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Effect of different Land-use Systems on Microbial Population and Urease Enzyme activity in a Mollisol

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ABSTRACT: The soil microbial properties and urease activity significantly influenced by different different treatments. Different land uses effect micrbial and urease enzyme activity, the present study was conducted at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar. The different treatment selected for study were T_1 (rice–potato–okra), T_2 (rice–pea (vegetable)–maize), T_3 (sorghum multi-cut (fodder)–yellow sarson–black gram), T_4 (rice-wheat–green gram), T_5 (rice–berseem + oat + mustard (fodder)–maize + cowpea (fodder)), T_6 (guava + lemon), S_7 (poplar + turmeric), T_8 (eucalyptus + turmeric), T_9 (fallow). The highest value of soil bacteria (4.29×10^8 cfu g^{-1} soil), fungi (3.99×10^5 cfu g^{-1} soil), actinomycetes (3.46×10^6 cfu g^{-1} soil), total microbial count (4.78×10^8 cfu g^{-1} soil). More over, urease enzyme activity (9.23mg urea g^1 soil $24h^{-1}$) observed under the T_8 treatment, which was significantly differ from T_9. Value of T_7 treatment was obtained significantly at par with T_8 treatment with respect to bacterial count. According to this finding, the soil under crop and crop + forest based treatments was found better with respect to soil microbial population popuand urease enzyme activity followed by crops, and uncultivated land.

The high amount chemical fertilize application in crop adversely are influence of soil health, production potential, water pollution, increase environmental challenge, land degradation, the areas increase of problematic soil and loss of soil biodiversity. This all are the challenge related to monocroping in particular area. Resultant most fertile soil become unproductive, Therefore, solution of this problems is that we should bring different land uses systems into practice, which will develop in the soil health and the quality of the soil. On the basis of result of this experiment, we can say that more soil health was found in the crop and forestry base treatments, as well as it was found that with this type of system, we can also generate additional income like different products from different systems. which is sold in different markets It has been concluded from this experiment that the number of fungi, bacteria, actinomycetes, total mircobial count and uraceae enzyme activity has been observed more in the crop and forestry based land uses systems because the forestry system increases the amount of organic carbon in the soil as well as in the amount of food for microbes. The forestry system improves other properties of the soil such as physical, chemical and biological properties, resultant increase the productivity and health of the soil.

Keywords: Land-use Systems, Microbial count, urease enzyme activity.

INTRODUCTION

Soil is a complex mixer of minerals consisting of different form of minerals, OM, soil separates, water retention and void in soil. Nutrients are contribute in soil from mineral by decomposition, mineralisation, immobilisation, absorption, and desorption (IFOAM, 2002). Soil is highly diverse in nature because it is composed of physical, chemical and biological properties (Goovaerts, 1998). Any process in soil affect soil properties; therefore, knowledge of soil properties is essential with different land-use systems (Amusan *et al*., 2006). Biological properties influence soil fertility by different processes like solubilization, absorption-desorption, and mineral and organic matter transformation. In addition, soil biological properties provide information regarding nutrient dynamics, nutrient availability, soil quality and health, root growth, soil erosion and seed germination. Since many soil biological processes became the founder of other soil processes, which may be variations induced by the different treatments. The present study was conduct for study of soil microbial population and urease under different different treatment. The Bacteria, actinomycetes, fungi and algae are part of soil microbial biomass, active carbon fraction of soil organic matter and nutrient cycling (Henrot and Robertson 1994). Soil nutrient content and its

availability are highly correlated with microbial biomass present in the soil. Therefore it is consider as indicator of soil quality under agricultural land (Rice *et al.,* 1986) and directly effect on soil health (Marschner *et al.,* 2001). Biochemical dynamics of carbon, nitrogen, and phosphorus(P) mineralization of nutrient are associated with microbial population (Schoenholtz *et al.,* 2000). Micro and essential nutrient in present in complex forms in soil and that are not easily available to the plants as water soluble form. Microbes helping in making complex form to water soluble forms (Grayston *et al.,* 1998). Micro and essential nutrient in present in complex forms in soil and that are not easily available to the plants as water soluble form. Microbes helping in making complex form to water soluble forms (Grayston *et al.,* 1998). Conventional tillage, irrigation, fertilizer application and human related activity influenced on microbial populations well activity of microbes in soil (Arunachalam 2003; Liebig *et al.,* 2004). The alteration of microbial population is due to different land use, continue cultivation and loss of soil organic matter in cultivated soil **(**Srivastava and Singh 1989). Agroforestry and management practice influenced on biological properties degraded land due to addition of high quality crop and organic residue in soil **(**Mendonça *et al.,* 2001). Fisher (1995) reported that trees based land use influenced soil biological properties by different ways such as many trees species fix nitrogen from atmosphere therefore increase nitrogen content in soil. Trees may also enhance the above and below ground microclimate around plant roots and may alter the soil biological properties. In Kenya, Belsky *et al.* (1989) reported 35% to 60% more soil microbial biomass under *Adansonia digitata* and *Acacia tortilis* crowns than in the grassland areas because of trees provide good bioclimate. Trees influenced above and below microclimate near root zone area ultimately that alter soil biological properties. kenya Belsky *et al.* (1989) reported 35 - 60% more microbial biomass with *Acacia tortilis* and *Adansonia digitata* cownns thanin the graasland area because of trees provide favourable bioclimate Kaur *et al.* (2000) reported soil microbial biomass under mono cropping of rice, forestry, and agro forestry in India. microbial biomass data was increased by 42% (microbial-C) and 13% (microbial-N) in agro forestry compared to cropping system. The agro-forestry based land use obtained more microbial biomass and population in soil.

From the results of this experiment, it has been concluded that adopting agroforestry in future, instead of any one cropping system, which we will be able to conserve soil, soil productivity, and crop production will also increase.

MATERIALS AND METHODS

A. Physiographic description of the study area

The that study was conducted at Norman E. Borlaug Crop Research Centre of Govind Ballabh Pant University, Pantnagar, and District U.S. Nagar of Uttarakhand. Soil order was Mollisol. Pantnagar falls under sub-humid and sub-tropical climate (Puri & Mahajan 1960). Soil samples were collected from the 0-20 cm depth.

B. Treatment details

Nive land-use system have been taken as a treatment with three replication. The treatment selected for study were T_1 (rice–potato–okra), T_2 (rice–pea (vegetable)–maize), T_3 (sorghum multi-cut (fodder)–yellow sarson–black gram), T_4 (rice-wheat–green gram), T_5 (rice–berseem + oat + mustard (fodder)–maize + cowpea (fodder)), T_6 (guava + lemon), S_7 (poplar + turmeric), T_8 (eucalyptus + turmeric), T_9 (fallow (uncultivated land).

C. Microbial population

Serial dilution pour plate method use for measurment of microbial count (Wollum, 1983). Serial dilutions were performedin the Laminar's flow chamber in the laboratory. 90 mL sterile water blank mix with 10 g of soil. For dilution 10^{-2} dilution, 10 mL of soil suspension was put to a 90 mL sterile water blank. It was shake uniformly for 10^{-3} dilutions 1mL was transferred to 9 mL water. The procedure was repeated to get dilution upto 10^{-8}.; 10^{-4}, 10^{-5} and 10^{-6} for actinomycetes and 10^{-6}, 10^{-7} and 10^{-8} for bacteria.Then 1 mL of required dilution 10^{-3}, 10^{-4} and 10^{-5} for fungi was transferred into sterile well-labelled Petri plates. Then 20-25 mL of selective media for specific organisms (Nutrient Agar medium, Martin's Rose-Bengal medium and Ken-knight's for bacteria, fungy and actinomycetes repectively cooled to 45ºC was poured uniformly into Petri plates. The medium was allowed to solidify and, after solidification, incubated at 28 ± 2ºC temperature. The colonies formed were counted for bacteria after 48 hours, for fungi after 92-96 hours and for actinomycetes after a week's incubation. cfu g^{-1} soil unit use for repersent of microbial population.

D. Urease activity

Urease enzyme activity was determined colourimetrically (Bremner and Douglas, 1971); in this process,urea react with diacetylmonoxime(DAM) in the thiosemicarbazide phosphoric acid (TSC) with sulphuric acid. 5g soil sample was use in 125 mL polypropylene (PP) bottle and treated with 5 mL urea solution (10 ppm urea). Then it was incubated at 37-40°C for 5-6 hours. After that 50 mL of 2*M*KCl-PMA (Phenyl mercuric acetate) solution was add up. The bottle was appropriately capped then after for one hour keep for shaking. After one hour, it was filtered. Then 2 mL extract was pipette out in 50 mL volumetric flask, and volume was made upto 10 mL with 2*M*KCl-PMA solution, after that 30 mL of colouring reagent diacetylmonoxime and thiosemicarbazide solution was added in it. The flask was swirled and kept in a hot waterbath for half an hour. After that flask was cooled immediately by keeping it in cold water (using ice) for 15-30 minutes, and volume was made up to 50 mL with water. The intensity red colour was measured at 527 nm wavelength by spectrophotometer (Chhonkar & Tarafdar 1984). Standard curve reading use for calculaton of extracted. Urease activity was calculate in mg urea g^{-1} soil 24 hr^{-1}.

E. Statistical analysis

Experiment was conducted according to the complete randomized block design (CRBD). The data of this

experimental data were statistically analyzed using of variance analysis technique that know as ANOVA (Panse and Suchatme, 1978). The difference in between treatments was measured by applying "F"test of significance at 5 per cent level of significance (0.05 LSD).

RESULTS AND DISCUSSION

A. Bacteria population

The data of the bacterial population under different tratment is given in Table 1. It is found from the data that the bacterial population in soil significantly varied under different treatments. The bacterial population in soil ranged between 1.56 to 4.29 × 10^8 cfu g^{-1} soil at 0-20 cm depth. The highest bacterial population was 4.29 × 10^8 cfu g^{-1}obtained under the treatment T_8eucalyptus + turmeric treatment, that was significantly superior than all other treatments of experment. It was significantly higher than that under T_1 (2.60× 10^8 cfu g^{-1} soil), T_2 (1.83 × 10^8 cfu g^{-1} soil), T_3 (1.93 × 10^8 cfu g^{-1} soil), T_4 (2.10 × 10^8 cfu g^{-1} soil), T_5 (2.34 × 10^8 cfu g^{-1} soil), T_6 (1.61 × 10^8 cfu g^{-1} soil), T_7 (4.16 × 10^8 cfu g^{-1} soil) and T_9 (1.56 × 10^8 cfu g^{-1} soil) treatment. In case of agro-forestry systems, the highest bacterial population was reported under the eucalyptus + turmeric treatment, followed by the poplar + turmeric tratment. Several research have reported that microbial diversity in soil is greater under agro + forestry systems due to the effects of tree with crop and organic matter inputs and also difference in litter fall, and root exudates of plants. (Ferreira *et al.,* 2012). The bacterial population significantly influenced under different land use systems and highest bacterial population obtained under forest land use than cultivated soil recorded by Bello *et al.,* (2013); Nwafor *et al.* (2015); Kumar *et al.* (2017); Pandey *et al.* (2019). Soil microbial count more obtain under agro forestry based land use systems as compare to field crops and horticultural crops.

B. Fungi population

The fungal count under different treatments is illustrated in Table 1. On the basis on data, different treatment was significantly differed with fungal population in soil. The fungal count in soil ranged between 1.54 to 3.99 × 10^5 $cfug^{-1}$ soil at 0-20 cm depth. The highest fungal population was obtained under T_8 (3.99 × 10^5 $cfug^{-1}$ soil) treatment and it was significantly higher than that under T_1 (2.58 × 10^5 $cfug^{-1}$ soil), T_2 (1.79 × 10^5 $cfug^{-1}$ soil), T_3 (1.88 × 10^5 $cfug^{-1}$ soil), T_4 (2.07 × 10^5 $cfug^{-1}$ soil), T_5 (2.30 × 10^5 $cfug^{-1}$ soil), T_6 (1.58 × 10^5 $cfug^{-1}$ soil), T_7 (3.66 × 10^5 $cfug^{-1}$ soil) and T_9 (1.54 × 10^5 $cfug^{-1}$ soil) treatment. Bharadwal and Omanwar, (1992) found that maximum value of fungal population were obtained with (eucalyptus + turmeric) + (poplar + turmeric) based treatments that increase the macronutrients content in the soil, the resultant increase in the fungal population with eucalyptus + turmeric and poplar + turmeric land uses systems. The fungi are easily influenced by change in land use systems and environmental condition (Sui *et al*., 2012). Pandey *et al*. (2019) Soil microbial count more obtain under agro forestry based land use systems as compare to field crops and horticultural crops. Under forest area fungi count reported maximum because of less disturbance and low tillage practice Asadu & Chibuike (2015).

C. Actinomycetes population

The actinomycetes population in the soil with different treatment is classified in table 1.**A**ctinomycetes population in soil significantly varied under different different. The actinomycetes population in soil ranged between 1.36 to 3.46 × 10^6 cfu g^{-1} soil at 0-20 cm depth. The actinomycetes population in soil was recorded maximum with T_8 (3.46 × 10^6 cfu g^{-1} soil) treatment was significantly higher than that under T_1 (3.07 cfu g^{-1} soil), T_2 (2.70 × 10^6 cfu g^{-1} soil), T_3 (2.75 × 10^6 cfu g^{-1} soil), T_4 (2.81 × 10^6 cfu g^{-1} soil), T_5 (2.88 × 10^6 cfu g^{-1} soil), T_6 (2.54 × 10^6 cfu g^{-1} soil), T_7 (3.18 × 10^6cfu g^{-1} soil), and T_9 (1.36 × 10^6 cfu g^{-1} soil) treatment.

Table 1: Effect of different land-use systems on the microbial population at 20 cm soil depth.

Symbol	Treatment	Bacteria (×10^8cfu g^{-1} soil)	Fungus (×10^5cfu g^{-1} soil)	Actinomycetes (×10^6cfu g^{-1} soil)
T_1	Rice – potato – okra	2.60	2.58	3.07
T_2	Rice – pea vegetable – maize	1.83	1.79	2.70
T_3	Sorghum multi-cutfodder– yellow sarson – black gram	1.93	1.88	2.75
T_4	Rice – wheat – green gram	2.10	2.07	2.81
T_5	Rice– berseem + oat + mustard – maize+cowpea fodder	2.34	2.30	2.88
T_6	Guava + lemon	1.61	1.58	2.54
T_7	Poplar + turmeric	4.16	3.66	3.18
T_8	Eucalyptus + turmeric	4.29	3.99	3.46
T_9	Fallow uncultivated land	1.56	1.54	1.36
SEm±		0.046	0.042	0.083
CD at 5%		0.140	0.127	0.251

Among the agroforestry systems, actinomycetes population was reported maximum with eucalyptus + turmeric treatment due to higher OM and more litter fall by the tree that increase microbial population content in the soil. This study supported by Joshi and Yadav (2005).

The actinomycetes population value was obtained highest in surface and subsurface soil under agro forestry based land use systems Kumar *et al.* (2017) that result also supported by Okonkwo (2010). Pandey *et al.* (2019) Soil microbial count more obtain under

agro forestry based land use systems as compare to field crops and horticultural crops.

D. Total microbial population

The total microbial population of the surface soil under different treatment is presented in Table 2. According to data the total microbial population in soil was significantly varied under different treatments. The total microbial count in soil was ranged between 1.68 to 4.78 × 10^8 cfu g^{-1} soil at 0-20 cm depth. The highest microbial population was measured under T_8 (4.78 × 10^8 cfu g^{-1} soil) treatment was significantly higher than T_1 (4.10 × 10^8 cfu g^{-1} soil), T_2 (2.06 × 10^8 cfu g^{-1} soil), T_3 (2.30 × 10^8 cfu g^{-1} soil), T_4 (3.10 × 10^8 cfu g^{-1} soil), T_5 (3.39 × 10^8 cfu g^{-1} soil), T_6 (1.71 × 10^8 cfu g^{-1} soil), T_7 (4.28 × 10^8 cfu g^{-1} soil), and T_9 (1.68 × 10^8 cfu g^{-1} soil) treatment. Bacteria were the most dominant group among different group of microbial populations. Same result also supported by Radhakrishnan and Varadharajan (2016); Nayak, (2017). Pandey *et al.*, (2019) reported soil microbial count more obtain under agro forestry based land use systems as compare to field crops and horticultural crops. Similar research finding supported by microbial population are influenced by soil type, moisture and plants species Wieland, *et al.* (2001); Girvan *et al.* (2003) reported that soil type is main determinative of soil microbial properties in soil. The population of bacteria higher in September and lower in July this was due to rain, temperature and land use and Chander *et al.* (1998) reported that under continue 12 year old agro forestry based land use system significantly influence on soil microbial population.

Table 2: Effect of different land-use systems on total microbial count and urease enzyme activity in the soil.

Symbol	Treatment	Total count (×10^8cfu g^{-1} soil)	Urease (mg urea g^1 soil $24h^{-1}$)
T_1	Rice – potato – okra	4.10	7.43
T_2	Rice – pea vegetable – maize	2.06	5.05
T_3	Sorghum multi-cutfodder– yellow sarson – black gram	2.30	5.26
T_4	Rice-wheat-green gram	3.10	5.46
T_5	Rice-berseem + oat + mustard-maize+cowpea fodder	3.39	6.14
T_6	Guava + lemon	1.71	4.95
T_7	Poplar + turmeric	4.28	8.20
T_8	Eucalyptus + turmeric	4.78	9.23
T_9	Fallow uncultivated land	1.68	4.16
SEm±		0.038	0.078
CD at 5%		0.115	0.235

E. Urease activity in soil

The data on urease enzyme activity in soil under different treatment is given in Table 2. Urease activity in surface soil significantly varied under different treatment. It varied from 4.16 to 9.23 mg urea g^{-1} soil $24h^{-1}$ at 0-20 cm depth. The highest urease activity was recorded under T_8 (9.23 mg urea g^{-1} soil), that was significantly more than all other trearments. On the other hand, urease activity recorded under T_7 (8.20 mg urea g^{-1} soil) treatment was significantly higher than that under T_1 (7.43 mg urea g^{-1} soil), T_2 (5.05 mg urea g^{-1} soil), T_3 (5.26 mg urea g^{-1} soil), T_4 (5.46 mg urea g^{-1} soil), T_5 (6.14 mg urea g^{-1} soil), T_6 (4.95 mg urea g^{-1} soil), and T_9(4.16 mg urea g^{-1} soil) treatment. Agro-forestry based treatments were obtained higher urease activity in the soil, i.e. eucalyptus + turmeric and poplar + turmeric treatments. This was due to high soil organic carbon and OM content. A similar finding was also observed by under forest soils compared to agricultural soils Blonska *et al*., (2017); Pandey *et al.* (2019). Soil microbial count and urease enzyme activity more were obtain under agro forestry based land use systems as compare to field crops and horticultural crops and The urease enzyme more obtained under agro-forest based land use systems because of more litter fall on soil and living dead root (Zahir *et al.*, 2001).

CONCLUSION

The bacterial, fungal, actinomycetes, total microbial population and urease activity differed significantly under different treatments.

The highest bacterial population, fungal population, actinomycetes, total microbial population and urease activity was reported under T_8 (eucalyptus + turmeric) land-use system while the lowest were obtained under T_9 (fallow uncultivated) treatment.The basis on of these result, concluded that among different treatment better microbial population and urease activity of soil were found under agro and forestry based treatment (T_8 and T_7 treatments). So, soil researchers should have been promoted the agroforestry land-use system in combination with agricultural systems.

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Conflict of Interest. None.

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