenum* were most commonly occurring fungi in both the soil types.

Liu *et al.* (2012) studied that variation in rhizosphere soil microbial index of tree species on seasonal flooding land: An *in situ* rhizobox approach. The result suggested that microbial activity of the tree rhizosphere provides important information relating to the selection of tree species for afforestation of the degraded land. This study was conducted using an *in situ* rhizobox approach, with the aims of establishing a viable technique for sampling desired rhizosphere soil and assessing the feasibility of rhizosphere soil microbial index (RSMI) as an indicator to screen tree species for the seasonal flood land of Yantse River,

China. The characteristics examined include soil pH, soil organic carbon (SOC), soil total nitrogen (TN), microbial biomass carbon (MBC), microbial biomass nitrogen (MBN), microbial quotients, enzyme activities (urease, proteinase, asparaginase and catalase) and relative growth rate of tree species, while the RSMI was calculated by principal component analysis. The results indicated that microbial properties of rhizosphere soil were significantly affected by trees species planted under seasonal flooding lands. Microbial biomass and its activity in the rhizosphere have a great ecological significance, and MBC, pH, MBN/TN, MBC/MBN and MBC/SOC could be most important properties for appraising rhizosphere soil quality. The RSMIs calculated by integrating microbial properties were different from various sampling positions of rhizosphere soil, and a significant difference in RSMI was observed among the five tree species for all sampling positions. The *in situ* rhizobox approach taken in this study can be used as an available method for sampling rhizosphere soil, and sampling the soil at 0–4 mm distance from the root mats as rhizosphere soil is reliable. Results from this study suggested that tree species having an RSMI > 0.5 would be used for afforestation at the seasonal flooding lands of Yangtse River.

Seasonal abundance of beneficial soil microflora in fodder production systems on red alfisols was done by Roy *et al.* (2007). The population dynamics of soil microbial flora, viz., actinomycetes, bacteria and fungi, were assessed during June 2002 to May 2004 in three fodder production systems (sown grassland, silvopasture and annual cultivated fodder crop) established at the central research farm of Indian Grassland and Fodder Research Institute, Jhansi, Uttar Pradesh, India. Ten soil (red Alfisols) samples (10 cm depth) were collected from each production systems. Eight genera of actinomycetes, ten genera of fungi and six types of bacteria were recorded. In silvopasture system, actinomycetes and fungi exhibited highest evenness in species distribution (0.5 and 0.7), Shannon-Wiener diversity index (0.9 and 1.4), and Simpson's index (2.1 and 2.9). In sown pasture, bacterial population exhibited highest Shannon-Weiner diversity index (0.76) and Simpson's index (1.87). The value of these indices was lowest for cultivated fodder cropping system. The peak population of actinomycetes

(1462-1232×10^5 cfu/g) and fungi (38-28×10^5 cfu/g) was recorded during monsoon months (July-August). The highest average population of actinomycetes was recorded in silvopasture (282×10^5 cfu/g), whereas highest average population of bacteria (129×10^5 cfu/g) and fungi (10.2×10^5 cfu/g) were recorded in sown pasture. In perennial fodder systems, fungi were found to be significantly correlated with soil water, relative humidity, rainfall, and soil respiration. In cultivated fodder cropping system, population of actinomycetes was significantly correlated with available phosphorus, potassium and soil pH.

Materials and Methods

3. MATERIALS AND METHODS

3.1 EXPERIMENTAL SITE

The present study was conducted in existing species trial plots of selected indigenous tree species in the sub-centre of Kerala Forest Research Institute, Nilambur, located in Malappuram district of the state at 11°16′37″ latitude and 76°13′33″ longitude. The area has an elevation of 41 m above mean sea level. The temperature varies between 17°C and 37°C, the mean annual rainfall ranges from 2500 to 3500mm.

3.2 EXPERIMENTAL MATERIALS

The study was conducted on four indigenous tree species namely *Hopea parviflora* Bedd., *Artocarpus hirsutus* Lamk., *Pterocarpus marsupium* Roxb, and *Pterocarpus santalinus* L.f. of thirty years of age and planted with 2 m× 2 m spacing. The field works extended over a period of one year (May 2013 to May 2014).

3.3 COLLECTION OF SOIL SAMPLES

The rhizosphere soil samples were collected within a radius of 30 cm from the tree and a depth from 0-30cm layer of the top soil from each tree species for microbial analysis. The samples were collected at quarterly interval for a period of one year. At each sampling, 15 samples were collected (4 tree species + tree less open area× 3 replications). Thus a total 75 samples (5 treatments× 3 replications× 5 sampling) were collected and analysed for soil microflora.

The soil samples for analyzing physico-chemical properties were collected at the start and again at the end of the study. The samples were analysed for soil pH, organic carbon, total and available nitrogen, available phosphorus, and exchangeable potassium using standard procedures. Also representative triplicate soil samples were collected from the contiguous treeless open area as control.

The sieved samples are then stored in a polythene bag for further physico-chemical analysis.

3.4 ISOLATION AND ENUMERATION OF SOIL MICROFLORA

The rhizosphere soils were collected from indigenous tree species plots namely *Hopea parviflora, Artocarpus hirsutus, Pterocarpus marsupium, Pterocarpus santalinus,* and also from the treeless control plots. Total bacteria, fungi, actinomycetes, nitrogen fixing bacteria, phosphate solubilizing microorganisms (PSM), and potash solubilizing bacteria (KSB) were isolated and enumerated using standard protocols (Johnson and Curl, 1972). The quantitative estimation of bacteria, fungi, actinomycetes, nitrogen fixers, phosphate solubilizing bacteria, potash solubilizing bacteria were carried out on Nutrient agar medium (bacteria), Martin's rose bengal medium (fungi), Kenknight munaier's mediaum (actinomycetes) (Johnson and Curl, 1972), Jensen's agar media (nitrogen fixing bacteria), Pikovskaya's agar medium (PSM) (Subbarao, 1988), and Glucose yeast extract agar medium (KSB). The dilution of $10^{-2}$was used for isolation of fungi and 10^{-3} for actinomycetes, nitrogen fixing bacteria, phosphate solubilizers, potash solubilizing bacteria, and 10^{-4} for bacteria.

3.5 PHYSICO-CHEMICAL PROPERTIES OF SOIL

The soil samples were analyzed for the following physico-chemical properties of soil.

3.5.1. **Soil moisture**

Soil moisture content was determined by weight loss after drying fresh soil at 100-110°C for 24 hour.

$$\text{Soil moisture content (\%)} = \frac{\text{Wet soil (g)} - \text{Dry soil (g)}}{\text{Dry soil (g)}} \times 100$$

3.5.2. **Bulk density**

Soil samples for bulk density measurements were done using a steel cylinder (Jackson, 1958). Bulk density was estimated by taking out a core of undisturbed soil by using steel cylinder. The soil was dried and weighed. The

volume of soil was calculated by measuring the volume of cylinder (πr^2h). The bulk density was calculated by dividing the oven dry weight of samples (g) by volume of the soil.

3.5.3. **Soil pH**

The pH of soil was determined using an aqueous suspension of soil (soil and water in 1:2.5 ratio) using an Elico pH analyser (Model Li 614).

3.5.4. **Organic Carbon**

Organic carbon content of the soil was determined by wet digestion method using 1 g soil (Walkley and Black, 1934). Soil organic matter was determined by multiplying the value of organic carbon by 1.334 (Van Bemmelen factor) and expressed in percentage.

3.5.5. **Total Nitrogen**

Total nitrogen content in soil samples was determined using continuous flow analyzer method (Skalar).

Sulphuric acid and Selenium powder mixture: 3.5 g Se powder was weighed. 1 litre of conc.H_2SO_4 was carefully poured into a two litre beaker. Selenium powder was then dissolved into the H_2SO_4 by heating the beaker for 4 to 5 hours at 300° C. The black colour of the solution changed to deep blue colour and then changed into light yellow. The solution was then cooled.

Digestion mixture: 10.8 g salicylic acid was weighed and added to 150 ml of hydrogen sulphide and selenium mixture.

Procedure: 0.4 g of the soil sample was weighed in the digestion tube. 2.5 ml of the digestion mixture was poured into the digestion tube. The tube was then swirled well and allowed to stand for 2 hours or overnight. It was then inserted into the digestion block and heated at 100°C for 2 hours. After cooling, the tubes were removed from the block and 1 ml of 30% H_2O_2 was added and again after reaction 1 ml of 30% H_2O_2 was added. After the reaction ceased, they were again

placed in the digestion block and heated at 330°C for 2 hours. The digest turned colourless, when the digestion was completed. The digest was made upto75 ml in a standard flask. The readings were then taken from the continuous flow analyzer (Skalar) directly using the reagents.

3.5.6. **Available Nitrogen and Available Phosphorus**

Available nitrogen and available phosphorus content in the soil were determined using continuous flow analyzer. Forty gram of soil samples was weighed in polyethylene shaking bottle, in that 200.00 ml of distilled water was poured and kept for shaking for 60 minutes. After shaking, the soil sample was filtered through filter paper. The readings were then taken from the continuous flow analyzer directly using the reagents.

3.5.7. **Exchangeable Potassium**

Exchangeable Potassium in the soils was extracted using 1*N* neutral ammonium acetate and estimated using flame photometry (Jackson, 1958).

3.6 GROWTH CHARACTERISTICS OF TREES IN THE PLOT

The tree height and girth at breast height were recorded at the start of the experiment and again after one year. The standing tree volume and mean annual increment were calculated from the total height and girth at breast height of trees.

3.7 STATISTICAL ANALYSIS

Statistical analysis was done using software package SPSS V. 20.0. Duncan's Multiple Range Test (DMRT) was used to compare among treatment means.

Results

4. RESULTS

The result of the study entitled "Soil productivity changes under selected indigenous tree species with special reference to beneficial microflora" carried out during the period of 2013-2014, at the sub-centre of Kerala Forest Research Institute, Nilambur, Malappuram, Kerala, India is presented under the following major titles.

4.1 Microbial population

4.2 Physico-chemical properties of soil

4.3 Growth characteristics of trees in the plot

4.1 MICROBIAL POPULATION

The population of various microflora such as bacteria, fungi, actinomycetes, nitrogen fixing bacteria, phosphate solubilizing microorganisms (PSM) and potash solubilizing bacteria (KSB) were investigated under different indigenous tree species like *Hopea parviflora* Bedd., *Artocarpus hirsutus* Lamk., *Pterocarpus marsupium* Roxb. and *Pterocarpus santalinus* L.f. The detailed results are given here under.

4.1.1. **Microbial population under different indigenous tree species**

4.1.1.1. ***Microbial population under different indigenous tree species during late summer- I (May, 2013) at Nilambur, Malappuram***

The highest bacterial population (Table.1) observed in *Pterocrapus santalinus* (11.67×10^4cfu g^{-1}) followed by *Artocarpus hirsutus* (11.33×10^4cfu g^{-1}) and lowest by treeless control plot (5.33×10^4cfu g^{-1}). The differences in bacterial population between the tree species (Table. 3) were not statistically significant. The fungi population observed highest in *Hopea parviflora* and *Artocarpus hirsutus* (25.00×10^2cfu g^{-1}) and with respect to fungi, significant

Table 1. Microbial population under different indigenous tree species during late summer- I (May, 2013), at Nilambur, Malappuram

Species	Bacteria ($\times 10^4$cfu g^{-1})	Fungi ($\times 10^2$cfu g^{-1})	Actinomycetes ($\times 10^3$cfu g^{-1})	Nitrogen fixing bacteria ($\times 10^3$cfu g^{-1})	Phosphate solubilizing microorganism ($\times 10^3$cfu g^{-1})	Potash solubilizing bacteria ($\times 10^3$cfu g^{-1})
Hopea parviflora	7.33 (2.08)	25.00^{a} (4.35)	3.67^{b} (1.15)	2.00^{a} (1.00)	7.00 (3.60)	13.67^{a} (0.57)
Artocarpus hirsutus	11.33 (4.61)	25.00^{a} (4.35)	7.67^{a} (1.52)	1.67^{ab} (0.57)	10.33 (3.21)	2.33^{c} (1.52)
Pterocarpus marsupium	9.00 (3.60)	19.67^{ab} (7.09)	6.33^{a} (1.52)	1.67^{ab} (0.57)	10.33 (1.52)	5.00^{bc} (2.64)
Pterocarpus santalinus	11.67 (7.23)	19.33^{ab} (3.05)	4.00^{b} (1.00)	2.00^{a} (1.00)	6.67 (2.88)	7.67^{b} (4.04)
Treeless control plot	5.33 (2.30)	14.33^{b} (2.08)	1.00^{c} (0.00)	0.33^{b} (0.57)	6.33 (0.57)	4.00^{bc} (1.00)

Values in the parenthesis are standard deviation of the mean.

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

variation observed between the tree species. Both, *Hopea parviflora* and *Artocarpus hirsutus* was significantly higher than treeless control plots. The fungal population in the treeless control plot (14.33×10^{2}cfu g^{-1}) was distinctively lowest than all the tree plots.

The highest actinomycetes population reported in *Artocarpus hirsutus* (7.67×10^{3}cfu g^{-1}) and lowest in treeless control plot (1.00×10^{3}cfu g^{-1}). Actinomycetes in *Artocarpus hirsutus* and *Pterocarpus marsupium* were significantly higher than *Hopea parviflora, Pterocrapus santalinus* and treeless control plot.

The highest population of nitrogen fixing bacteria observed in *Hopea parviflora* and *Pterocrapus santalinus* (2.00×10^{3}cfu g^{-1}). Nitrogen fixing bacteria in *Hopea parviflora* and *Pterocrapus santalinus* was significantly higher than treeless control plot. The population in *Hopea parviflora* was at par with remaining tree control plots. The treeless control plot (0.33×10^{3}cfu g^{-1}) remained significantly lower compared to the tree plots.

The highest phosphate solubilizing microorganisms (PSM) population noticed in *Artocarpus hirsutus* and *Pterocrapus marsupium* (10.33×10^{3}cfu g^{-1}) followed by *Hopea parviflora* (6.67×10^{3}cfu g^{-1}) and lowest by treeless control plot (6.33×10^{3}cfu g^{-1}). However, the PSM populations between the treatments were not statistically significant.

The highest quantity of potash solubilizing bacteria (KSB) observed in *Hopea parviflora* (13.67×10^{3}cfu g^{-1}) and lowest in *Artocarpus hirsutus* (2.33×10^{3}cfu g^{-1}). The KSB in *Hopea parviflora* was significantly higher than *Pterocrapus santalinus* and *Artocarpus hirsutus*. The population in *Pterocrapus santalinus* was at par with *Pterocrapus marsupium* and treeless control plot. While comparing all microflora population in late summer-I sampling (May, 2013), *Artocarpus hirsutus* recorded highest microflora population and lowest by treeless control plot.

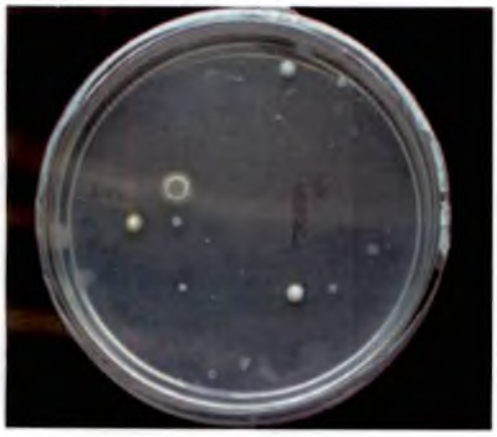
Hopea parviflora

Pterocarpus santalinus

Artocarpus hirsutus

Pterocarpus marsupium

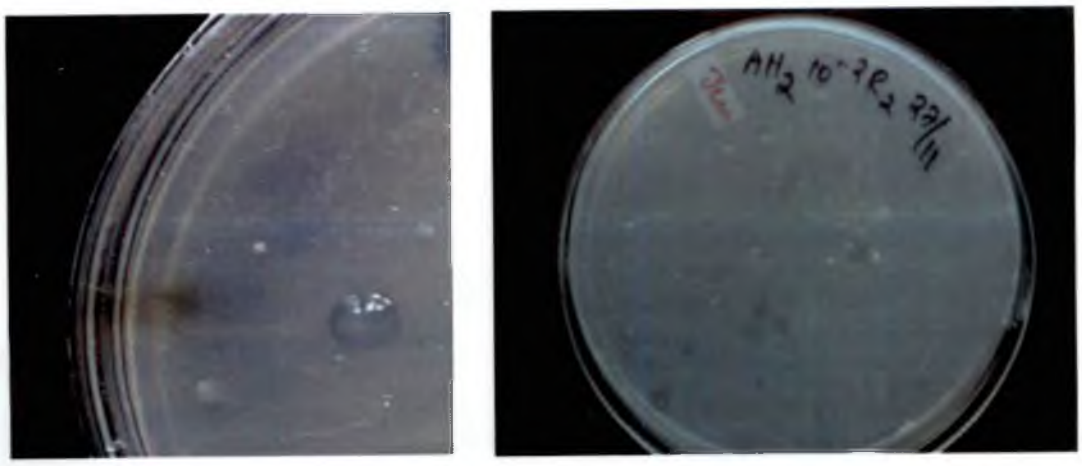
Plate 1. Fungi colonies in different indigenous tree species



Artocarpus hirsutus

Pterocarpus marsupium

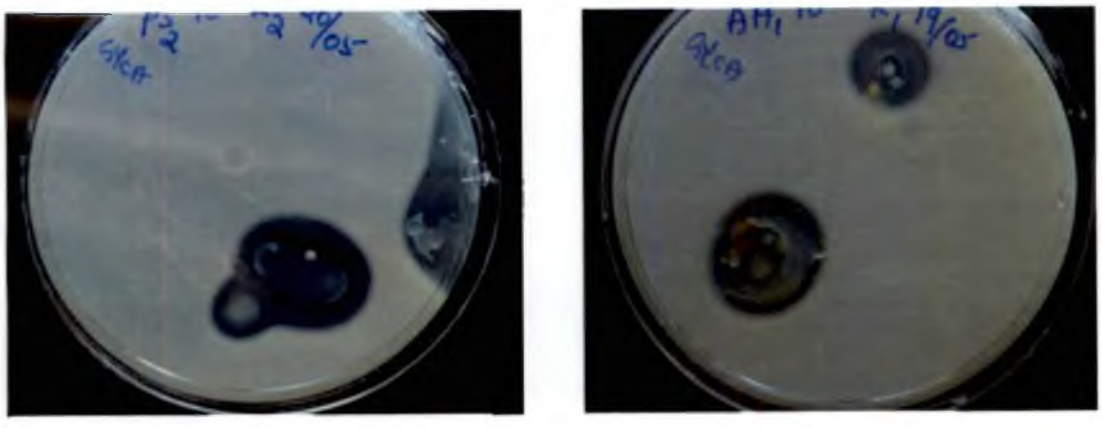
Plate 2. Actinomycetes colonies in different indigenous tree species



Pterocarpus marsupium *Artocarpus hirsutus*

Plate 3. Nitrogen fixing bacteria colonies in different indigenous tree species

Hopea parviflora *Pterocarpus marsupium*



Pterocarpus santalinus *Artocarpus hirsutus*

Plate 4. Potash solubilizing bacteria colonies in different indigenous tree species

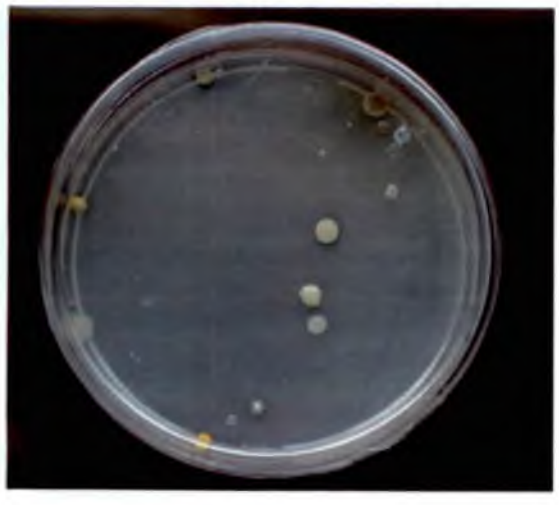
Hopea parviflora

Pterocarpus santalinus

Artocarpus hirsutus

Pterocarpus marsupium

Plate 5. Phosphate solubilizing bacteria colonies in different indigenous tree species



Artocarpus hirsutus

Hopea parviflora

Plate 6. Bacteria colonies in different indigenous tree species

4.1.1.2. ***Microbial population under different indigenous tree species during rainy season (August, 2013), at Nilambur, Malappuram***

The *Hopea parviflora* (51.33×10^4cfu g^{-1}) species was found as the highest bacterial population (Table. 2) followed by *Artocarpus hirsutus* (9.67×10^4cfu g^{-1}) and lowest by treeless control plot (3.67×10^4cfu g^{-1}). In bacterial population, there is a significant difference observed between tree plots and treeless control plots. The population in *Hopea parviflora* was significantly higher than *Artocarpus hirsutus* and treeless control plot.

The fungi population was highest in *Artocarpus hirsutus* (25.67×10^2cfu g^{-1}) and lowest in treeless control plot (0.33×10^2cfu g^{-1}). The population in *Artocarpus hirsutus* was significantly higher than all tree plots and treeless control plots.

The statistical analysis revealed that actinomycetes population (Table.2) was significantly highest in *Artocarpus hirsutus* (9.33×10^3cfu g^{-1}) and the lowest in treeless control plot (1.33×10^3cfu g^{-1}). *Artocarpus hirsutus* was significantly higher than *Hopea parviflora* and treeless control plot. The *Pterocrapus marsupium* also recorded significantly higher population than treeless control plot. The population in *Pterocarpus marsupium* was at par with *Hopea parviflora* and *Pterocarpus santalinus*. The *Pterocarpus santalinus* was at par with treeless control plot.

The highest nitrogen fixing bacteria was observed in *Artocarpus hirsutus* (2.00×10^3cfu g^{-1}) and lowest in treeless control plot (0.33×10^3cfu g^{-1}). Both *Artocarpus hirsutus* and *Pterocrapus santalinus* were significantly higher than treeless control plot. However, the population of nitrogen fixing bacteria in *Artocarpus hirsutus* and *Pterocrapus santalinus* were at par with *Hopea parviflora* and *Pterocrapus marsupium.*

Table 2. Microbial population under different indigenous tree species during rainy season (August, 2013) at Nilambur, Malappuram

Species	Bacteria ($\times 10^4$cfu g^{-1})	Fungi ($\times 10^2$cfu g^{-1})	Actinomycetes ($\times 10^3$cfu g^{-1})	Nitrogen fixing bacteria ($\times 10^3$cfu g^{-1})	Phosphate solubilizing microorganism ($\times 10^3$cfu g^{-1})	Potash solubilizing bacteria ($\times 10^3$cfu g^{-1})
Hopea parviflora	51.33^{a} (3.51)	8.00^{b} (2.64)	3.00^{bc} (2.00)	1.33^{ab} (0.57)	4.00 (3.60)	1.00^{ab} (0.00)
Artocarpus hirsutus	9.67^{b} (4.04)	25.67^{a} (2.51)	9.33^{a} (4.04)	2.00^{a} (1.00)	9.00 (3.00)	2.67^{a} (2.08)
Pterocarpus marsupium	8.00^{bc} (2.00)	8.67^{b} (3.78)	7.33^{ab} (2.08)	1.00^{ab} (0.00)	7.67 (2.08)	1.00^{ab} (0.00)
Pterocarpus santalinus	5.33^{bc} (2.51)	3.67^{c} (0.57)	5.33^{abc} (2.51)	1.67^{a} (0.57)	6.00 (3.46)	1.00^{ab} (0.00)
Treeless control plot	3.67^{c} (0.57)	0.33^{c} (0.57)	1.33^{c} (1.52)	0.33^{b} (0.57)	5.67 (3.05)	0.00^{b} (0.00)

Values in the parenthesis are standard deviation of the mean.

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

The highest population of phosphate solubilizing microorganism recorded by *Artocarpus hirsutus* (9.00×10^3cfu g^{-1}) followed by *Pterocrapus marsupium* (7.67×10^3cfu g^{-1}) and the lowest by *Hopea parviflora* (4.00×10^3cfu g^{-1}). However, the difference between the populations (Table. 2) was not statistically significant.

The highest potash solubilizing bacteria was noticed in *Artocarpus hirsutus* (2.67×10^3cfu g^{-1}) and lowest in treeless control plot. Potash solubilizing bacteria in *Artocarpus hirsutus* was significantly higher than treeless control plot. The population in *Artocarpus hirsutus* was at par with all tree plots. In general, the total microflora population in rainy season (August, 2013) sampling, was the highest in *Artocarpus hirsutus* compared to all the tree species and the treeless control plot.

4.1.1.3. *Microbial population under different indigenous tree species during winter (November, 2013) at Nilambur, Malappuram*

The highest bacterial population (Table. 3) was noticed in *Pterocrapus santalinus* (16.00×10^4cfu g^{-1}) and lowest in treeless control plot (3.00×10^4cfu g^{-1}). Bacterial population in *Pterocrapus santalinus* was significantly higher than all plots except *Artocarpus hirsutus*. The population in *Pterocrapus santalinus* was at par with *Artocarpus hirsutus*.

The highest fungal population observed in *Artocarpus hirsutus* (19.00×10^2cfu g^{-1}) and lowest in treeless control plot (2.33×10^2cfu g^{-1}). The fungi population in *Artocarpus hirsutus* was significantly higher than all other treatments. The population in *Pterocrapus santalinus* was at par with *Hopea parviflora and Pterocrapus marsupium.*

The actinomycetes population (Table. 3) was highest in *Pterocrapus marsupium* (11.67×10^3cfu g^{-1}) and lowest in treeless control plot (3.33×10^3 cfu g^{-1}). *Pterocrapus marsupium* and *Artocarpus hirsutus* was significantly higher than treeless control plots.

Table 3. Microbial population under different indigenous tree species during winter (November, 2013) at Nilambur, Malappuram

Species	Bacteria ($\times 10^4$cfu g^{-1})	Fungi ($\times 10^2$cfu g^{-1})	Actinomycetes ($\times 10^3$cfu g^{-1})	Nitrogen fixing bacteria ($\times 10^3$cfu g^{-1})	Phosphate solubilizing microorganism ($\times 10^3$cfu g^{-1})	Potash solubilizing bacteria ($\times 10^3$cfu g^{-1})
Hopea parviflora	9.00^{bc} (3.00)	7.33^{bc} (0.57)	6.00^{ab} (2.64)	2.33^{b} (1.52)	8.33^{ab} (2.08)	1.33 (0.57)
Artocarpus hirsutus	12.67^{ab} (3.78)	19.00^{a} (4.58)	11.00^{a} (2.64)	7.00^{a} (2.00)	9.67^{a} (4.61)	1.33 (0.57)
Pterocarpus marsupium	8.00^{bc} (2.00)	7.33^{bc} (2.51)	11.67^{a} (4.50)	2.67^{b} (0.57)	10.00^{a} (2.00)	1.67 (1.15)
Pterocarpus santalinus	16.00^{a} (5.29)	8.00^{b} (2.64)	8.33^{ab} (2.51)	2.67^{b} (1.15)	11.00^{a} (2.00)	1.00 (0.00)
Treeless control plot	3.00^{c} (2.00)	2.33^{c} (1.52)	3.33^{b} (2.30)	0.67^{b} (1.15)	4.00^{b} (2.64)	0.67 (0.57)

Values in the parenthesis are standard deviation of the mean.

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

The highest nitrogen fixing bacteria population was observed in *Artocarpus hirsutus* (7.00×10^3cfu g^{-1}) and lowest in treeless control plot (0.67×10^3cfu g^{-1}). The population in *Artocarpus hirsutus* was significantly different from other tree species and treeless control plot.

The highest population of phosphate solubilizing microorganisms was observed in *Pterocarpus santalinus* (11.00×10^3cfu g^{-1}) and lowest in treeless control plot (4.00×10^3cfu g^{-1}). The treeless control plot was significantly the lowest than other tree species except in *Hopea parviflora.*

The highest KSB recorded in *Pterocrapus marsupium* (1.67×10^3cfu g^{-1}) and lowest in treeless control plot (0.67×10^3cfu g^{-1}). The potash solubilizing bacteria population (Table.3) during the third sampling season was not statistically significant. In the winter (November, 2013) sampling also, *Artocrapus hirsutus* observed as highest total microflora population and treeless control plot the lowest.

4.1.1.4. ***Microbial population under different indigenous tree species during early summer (February, 2014), at Nilambur, Malappuram***

The highest bacteria population was recorded in *Pterocarpus marsupium* (5.33×10^4cfu g^{-1}) and lowest in treeless control plot (1.67×10^4 cfu g^{-1}). The bacterial population (Table. 4) in *Pterocarpus santalinus* was significantly higher than *Hopea parviflora*, *Artocarpus hirsutus* and treeless control plot. The population in *Pterocarpus santalinus* was at par with *Pterocarpus marsupium.*

The highest fungi population was observed in *Artocarpus hirsutus* (32.00×10^2cfu g^{-1}) and the lowest in treeless control plot (5.33×10^2cfu g^{-1}). Fungi population in *Artocarpus hirsutus* was significantly higher than all other treatments. The highest actinomycetes recorded in *Pterocarpus santalinus* and *Pterocarpus marsupium* (12.33×10^3cfu g^{-1}) and the lowest in treeless control plot (7.00×10^3 cfu g^{-1}).

Table 4. Microbial population under different indigenous tree species during early summer (February, 2014) at Nilambur, Malappuram

Species	Bacteria ($\times 10^4$cfu g^{-1})	Fungi ($\times 10^2$cfu g^{-1})	Actinomycetes ($\times 10^3$cfu g^{-1})	Nitrogen fixing bacteria ($\times 10^3$cfu g^{-1})	Phosphate solubilizing microorganism ($\times 10^3$cfu g^{-1})	Potash solubilizing bacteria ($\times 10^3$cfu g^{-1})
Hopea parviflora	4.33^{bc} (2.08)	9.67^{cd} (3.78)	7.33^{b} (1.52)	1.67^{a} (1.15)	2.67 (0.57)	1.33^{bc} (0.57)
Artocarpus hirsutus	5.00^{bc} (3.60)	32.00^{a} (3.00)	7.33^{b} (3.21)	1.33^{a} (0.57)	5.67 (1.15)	1.33^{bc} (0.57)
Pterocarpus marsupium	5.33^{ab} (2.51)	15.00^{b} (3.60)	12.33^{a} (2.08)	1.33^{a} (0.57)	5.67 (2.08)	2.67^{ab} (1.15)
Pterocarpus santalinus	5.00^{a} (1.73)	11.00^{bc} (1.00)	12.33^{a} (2.51)	1.33^{a} (0.57)	3.33 (1.52)	3.33^{a} (1.15)
Treeless control plot	1.67^{c} (1.15)	5.33^{d} (0.57)	7.00^{b} (1.00)	0.00^{b} (0.00)	5.00 (2.64)	0.67^{c} (0.57)

Values in the parenthesis are standard deviation of the mean

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

Actinomycetes population in *Pterocarpus santalinus* and *Pterocarpus marsupium* was significantly higher than *Hopea parviflora*, *Artocarpus hirsutus* and treeless control plot.

The nitrogen fixing bacteria was highest in *Hopea parviflora* (1.67×10^3cfu g^{-1}) and lowest in treeless control plot. However, nitrogen fixing bacteria in all trees species were significantly higher than treeless control plot.

The highest population of phosphate solubilizing microorganisms was recorded in *Pterocrapus marsupium* and *Artocarpus hirsutus* (5.67×10^3cfu g^{-1}) and lowest in *Hopea parviflora* (2.67×10^3cfu g^{-1}). The phosphate solubilizing microorganism population (Table.4) during the third sampling season was not statistically significant.

The highest potash solubilizing bacteria population observed in *Pterocarpus santalinus* (3.33×10^3cfu g^{-1}) and lowest in treeless control plot (0.67×10^3cfu g^{-1}). Population in *Pterocarpus santalinus* was significantly higher than *Hopea parviflora, Artocarpus hirsutus* and treeless control plot. The population in *Pterocarpus santalinus* was at par with *Pterocrapus marsupium.*

Early summer season (February, 2014) shown a distinct trend with regards to the total microflora population. *Pterocarpus santalinus* plot recorded highest microflora population.

4.1.1.5. ***Microbial population under different indigenous tree species during late summer-II (May, 2014) at Nilambur, Malappuram***

The highest bacterial population (Table. 5) was observed in *Artocarpus hirsutus* (37.00×10^4cfu g^{-1}) and lowest in treeless control plot (6.67×10^4cfu g^{-1}). Population in *Artocarpus hirsutus* was significantly higher than all other tree species and treeless control plot.

The highest fungi population observed in *Pterocarpus santalinus* (31.33×10^2cfu g^{-1}) and lowest in treeless control plot (6.67×10^2cfu g^{-1}). Fungi in *Pterocarpus santalinus* and *Artocarpus hirsutus* were significantly higher than *Hopea parviflora, Pterocarpus marsupium* and treeless control plot.

Table 5. Microbial population under different indigenous tree species late summer- II (May, 2014) at Nilambur, Malappuram

Species	Bacteria ($\times 10^4$cfu g^{-1})	Fungi ($\times 10^2$cfu g^{-1})	Actinomycetes ($\times 10^3$cfu g^{-1})	Nitrogen fixing bacteria ($\times 10^3$cfu g^{-1})	Phosphate solubilizing microorganism ($\times 10^3$cfu g^{-1})	Potash solubilizing bacteria ($\times 10^3$cfu g^{-1})
Hopea parviflora	23.33^{b} (4.50)	12.00^{b} (5.00)	9.67^{a} (1.52)	2.00^{b} (0.00)	3.33 (1.15)	5.00^{ab} (3.46)
Artocarpus hirsutus	37.00^{a} (3.00)	27.67^{a} (3.05)	8.33^{a} (1.52)	5.33^{a} (3.51)	6.67 (3.05)	8.00^{a} (2.64)
Pterocarpus marsupium	24.33^{b} (6.80)	11.67^{b} (2.51)	9.00^{a} (1.00)	1.33^{b} (0.57)	4.67 (1.52)	1.67^{bc} (1.15)
Pterocarpus santalinus	22.33^{b} (6.50)	31.33^{a} (3.51)	10.00^{a} (1.00)	1.33^{b} (0.57)	5.33 (0.57)	2.33^{bc} (1.15)
Treeless control plot	6.67^{c} (1.15)	6.67^{b} (1.52)	5.33^{b} (1.52)	0.33^{b} (0.57)	4.33 (2.08)	0.67^{c} (0.57)

Values in the parenthesis are standard deviation of the mean.

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

The highest actinomycetes population observed in *Pterocarpus santalinus* (10.00×10^3cfu g^{-1}) and lowest in treeless control plot (5.33×10^3 cfu g^{-1}). Actinomycetes in treeless control plot was significantly lower than all the tree species plots

The highest population of nitrogen fixing bacteria was observed in *Artocarpus hirsutus* (5.33×10^3cfu g^{-1}) and lowest in treeless control plot (0.33×10^3cfu g^{-1}). The nitrogen fixing bacteria population in *Artocarpus hirsutus* was significantly different from other tree species and treeless control plot.

The highest population of phosphate solubilizing microorganisms' (Table. 5) was recorded in *Artocarpus hirsutus* (6.67×10^3cfu g^{-1}) and lowest in *Hopea parviflora* (3.33×10^3cfu g^{-1}). The phosphate solubilizing bacterial population (Table.5) during the late summer-II sampling season was not statistically significant.

The highest KSB population observed in *Artocarpus hirsutus* (8.00×10^3cfu g^{-1}) and lowest in treeless control plot (0.67×10^3cfu g^{-1}). The potash solubilizing bacteria population in *Artocarpus hirsutus* was significantly higher than other treatments expect *Hopea parviflora*. The population in *Artocarpus hirsutus* was at par with *Hopea parviflora*.

While comparing microflora population between tree species during late summer-II season (May, 2014) *A. hirsutus* recorded the highest population and the second highest recorded in *P. santalinus*.

4.1.2. **Seasonal changes in microbial population under different indigenous tree species**

Seasonal changes in microbial population were analysed using soil samples collected quarterly for one year period. Late summer-I, rainy, winter, early summer and late summer-II samples were collected in the months of May-2013, August-2013, November-2013, February-2014 and May-2014 respectively.

4.1.2.1. ***Seasonal changes in bacteria population***

Bacterial population (Fig. 1) in *Hopea parviflora* was highest in rainy season (51.33×10^4cfu g^{-1}) followed by late summer- II, winter, late summer-I and lowest in early summer (4.33×10^4cfu g^{-1}). The population of bacteria in *Artocarpus hirsutus* was highest in late summer-II (37.00×10^4cfu g^{-1}) followed by winter, late summer-I, rainy season and lowest was recorded in early summer (5.00×10^4cfu g^{-1}). The population in *Pterocarpus marsupium* observed highest in late summer-II (24.33×10^4cfu g^{-1}) followed by late summer-II and lowest by winter (5.33×10^4cfu g^{-1}). The winter and early summer of the same species reported an equal number of bacterial populations (8.00×10^4cfu g^{-1}). The bacterial population in *Pterocarpus santalinus* observed highest in late summer-II (22.33×10^4cfu g^{-1}) followed by winter, late summer-I, rainy season and lowest by early summer (5.00×10^4cfu g^{-1}). The bacterial population in treeless control plot reported comparatively lower values than other tree species. The highest value observed in late summer-II (6.67×10^4cfu g^{-1}) followed by late summer-I, rainy season, winter and lowest in early summer (1.67×10^4cfu g^{-1}). While comparing different sampling seasons, the highest bacterial population was present in late summer-II (May-2014) in all treatments and early summer (February-2014) reported lowest bacterial population. In general, the highest bacteria population among the tree species during the entire study period recorded in *A. hirsutus*.

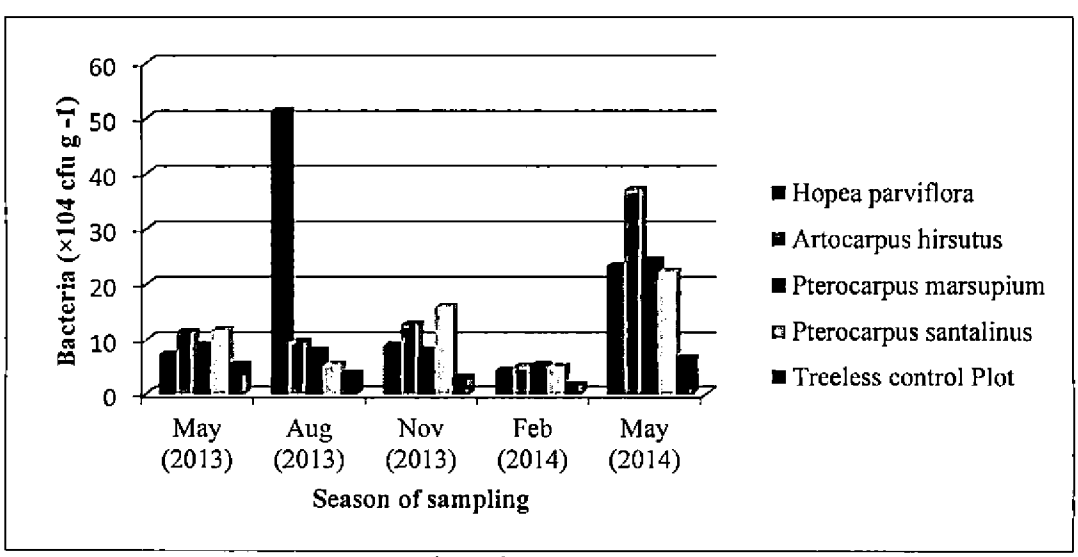


Fig.1. Seasonal changes in bacteria ($\times10^4$cfu g^{-1}) population under indigenous tree species

Table 6. Seasonal changes in bacterial ($\times 10^4$cfu g^{-1}) population under indigenous tree species at Nilambur, Malappuram

Bacteria ($\times 10^4$cfu g^{-1})						
Species	Late summer-I (May, 2013)	Rainy (Aug, 2013)	Winter (Nov, 2013)	Early Summer (Feb, 2014)	Late summer-II (May, 2014)	Mean bacterial population (over 1 year)
Hopea parviflora	7.33	51.33	9.00	4.33	23.33	19.06
Artocarpus hirsutus	11.33	9.67	12.67	5.00	37.00	15.13
Pterocarpus marsupium	9.00	8.00	8.00	5.33	24.33	10.93
Pterocarpus santalinus	11.67	5.33	16.00	5.00	22.33	12.06
Treeless control plot	5.33	3.67	3.00	1.67	6.67	4.06

Table 7. Seasonal changes in fungal ($\times 10^2$cfu g^{-1}) population under indigenous tree species at Nilambur, Malappuram

Fungi ($\times 10^2$cfu g^{-1})						
Species	Late summer-I (May,2013)	Rainy (Aug, 2013)	Winter (Nov, 2013)	Early summer (Feb, 2014)	Late summer-II (May, 2014)	Mean fungal population (over 1 year)
Hopea parviflora	25.00	8.00	7.33	9.67	12.00	12.40
Artocarpus hirsutus	25.00	25.67	19.00	32.00	27.67	25.86
Pterocarpus marsupium	19.67	8.67	7.33	15.00	11.67	12.46
Pterocarpus santalinus	19.33	3.67	8.00	11.00	31.33	14.66
Treeless control plot	14.33	0.33	2.33	5.33	6.67	5.79

4.1.2.2. ***Seasonal changes in fungi population***

Fungi population (Fig. 2) in *Hopea parviflora* was highest in late summer-I (25.00×10^2cfu g^{-1}) followed by late summer-II, early summer, rainy season and lowest in winter (7.33×10^2cfu g^{-1}). The population of fungi in *Artocarpus hirsutus* observed highest in early summer (32.00×10^2cfu g^{-1}) followed by late summer-II, rainy season, late summer-I and least value observed in winter (19.00×10^2cfu g^{-1}). The population in *Pterocarpus marsupium* recorded highest in late summer-I (19.67×10^2cfu g^{-1}) followed by early summer, late summer-II, rainy season and lowest in winter (7.33×10^2cfu g^{-1}). The highest quantity of fungi population observed in late summer-II (31.33×10^2cfu g^{-1}) of *Pterocarpus santalinus*, followed by late summer-I, early summer, winter and lowest recorded in rainy season (3.67×10^2cfu g^{-1}). The fungi population in treeless control plot observed highest in late summer-I (14.33×10^2cfu g^{-1}) followed by late summer-II, early summer, winter and least was reported in rainy season (0.33×10^2cfu g^{-1}). While comparing the various sampling seasons, late summer-I (May-2013) and late summer-II (May-2014) reported comparatively higher fungal population in all treatments. In general, the highest fungal population among the tree species during the entire study period recorded in *A. hirsutus*. The second highest fungal population recorded in *P. marsupium.*

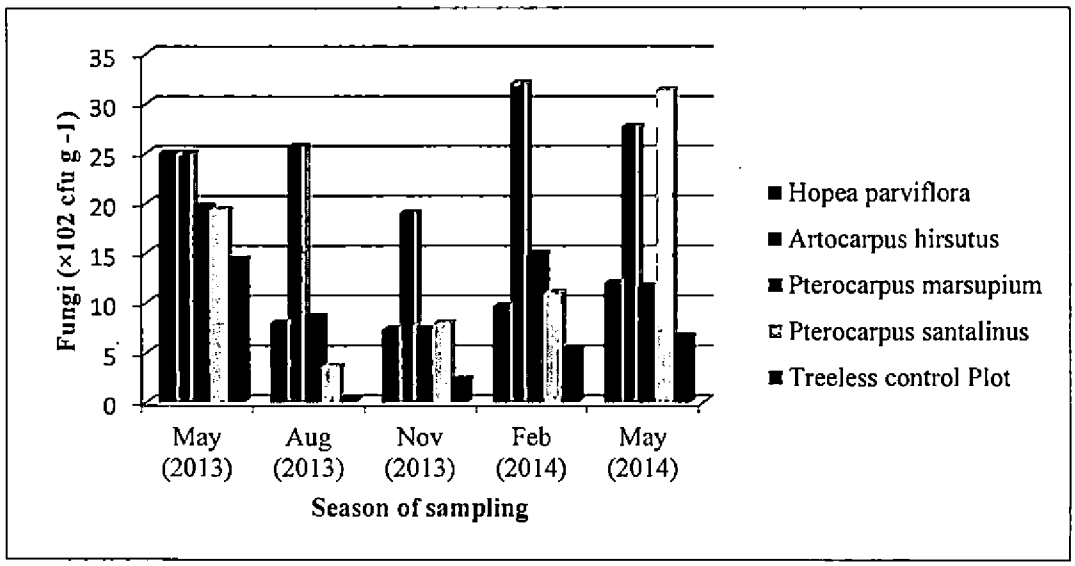


Fig.2. Seasonal changes in fungi ($\times10^2$cfu g^{-1}) population under indigenous tree species

4.1.2.3. ***Seasonal changes in actinomycetes population***

The actinomycetes population (Fig. 3) in *Hopea parviflora* observed highest in late summer-II (9.67×10^3cfu g^{-1}) followed by early summer, winter, late summer-I and lowest in rainy season (3.00×10^3cfu g^{-1}). The population in *Artocarpus hirsutus* was highest in winter (11.00×10^3cfu g^{-1}) followed by rainy season, late summer-II, late summer-I and lowest in winter (7.33×10^3cfu g^{-1}). Actinomycetes in *Pterocarpus marsupium* were highest in early summer (12.33×10^3cfu g^{-1}) followed by winter, late summer-II, rainy season and least observed in late summer-I (6.33×10^3cfu g^{-1}). Actinomycetes in *Pterocarpus santalinus* observed highest in early summer (12.33×10^3cfu g^{-1}) followed by late summer-II, winter, rainy season and lowest in late summer-I (4.00×10^3cfu g^{-1}). In treeless control plot, early summer (7.00×10^3cfu g^{-1}) recorded highest population followed by late summer-II, winter, rainy and least recorded in late summer-II (1.00×10^3cfu g^{-1}). While comparing different sampling seasons, early summer (February-2014) reported highest actinomycetes population in all treatments and late summer-I (May-2013) shows comparatively lowest actinomycetes population. In general, the highest actinomycetes population among the trees species during the entire study period was recorded in *A. hirsutus* and *P. marsupium.*

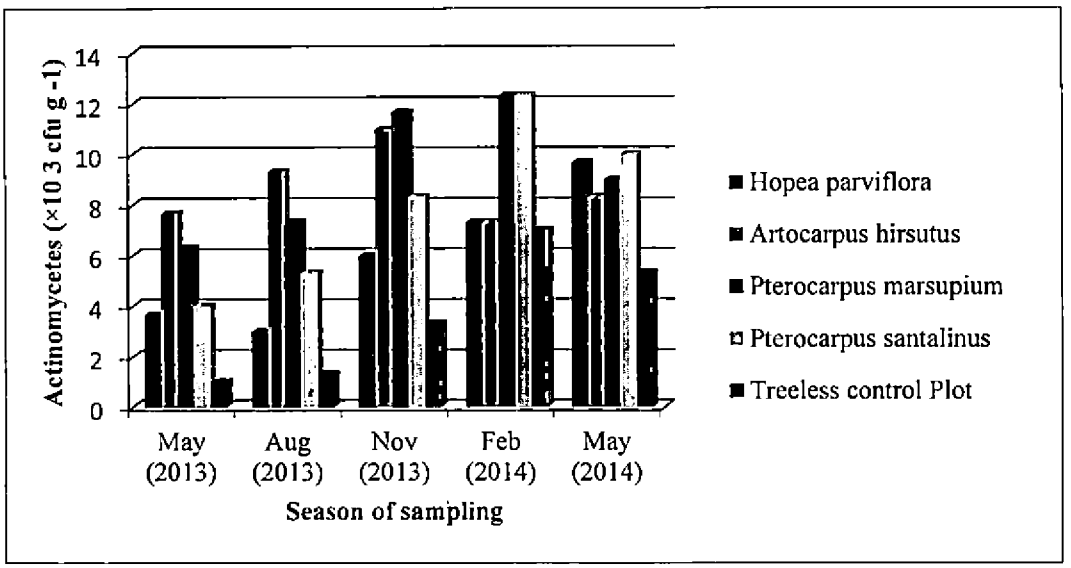


Fig.3. Seasonal changes in actinomycetes ($\times10^3$cfu g^{-1}) population under indigenous tree species

4.1.2.4. ***Seasonal changes in nitrogen fixing bacterial population***

The nitrogen fixing bacterial population (Fig. 4) in *Hopea parviflora* observed highest in winter (2.33×10^3cfu g^{-1}) followed by late summer-I and late summer-II, early summer and lowest in rainy season (1.33×10^3cfu g^{-1}). The population in *Artocarpus hirsutus* was highest in winter (7.00×10^3cfu g^{-1}) followed by late summer-II, rainy season, late summer-II and lowest recorded in early summer (1.33×10^3cfu g^{-1}). Nitrogen fixing bacteria in *Pterocarpus marsupium* was highest in winter (2.67×10^3cfu g^{-1}) followed by rainy season, early summer and late summer-II and least observed in rainy season (1.00×10^3cfu g^{-1}). Nitrogen fixing bacteria in *Pterocarpus santalinus* was highest in winter (2.67×10^3cfu g^{-1}) followed by late summer-II, rainy season and lowest was in early summer and late summer-II (1.33×10^3cfu g^{-1}). In treeless control plot, winter (0.67×10^3cfu g^{-1}) recorded comparatively highest population followed by late summer-I, rainy season and late summer-II least recorded in early summer (0.00×10^3cfu g^{-1}). While comparing different sampling seasons, winter (November-2013) was reported highest nitrogen fixing bacteria population in all treatments and early summer (February-2014) shows comparatively lowest population. In general, the highest nitrogen fixing bacteria population among the trees species during the entire study period recorded in *A. hirsutus* and second largest in *P. santalinus*.

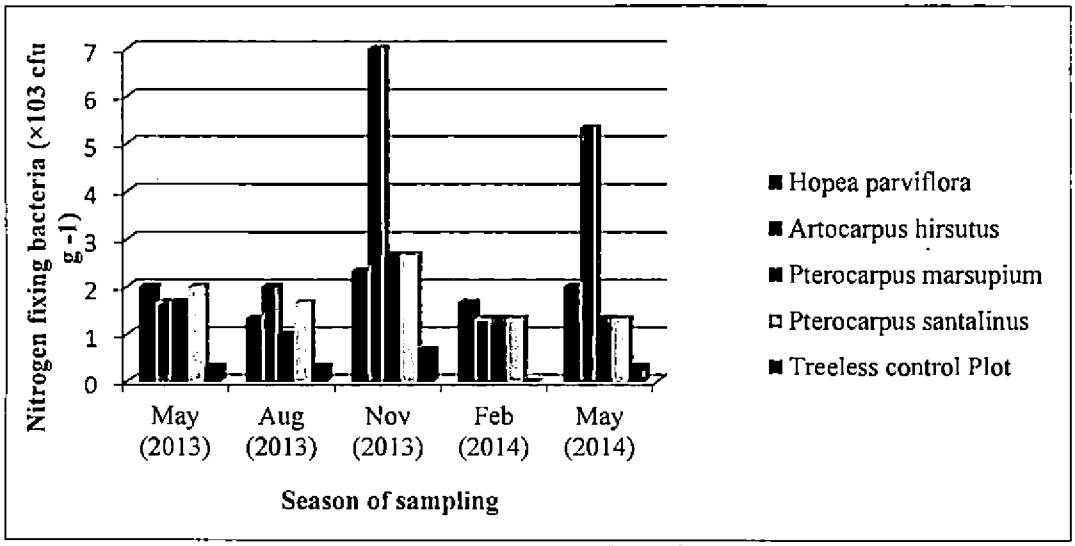


Fig.4. Seasonal changes in nitrogen fixing bacteria ($\times10^3$cfu g^{-1}) population under indigenous tree species

Table 8. Seasonal changes in actinomycetes ($\times 10^3$cfu g^{-1}) population under indigenous tree species at Nilambur, Malappuram

Actinomycetes ($\times 10^3$cfu g^{-1})						
Species	Late summer-I (May, 2013)	Rainy (Aug, 2013)	Winter (Nov, 2013)	Early summer (Feb, 2014)	Late summer-II (May, 2014)	Mean actinomycetes population (over 1 year)
Hopea parviflora	3.67	3.00	6.00	7.33	9.67	5.93
Artocarpus hirsutus	7.67	9.33	11.00	7.33	8.33	8.73
Pterocarpus marsupium	6.33	7.33	11.67	12.33	9.00	9.33
Pterocarpus santalinus	4.00	5.33	8.33	12.33	10.00	7.99
Treeless control plot	1.00	1.33	3.33	7.00	5.33	3.59

Table 9. Seasonal changes in nitrogen fixing bacteria ($\times 10^3$cfu g^{-1}) population under indigenous tree species at Nilambur, Malappuram

Nitrogen fixing bacteria ($\times 10^3$cfu g^{-1})						
Species	Late summer-I (May, 2013)	Rainy (Aug, 2013)	Winter (Nov, 2013)	Early summer (Feb, 2014)	Late summer-II (May, 2014)	Mean nitrogen fixing bacterial population (over 1 year)
Hopea parviflora	2.00	1.33	2.33	1.67	2.00	1.86
Artocarpus hirsutus	1.67	2.00	7.00	1.33	5.33	3.46
Pterocarpus marsupium	1.67	1.00	2.67	1.33	1.33	1.60
Pterocarpus santalinus	2.00	1.67	2.67	1.33	1.33	1.80
Treeless control plot	0.33	0.33	0.67	0.00	0.33	0.33

4.1.2.5. ***Seasonal changes in phosphate solubilizing microorganisms (PSM) population***

The phosphate solubilizing microorganisms population (Fig. 5) in *Hopea parviflora* observed highest in winter (8.33×10^3cfu g^{-1}) followed by late summer-I, rainy season, late summer-II and lowest in early summer (3.33×10^3cfu g^{-1}). The population in *Artocarpus hirsutus* was highest in late summer-I (10.33×10^3cfu g^{-1}) followed by winter, rainy season, late summer-II and lowest recorded in early summer(5.67×10^3cfug^{-1}). Phosphate solubilizing microorganisms in *Pterocarpus marsupium* was highest in late summer-I (10.33×10^3cfu g^{-1}) followed by winter, rainy season, early summer and least observed in late summer-II (4.67×10^3cfu g^{-1}). Phosphate solubilizing microorganisms in *Pterocarpus santalinus* was highest in winter (11.00×10^3cfu g^{-1}) followed by late summer-I, rainy season, late summer-II and lowest was in early summer (1.33×10^3cfu g^{-1}). In treeless control plot, late summer-II (6.33×10^3cfu g^{-1}) recorded comparatively highest population followed by rainy season, early summer, late summer-II and least was recorded in winter (4.00×10^3cfu g^{-1}). While comparing different sampling seasons, winter was reported highest phosphate solubilizing microorganism population in all treatments and early summer (February-2014) shows comparatively lowest population. In general, the highest PSM population among the trees species during the entire study period recorded in *A. hirsutus* and second highest in *P. marsupium*.

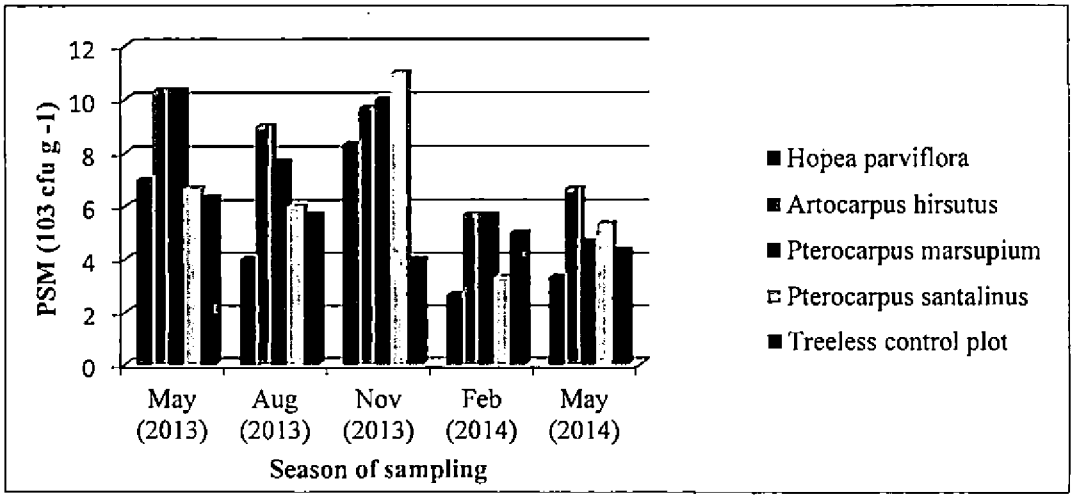


Fig.5. Seasonal changes in PSM ($\times10^3$cfu g^{-1}) population under indigenous tree species

Table 10. Seasonal Changes in phosphate solubilizing microorganisms ($\times 10^3$cfu g^{-1}) population under indigenous tree species at Nilambur, Malappuram

Phosphate solubilizing microorganisms ($\times 10^3$cfu g^{-1})						
Species	Late summer-I (May, 2013)	Rainy (Aug, 2013)	Winter (Nov, 2013)	Early summer (Feb, 2014)	Late summer-II (May, 2014)	Mean PSM population (over 1 year)
Hopea parviflora	7.00	4.00	8.33	2.67	3.33	5.06
Artocarpus hirsutus	10.33	9.00	9.67	5.67	6.67	8.26
Pterocarpus marsupium	10.33	7.67	10.00	5.67	4.67	7.66
Pterocarpus santalinus	6.67	6.00	11.00	3.33	5.33	6.46
Treeless control plot	6.33	5.67	4.00	5.00	4.33	5.06

Table 11. Seasonal changes in potash solubilizing bacteria ($\times 10^3$cfu g^{-1}) population under indigenous tree species at Nilambur

Potash solubilizing bacteria ($\times 10^3$cfu g^{-1})						
Species	Late monsoon-I (May, 2013)	Rainy (Aug, 2013)	Winter (Nov, 2013)	Early summer (Feb, 2014)	Late summer-II (May, 2014)	Mean KSB population (over 1 year)
Hopea parviflora	13.67	1.00	1.33	1.33	5.00	4.66
Artocarpus hirsutus	2.33	2.67	1.33	1.33	8.00	3.13
Pterocarpus marsupium	5.00	1.00	1.67	2.67	1.67	2.40
Pterocarpus santalinus	7.67	1.00	1.00	3.33	2.33	3.06
Treeless control plot	4.00	0.00	0.67	0.67	0.67	1.20

4.1.2.6. ***Seasonal changes in potash solubilizing bacteria (KSB) population***

The potash solubilizing bacteria population (Fig. 6) in *Hopea parviflora* observed highest in late summer-I (13.67×10^3cfu g^{-1}) followed by late summer-II, winter and early summer and lowest in rainy season (1.00×10^3cfu g^{-1}). The population in *Artocarpus hirsutus* was highest in late summer-II (8.00×10^3cfu g^{-1}) followed by rainy season, late summer-I, and lowest was recorded in early summer and winter (1.33×10^3cfu g^{-1}). Potash solubilizing bacteria in *Pterocarpus marsupium* was highest in late summer-I (5.00×10^3cfu g^{-1}) followed by early summer, late summer-II and winter and least observed in rainy season (1.00×10^3cfu g^{-1}). Potash solubilizing bacteria in *Pterocarpus santalinus* was highest in late summer-I (7.67×10^3cfu g^{-1}) followed by early summer, late summer-II, and lowest in rainy season and winter (1.00×10^3cfu g^{-1}). In treeless control plot, late summer-I (4.00×10^3cfu g^{-1}) recorded highest population followed by winter, early summer, and late summer-II. While comparing different sampling seasons, late summer-II (May-2013) reported highest potash solubilizing bacteria population in all treatments and rainy season (August-2013) showed comparatively lowest population. In general, the highest KSB population among the tree species during the entire study period recorded in *A. hirsutus* and second highest in *H. parviflora.*

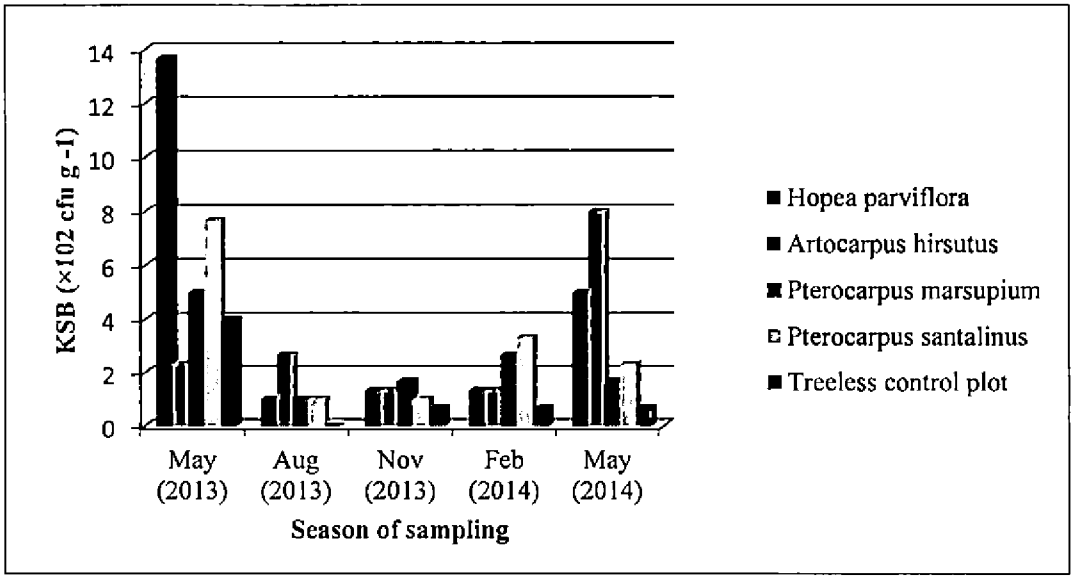


Fig.6. Seasonal changes in KSB ($\times10^3$cfu g^{-1}) population under indigenous tree species

4.2 PHYSICO-CHEMICAL PROPERTIES OF SOIL

4.2.1 **Physical properties of soil**

4.2.1.1 ***Physical properties of initial soil sample under different indigenous tree species during late summer-I (May, 2013) at Nilambur, Malappuram***

The soil moisture content (Table. 12) in *Hopea parviflora* (9.11%) was significantly higher than remaining tree species and treeless control plot (3.76%). The difference in moisture content (%) of tree plots and the treeless control was very high. For instance, the moisture content (%) in *Hopea parviflora* was more by 5.35% as compared to the treeless control plot.

Bulk density in treeless control plot and *Artocarpus hirsutus* was significantly higher than *Hopea parviflora*, *Pterocarpus marsupium*, *Pterocarpus santalinus*. The highest value reported in treeless control plot (1.57%) and lowest in *Hopea parviflora* (1.23%). With regard to bulk density, the tree plots maintained the most ideal condition for plant growth that is a lower bulk density compared to the treeless control plots.

4.2.1.2 ***Physical properties of final soil sample under different indigenous tree species during late summer-II (May, 2014) at Nilambur, Malappuram***

The soil moisture content (Table. 13) in *Hopea parviflora* (13.39%) was significantly higher than all remaining tree species and treeless control plot (10.76%). Bulk density in treeless control plot was significantly higher than *Hopea parviflora*. The highest value reported in treeless control plot (1.37%) and lowest in *Hopea parviflora* (1.13%).

4.1.2.6. ***Seasonal changes in potash solubilizing bacteria (KSB) population***

The potash solubilizing bacteria population (Fig. 6) in *Hopea parviflora* observed highest in late summer-I (13.67×10^3cfu g^{-1}) followed by late summer-II, winter and early summer and lowest in rainy season (1.00×10^3cfu g^{-1}). The population in *Artocarpus hirsutus* was highest in late summer-II (8.00×10^3cfu g^{-1}) followed by rainy season, late summer-I, and lowest was recorded in early summer and winter (1.33×10^3cfu g^{-1}). Potash solubilizing bacteria in *Pterocarpus marsupium* was highest in late summer-I (5.00×10^3cfu g^{-1}) followed by early summer, late summer-II and winter and least observed in rainy season (1.00×10^3cfu g^{-1}). Potash solubilizing bacteria in *Pterocarpus santalinus* was highest in late summer-I (7.67×10^3cfu g^{-1}) followed by early summer, late summer-II, and lowest in rainy season and winter (1.00×10^3cfu g^{-1}). In treeless control plot, late summer-I (4.00×10^3cfu g^{-1}) recorded highest population followed by winter, early summer, and late summer-II. While comparing different sampling seasons, late summer-II (May-2013) reported highest potash solubilizing bacteria population in all treatments and rainy season (August-2013) showed comparatively lowest population. In general, the highest KSB population among the tree species during the entire study period recorded in *A. hirsutus* and second highest in *H. parviflora.*

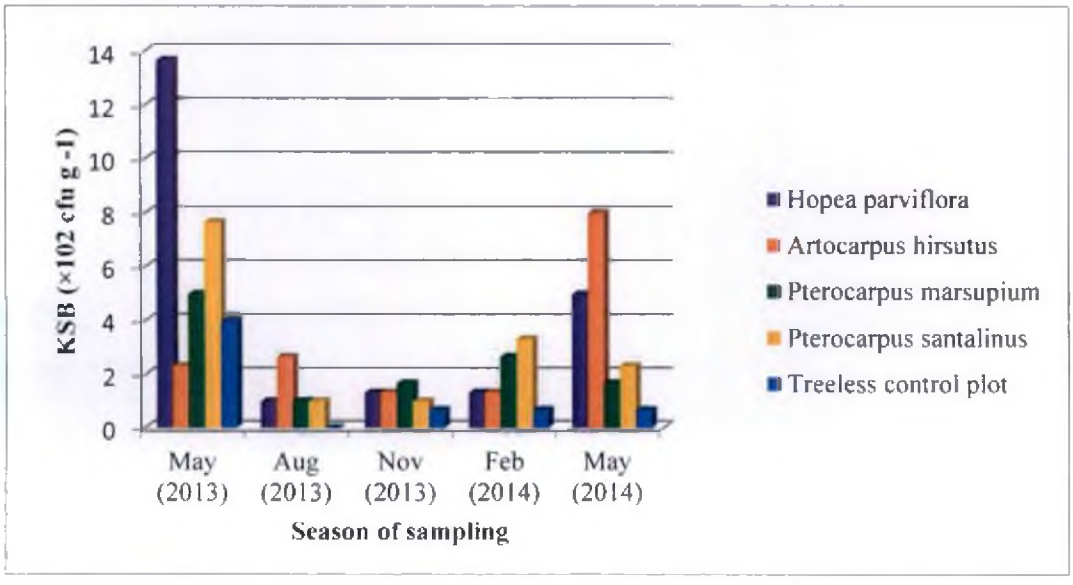


Fig.6. Seasonal changes in KSB ($\times10^3$cfu g^{-1}) population under indigenous tree species

4.2 PHYSICO-CHEMICAL PROPERTIES OF SOIL

4.2.1 **Physical properties of soil**

4.2.1.1 ***Physical properties of initial soil sample under different indigenous tree species during late summer-I (May, 2013) at Nilambur, Malappuram***

The soil moisture content (Table. 12) in *Hopea parviflora* (9.11%) was significantly higher than remaining tree species and treeless control plot (3.76%). The difference in moisture content (%) of tree plots and the treeless control was very high. For instance, the moisture content (%) in *Hopea parviflora* was more by 5.35% as compared to the treeless control plot.

Bulk density in treeless control plot and *Artocarpus hirsutus* was significantly higher than *Hopea parviflora*, *Pterocarpus marsupium*, *Pterocarpus santalinus*. The highest value reported in treeless control plot (1.57%) and lowest in *Hopea parviflora* (1.23%). With regard to bulk density, the tree plots maintained the most ideal condition for plant growth that is a lower bulk density compared to the treeless control plots.

4.2.1.2 ***Physical properties of final soil sample under different indigenous tree species during late summer-II (May, 2014) at Nilambur, Malappuram***

The soil moisture content (Table. 13) in *Hopea parviflora* (13.39%) was significantly higher than all remaining tree species and treeless control plot (10.76%). Bulk density in treeless control plot was significantly higher than *Hopea parviflora*. The highest value reported in treeless control plot (1.37%) and lowest in *Hopea parviflora* (1.13%).

Table 12. Physical properties of initial soil sample under different indigenous tree species during late summer-I (May, 2013) at Nilambur, Malappuram

Species	Moisture Content (%)	Bulk Density (%)
Hopea parviflora	9.11[a] (1.05	1.23[b] (0.04)
Artocarpus hirsutus	6.05[b] (0.80)	1.49[a] (0.04)
Pterocarpus marsupium	4.63[b] (1.26)	1.28[b] (0.08)
Pterocarpus santalinus	4.19[b] (0.53)	1.35[b] (0.04)
Treeless control plot	3.76[b] (2.93)	1.57[a] (0.11)

Values in the parenthesis are standard deviation of the mean.

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

Table 13. Physical properties of final soil sample under different indigenous tree species during late summer-II (May, 2014) at Nilambur, Malappuram

Species	Moisture Content (%)	Bulk Density (%)
Hopea parviflora	13.39[a] (0.45)	1.13[b] (0.16)
Artocarpus hirsutus	11.70[b] (0.82)	1.25[ab] (0.06)
Pterocarpus marsupium	10.76[b] (0.54)	1.18[ab] (0.4)
Pterocarpus santalinus	10.94[b] (0.26)	1.18[ab] (0.4)
Treeless control plot	11.23[b] (1.34)	1.37[a] (0.14)

Values in the parenthesis are standard deviation of the mean.

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

4.2.2 Chemical properties of Soil

4.2.2.1 *Chemical properties of initial soil sample under different indigenous tree species during late summer-I (May, 2013)*

Soil organic carbon in *Hopea parviflora* was significantly higher than all remaining tree species and treeless control plot (Table. 14). The carbon content in *Pterocarpus marsupium* was at par with *Artocarpus hirsutus* and *Pterocarpus*

santalinus. The highest value observed in *Hopea parviflora* (2.38%) and lowest in treeless control plot (1.33%).

On statistical analysis, the available nitrogen content during the first sampling season was not observed a significant variation between the species. The highest value observed in *Hopea parviflora* and lowest in treeless control plot.

The availabile phosphorus content in *Artocarpus hirsutus* was significantly higher than all remaining species and treeless control plot. The highest value observed in *Artocarpus hirsutus* and lowest in treeless control plot.

The total nitrogen content in *Hopea parviflora* was significantaly higher than *Artocarpus hirsutus*, *Pterocarpus marsupium*, *Pterocarpus santalinus* and treeless control plot. The highest value observed in *Hopea parviflora* (0.13%) and lowest in *Artocarpus hirsutus*, *Pterocarpus santalinus* and treeless control plot (0.06%).

The exchangeable potassium in *Hopea parviflora*, *Artocarpus hirsutus*, *Pterocarpus marsupium* were significantly higher than *Pterocarpus santalinus* and treeless control plot. The highest value noticed in *Hopea parviflora* and lowest in treeless control plot.

Soil pH in *Artocarpus hirsutus* was significantly higher than remaining tree species and treeless control plot. Soil pH in treeless control plot was at par with *Hopea parviflora*. The highest value observed in *Artocarpus hirsutus* and lowest in *Pterocarpus santalinus*.

4.2.2.2 ***Chemical properties of final soil sample under different indigenous tree species during late summer-II (May, 2014) at Nilambur, Malappuram***

Soil organic carbon in *Hopea parviflora* was significantly higher than all remaining tree species and treeless control plot (Table. 15). Carbon content in *Artocarpus hirsutus* was at par with *Pterocarpus marsupium* and carbon content in *Pterocarpus santalinus* was at par with treeless control plot. The highest value observed in *Hopea parviflora* (2.25%) and lowest in treeless control plot (1.38%).

The available nitrogen content in *Hopea parviflora* was significantly higher than all remaining tree species and treeless control plot. The highest value observed in *Hopea parviflora* and lowest in treeless control plot.

The available phosphorus content in *Artocarpus hirsutus* was significantly higher than all remaining tree species and treeless control plot. The highest value observed in *Artocarpus hirsutus* and lowest in treeless control plot.

The total nitrogen content in *Hopea parviflora* and treeless control plot were significantly higher than *Pterocarpus marsupium*. The total nitrogen content in *Hopea parviflora* and treeless control plot were at par with *Artocarpus hirsutus* and *Pterocarpus santalinus*. The highest value reported in *Hopea parviflora* (0.16%) and lowest in *Pterocarpus marsupium* (0.06%).

The exchangeable potassium in *Hopea parviflora* and *Artocarpus hirsutus* was significantly higher than *Pterocarpus marsupium*, *Pterocarpus santalinus* and treeless control plot. The highest value observed in *Artocarpus hirsutus* and lowest in *Pterocarpus santalinus*.

Soil pH in *Artocarpus hirsutus* was significantly higher than all remaining tree species and treeless control plot. The highest value observed in *Artocarpus hirsutus* and lowest in *Hopea parviflora*.

Table 14. Chemical properties of soil under different indigenous tree species during late summer-I (May, 2013) at Nilambur

Species	Organic Carbon (%)	Available Nitrogen (kg/ha)	Available Phosphrous (kg/ha)	Total Nitrogen (%)	Exchangeable Potassium (kg/ha)	pH
Hopea parviflora	2.38^{a} (0.21)	18.32 (5.98)	2.05^{b} (0.03)	0.13^{a} (0.01)	81.57^{a} (12.27)	4.79^{bc} (0.121)
Artocarpus hirsutus	1.59^{bc} (0.11)	14.64 (4.96)	2.25^{a} (0.12)	0.06^{b} (0.02)	80.92^{a} (3.76)	5.89^{a} (0.145)
Pterocarpus marsupium	1.65^{b} (0.17)	15.11 (4.77)	1.99^{b} (0.02)	0.08^{b} (0.01)	77.09^{a} (2.34)	4.75^{c} (0.199)
Pterocarpus santalinus	1.40^{bc} (0.69)	12.58 (2.75)	1.97^{b} (0.01)	0.06^{b} (0.01)	47.69^{b} (2.10)	4.73^{c} (0.170)
Treeless control plot	1.33^{c} (0.12)	12.23 (1.89)	1.95^{b} (0.02)	0.06^{b} (0.02)	43.96^{b} (6.14)	5.04^{b} (0.087)

Values in the parenthesis are standard deviation of the mean. Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

Table 15. Chemical properties of soil under different indigenous tree species during late summer-II (May, 2014) at Nilambur

Species	Organic Carbon (%)	Available Nitrogen (kg/ha)	Available Phosphrous (kg/ha)	Total Nitrogen (%)	Exchangeable Potassium (kg/ha)	pH
Hopea parviflora	2.25^{a} (0.16)	17.80^{a} (0.74)	2.01^{b} (0.03)	0.16^{a} (0.05)	70.70^{a} (2.47)	4.97^{b} (0.27)
Artocarpus hirsutus	1.96^{b} (0.22)	14.93^{b} (0.64)	2.23^{a} (0.11)	0.11^{ab} (0.02)	76.94^{a} (4.40)	5.73^{a} (0.06)
Pterocarpus marsupium	1.73^{bc} (0.12)	15.82^{b} (0.26)	1.90^{b} (0.02)	0.06^{b} (0.00)	44.94^{b} (7.14)	5.02^{b} (0.15)
Pterocarpus santalinus	1.52^{cd} (0.19)	14.66^{b} (0.68)	1.91^{b} (0.02)	0.12^{ab} (0.01)	35.28^{c} (3.14)	5.20^{b} (0.25)
Treeless control plot	1.38^{d} (0.03)	12.97^{c} (0.77)	1.55^{c} (0.04)	0.13^{a} (0.04)	35.35^{c} (3.42)	5.10^{b} (0.11)

Values in the parenthesis are standard deviation of the mean. Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05

4.3. GROWTH CHARACTERISTICS OF TREES IN THE PLOT

The standing tree volume was calculated from the height and diameter of trees at the start of the study and again after one year. The details of the tree growth characteristics are given below.

4.3.1 **Growth characteristics of trees at the start of the experiment (May, 2013)**

Table.16 shows the height, diameter at breast height, volume and mean annual increment were observed during the initial sampling season (May, 2013). The results showed that, the maximum tree height observed in *Pterocarpus santalinus* (12.41m) and lowest in *Hopea parviflora* (8.94 m). The height of *Pterocarpus santalinus* was significantly higher than *Hopea parviflora.*

The maximum diameter at breast height was also observed in *Pterocarpus santalinus* (16.25 cm) and lowest in *Hopea parviflora* (8.87 cm). The tree diameter shows significant variation between the species. Both *Pterocarpus santalinus* and *Pterocarpus marsupium* recorded significantly higher radial growth compared to other tree plots.

The highest mean tree volume ($0.31m^3$/tree) and MAI ($0.010m^3$/tree/year) was reported in *Pterocarpus santalinus* and lowest in *Hopea parviflora.* The tree volume and MAI of *Pterocarpus santalinus* and *Pterocarpus marsupium* plots observed significantly higher than *Artocarpus hirsutus* and par with *Hopea parviflora.*

Table 16. Growth characteristics of trees at the start of the experiment (May, 2013) at Nilambur, Malappuram

Species	Height (m)	Diameter (cm)	Volume (m^3/tree)	MAI(m^3/tree/Year)
Hopea parviflora	8.94^{b} (3.44)	8.87^{b} (4.07)	0.08^{b} (0.08)	0.002^{b} (0.00)
Artocarpus hirsutus	9.94^{ab} (4.91)	10.89^{b} (6.41)	0.17^{ab} (0.27)	0.006^{ab} (0.01)
Ptrocarpus marsupium	11.20^{ab} (4.31)	16.05^{a} (8.58)	0.37^{a} (0.43)	0.012^{a} (0.01)
Pterocarpus santalinus	12.41^{a} (2.80)	16.25^{a} (5.53)	0.31^{a} (0.23)	0.010^{a} (0.00)

Values in the parenthesis are standard deviation of the mean.

Values followed by same superscript in a column do not differ significantly (LSD, P, 0.05)

As expected, the growth observations recorded after the experiment (May, 2014) did not show any appreciable increment in the total tree height and diameter and follows the same trend as reported at the start of the experiment. The tree growth observations were recorded as a basic reference to understand about the condition of the tree plots.

Discussion

5. DISCUSSION

The results of the study entitled "Soil productivity changes under selected indigenous tree species with special reference to beneficial microflora" are discussed in this chapter.

5.1. Microbial population

5.1.1. *Microbial population under different indigenous tree species*

The microorganism viz., bacteria, fungi, actinomycetes, nitrogen fixing bacteria, phosphate solubilizing microorganisms (PSM), and potash solubilizing bacteria (KSB) were isolated and enumerated over a period of one year. The collections were made from the rhizosphere soil under four indigenous tree species namely *Hopea parviflora* Bedd., *Artocarpus hirsutus* Lamk., *Pterocarpus marsupium* Roxb, and *Pterocarpus santalinus* L.f. of thirty years of age and planted with 2m × 2m spacing. The results indicated differences in the composition of the microbial communities under different tree species. Microbial population was different in soils under different plant cover and soil types. The diversity and abundance of soil borne microbes may be strongly influenced by some abiotic and biotic factors (Melini *et al.*, 2012).

The highest bacterial population during initial sampling (late summer-I, May-2013) was observed in *Pterocarpus santalinus* (11.67×10^4 cfu g^{-1}) and *Artocarpus hirsutus* (11.33×10^4 cfu g^{-1}). The treeless control plot recorded lowest bacterial population and it exhibited a significant difference from the other tree species. The higher population in the wooded land might be due to the presence of root exudates produced by the host plants. Curl and Truelove (1986) observed that root exudates enhance nutrient availability indirectly through their use as carbon substrates, by increasing microbial growth and activity in the rhizosphere. Differences in the substrates exuded between plant species affect the composition of rhizosphere microbial populations and may result in microflora specific to plant species and genotypes (Neal *et al.*, 1970; Neal *et al.*, 1973). The presence of

microorganisms in the rhizosphere of plants increases root exudation (Rovira *et al.*, 1983). This stimulation of exudation occurs in the presence of free-living nitrogen fixing organisms in both herbaceous plants (Lee and Pankhurst, 1992) and trees (Leyval and Berthelin, 1993).

The highest bacterial population in rainy season was noticed in *H. parviflora* (51.33×10^4 cfu g^{-1}). However, all other plots recorded comparatively lower population than the late summer-I readings. Thoms and Gleixer (2013) opined that the highest level of soil microbial biomass was observed during summer, decreasing through winter to the minimum during the rainy season.

The highest bacterial population in winter season noticed in *P. santalinus* (16.00×10^3cfu g^{-1}) followed by *A. hirsutus* and least by treeless control plot (3.00×10^3 cfu g^{-1}). While considering bacterial population of other two tree species, these two species had shown an increasing tendency than rainy season. This might be due to the increased organic matter and moisture content of the soil. When rain water infiltrate and percolate through soil layers, which brings organic matter from surrounding area to the rhizosphere and contributes to the organic carbon content in rhizosphere soil (Shilpkar et al., 2010).

During the entire period of study (mean over one year), the maximum bacterial population was noticed in *Artocarpus hirsutus* followed by *Hopea parviflora.* Among the tree species, the bacterial population during the entire study period was the lowest in *P. marsupium* and it always supported a minimum population. It may be due to the antibacterial activity of the bark and leaves of the species. According to Ramya *et al.* (2008) phytochemical extracts of *P. marsupium* exhibited significant anti-bacterial activity.

With regard to the fungi, the highest population in late summer-I observed in two tree species namely, *Hopea parviflora* (25.00×10^2 cfu g^{-1}) and *Artocarpus hirsutus* (25.00×10^4 cfu g^{-1}) and least was in treeless control plot. This might be due to the percentage of soil moisture under these two tree species was significantly higher than remaining tree species and treeless control plot.

The highest fungi population in rainy season observed in *A. hirsutus* (25.67×10^2 cfu g^{-1}) followed by *P. marsupium* and lowest in treeless control plot (0.33×10^2 cfu g^{-1}). While comparing fungi population between species, *A. hirsutus* was the only species that recorded a slight increase. Ruma *et al.*, (2011) reported that, about 106 endophytic fungi from *Artocarpus hirsutus* and *Vateria indica*, two endemic medicinal plants of Western Ghats, were documented using traditional morphological methods

In the winter samples also, the highest fungi population reported in *A. hirsutus* (19.00×10^2 cfu g^{-1}) and lowest recorded in treeless control plot (2.33×10^2 cfu g^{-1}). *A. hirsutus* had showed significant differences than treeless control plot. This is supported by the increased root activity in *A. hirsutus* at 30 cm depth as reported by Jamaludheen *et al* (1994).

The highest fungi population during early summer season was reported in *A. hirsutus* (32.00×10^2 cfu g^{-1}). All the tree species recorded a higher fungi population compared to the winter season. It may due to the raising of soil temperature and making a good micro climate. *A. hirsutus* species recorded significantly higher fungal population than the treeless control plot (5.33×10^2 cfu g^{-1}).

The highest fungi population during the late summer-II season noticed in *P. santalinus* followed by *A. hirsutus.* The second highest fungi populations during the entire study period noticed in summer seasons. It might be because; the summer showers were reported during this season. Another possible reason that can be attributed for higher population of fungi in *P. santalinus* in the late summer season is the best growing natural tracts of this tree species is dry tracts.

During the entire period of study (mean over the seasons), the maximum fungi population was noticed in *Artocarpus hirsutus* followed by *Pterocarpus santalinus.* Among the tree species, the fungi population during the entire study period was the lowest in *Hopea parviflora.*

Issac and Nair (2004) also reported the higher populations of microflora and earthworms under the wild jack (*A. hirsutus)* tree canopy. They reported that, among the various species of organisms, highest fungi (33.20×10^3cfu per g soil) were reported during rainy season and bacteria (48.80×10^6 cfu per g soil) were noticed in rainy season and winter season in. The highest actinomycetes recorded during early summer (21.60×10^4 cfu per g soil) and winter season (20.20×10^4 cfu per g soil).

The actinomycetes population in late summer season-I reported highest in *A. hirsutus* followed by *P. marsupium* and least by treeless control plot. The lowest actinomycetes population recorded during the late summer-I season. It might be related to the lowest moisture content recorded during this season. Interestingly, the actinomycetes population noticed an increasing trend from rainy season to early summer and the late summer season. The highest population noticed in *A. hirsutus* (9.33×10^3 cfu g^{-1}) and lowest in treeless control plot.

Among the microbes, actinomycetes recorded the highest population during winter season as compared to the nitrogen fixing bacteria, PSM and KSB population The highest actinomycetes population was recorded in *P. marsupium* (11.67×10^2 cfu g^{-1}) followed by *A. hirsutus* (11.00×10^2 cfu g^{-1}) and lowest in treeless control plot (3.33×10^2 cfu g^{-1}). Silpkar *et al.* (2010) reported that the number of actinomycetes increased in post-monsoon than monsoon and varied between 0.0098 to 0.0104 x 10^5 cfu g^{-1}soil. Lower soil temperature during monsoon and post- monsoon seasons resulted in lower oxidation of organic matter and hence, organic carbon content increased in these seasons compared to pre-monsoon.

In the present study, winter and early summer season was the best season noticed for the growth of rhizosphere actinomycetes population. The highest actinomycetes population during the entire study period reported from early summer season in *P. marsupium* and *P. santalinus* (12.33×10^3 cfu g^{-1}) plots. Shilpkar *et al.*, (2010) reported that the number of actinomycetes in rhizosphere soil of *Aegle marmelos* was found maximum in post-monsoon.

During the entire period of study (mean over the seasons), the maximum actinomycetes population was noticed in *P. marsupium* (Table. 8) followed by *A. hirsutus.* Among the tree species, the actinomycetes population during the entire study period was the lowest in *H. parviflora* and it always supported a minimum population.

The nitrogen fixing bacteria observed in all the four tree species. The activity of nitrogen fixers reported highest in *P. santalinus* and *H. parviflora.* While comparing the pH values of these two tree species a significant difference reported and was lesser than that of other tree species and treeless control plots. Microbial composition may be affected indirectly through an influence of tree species on soil pH as reported by Thoms and Gleixer (2013). Kahindi *et al.* (1997) reported that rhizobia are competent free-living bacteria, although few fix nitrogen in the free-living state, and the major factors that determine their population sizes in the absence of legume hosts are environmental stresses (such as soil acidity factors.

The nitrogen fixing bacteria population in rainy season observed highest in *A. hirsutus* (2.00×10^3 cfu g^{-1}). This species observed a slight increase in population from the late summer-I samples.

During the entire period of study (mean over the seasons), the maximum nitrogen fixing bacteria population was noticed in *A. hirsutus* (Table. 9) followed by *H. parviflora.* Among the tree species, the nitrogen fixing bacteria population during the entire study period was the lowest in *P. marsupium* and it always supported a minimum population.

The highest PSM during the late summer-I observed in *A. hirsutus* and *P. marsupium* (10.33×10^3 cfu g^{-1}). This is supported by the significantly higher 'P' in *P. marsupium* plots as reported by Jamaludheen, (1994). The two higher tree foliar 'P' concentrations were also reported for *P. marsupium* and *A. hirsutus*

The highest KSB population in late summer-I season was reported in *H. parviflora* (13.67×10^3 cfu g^{-1}). The lowest value was recorded in *A. hirsutus* and treeless control plot. It might be due to the severe dry climate reported in that particular month.

The highest PSM and KSB populations in rainy season observed in *A. hirsutus* followed by *P. marsupium*. Interestingly, KSB population was not observed in treeless control plot during rainy season. Jamaludheen (1994) reported that regarding foliar P and K concentration, *P. marsupium* and *A. hirsutus* were the toppers in respect of both these nutrients. In the present study also, both these species recorded highest soil k content than the other species.

The highest PSM population during the entire study period observed from winter season in *P. santalinus* (11.00×10^3 cfu g^{-1}) followed by *P. marsupium* (10.00×10^3 cfu g^{-1}) and lowest in treeless control plot. So the *A. hirsutus* and *H. parviflora* plots had shown an increased population of phosphate solubilizing microorganisms. Population of PSB depends on different soil properties (physical and chemical properties, organic matter, and P content) and cultural activities (Kim *et al.*, 1998). Wide range of microbial P solubilization mechanisms exist in nature and much of the global cycling of insoluble organic and inorganic soil phosphates is attributed to bacteria and fungi (Banik and Day, 1982).

Besides providing P to the plants, the phosphate solubilizing bacteria also augment the growth of plants by stimulating the efficiency of biological nitrogen fixation (BNF), enhancing the availability of other trace elements by synthesizing important plant growth promoting substances (Ahmad *et al.*, 2008).

During the entire period of study (mean over the seasons), the maximum phosphate solubilizing bacteria population was noticed in *A. hirsutus* (Table. 10) followed by *P. marsupium*.Among the tree species, the phosphate solubilizing bacteria population during the entire study period was the lowest in *H. parviflora* .

The KSB population during winter season was highest in *P. marsupium* (1.67×10^3 cfu g^{-1}) followed by *A. hirsutus* and *H. parviflora* (1.33×10^3 cfu g^{-1}). The potash solubilizing bacteria population during the winter season was not statistically significant. Jamaludheen *et al* (1997) reported that *C. equisetifolia, P. marsupium* plots had significantly higher 'P'. Soil potassium levels were more or less uniform but for *A. hirsutus* plots, which registered markedly higher potassium levels.

However, the KSB maintained comparatively similar population in the early summer season also except in *P. marsupium* and *P. santalinus*, where these tree species recorded a higher population than winter. The *P. santalinus* observed significantly higher KSB population than treeless control plot.

The highest nitrogen fixing bacteria, PSM and KSB during late summer-II season noticed in *A. hirsutus*. The *A. hirsutus* registered the highest 'P' and 'K' accumulation in the main trunk or bole of the tree. This species was least efficient for both of these nutrients (P and K) use efficiency (Jamaludheen, 1994). The highest KSB population noticed in late summer-I season (May, 2013) and late summer-II season (May, 2014) during the study period. While considering actinomycetes, nitrogen fixing bacteria, PSM and KSB population, the actinomycetes recorded highest population in all indigenous tree species during summer season of the study.

During the entire period of study (mean over the seasons), the maximum potash solubilizing bacteria population was noticed in *H. parviflora* (Table. 11) followed by *A. hirsutus.*Among the tree species, the potash solubilizing bacteria population during the entire study period was the lowest in *P. marsupium* and it always supported a minimum population.

With regard to the population of different microbes under different indigenous tree species, the bacteria were dominated consistently and recorded the highest population in all the four indigenous tree species studied.

5.1.2 SEASONAL CHANGES IN MICROBIAL POPULATION UNDER DIFFERENT INDIGENOUS TREE SPECIES

5.1.2.1. **Seasonal changes in bacteria population**

The highest bacterial population observed in the late summer-II season (May, 2014). This might be due the most ideal condition of higher soil temperature coupled with the summer showers received during the month of May, 2014. *Artocarpus hirsutus* and *Pterocarpus santalinus* recorded comparatively higher bacterial population throughout the study period. The lowest bacterial population was recorded in the early summer season (February, 2014) and increased substantially towards the late summer season-II. As expected, the treeless control plot recorded significantly lower bacterial population than tree plots during all the sampling seasons.

5.1.2.2 **Seasonal changes in fungi population**

Generally, the highest fungal population observed in the late summer-I season (May, 2013). Then fungal population found to decrease in the rainy season and the winter season and again increase gradually towards the early summer and late summer-II. *A. hirsutus* plots recorded a very high fungi population throughout the study period and was least affected by seasons. Ruma *et al.*, (2011) reported about106 endophytic fungi from *Artocarpus hirsutus* and *Vateria indica* using traditional morphological methods. The treeless control plot observed significantly lower fungi population than tree plots in all sampling seasons.

5.1.2.3. **Seasonal changes in actinomycetes population**

Compared to all other microbes, the actinomycetes population was found less responsive to the seasonal changes. However, a general increase in the population was noticed from the late summer-I (May, 2013) through the rainy season and the winter and the early summer and the late summer-II season (May, 2014). The actinomycetes population maintained a higher level in the late summer-II season. This increased level of the actinomycetes population may be attributed to the summer showers and the consequent increase in the soil moisture

content. This is agreement with the reports of Silpkar *et al* (2010) where the highest actinomycetes population was observed in the post monsoon season. In general, the highest actinomycetes population among the trees species during the entire study period was recorded in *A. hirsutus* and *P. marsupium.*

5.1.2.4. **Seasonal changes in nitrogen fixers**

The highest nitrogen fixing bacteria population observed in the winter season. Then it reduced slightly towards the early summer and later summer season-II except for *A. hirsutus*. The lowest nitrogen fixing bacterial population recorded in early summer season. In the present study, all the tree species reported comparatively similar nitrogen fixing bacteria population throughout the season except in *A. hirsutus*. The possible utilization by these abundant populations of nitrogen fixers might have resulted in lower nitrogen content in the soil under this tree species. The treeless control plot observed significantly lower nitrogen fixing bacteria population than tree plots.

5.1.2.5. **Seasonal changes in phosphate solubilizing microorganism**

The highest population of phosphate solubilizing microorganism recorded in winter season and the lowest in the early summer. The late summer-I, rainy season and winter season recorded very high phosphate solubilizing bacterial population compared to the early summer season. In the overall study period *A. hirsutus* and *P. marsupium* recorded highest PSM population.

5.1.2.6. **Seasonal changes in potash solubilizing bacteria**

The highest potash solubilizing bacteria recorded in the summer seasons (late summer-I and late summer-II seasons). With the onset of rainy season, the KSB population found to decrease drastically and found to maintain the lower levels in the winter season also. Then very slowly the population picked up in the early summer season and reached the peak population in the late summer season-II. The potassium, being highly mobile in the soil, seems to be low in the rainy season (Jamaludheen, 1994). The lower availability of potassium might have limited the growth and high population of potash solubilizing bacteria.

Table 17. Seasonal changes in microorganism population under indigenous tree species at Nilambur, Malappuram

Tree species	Bacteria ($\times 10^4$ cfu g^{-1})					Fungi ($\times 10^2$ cfu g^{-1})					Actinomycetes ($\times 10^3$ cfu g^{-1})				
	Season														
	S1	S2	S3	S4	S5	S1	S2	S3	S4	S5	S1	S2	S3	S4	S5
T1	7.33	51.33	9.00	4.33	23.33	25.00	8.00	7.33	9.67	12.00	3.67	3.00	6.00	7.33	9.67
T2	11.33	9.67	12.67	5.00	37.00	25.00	25.67	19.00	32.00	27.67	7.67	9.33	11.00	7.33	8.33
T3	9.00	8.00	8.00	5.33	24.33	19.67	8.67	7.33	15.00	12.46	6.33	7.33	11.67	12.33	9.00
T4	11.67	5.33	16.00	5.00	22.33	19.33	3.67	8.00	11.00	14.66	4.00	5.33	8.33	12.33	10.00
T5	5.33	3.67	3.00	1.67	6.67	14.33	0.33	2.33	5.33	5.79	1.00	1.33	3.33	7.00	5.33

Table 18. Seasonal changes in beneficial microorganism population under indigenous tree species at Nilambur, Malappuram

Tree species	NFB ($\times 10^3$ cfu g^{-1})					PSM ($\times 10^3$ cfu g^{-1})					KSB ($\times 10^3$ cfu g^{-1})				
	Season														
	S1	S2	S3	S4	S5	S1	S2	S3	S4	S5	S1	S2	S3	S4	S5
T1	2.00	1.33	2.33	1.67	2.00	7.00	4.00	8.33	2.67	3.33	13.67	1.00	1.33	1.33	5.00
T2	1.67	2.00	7.00	1.33	5.33	10.33	9.00	9.67	5.67	6.67	2.33	2.67	1.33	1.33	8.00
T3	1.67	1.00	2.67	1.33	1.33	10.33	7.67	10.00	5.67	4.67	5.00	1.00	1.67	2.67	1.67
T4	2.00	1.67	2.67	1.33	1.33	6.67	6.00	11.00	3.33	5.33	7.67	1.00	1.00	3.33	2.33
T5	0.33	0.33	0.67	0.00	0.33	6.33	5.67	4.00	5.00	4.33	4.00	0.00	0.67	0.67	0.67

Note: T1- *Hopea parviflolra*, T2- *Artocarpus hirsutus*, T3- *Pterocarpus marsupium*, T4- *Pterocarpus santalinus*, T5- Treeless control plot
S1- Late summer-I (May,2013), S2- Rainy (Aug, 2013), S3- Winter (Nov, 2013), S4- Early summer (Feb, 2014), S5- Late summer- II (May, 2014)
NFB- Nitrogen Fixing Bacteria, PSM- Phosphate Solubilizing Microorganism, KSB- Potash Solubilizing Bacteria

5.2. PHYSICO-CHEMICAL PROPERTIES OF SOIL

5.2.1. **Physical properties of initial soil sample under different indigenous tree species during late summer-I (May, 2013)**

The activity and species composition of microbes are generally influenced by many factors including physico-chemical properties of the soil like soil moisture, temperature and vegetation (Melini *et al.*, 2012). The highest soil moisture content was noticed in *H. parviflora* (9.11%) followed by *A. hirsutus* (6.05%). While comparing rhizosphere moisture content in *Hopea parviflora,* it was almost 5.35% more than the treeless control plot. The increased moisture content in these two tree species might have facilitated an increased population of both the bacteria and fungi (Issac and Nair, 2004) as compared to other tree species and the treeless control pot.

The maximum bulk density observed in treeless control plot (1.57%) and the minimum in *H. parviflora* (1.23%), which is ideal for better plant growth. Melini *et al* (2012) reported that the more organic matter content in soil the more will be the pore space and there by resulting in a lower bulk density of soil.

5.2.2. **Physical properties of final soil sample under different indigenous tree species during late summer-II (May, 2014)**

While comparing the late summer-I and late summer-II moisture content, there was an increase in the moisture content in all the tree species and the treeless control plot. It might be due the summer showers reported during the season. The bulk density also remained stable and recorded almost similar value as in the initial season.

5.2.3. **Chemical properties of initial soil sample under different indigenous tree species during late summer-I (May, 2013) sampling**

Soil organic carbon in *Hopea parviflora* was significantly higher (2.38%) than all other tree species and treeless control plot (1.33%). Melini *et al.*, (2012) reported a similar result as the soil organic matter was higher in the forest ecosystem soils and the lowest in the agroecosystems soils.

The higher available nitrogen, available phosphorus, total nitrogen and exchangeable potassium also recorded in *H. parviflora* followed by *P. marsupium* and least in treeless control plot. Jamaludheen (1994) also reported a comparatively higher N status of N fixing tree plots may probably due to release of fixed N in to rhizosphere. *P. marsupium* plots were having significantly higher P and the Soil K was almost uniform and was statistically at par for most of the species except a markedly higher level in *Artocarpus hirsutus* and *Acacia auriculiformis*.

Apart from this, the soil pH has a greater role in the population and diversity of soil microflora. In this study, maximum soil pH reported in *A. hirsutus* (5.89) and least recorded in *P. marsupium* (4.73). This soil pH had a higher influence on the microflora population under *A. hirsutus* species and *P. marsupium* species. Especially in *H. parviflora,* the soil pH might have influenced the microflora population. Most of the soil nutrients were also higher under this tree species. However, a higher pH concentration in treeless control plot was not influenced the microflora in treeless control plot. This result may support the importance of tree microflora interactions and its essentiality in soil fertility and productivity in wooded land as compared to a treeless open area.

5.2.4. **Chemical properties of final soil sample under different indigenous tree species during late summer-II (May, 2014) sampling**

There was no marked difference in organic carbon content between the initial and summer (final) season. However, in *H. parviflora* organic carbon percentage was noticed a reduction from the initial season. While considering all the tree species and treeless control plot, *H. parviflora* was observed highest available nitrogen and phosphorus, total nitrogen and exchangeable potassium. All the tree species (except *H. parviflora*) and treeless control plot was noticed a slight increase in organic carbon percentage, available nitrogen and phosphorus, total nitrogen and exchangeable potassium in summer season. This may be due to the summer shower reported during the final sampling.

The pH of all the plots except *H. parviflora* was noticed a slightly higher value than the initial season. Root exudates neutralise the soil pH and alters the microclimate of the rhizosphere through liberation of water and carbon dioxide (Subba Rao 2001). Higher moisture content during monsoon might have enhanced soil pH of rhizosphere due to dilution effect.

5.3. GROWTH CHARACTERISTICS OF TREES IN THE PLOT

5.3.1 **Growth characteristics of trees at the start of the experiment (May, 2013)**

The height, dbh, volume and MAI were observed during the initial sampling season (May, 2013). The results showed that, the maximum tree height (12.41m) and dbh (16.25 cm) observed in *Pterocarpus santalinus* and the lowest in *Hopea parviflora* (8.94 m and 8.87 cm respectively). The tree diameter showed significant variation between the species. Both *Pterocarpus santalinus* and *Pterocarpus marsupium* recorded significantly higher radial growth compared to other tree plots. This may be due to the differential requirement of these species for their optimum growth. For instance, *A. hirsutus, P. marsupium* and *H. parviflora* are ideally grown in a comparatively moist and semi-evergreen to evergreen conditions and require a larger space for their optimum growth. *P. santalinus*, on the other hand, grows on a drier location and requires lesser space for growth.

As expected, the growth observations recorded after the experiment (May, 2014) did not show any appreciable increment in the total tree height and diameter and follows the same trend as reported at the start of the experiment. The tree growth observations were recorded as a basic reference to understand about the condition of the tree plots where the present investigation was carried out.

Summary

6. SUMMARY

A field study with the objective to monitor the soil productivity changes, due to long term occupancy of the tree species with special reference to the quantity and quality of the soil microflora, was conducted for a period of one year (May 2013 to May 2014) with four important indigenous tree species *viz. Hopea parviflora*, *Artocarpus hirsutus*, *Pterocarpus marsupium* and *Pterocarpus santalinus* of about 30 years age and maintained at Kerala Forest Research Institute sub-centre Nilambur, Malappuram.

The salient findings of the study are summarised as below:

1. The highest microbial population, during the entire study period, was recorded in *Artocarpus hirsutus* plots and the lowest in treeless control plot.

2. At the initial sampling, *Artocarpus hirsutus* recorded the maximum bacteria, fungi, actinomycetes and phosphate solubilising microorganism. The highest nitrogen fixing bacteria and potash solubilizing bacteria were recorded in *Hopea parviflora* plots.

3. The highest bacterial population observed in late summer-II (May-2014) season and lowest recorded during early summer season. However, the highest fungal population recorded in late summer-I (May-2013) season and the lowest during winter season (November, 2013).

4. *A. hirsutus* and *P. marsupium* recorded highest actinomycetes population. Early summer season recorded the highest actinomycetes population and lowest in late summer-I season.

5. The highest population of nitrogen fixing bacteria and the phosphate solubilizing microorganism recorded in *A. hirsutus*.

6. The highest population of nitrogen fixing bacteria and phosphate solubilising microorganism observed in the winter season (November, 2013) and the lowest population during early summer season (February, 2014).

7. Potash solubilizing bacteria recorded highest during the summer seasons (late summer-I and late summer-II seasons) and lowest in the rainy season.

8. *A. hirsutus* and *H .parviflora* recorded highest Potash solubilizing bacteria.

9. In the final sampling (late summer-II), *A. hirsutus* was found to harbour maximum bacteria, nitrogen fixing bacteria, phosphate solubilising bacteria and potash solubilising bacteria. However, the highest fungi and actinomycetes were associated with *Pterocarpus santalinus.*

10. The soil physical properties like soil moisture and bulk density were distinctively superior in the wooded lands as compared to the treeless open area.

11. The organic carbon, available nitrogen, available phosphorus, total nitrogen and exchangeable potassium contents were greatly improved in the tree plots compared to the nearby treeless control plot.

12. The potential ability of these indigenous tree species for improving the soil productivity was very much evident.

References

REFERENCES

Ahmad, F., Ahmad, I., and Khan, M. S. 2008. Screening of free-living rhizospheric bacteria for their multiple plant growth promoting activities. *Microbiol. Res.* 163: 173-18.

Alam, S., Khalil, S., Ayub, N., and Rashid, M. 2002. In vitro solubilization of inorganic phosphate by phosphate solubilizing microorganism (PSM) from maize rhizosphere. *Int. J. Agric Biol.* 4: 454-458.

Alongi, D. M., Boto, K. G., and Robertson, A. I. 1992. Nitrogen and phosphorus cycles. In: Robertson, A. I. and Alongi, D. M. (eds.), *Tropical Mangrove Ecosystems*, American. Geophysical Union, Washington, DC, pp. 251-292.

Aponte, C., García, L.V., and Marañón, T. 2013. Tree species effects on nutrient cycling and soilbiota: A feedback mechanism favoring species coexistence. *For. Ecol. Manage.* 309: 36-46.

Balloni, W. and Favilli, F. 1987. Effects of agricultural practices on physical, chemical and biological properties of soils: the effect of some agricultural practices on the biological soil fertility. In: Barth, H., L'Hermite, P. (eds.), *Scientific Basis for Soil Protection in the European Community*, Elsevier, London, pp.161-175.

Banik, S. and Day, B. K. 1982. Available phosphate content of an alluvial soil as influenced by inoculation of some isolated phosphate solubilizing microorganisms. *Plant Soil.* 69(3): 353-364.

Basak, B. B., and Bisws, D. R. 2009. Influence of potassium solubilizing microorganism (*Bacillus mucilaginosus*) and waste mica on potassium

uptake dynamics by sudan grass (*Sorghum vulgare* Pers.) grown under two alfisols. *Plant soil.* 317: 235-255.

Basak, B. B. and Bisws, D. R. 2010. Co-inoculation of potassium solubilizing and nitrogen fixing bacteria on solubilization of waste mica and their effect on growth promotion and nutrient acquisition by a forage crop. *Biol. fertile soils* 46: 641-648.

Beheraa, B. C., Singdevsachanb, S. K., Mishrac, R. R., Duttad, and Thatoib, S. K. 2014. Diversity, mechanism and biotechnology of phosphate solubilising microorganism in mangrove: a review. *Biocatalysis Agric Biotech.* 3: 97-110.

Binkley, D. and Giardina, C. 1997. Nitrogen fixation in tropical forest plantations. In: Nambiar, E. K. S., Brown, A. G. (eds.), *Management of soil, Nutrients and water in tropical plantation forests.* Australian Centre for International Agricultural Research, Canberra, pp 297-337.

Bloem, J., Hopkins, D. W., and Benedetti, A. 2006. *Microbiological Methods for Assessing Soil Quality.* CABI Publishing, Oxfordshire, UK, 120p.

Bojinova, D., Velkova, R., Grancharov, K., and Zhelev, S. 1997. The bio conservation of Tunisian phosphorite using *Aspergillus niger*. *Nutr. Cyc. Agro ecosyst.* 42: 227-232.

Bonanomi, G., Giannino, F., and Mazzoleni, S. 2005. Negative plant soil feedback and species coexistence. *Oikos* 111:311-321.

Boudiaf, I. E., Baudoin, E., Sanguin, H., Beddiar, A., Thioulouse, J., Galiana, A., Prin, Y., LeRoux, C., Lebrun, M., and Duponnois, R. 2013. The exotic legume tree species, *Acacia mearnsii*, alters microbial soil functionalities

and the early development of a native tree species, *Quercus suber*, in North Africa. *Soil Biol. Biochem.* 65: 172-179.

Brandt, A. J., de Kroon, H., Reynolds, H. L., and Burns, J. H. 2013. Soil heterogeneity generated by plant soil feedbacks has implications for species recruitment and coexistence. *J. Ecol.* 101: 277-286.

Carroll, G. C. and Wicklow, D. T. 1992. The fungal community, its organisation and role in the ecosystem. (2nd ed.). New York: Marcel Dekker.

Chabot, R., Antoun, H., and Cescas, M. P. 1996. Growth promotion of maize and lettuce by phosphate-solubilizing Rhizobium leguminosarum biovar phaseoli. *Plant Soil.* 184: 311-321.

Chen, Y. P., Rekha, P.D., Arun, A.B., Shen, F. D., Lai, W. A., and Young, C.C. 2006. Phosphate solubilizing bacteria from subtropical soil and their tricalcium phosphate solubilizing abilities. *Appl. Soil Ecol.* 34: 33-41.

Colonna, J. P., Thoen, D., Ducousso, M., and Badji, S. 1991. Comparative effects of *Glomus mosseae* and P on fertilized foliar mineral composition of *Acacia Senegal* seedlings inoculated with rhizobium. *Mycorrhiza.* 1:35-38

Cossalter, C. 1987. Introduction of Australian acacias into dry tropical West Africa. *For. Ecol. Manage.* 16: 367-389.

Curl, E. A. and Truelove, B. 1986. *The Rhizosphere. Springer*, New York, 288 pp.

Curtis, T. P., Sloan, W. T., and Scannel, J. W. 2002. Estimating prokaryotic diversity and its limits. *Proc. Natl. Acad. Sci.* U.S.A. 99: 104914-110499.

De Deyn, G. B., Cornelissen, J. H. C., and Bardgett, R. D. 2008. Plant functional traits and soil carbon sequestration in contrasting biomes. *Ecol. Lett.* 11: 516-531.

Dirzo, R. and Raven, P. H. 2003. Global state of biodiversity and loss. *Annual Rev. Environ. Resour.* 28: 137-167.

Doran, J.W. and Parkin, T.B. 1994. Defining and assessing soil quality. In: Doran, J.W. (ed.), *Defining Soil Quality for Sustainable Environment*, SSSA Special Publication, Madison, pp. 3-23.

Duponnois, R., Founoune, D., and Lesueur. 2002. Influence of the controlled dual ectomycorrhizal and rhizobial symbiosis on the growth of *Acacia mangium* provenances, the in digenous symbiotic microflora and the structure of plant parasitic nematode communities, *Geoderma* 109: 85-102.

Fierer, N., Schimel, J.P., and Holden, P. A. 2003. Variations in microbial community composition through two soil depth profiles. *Soil Biol. Biochem.* 35: 167-176.

Fisher, R. F. and Bankley, D. 2000. *Ecology and management of forest soils.* John Wiley and Sons, New York, 158p.

Goldstein, A. H. 1986. Bacterial solubilization of mineral phosphates: historical perspective and future prospects. *Am. J. Alt. Agric.* 1: 51-57.

Goldstein, A. H. 1995. Recent progress in understanding the molecular genetics and biochemistry of calcium phosphate solubilization by Gram-negative bacteria. *Biol. Agric. Hort.* 12: 185-193.

Grayston, S. J. and Prescott, C.E. 2005. Microbial communities in forest floors under four tree species in coastal British Columbia. *Soil Biol Biochem.* 37: 1157-1167.

Han, H. S. and Lee, K. D. 2005. Phosphate and potassium solubilizing bacteria effect on mineral uptake, soil availability and growth of eggplant. *Res. J. Agric. Biol. Sci.* 1(2): 176-180.

Han, H. S., Supanjani, L., and Lee, K. D. 2006. Effect of co-inoculation with phosphate and potassium solubilizing bacteria on mineral uptake and growth of pepper and cucumber. *Plant Soil Environ.* 52 (3): 130-136.

Hesse, P. R. 1962. Phosphorus fixation in mangrove swamp muds. *Nature.* 193: 295-296.

Hilda, R. and Fraga, R. 1999. Phosphate solubilizing bacteria and their role in plant growth promotion. *Biotech Adv.* 17: 319-359.

Holguin, G., Vazquez, P., and Bashan, Y. 2001. The role of sediment microorganisms in the productivity, conservation and rehabilitation of mangrove ecosystems: an overview. *Biol. Fert. Soils.* 33: 265-278.

Illmer, P. 1995. Solubilization of hardly-soluble AlPO4 with P- solubilizing microorganism. *Soil Biol. Biochem.* 27: 265-27.

Isaac, S. R. and Nair, M. A. 2004. Decomposition of wild jack (*Artocarpus hirsutus* Lamk.) leaf litter under subcanopy and open conditions. *J. Trop Agric.* 42(1-2): 29-32.

Jackson, M.L. 1958. *Soil Chemical Analysis*. Prentice Hall of India private ltd., New Delhi, 498p.

Jamaludheen, V. 1994. Biomass production and root distribution pattern of selected fast growing multipurpose tree species. MSc (For.) Thesis, Kerala Agricultural University, Thrissur, 180p.

Jamaludheen, V. Kumar, B. M., Wahid, P. A. and Kamalam, N. V. 1997. Root distribution pattern of the wild jack tree (*Artocarpus hirsutus*) as studied by 32_p soil injection method. *Agroforestry systems* 329-336.

Jones, D. L., Hodge, A., and Kuzyakov, Y. 2004. Plant and mycorrhizal regulation of rhizodeposition. *New Phytologist* 163: 459-480.

Johnson, L.F. and Curl, E.A. 1972. Isolation of groups of microorganisms from soil. Methods for research on the ecology of soil borne plant pathogens. Burgees publishing company, New York, pp 6-13.

Kahindi, J. H. P., George, W. T., Moreira, F. M., de, S., and Karanja, N. K. and Giller. K. E. 1997. Agricultural intensification, soil biodiversity and ecosystem function in the tropics: the role of nitrogen-fixing bacteria. *Appl. Soil Ecol.* 6: 55-76.

Karmakar, R. Sekhar, S., Kumara, K., Sampath, K., Niranjana, S. R., and Prakash, H. S. 2011. Diversity of fungal endophytes from two endemic tree species *Artocarpus hirsutus* Lam. and *Vateria indica* Linn. of Western Ghats, India. *World J. Agric. Sci.* 7 (5): 577-582.

Katznelson, H., Peterson, E. A., and Rovatt, J. W. 1962. Phosphate dissolving microorganisms on seed and in the root zone of plants. *Can. J. Bot.* 40: 1181-1186.

Kim, K. Y., Jordan, D., and McDonald, G. A. 1998. Effect of phosphate solubilizing bacteria and vesicular-arbuscular mycorrhizae on tomato growth and soil microbial activity. *Biol. Fert. Soils.* 26: 79-87.

Kinsbursky, R. S., Degani, R., Baranes, G., and Steinberger, Y. 1990. Root-microbial population dynamics in a soil profile under the canopy of the desert shrub *Zygophyllum dumosum. J. Arid Environ.* 19(3): 261-267.

Koranda, M., Kaiser, C., Fuchslueger, L., Kitzler, B., Sessitsch, A., Sophie Zechmeister-Boltenstern, S., and Richter, A. 2013. Seasonal variation in functional properties of microbial communities in beech forest soil. *Soil Biol. Biochem.* 60: 95-104.

Kpomblekou, K. and Tabatabai, M. A. 1994. Effect of organic acids on release of phosphorus from phosphate rocks. *Soil Sci.* 158: 442-453.

Krivtsov, V., Brendler, A., Watling, R., Liddell, K., and Staines, H. J. 2007. Some aspects of forest soil and litter ecology in the Dawyck Cryptogamic Sanctuary with a particular reference to fungi. Acta Ecologigica Sinica, 27(3): 813-836.

Kucey, R. W. N., Tanez, H. H., and Leggett, M. E. 1989. Microbially mediated increase in plant available phosphorus. *Adv. Agron.* 42: 199-228.

Lacombe, S., Bradley, R. L., Hamel, C., and Beaulieu, C. 2009. Do tree-based intercropping systems increase the diversity and stability of soil microbial communities? *Agric. Ecosyst. Environ,* 131: 25-31.

Lee, K.E. and Pankhurst, C.E. 1992. Soil organisms and sustain- able productivity. Aust. J. Soil Res. 30: 855-892.

Lewis, S. L., Lloyd, J., Sitch, S., Mitchard, E. T. A., and Laurance, W. F. 2009. Changing ecology of tropical forests: evidence and drivers. *Ann. Rev. Ecol, Evol. Syst.* 40: 529-549.

Leyval, C., and Berthelin, J. 1993. Rhizodeposition and net release of soluble organic compounds by pine and beech seedlings inoculated with rhizobacteria and ectomycorrhizal fungi. *Biol. Fertil. Soils.* 15: 259-267.

Manoj. K., Nandakumar, M. K., Remya, M. P., Shinila, K., and Lakshmi, D. P. 2012. Phytosociological analysis of riparian tree species of Alakyam stream; Pariyaram, Kerala, India. *Int. J. Environ. Sci.* 2: 4-10.

Marschner, P. and Rengel, Z. 2007. Contributions of rhizosphere interactions to soil biological fertility. In: Abbott, L.K., Murphy, D.V. (eds.), Soil biological fertility a key to sustainable land use in agriculture. Springer, Dordrecht, The Netherlands, pp.81-98.

Marzaioli, R., D'Ascoli, R., De Pascale, R. A., and Rutigliano, F. A. 2010. Soil quality in a Mediterranean an area of Southern Italy as related to different land use types. *Appl. Soil Ecol.* 44: 205-212.

Mathew, S.P., Mohandas, A., Shareef, S.M., and Nair, G. M. 2006. Bicultural diversity of the endemic 'Wild Jack Tree' on the Malabar coast of South India. *Ethnobotany Res. Appli.* 4:25-40.

Meliani, A. Bensoltane., K. and Mederbel. 2012. Microbial Diversity and Abundance in Soil: Related to Plant and Soil Type. *Am. J. Plant Nutr. Fert. Technol.* 2 (1): 10-18.

Melillo, J. M., Aber, J. D., and Muratore, J. F. 1982. Nitrogen and lignin control of hardwood leaf litter decomposition dynamics. *Ecology* 63(3): 621-626.

Midgley, S. J. and Turnbull, J.W. 2003. Domestication and use of Australian acacias: case studies of five important pieces. *Aust. Syst. Bot*, 16: 89-102.

Mokrane, S., Bouras, N., Sabaou, N., and Mathieu, F. 2013. Actinomycetes from saline and non-saline soils of Saharan palm groves: taxonomy, ecology and antagonistic properties. *African J. Microbiol. Res,* 7(20): 2167-21.

Muthukumar, T., Udaiyan, K., and Rajeshkannan, V. 2001. Response of Neem (*Azadirachta indica* A. Juss) to indigenous arbuscular mycorrhizal fungi, phosphate-solubilizing and asymbiotic nitrogen-fixing bacteria under tropical nursery conditions. *Biol Fertil Soils*. 34: 417-426.

Nayar, M. P. 1996. Hot Spots of Endemic Plants of India, Nepal and Bhutan. Tropical Botanic Garden and Research Institute, Trivandrum, India

Neal, J. R., Atkinson, T. G., and Larson, R. I. 1970. Changes in the rhizosphere microflora of spring wheat induced by disomic substitution of a chromosome. *Can. J. Microbiol.* 16: 153-158.

Neal, J. R., Larson, R. I., and Atkinson, T. G. 1973. Changes in rhizosphere populations of selected physiological groups of bacteria related to substitution of specific pairs of chromosomes in spring wheat. *Plant Soil.* 39: 209-212.

Parr, J. F. and Papendick, R. I. 1997. Soil quality: relationship and strategies for sustainable dryland farming systems. *Ann. Arid Zones* 36: 181-191.

Parr, J. F. and Smith, S. S. 1969. A multi-purpose manifold assembly: use in evaluation microbial effects of pesticides. *Soil Sci.* 107: 271-276.

Prescott, C. E. and Grayston, S. J. 2013. Tree species influence on microbial communities in litter and soil: Current knowledge and research needs. *For. Ecol. Manage*. 309: 9-27.

Prescott, C. E. and Vesterdal, L. 2013. Tree species effects on soils intemperate and boreal forests: Emerging themes and research needs. *For. Ecol. Mgmt.* 309: 1-3.

Raghu, K., and Rae, I. C. M. 1966. Occurrence of phosphate-dissolving microorganisms in the rhizosphere of rice plants and in submerged soils. *J. Appl. Bact,* 29: 582-586.

Rejili. M., Mahdhi. M., Fterich. A., Dhaoui. S., Guefrachi. I., Abdeddayem. R., and Mars. M. 2012. Symbiotic nitrogen fixation of wild legumes in Tunisia: Soil fertility dynamics, field nodulation and nodules effectiveness. *Agric, Ecosyst. Environ*. 157: 60-69.

Reynolds, H. L., Packer, A., Bever, J. D., and Clay, K. 2003. Grass roots ecology: plant microbe soil interactions as drivers of plant community structure and dynamics. *Ecology* 84: 2281- 2291.

Richardson, D. M. and Rejmanek, M. 2011. Trees and shrubs as invasive alien species global review. *Diversity Distributions* 17: 788-809.

Rodriguez, H. and Fraga, R. 1999. Phosphate solubilizing bacteria and their role in plant growth promotion. *Biotechnol Adv*.17:319-339.

Rousk, J., Baath, E., Brookes, P.C., Lauber, C.L., Lozupone, C., Caporaso, J.G., Knight, R., and Fierer, N. 2010. Soil bacterial and fungal communities across a pH gradient in an arable soil. *ISME J.* 4: 1340-1351.

Rovira, A. D., Bowen, G. D. and Foster, R. C. 1983. The significance of rhizosphere microflora and mycorrhizas on plant nutrition. In: A. Lanchii and R. L. Bielski (eds.), *Encyclopedia Plant Physio.* 12: 61-93.

Roy, S., Bano, R., Saxena, P and Roy, M. M. 2007. Seasonal abundance of beneficial soil microflora in fodder production systems on red alfisols. *Range Management and Agroforestry,* 28: 10-15.

Ruma, K., Shailasree, S., Sampath, K. K., Niranjana, S. R. and Prakash, H. S. 2011. Diversity of Fungal Endophytes from Two Endemic Tree Species Artocarpus hirsutus Lam. And Vateria indica Linn. of Western Ghats, India. *World J. Agrl. Sci.* 7(5): 577-582.

Russoa, S. E., Leggeb, R.,Webera, K. A., Brodied, E. L., Goldfarbd, K. C., Bensonb, A. K., and Tan. S. 2012. Bacterial community structure of contrasting soils underlying Borneanrain forests: Inferences from micro array and next-generation sequencing methods. *Soil Biol. Biochem.* 55: 48-59.

Sahoo, K. and Dhal, N.K. 2009. Potential microbial diversity in mangrove ecosystem: a review. *Indian J. Marine Sci.* 38: 249-256.

Sam, P., Mathew, A., Mohandas, S., Shareef, M., and Nair, G. M. 2006. Bio cultural diversity of the Endemic 'Wild Jack Tree' on the Malabar Coast of South India. *Ethnobotany Res. Appl.* 4: 25-40.

Schloter, M., Dilly, O., and Munch, J. C. 2003. Indicators for evaluating soil quality. *Agric. Ecosyst. Environ.* 98: 255-262.

Sharma, D. D., Chaudari, A. K., Chowdary, N. B., Mala, V. R., and Qadri, S. M. H. 2010 Comparative study of rhizosphere and rhizoplane microflora in

healthy and diseased mulberry (Morusspp) gardens. *Indian. J. Seric,* 49(2): 203-207.

Sheng, X. F. and Huang, W.Y. 2002. Mechanism of potassium release from feldspar affected by the strain NBT of silicate bacterium. Acta pedologiea sinica. 39: 863-871.

Shi, S., O'Callaghan, M., Jones, E. E., Richardson, A. E., Walter, C., Stewart, A., and Condron, L. 2012. Investigation of organic anions in tree root exudates sand rhizosphere microbial communities using in situ and destructive sampling techniques. *Plant and Soil.* 359: 149–163.

Shilpkar P., Shah, M. C., Modi K. R., and Patel S. M. 2010. Seasonal changes in microbial community structure and nutrients content in rhizospheric soil of Aegle marmelos tree. *Ann. For. Res.* 53(2): 135-140.

Silva, D. K. A., Freitas, N. O., deSouza, R. G., Silva, F. S. B., Araujo, A. S. F., and Maia, L. C. 2012. Soil microbial biomass and activity under natural and regenerated forests and conventional sugar cane plantations in Brazil. *Geoderma.* 189–190, 257–261.

Singh, S., and Kappor, K. K. 1998. Effects of inoculation of phosphate-solubilizing microorganisms and an arbuscular mycorrhizal fungus on mungbean grown under natural soil conditions. *Mycorrhiza* 7: 249–253.

Singleton, P. W., Abdel-Magid, H. M., and Tavares, J. W. 1985. Effect of phosphorus on the effectiveness of strains of *Rhizobium japonicum. Soil Sci. Soc. Am. J.* 49: 613-616.

Sinha, S., Masto, R. E., Ram, L. C., Selvi, V. A., Srivastava, N. K., Tripathi, R. C., George, J. 2009. Rhizosphere soil microbial index of tree species in a coal mining ecosystem. *Soil Biol. Biochem.* 41: 1824–1832.

Siviero, M.A., Motta, A.M., Lima, D.D.S., Birolli, R.R., Huh, S.Y., Santinoni, I.A., Murate, L.S., Antonia de Castro, C.M., Miyauchi, M.Y.H., Zangaro, W., Nogueira, M.A. and Andrade, G. 2008. Interaction among N-fixing bacteria and AM fungi in Amazonian legume tree (Schizolobium amazonicum) in field conditions. Appl. Soil Ecol. 39: 144-152.

Spark, D. L. 1987. Potassium dynamics in soils. *Adv soil sci.* 6: 1-63.

Strickland, M.S., Osburn, E., Lauber, C., Fierer, N., and Bradford, M. A. 2009. Litter quality is in the eye of the beholder: initial decomposition rates as a function of inoculums characteristics. *Functional Ecology.* 23: 627-636.

Sturz, A. V., and Christie, B. R. 2003. Beneficial microbial allelopathies in the root zone: the management of soil quality and plant disease with rhizobacteria. *Soil Tillage Research.* 72: 107-123.

Subbarao, N. S. 1988. Phosphate solubilizing microorganism, biofertilizers in agriculture and forestry. Regional Biofert. Dev. Centre, Hissar, India. pp. 133–142.

Subbarao S. N. S., 2001. *Soil Microbiology.* Oxford and IH publishing Pvt. Ltd, New Delhi.p 22-26.

Sugumaran, P., and Janarthanam, B. 2007. Solubilization of potassium containing minerals by bacteria and their effect on plant growth. *Wld. J. Agric. Sci.* 3(3): 350-355.

Sundara-Rao, W.V.B., and Sinha M.K. 1963. Phosphate dissolving micro-organisms in the soil and rhizosphere. *Indian J. Agric Sci.* 33:272–278.

Tian, J., Fan, M., Guo, J., Marschner, P., Li, X. and Kuzyakov, Y. 2012. Effects of land use intensity on dissolved organic carbon properties and microbial community structure. *European J. Soil Biol.* 52: 67-72.

Thombre, B. B., and Joshi, M. S. 2011. Quantification of rhizosphere microflora of coconut in sandy and lateritic soils. *Indian Coconut J.* 53(10): 19-21.

Thoms, C., Gattinger, A., Jacob, M., Thomas, F. M., and Gleixner, G. 2010. Direct and indirect effects of tree diversity drive soil microbial diversity in temperate deciduous forest. *Soil Biol. Biochem.* 42: 1558-1565.

Thoms, C. and Gleixner, G. 2013. Seasonal differences in tree species influence on soil microbial communities. *Soil Biol. Biochem.* 66: 239-248.

Ushio, M., Wagai, R., Balser, T. C., and Litayama, L. 2008. Variations in the soil microbial community composition of a tropical montane forest ecosystem: does tree species matter? *Soil Biol. Biochem.* 40: 2699-2702.

Vazquez, P., Holguin, G., Puente, M. E., Lopez Cortes, A., and Bashan, Y. 2000. Phosphate solubilizing microorganism associated with the rhizosphere of mangroves in a semi-arid coastal lagoon. *Biol. Fert. Soils.* 30: 460–468.

Walker, J. C. G., Klein, C., Schildlowski, M., Schopf, J. W., Stevensen, J. D., and Walker, R. M. 1983. Environmental evolution of the Archean- Early-Proterozoic Earth. In: Schoph, J. W. (ed.), *Earth's Earlist Biosphere.* Princeton University Press, Princeton.p 68-72.

Walkley, A.J. and Black, J.A. 1934. Estimation of soil organic carbon by chromic acid titration method. *Soil Sci.* 31: 29-38.

Wardle, D. A., Bardgett, R. D., Klironomos, J. N., Setala, H., Vander Putten, W. H., and Wall, D. H. 2004. Ecological linkages between above ground and below ground biota. *Science*. 304: 1629–1633.

Yu, X., Xu Liu, X., Zhu, T. H., Liu, G. H., and Mao, C. 2011. Isolation and characterization of phosphate-solubilizing bacteria from walnut and their effect on growth and phosphorus mobilization. *Biol Fertil Soils*. 47: 437–446.

YuanYuan, S., Li, Z., ZhiYing, W., ShaoPing, W. 2011. Dynamics of soil nutrient and microbial community of larch plantation. *J. Northeast Forestry University*. 39: 82-98.

Zhang, D., Zhang, J., Yang, W., and Wu, F. 2012. Effects of Afforestation with *Eucalyptus grandis* on Soil Physicochemical and Microbiological Properties. *Soil Res.* 50(2): 167-176.

SOIL PRODUCTIVITY CHANGES UNDER SELECTED INDIGENOUS FOREST TREE SPECIES WITH SPECIAL REFERENCE TO BENEFICIAL MICROFLORA

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ABSTRACT OF THESIS

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ABSTRACT

A field investigation was conducted with four important indigenous tree species viz. *Hopea parviflora* Bedd., *Artocarpus hirsutus* Lamk., *Pterocarpus marsupium* Roxb, and *Pterocarpus santalinus* L.f. of about 30 years of age and planted at 2 m×2 m spacing at Kerala Forest Research Institute sub-centre Nilambur, India for a period of one year (May 2013 to May 2014). The specific objective of the study was to monitor the soil productivity changes due to long term occupancy of four indigenous trees with special reference to the beneficial soil microflora. The rhizosphere soil samples were collected for the isolation and enumeration of microbial population at quarterly interval for a period of one year. The population of bacteria, fungi, actinomycetes, nitrogen fixing bacteria, phosphate solubilising bacteria and potash solubilising bacteria were estimated by serial dilution method. The soil physico-chemical properties and the growth of trees were also observed.

The highest microbial population, during the entire study period, was recorded in *Artocarpus hirsutus* and the lowest in treeless control plot. *Artocarpus hirsutus* recorded the maximum bacteria, fungi, actinomycetes, nitrogen fixing bacteria and phosphate solubilising microorganism. Potash solubilizing bacteria were recorded maximum in *Hopea parviflora* plots. The highest bacterial population observed in late summer and rainy season and the lowest recorded during early summer season. The highest fungal population recorded in late summer season and the lowest during winter season. Early summer season recorded the highest actinomycetes population and lowest in late summer season. The highest population of nitrogen fixing bacteria and phosphate solubilising microorganism observed in the winter season and the lowest population during early summer season. Potash solubilizing bacteria recorded highest during the summer seasons (late summer-I and late summer-II seasons) and lowest in the rainy season. In the final sampling (late summer) also, *A. hirsutus* was found to harbour maximum bacteria, nitrogen fixing bacteria, phosphate solubilising

bacteria and potash solubilising bacteria. However, the highest fungi and actinomycetes associated with *Pterocarpus santalinus.*

The long term occupancy of the indigenous tree species was found to have influenced the soil physico-chemical properties. The soil moisture and bulk density was distinctively superior in the wooded lands as compared to the treeless open area. The soil organic carbon (2.25%), available nitrogen (17.80 kg ha^{-1}), total nitrogen (0.16%) and exchangeable potassium (70.70 kg ha^{-1}), were also significantly higher in *H. parviflora.* The most acidic soil was also found in *H. parviflora* while the least acidic was *A. hirsutus* plots. The maximum height (12.41m) and the dbh (16.25 cm) were recorded in *Pterocarpus santalinus*

The present study throws light into the intimate relation between the types and nature of soil microflora populations and their positive influence on the microsite enrichment aspects of promising indigenous tree species. The information will aid in preferential selection of these tree species along with crops into different tree farming systems where the ecosystem sustainability is of greater relevance. In general, all the four indigenous tree species recorded significantly higher microflora population and greatly improved physico-chemical properties than treeless plot due to long term occupancy of trees.