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Research Article

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Microbial Diversity in Selected Agroforestry Systems of Central Rajasthan

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Abstract: Agroforestry is a sustainable land use system in which crops, trees and livestock are maintained together on the same land to increase total yield and income. Agroforestry can alter the microclimate of soil under tree canopy. It plays an important role in enhancement of farm productivity, climate change mitigation, carbon sequestration, biodiversity conservation, phytoremediation, water conservation, improvement in quality of soil by addition of plant and animal waste. Diversification in plant species enhances microbial activity in soil, provides habitat to beneficial insects, modification in micro climate, nitrogen fixation etc. This agroecological approach breaks the monoculture structure and enhances complex interaction among various species of microflora, fauna, crops and tree species. This approach enhances natural regulation of harmful organisms, biomass production and nutrient cycling resulting in ecological sustainability. This study was undertaken to assess microbial diversity in different types of soil systems in Central Rajasthan. The different land use systems were agroforestry, Agrosilvopastoral, monoculture and barren land. Samples were taken from 0-15 cm depth and assessment of microbial diversity was carried out by characterization method by using Biomerieux VITEK 2 Compact System. Various strains of gram positive and gram negative bacterial species were identified. Most of the species belong to Bacilli. Result shows that microbial diversity was higher in agroforestry and agrosilvopastoral systems as compared to monoculture and barren land. This shows that agroforestry systems are more suitable for agricultural practices than monocropping system to enhance soil productivity and biodiversity.

Keywords: Agroforestry, Agrosilvopastoral System, Biodiversity, Soil Microorganisms, Soil Nutrients, Soil Productivity

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1. INTRODUCTION

According to Alao and Shuaibu (2013) Agroforestry is described as a dynamic ecologically dependent natural resource management system that diversifies and promotes development for increased environmental, social and economic benefits for farmers at all levels through the plantation of trees on farms and in the agricultural fields. In order to improve overall production, agroforestry adopts effective management practices. It is an integrated system of land use management in which certain trees, types of forest trees and livestock are raised on the same soil.[1]Tree imparted benefits of agroforestry systems are related to farm use of fodder, firewood, live fence, timber, medicinal plants and fruits etc. It supports the production of various products like fuel, fodder, timber, fruits, fiber, gums, resin, craft products, gardening material, medicinal products, ecological services, recreation etc.[2] In context to soil nutrient dynamics it minimizes nutrient loss and maximizes internal cycling of nutrients. It enhances pest , disease control and management and reduces dependence on chemical fertilizer and pesticides and other chemical inputs[3]. Agroforestry can enhance and manage soil productivity, fertility and sustainability for a long time. It can enhance soil chemical, physical and biological properties by addition and decay of organic matter. It promotes cycling of nutrients into the soil and makes it available to the crops. Nitrogen fixing tree species increases quantity of nitrogen into the soil and improves quality of soil and crop productivity.[4] The soil's biological aspect is essential for ecosystem conservation and activity. Soil organisms sustain soil cycles such as capture and storage of carbon, cycling of nutrients, fixation of nitrogen, infiltration of water, aeration, and degradation of organic matter.[5] Agroforestry is a system in which trees are integrated in the agricultural system. This had been practiced by farmers since ancient times. In an agroforestry system, a wide range of tree species are grown on farms. It includes fodder trees, fruit trees, medicinal trees, fertilizer trees to improve soil health, timber trees for fuel wood and trees for minor products like resin, gums etc. It is a form of multiple cropping in which three basic conditions are included: (i) existence of minimum two plant species which interact biologically (ii) one plant species is managed for crop production (iii) one plant species is a woody perennial.[6] Agroforestry systems may provide opportunities to improve living conditions by simultaneously producing food, fodder and firewood and mitigating the impact of climate change. Multifunctional agroforestry systems in the tropical region offer countless ecological benefits such as carbon sequestration, climate change mitigation, soil fertility and water efficiency enhancement, biodiversity conservation, bio-pest control, sustainable land use, shelter and windbreaks, micro-climate improvement, poverty breakdown poverty and food insecurity. Agroforestry, if built on depleted property, will not only minimize the anthropogenic burden on existing forest supplies, but will also increase the potential for CO_2 emissions.[7] The hot arid zones of India have disadvantages from an environmental and economic point of view. But even after hostile climatic conditions , Indian hot arid regions are well vegetated and have higher tree species diversity as compared to other hot arid zones of the world. In hot Indian arid zones there are majority of tree species which are multi-purpose and fulfill the needs of rural folk by providing fodder, fuel wood, timber, food and other products. Different species of trees were introduced in hot arid zones of India from iso-climatic regions of the world. Plantation of trees in different arid landforms helps in combating the issue of desertification and provides ecosystem services. These trees play a vital role in sustainability, productivity and livelihood. These trees utilize incoming solar radiations, recycle litter and enrich soil, modify microclimate which is favorable to soil, plant and animal species.[8] Microbial adjustment to natural conditions permits microbial examination to be segregating in soil wellbeing evaluation, and changes in microbial population and exercises may thus work as a superb pointer of progress in soil wellbeing.[9,10] Agroforestry frameworks advance the upkeep of, or on the other hand can even improve, soil natural quality, and is more able to maintain than the cut and-consume cultivating frameworks over the long period of time The multilayered structures of agroforestry can keep up the solidness of inside microclimates which are solid resources for extraordinary climate adaptations. Trees cause significant changes in microclimate, mesoclimate and macroclimate, in addition, trees at wide dispersing additionally encourages them to grow increasingly stable root frameworks to oppose harm from tempests and normal pruning of lower branches assists with keeping away from wind toss.[11] The soil's biological aspect is essential for ecosystem conservation and activity. Soil organisms sustain soil cycles such as capture and storage of carbon, cycling of nutrients, fixation of nitrogen, infiltration of water, aeration, and degradation of organic matter.[12] The agroforestry system is an effective system that helps to prevent degradation of land while ensuring the continuous use of land for productive development of crops and livestock. The system improves the concentration of organic carbon in soils by including crops and permanent trees, which is supposed to increase microbial biomass in soil. Agroforestry encourages litter's permanent contribution to increase the soil's organic matter content and influence the soil microbial population by supplying a wide source of energy and carbon. The use of microorganisms is intended to improve the supply of nutrients to plants. Arbuscular mycorrhizal fungi, rhizobacteria and leguminous plants with rhizobium are important for increase in agricultural production. Improvement in the status of soil microorganisms is significant as microorganisms provide many functions in the soil environment, including decomposition of organic matter, nitrogen fixation, mycorrhiza absorption of phosphorus and plant growth promotion. Soil microorganisms affect the fitness of plants and quality of soil. They ensure the productivity and stability of natural and agricultural ecosystem.[13] Agroforestry promotes food and nutritional protection by: (1) Growing farmer's income by selling tree products (2) Direct supply of tree foods such as fruits and vegetables and by promoting crop production (3) Supplying fuel for cooking (4) Supporting different ecosystem services like pollination ,which are important for the growth of certain crop plants.[14] Diversification in plant species enhances microbial activity in soil, provides habitat to beneficial insects, modification in micro climate, nitrogen fixation etc. This agroecological approach breaks the monoculture structure and enhances complex interaction among various species of microflora, fauna, crops and tree species. This approach enhances natural regulation of harmful organisms, biomass production and nutrient cycling resulting in ecological sustainability.

2. MATERIALS AND METHODS

Soil samples collected from four different fields namely Agroforestry, Agrosilvopastoral, Monoculture and barren land. Soil was collected from depth upto 15 cm by sampling

tools from four corners of the field and mixed in sterile petri plates. Sample was collected and brought to the lab on the same day. The same was processed further as per the method of Laboratory manual of Microbiology (Cappuccino and Sherman).[15] Nutrient agar media was prepared by adding 9.8 g nutrient agar in 350 ml distilled water and boiling. Nutrient agar media was poured into autoclaved petri plates under Laminar Air Flow (LAF) and kept aside to solidify. 1 g of soil sample was mixed into 99 ml autoclaved tap H_2O. Serial dilution of soil samples (10^{-2}, 10^{-4}, 10^{-5}, 10^{-6}, 10^{-7} and 10^{-8}) in autoclave test tubes containing tap water was done. Plating was done by transferring 0.1 ml diluted soil sample on nutrient agar media plates under LAF. After plating, agar media plates were kept in the oven in an inverted position overnight. Result was observed. Colonies were counted on the Quebec Colony Counter. Pure culture of microorganisms was obtained by streaking and plating. Result of pure culture was observed. Gram staining was performed. Micro-organisms were identified by characterization method. Microorganisms were transferred on glass slides with sterile cooled loops and smear was prepared. Smear was heat fixed. Smear was gently flooded by crystal violet and kept for one minute. It was then washed with tap water. It was then gently flooded by Gram's iodine and kept for one minute. It was again washed with tap water. It was then decolorized by 95% ethyl alcohol followed by washing with tap water. Counterstain with safranin for 45 seconds was performed. It was then examined under oil immersion objective of microscope Microorganisms were then identified by using Biomerieux VITEK 2 Compact System. It is an automated microbial identification system that provides highly accurate and reproducible results. With its colorimetric reagent cards and associated hardware and software advances, the VITEK 2 offers platform for phenotypic identification methods.

3. RESULT

On the basis of gram value and cell morphology three types of cards were used in Biomerieux VITEK 2 Compact System namely BCL (Bacillus), GP (Gram positive) and GN (Gram negative) (table 1). On the basis of cell morphology, Bacillus and Coccus types of bacterial species were identified (table 1). In type-1 card (BCL) 21 types of bacteria species were identified (table 2). In type- 2 card (GN) two types of bacteria species were identified (table 3). In type-3 card (GP) two types of bacteria species were identified (table 4). Total 25 bacterial strains were found in four types of study field (table 5). Soil microbial analysis of four different systems namely agroforestry, agrosilvopastoral, monoculture and barren land are as follows:

Table-1. On the basis of Gram value and cell morphology, three types of cards were used for identifying different bacterial strains in four types of study fields

S. No.	Isolates	Gram value (+/-)	Cell morphology (Bacillus/ Coccus)	Card type
A.	**Agroforestry**			
	A1	+	Bacillus	BCL
	A2	+	Bacillus	BCL
	A3	+	Bacillus	BCL
	A4	+	Bacillus	BCL
	A5	+	Bacillus	BCL
	A6	+	Bacillus	BCL
	A7	+	Bacillus	BCL
B.	**Agrosilvopastoral**			
	B1	+	Bacillus	BCL
	B2	+	Bacillus	BCL
	B3	+	Bacillus	BCL
	B4	+	Bacillus	BCL
	B5	+	Bacillus	BCL
	B6	+	Bacillus	BCL
	B7	+	Bacillus	BCL
C.	**Monoculture**			
	C1	-	Bacillus	GN
	C2	-	Bacillus	GN
	C3	+	Coccus	GP
	C4	+	Bacillus	BCL
	C5	+	Bacillus	BCL
D.	**Barren land**			
	D1	+	Bacillus	BCL
	D2	+	Bacillus	BCL
	D3	+	Bacillus	BCL
	D4	+	Bacillus	BCL
	D5	+	Coccus	GP
	D6	+	Bacillus	BCL

CL- Gram-positive spore forming bacilli, GP- Gram-positive cocci and non-spore forming bacilli, GN- Gram-negative fermenting and non-fermenting bacilli

Table- 2 Result for Card -1(BCL) showing Gram positive spore forming bacillus bacteria in four types of study field by charaterisation method

Well	Test	Isolate																			
		Agroforestry							Agrosilvopastoral						Monoculture			Barren land			
		A1	A2	A3	A4	A5	A6	A7	B1	B2	B3	B4	B5	B6	B7	C4	C5	D1	D2	D3	D4	D6
1	BETA-XYLOSIDASE	+	+	+	-	+	-	-	+	-	-	-	+	-	+	-	+	+	+	+	-	-
3	L-Lysine-ARYLAMIDASE	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	L-Aspartate ARYLAMIDASE	-	-	-	+	+	-	+	-	-	(-)	-	-	-	+	-	(+)	-	-	-	-	-
5	Leucine-ARYLAMIDASE	-	+	-	-	-	-	+	-	+	+	+	+	+	-	-	+	-	+	+	(-)	-
7	Phenylalanine ARYLAMIDASE	+	+	+	-	(-)	+	+	+	+	+	-	+	-	+	-	+	-	+	+	+	-
8	L-Proline ARYLAMIDASE	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	BETA-GALACTOSIDASE	(+)	(+)	+	-	-	+	(-)	+	-	+	-	-	-	+	-	-	+	+	+	-	+
10	L-Pyrrolidonyl-ARYLAMIDASE	-	+	+	-	+	+	+	-	+	+	+	(+)	+	-	+	+	(-)	+	+	-	+
11	ALPHA-GALACTOSIDASE	+	+	-	-	(-)	+	+	+	-	+	-	+	-	+	-	-	(-)	(-)	+	-	+
12	Alanine ARYLAMIDASE	-	-	-	-	-	-	(-)	-	+	-	+	-	-	-	-	+	-	-	-	+	-
13	Tyrosine ARYLAMIDASE	+	(-)	-	+	+	+	+	+	+	+	+	(+)	-	-	-	+	-	(+)	-	+	+
14	BETA-N-ACETYL-GLUCOSAMINIDASE	+	-	-	-	-	-	+	-	+	(-)	-	(-)	-	+	-	-	-	(+)	-	+	-
15	Ala-Phe-Pro ARYLAMIDASE	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
18	CYCLODEXTRIN	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-
19	D-GALACTOSE	-	-	-	-	-	+	-	-	+	(+)	-	-	+	-	-	-	-	-	-	-	+
21	GLYCOGEN	-	+	+	-	-	+	-	-	-	+	-	+	-	(-)	-	-	+	+	+	-	+
22	Myo-INOSITOL	-	+	+	-	-	+	-	-	(-)	-	-	+	-	+	-	-	+	+	+	-	-
24	METHYL-A-D-GLUCOPYRANOSIDE acidification	+	+	+	-	-	-	-	-	-	-	-	+	-	(-)	-	-	+	+	+	-	-
25	ELLMAN	-	-	-	-	-	-	-	-	-	-	+	-	-	-	+	+	-	(-)	-	+	-
26	METHYL-D-XYLOSIDE	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
27	ALPHA-MANNOSIDASE	+	-	-	-	(+)	-	(-)	-	-	-	-	-	-	-	-	-	-	-	-	-	-
29	MALTOTRIOSE	-	+	+	-	-	(+)	+	-	+	(+)	-	+	+	+	+	-	+	+	+	-	+
30	Glycine ARYLAMIDASE	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	(+)	-	-
31	D-MANNITOL	+	+	+	+	-	+	-	-	-	+	+	+	-	+	+	-	+	+	+	-	+
32	D-MANNOSE	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+
34	D-MELEZITOSE	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-
36	N-ACETYL-D-GLUCOSAMINE	-	-	+	-	-	+	+	-	+	-	-	-	+	+	-	-	-	+	-	-	(+)
37	PALATINOSE	-	+	+	-	-	-	-	-	-	+	-	+	-	+	-	-	+	+	+	-	(-)
39	L-RHAMNOSE	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
41	BETA-GLUCOSIDASE	+	+	+	-	+	+	-	+	-	+	-	+	-	+	-	-	+	+	+	-	+
43	BETA-MANNOSIDASE	(-)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
44	PHOSPHORYL CHOLINE	-	-	-	-	-	-	(-)	-	-	-	-	-	-	(+)	-	-	-	-	-	-	-
45	PYRUVATE	+	+	-	(-)	-	+	-	-	-	+	-	+	-	+	-	-	+	+	+	-	+
46	ALPHA-GLUCOSIDASE	-	-	-	-	+	+	-	+	-	+	+	-	(-)	-	+	+	(+)	(+)	(-)	+	+
47	D-TAGATOSE	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
48	D-TREHALOSE	+	+	+	-	-	+	+	-	+	+	+	+	+	+	+	-	+	+	+	-	+
50	INULIN	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	(+)	-

53	D-GLUCOSE	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	(+)	+
54	D-RIBOSE	+	+	+	(+)	+	+	+	+	+	(+)	-	+	+	+	-	-	+	+	+	-	+
56	PUTRESCINE assimilation	-	-	-	(+)	-	(-)	-	-	(-)	+	-	-	-	-	-	-	-	-	-	-	(+)
58	GROWTH IN 6.5% NaCl	+	+	+	+	-	+	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+
59	KANAMYCIN RESISTANCE	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(-)	-	-	-
60	OLEANDOMYCIN RESISTANCE	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
61	ESCULIN hydrolysis	+	+	+	(+)	-	+	-	-	-	-	-	+	+	-	-	(+)	+	+	+	-	+
62	TETRAZOLIUM RED	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	(-)	-	-	+	-
63	POLYMIXIN_B RESISTANCE	+	+	+	-	-	-	+	-	+	-	-	+	+	+	-	-	+	+	+	-	-

"+" means Positive, "-" means Negative, "(+)" means weak positive, "(-)" means weak negative

Table-3 Result for Card -2(GN) showing Gram negative fermenting and non-fermenting bacillus bacteria in four types of study field by characterization method

Well	Test	Isolate Monoculture	
		C1	C2
2	Ala-Phe-Pro-ARYLAMIDASE	-	-
3	ADONITOL	-	-
4	L-Pyrrolidonyl-ARYLAMIDASE	+	+
5	L-ARABITOL	-	-
7	D-CELLOBIOSE	-	-
9	BETA-GALACTOSIDASE	-	-
10	H2S PRODUCTION	-	-
11	BETA-N-ACETYL-GLUCOSAMINIDASE	-	-
12	Glutamyl Arylamidase pNA	-	-
13	D-GLUCOSE	-	-
14	GAMMA-GLUTAMYL-TRANSFERASE	-	-
15	FERMENTATION/GLUCOSE	-	-
17	BETA-GLUCOSIDASE	-	-
18	D-MALTOSE	-	-
19	D-MANNITOL	-	-
20	D-MANNOSE	-	-
21	BETA-XYLOSIDASE	-	-
22	BETA-Alanine arylamidase pNA	-	-
23	L-Proline ARYLAMIDASE	-	-
26	LIPASE	-	-
27	PALATINOSE	-	-
29	Tyrosine ARYLAMIDASE	-	-
31	UREASE	-	-
32	D-SORBITOL	-	-
33	SACCHAROSE/SUCROSE	-	-
34	D-TAGATOSE	-	-
35	D-TREHALOSE	-	-
36	CITRATE (SODIUM)	-	-
37	MALONATE	-	-
39	5-KETO-D-GLUCONATE	-	-
40	L-LACTATE alkalinisation	-	-
41	ALPHA-GLUCOSIDASE	-	-
42	SUCCINATE alkalinisation	-	-
43	BETA-N-ACETYL-GALACTOSAMINIDASE	-	-
44	ALPHA-GALACTOSIDASE	-	-
45	PHOSPHATASE	-	-
46	Glycine ARYLAMIDASE	-	-
47	ORNITHINE DECARBOXYLASE	-	-
48	LYSINE DECARBOXYLASE	-	-
52	DECARBOXYLASE BASE	-	-
53	L-HISTIDINE assimilation	-	-
56	COUMARATE	-	-
57	BETA-GLUCuRONIDASE	-	-
58	O/129 RESISTANCE (comp.vibrio.)	-	-
59	Glu-Gly-Arg-ARYLAMIDASE	-	-
61	L-MALATE assimilation	-	-
62	ELLMAN	+	+
64	L-LACTATE assimilation	-	-

Table-4 Result for Card -3(GP) showing Gram positive cocci and non-spore forming bacillus bacteria in four types of study field by characterization method

Well	Test	Isolate	
		Monoculture	Barren land
		C3	D5
2	D-AMYGDALIN	-	-
4	PHOSPHATIDYLINOSITOL PHOSPHOLIPASE C	-	-
5	D-XYLOSE	-	-
8	ARGININE DIHYDROLASE 1	+	-
9	BETA-GALACTOSIDASE	-	+
11	ALPHA-GLUCOSIDASE	-	+
13	Ala-Phe-Pro ARYLAMIDASE	-	-
14	CYCLODEXTRIN	-	-
15	L-Aspartate ARYLAMIDASE	-	-
16	BETA GALACTOPYRANOSIDE	-	-
17	ALPHA-MANNOSIDASE	-	-
19	PHOSPHATASE	-	-
20	Leucine ARYLAMIDASE	-	-
23	L-Proline ARYLAMIDASE	-	-
24	BETA GLUCURONIDASE	-	-
25	ALPHA GALACTOSIDASE	-	+
26	L-Pyrrolidonyl-ARYLAMIDASE	-	-
27	BETA-GLUCURONIDASE	-	-
28	Alanine ARYLAMIDASE	-	-
29	Tyrosine ARYLAMIDASE	-	-
30	D-SORBITOL	-	-
31	UREASE	+	-
32	POLYMIXIN B RESISTANCE	+	-
37	D-GALACTOSE	+	-
38	D-RIBOSE	-	+
39	L-LACTATE alkalinization	-	-
42	LACTOSE	-	-
44	N-ACETYL-D-GLUCOSAMINE	-	-
45	D-MALTOSE	+	-
46	BACITRACIN RESISTANCE	+	-
47	NOVOBIOCIN RESISTANCE	-	-
50	GROWTH IN 6.5% NaCl	+	-
52	D-MANNITOL	-	-
53	D-MANNOSE	-	-
54	METHYL-B-D-GLUCOPYRANOSIDE	-	-
56	PULLULAN	-	-
57	D-RAFFINOSE	-	-
58	O/129 RESISTANCE (comp.vibrio.)	+	+
59	SALICIN	-	-
60	SACCHAROSE/SUCROSE	+	-
2	D-TREHALOSE	-	-
63	ARGININE DIHYDROLASE 2	-	-
64	OPTOCHIN RESISTANCE	+	+

Table 5: Bacteria identified in four different soil types in selected agroforestry systems

	Agroforestry	Agrosilvopastoral	Monoculture	Barren land
1.	*Bacillus pumilus*	*Unidentified*	*Francisella tularensis*	*Bacillus subtilis*
2.	*Bacillus subtilis*	*Bacillus thuringiensis*	*Aeromonas salmonicida*	*Bacillus licheniformis*
3.	*Unidentified*	*Bacillus megaterium*	*Staphylococcus epidermidls*	*Bacillus atrophaeus*
4.	*Fic Bacillus gelatin*	*Bacillus firmus*	*Unidentified*	*Bacillus firmus*
5.	*Unidentified*	*Bacillus amyloliquefaciens*	*Bacillus firmus*	*Leuconostoc pseudomesenteroides*
6.	*Bacillus megaterium*	*Unidentified*	-	*Bacillus megaterium*
7.	*Bacillus cereus*	*Unidentified*	-	-

4. DISCUSSION

In the study carried out in four different types of land use system it was found that the bacterial diversity was maximum in agroforestry and agrosilvopastoral systems and least in monocropping system (Table 5). The *usar* or wasteland also showed significant bacterial diversity (Table 5)which can be attributed to the presence of sufficient diversity in terms of flora that are predominantly weeds and fauna represented mainly by dead animals body parts (bones, skeleton, hooves). All of these contribute much to the soil after decay and decomposition and that explains the existence of bacterial populations in that area. Some scholars have stated that, in agroforestry systems, soil microbial productivity and microbial abundance are greater due to the impact of trees and organic matter supplies and variations in quality and quantity of litter and root exudates. In agroforestry systems, soil microbial biomass rates were controlled by litter content. The existence of organic compounds and substrates such as sugars, amino acids and organic acids from the roots to the soil is essential for energy supply to the microbial communities (Radhakrishnan et al, 2016)[16]. The transition of land-use influences not only physicochemical properties of soil but also soil microorganisms. Soil microbes play a major role in improving fertility and productivity of soil and can affect plant growth indirectly or explicitly (Liu et al, 2019)[17]. The influence of agroforestry on the availability of soil fauna and diversity was found to be generally positive; if paired with a cropping method without Forest. Agroforestry systems give diverse circumstances of spatial connections of trees and crop / pasture and the various wildlife populations they sustain that can be anticipated to cause unique spatial mechanisms of soil biodiversity and contact networks (Marsden et al, 2019)[18]. Substrate storage ability and microbial population composition are influenced by vegetation and land use, and the productive potential of degraded soils may be preserved by successful soil management, such as forest planting (2014)[19]. Agroforestry and agrosilvopastoral systems are dynamic systems wherein definite trophic structure exists in terms of eating and being eaten and due to these inter relationships they survive as robust systems relying much on the bacterial diversity that has been discovered and the unexplored fungal diversity if any. The presence of less bacterial diversity in monocropping systems can be explained similarly in terms of less dependence and less providers. In monocropping system due to less organic matter and tree abundance, soil microbial diversity is lesser as compared to agroforestry systems.

5. CONCLUSION

This study therefore clearly indicates that the first two land use systems namely agroforestry and agrosilvo pastoral are much more stable as compared to the other two systems. Diversity of soil microorganisms was found to be higher in these two systems indicates that agroforestry systems provide favorable conditions to soil microflora to flourish as compared to other systems.

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7. AUTHOR CONTRIBUTION STATEMENT

Ankita Choudhary and Shilpi Rijhwani designed the study, Ankita Choudhary collected data, performed the experiments, Ankita Choudhary wrote the manuscript with support from Shilpi Rijhwani. Shilpi Rijhwani supervised the research.

8. CONFLICT OF INTEREST

Conflict of Interest declared none

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