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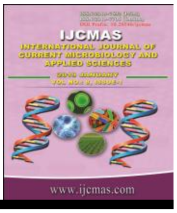

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Study of Microbial Count in Soil under Different Land Use Systems in a Mollisol

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ABSTRACT

Keywords

Microbial, Count, Land use systems, Mollisol

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Present study was undertaken to assess the microbial count in soil under different land use systems in a Mollisol at Norman E. Borlaug Crop Research Centre, G.B. Pant University, Pantnagar. The land use systems were rice–wheat–green gram, rice–pea (vegetable)-maize, rice-potato –okra, rice–berseem + oat + mustard (fodder)-maize + cowpea (fodder), maize–wheat–cowpea, sorghum (fodder)-yellow sarson-black gram, guava + lemon, poplar + turmeric, eucalyptus + turmeric and fallow (uncultivated land). Samples were taken from 0-20cm depth and counts of microorganisms were carried out by using serial dilution pour plate method. Results indicated that soils under agroforestry based systems showed best results with respect to soil biological health followed by field crops, horticultural crops and the uncultivated land.

Introduction

Soil, a part of land, is the most important production factor for crops and at the same time influenced most by the farm practices. There is a considerable decline in soil fertility because of continuous growing of crops one after another without giving much consideration to the nutrient requirement of the crops grown (Ghosh *et al.,* 2003). Microorganisms in the soil strongly influence soil processes (Garbeva *et al.,* 2004), fulfill key roles in the decomposition of organic matter, the cycling of carbon and nitrogen and the formation and stabilization of soil structure (Loranger-Merciris *et al.,* 2006). The constituents of soil microorganisms, such as microbial community diversity, have often been identified as sensitive indicators of biological indices for maintaining soil health and quality (Bending *et al.,* 2004).

The soil microbial diversity is the most important functional component of the soil biota (Tate, 2000). Microbial adaptation to environmental conditions allows microbial analysis to be discriminating in soil health assessment, and changes in microbial populations and activities may therefore function as an excellent indicator of change in soil health (Kennedy *et al.,* 1995; Pankhurst *et al.,* 1995).

Therefore, the present study was undertaken with the objective of assessment of soil microbial count under different land use systems.

Materials and Methods

Present study was undertaken at Norman E. Borlaug Crop Research Centre at Pantnagar in Mollisol soil. Five composite soil samples (0-20 cm depth) representing the whole area were collected randomly from different land use systems comprising of field crops, horticultural crops, agroforestry crops and fallow (uncultivated land) of the same block during kharif, 2017-18. Each composite soil sample was air dried, processed with the help of pestle and mortar, passed through 2 mm sieve and used for the analysis of biological properties.

The count of microorganisms (bacteria, fungi and actinomycetes) was carried out by using serial dilution pour plate method (Wollum, 1982).

The data were analysed statistically by using complete randomized design (C.R.D). The data collected on different soil properties were analysed applying ANOVA technique (Pansa and Sukhatme, 1985). The overall difference was tested by F test of significance at 5 % level of probability. In case of significant F test, C.D. at 5 % was calculated for comparing treatment means.

Results and Discussion

Bacterial population

Bacterial population in soil significantly differed under different land use systems and ranged between 1.62 to 4.75 × 10^8cfu g^{-1}soil (Table 1). Highest bacterial population was seen under eucalyptus + turmeric system which was significantly higher than population under all other land use systems. Bacterial population noted under poplar + turmeric system was significantly higher than that under rice-potato –okra, rice–wheat–green gram, rice–berseem + oat + mustard(fodder)-maize + cowpea(fodder), sorghum(fodder)-yellow sarson-black gram, rice–pea(vegetable)-maize, maize–wheat–cowpea, guava + lemon and fallow(uncultivated) land use system. Bacterial population noted under maize–wheat–cowpea system was significantly higher than that under guava + lemon and fallow (uncultivated) land use system (Table 1).

Several researchers have reported that microbial diversity in soil is greater under agroforestry systems due to the effect of trees and organic matter inputs and also difference in litter quality, quantity and root exudates. The availability of carbonaceous materials and substrates such as amino acids, sugars and organic acids are important for supplying energy for the microbial population (Ferreira *et al.*, 2012).

Fungal population

Fungal population in soil significantly varied under different land use systems and ranged between 1.35 to 4.15 × 10^5cfug^{-1}soil (Table 1). Highest fungal population was recorded under poplar + turmeric and eucalyptus + turmeric land use system. Fungal population noted under rice-potato-okra system was significantly higher than that under rice–wheat–green gram, rice–berseem + oat + mustard(fodder)-maize + cowpea (fodder), sorghum(fodder)-yellow sarson-black gram, maize–wheat–cowpea, rice–pea (vegetable)-maize, guava + lemon and fallow (uncultivated) land use system (Table 1). Fungal count recorded under rice–pea (vegetable)-maize and guava + lemon system were significantly higher than that under fallow (uncultivated) land use system.

Bharadwaj and Omanwar (1992) observed that increase in the content of macronutrients in the soil caused increase in the fungal population. This might be the reason for higher fungal population under eucalyptus + turmeric and poplar + turmeric based land use system.

Actinomycetes population

Actinomycetes population in soil varied significantly under different land use systems and ranged between 1.87 to 4.51 × 10^6cfu g^{-1} soil (Table 1). Highest actinomycetes population in soil was noted under eucalyptus + turmeric system which was significantly higher than population noted under poplar + turmeric, rice–wheat–green gram, rice–berseem + oat + mustard (fodder)-maize + cowpea(fodder), sorghum (fodder)-yellow sarson-black gram, rice–pea (vegetable)-maize, guava + lemon, maize–wheat–cowpea and fallow (uncultivated) land use system. Actinomycetes population noted under guava + lemon system was significantly higher than that under fallow (uncultivated) land use system (Table 1). Higher actinomycetes population under eucalyptus + turmeric land use system might be due to higher organic matter content of the soil and due to organic matter added to the soil through leaf litter which serves as a source of energy for microbial population. Similar results were also reported by Joshi and Yadav (2005).

Total microbial population

Total microbial population in soil significantly differed under different land use systems and ranged between 1.64 to 4.80 × 10^8 cfu g^{-1}soil. The highest microbial population was noted under eucalyptus + turmeric system which was significantly higher than total microbial population noted under all other land use systems. Total microbial population noted under guava + lemon was significantly higher than that under fallow (uncultivated) land use system (Table 1).

Among different groups of microbial population, the population of bacteria was recorded maximum followed by actinomycetes followed by fungal population. Similar order was also observed by Radhakrishnan *et al.*, (2016) and Nayak (2017).

Functional groups of microbes

Azotobacter

Azotobacter population in soil significantly varied under different land use systems and ranged between 1.25 to 3.99 ×10^5cfu g^{-1}soil. The highest population of *Azotobacter* was noted under eucalyptus + turmeric land use system which was significantly higher than that under rice–wheat–green gram, rice-potato – okra, sorghum (fodder)-yellow sarson-black gram, rice–pea (vegetable)-maize, rice–berseem + oat + mustard (fodder)-maize + cowpea (fodder), maize–wheat–cowpea, guava + lemon and fallow (uncultivated) land use system. *Azotobacter* population observed recorded under guava + lemon system was significantly higher than that under fallow (uncultivated) land use system (Table 2).

Higher population of *Azotobacter* was noted under eucalyptus + turmeric system followed by poplar + turmeric as compared to other systems. This might be due to the high soil organic carbon content under these systems. *Azotobacter* population ranged from 10 ×10^4 to 13 ×10^4cfu g^{-1} soil in rhizospheric soil due to high organic matter content of the soil (Maurya *et al.*, 2012).

Phosphorous solubilizing bacteria (PSB)

PSB population in soil significantly differed under different land use systems and ranged between 1.63 to 4.13 × 10^3cfu g^{-1} soil. Highest population of PSB was recorded under eucalyptus + turmeric system which was significantly higher than that under all other land use systems.

PSB population noted under poplar + turmeric and rice-potato-okra system was significantly higher than that under rice–berseem + oat + mustard(fodder)-maize + cowpea(fodder), rice–wheat–green gram, sorghum(fodder)-yellow sarson-black gram, rice–pea (vegetable)-maize, maize–wheat–cowpea, guava + lemon and fallow(uncultivated) land use system. PSB population observed under maize–wheat–cowpea system was significantly higher than that under fallow (uncultivated) land use system (Table 2).

Table.1 Bacterial, fungal and actinomycetes population in soil under different land use systems at 0 – 20 cm depth

Land use systems	Bacteria (×10^8cfu g^{-1} soil)	Fungus (×10^5cfu g^{-1} soil)	Actinomycetes (×10^6cfu g^{-1} soil)	Total count (×10^8cfu g^{-1} soil)
Rice – wheat – green gram	3.46	3.54	3.18	3.49
Rice – pea (vegetable) –maize	3.16	2.47	2.94	3.19
Rice – potato – okra	4.10	3.95	4.41	4.15
Rice – berseem + oat + mustard (fodder) –maize+cowpea (fodder)	3.42	2.91	3.06	3.46
Maize – wheat – cowpea	2.94	2.69	2.33	2.97
Sorghum (fodder) – yellow sarson – black gram	3.30	2.72	3.02	3.34
Guava + lemon	2.72	2.46	2.47	2.74
Poplar + turmeric	4.46	4.15	3.27	4.50
Eucalyptus + turmeric	4.75	4.15	4.51	4.80
Fallow (uncultivated land)	1.62	1.35	1.87	1.64
SEm±	0.06	0.06	0.05	0.06
CD at 5%	0.16	0.17	0.15	0.16

Table.2 Azotobacter and phosphate solubilising bacterial count in soil under different land use systems at 0–20 cm depth

Land use systems	*Azotobacter* (×10^5cfug^{-1} soil)	Phosphate solubilising bacteria (×10^3 cfu g^{-1} soil)
Rice – wheat – green gram	3.80	3.07
Rice – pea (vegetable) –maize	3.01	2.69
Rice – potato – okra	3.69	3.75
Rice – berseem + oat + mustard (fodder) – maize+cowpea(fodder)	2.90	3.25
Maize – wheat – cowpea	2.65	2.38
Sorghum (fodder) – yellow sarson – black gram	3.16	3.04
Guava + lemon	2.49	2.38
Poplar + turmeric	3.94	3.81
Eucalyptus + turmeric	3.99	4.13
Fallow (uncultivated land)	1.25	1.63
SEm±	0.06	0.03
CD at 5%	0.16	0.10

PSB population of the soil was reported higher under systems with more organic carbon and nitrogen content which might be possible because organic carbon in soil supports the growth of phosphate solubilizing microbes. Similar results were observed by Vikram *et al.*, (2007) and Venkateswarlu *et al.*, (1984).

In conclusion, it is evident from the study that different land use systems have significant impact on soil biological health. Soils under agroforestry based systems showed best results with respect to soil biological environment followed by field crops, horticultural crop and the uncultivated land. The study indicates that dense cover and high litter fall in agroforestry systems led to higher organic matter content in soil which further favoured the microbial growth. Study may be helpful in evaluation of soil health and thereby enhancing cropping system sustainability.

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