Original Research Article

Impact of soil biological parameters on soil health in the intensively cultivated deltaic Inceptisol

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ABSTRACT

An experiment was conducted during 2021-22 at Agricultural Research Station, Kattuthottam, Thanjavur, Tamil Nadu to identify the impact of biological parameters on different cropping sequences. Soil samples are taken from different cropping sequences from the experiment plot during active vegetative stage. Samples were analysed for soil biological parameters viz., Urease, Acid phosphatase, Dehydrogenase, Soil microbial count (Bacteria, fungi and actinomycetes) and Microbial Biomass Carbon. Different cropping sequences showed their effect as variations in soil biological properties. The cropping sequence T_4, sunhemp-rice+dhaincha(10:1)-green gram showed more biological activity with urease activity 40.6 NH_4 µg/g/h, acid phosphatase activity 43.1 P-NP µg/g/h, dehydrogenase activity 137.9 TPF µg/g/day, microbial biomass carbon value 307 mg kg^{-1}, bacterial count 55.6 cfu g^{-1} soil, fungal count 23.5 cfu g^{-1} soil and actinomycetes count 41.2 cfu g^{-1} soil. Rice-rice-sesame sequence was observed to have less biological activity than other cropping sequences.

Keywords: Biological properties, cropping sequence, enzyme activity, microbial biomass carbon, microbial population, soil health

1. INTRODUCTION

'Soil health' is described as a condition of dynamic balance between flora and fauna and their surrounding soil environment, in which all the former's metabolic functions run smoothly without any interference, impedance from the latter [1]. Soil health is the ability of soil to continue and operate as a vibrant living ecosystem that supports plants, animals and humans. Soil health is a word used frequently in conversations about sustainable agriculture to indicate the overall state and quality of the soil resource. We have clean air and water, abundant crops and forests, productive grazing grounds, diversified fauna and attractive vistas because of healthy soil. All agricultural systems require management to function properly. Despite this, there is evidence of extensive damage of the environment due to erosion and degradation of organic matter in agricultural soils. Pollution, compaction and salinity increasing as well as other negative consequences.

Rice (*Oryza sativa*) is a component of widely varying cropping sequences. Rice-based cropping sequences form an integral part of agriculture in Tamil Nadu. Several intense rice-based cropping sequences have been noticed and are being practiced by the farmers. While intensive agriculture, those involving exhaustive high yielding varieties of rice and other crops, has led to heavy withdrawal of nutrients from the soil by crops, imbalanced and indiscriminate use of chemical fertilizers has resulted in deterioration and degradation of soil health [2]. According to the FAO, global rice demand in 2020 would be 800 MT, whereas current output is 600 MT. To satisfy future requirements, an extra 200 million tonnes must be generated by boosting productivity per hectare [3]. Even when rice is planted with appropriate N, P and K, the productivity of the crop is dropping. Previously conducted experiment in the same established field which comprising seven different crop rotations *viz.*, rice-black gram, rice-sesame, rice+dhaincha-maize+green gram, rice+dhaincha-bhendi, rice+dhaincha-ragi, rice+dhaincha-varagu, rice+dhaincha-fodder cowpea with first crop of green manure in all rotations. The results revealed that crop rotations had a significant impact on soil quality by altering their properties [4]. Suitable rice-based cropping sequence has to be evaluated, to assess the stability in production. Hence with this context, a research work was carried out to evaluate the soil biological properties in different cropping sequences.

2. MATERIALS AND METHODS

2.1. Study site

The present investigation was carried out at Department of Soil Science and Agricultural Chemistry at Tamil Nadu Agricultural University, Coimbatore. For this study, the soil samples were collected from Agricultural Research Station, Thanjavur which is 272 km away from the Coimbatore in the eastern direction. The soil initial analysis showed it was sandy loam soil with 10 cropping sequences replicated thrice in Randomized Block Design. The area of each plot is about 40 m^2. Samples were collected at active vegetative stage from the root zone at 0-15 cm which were considered as surface samples, during *kharif, rabi and* summer seasons of 2021-22. The cropping sequences were established with recommended dosage of fertilizer. The details of the cropping sequences are as follows (Table 1)

Table 1. List of treatments in cropping sequence

Treatments	*Kharif*	*Rabi*	Summer
T_1	Rice (Co 51)	Rice (ADT 46)	Black gram (ADT 5)
T_2	Rice (Co 51)	Rice (ADT 46)	Sesame (VRI 2)
T_3	Dhaincha	Rice+dhaincha (5:1) (ADT 46)	Black gram (ADT 5)
T_4	Sun hemp	Rice+dhaincha (10:1) (ADT 46)	Green gram (Co 6)
T_5	Black gram (ADT 5)	Rice (ADT 46)	Groundnut (TMV 13)
T_6	Green gram (Co 6)	Rice (Bio fortified-CR Dhan45)	Sesame (VRI 2)
T_7	Fodder Cowpea Co(FC) 9	Rice (ADT 46)	Fodder Maize (African tall)
T_8	Fodder Sorghum Co(FS) 29	Rice (Co 52)	Fodder Cowpea Co(FC) 9
T_9	Maize hybrid (Co 6)	Rice (Seeraga samba)	Bhendi (Co 4)+black gram (ADT 5) (5:1)
T_{10}	Ragi (Co 15)	Rice (Navara)	Cluster bean (MDU1)+black gram (ADT 5) (5:1)

2.2. Soil analysis

The soil analysis was carried out at the laboratory of Department of Soil Science and Agricultural Chemistry in Tamil Nadu Agricultural University, Coimbatore. Urease was determined by calculating µg of TPF /g/day [5]. Acid Phosphatase enzyme activity was determined using *p*-nitro phenyl phosphate as substrate colorimetrically at 410 nm [6]. The Dehydrogenase of the soil was determined as µg of NH^{4+} released /g/hr [7]. Microbial population (bacteria, fungi and actinomycetes) of soil were determined by [8] [9] [10] and [11] in cfu g^{-1} soil. Microbial biomass carbon of the soil sample was analysed by using fumigation extraction technique [12].

3. RESULTS AND DISCUSSION

3.1. Urease and Acid Phosphatase

From table 2, the values of urease activity in the soil ranged from 18.6 to 39.8 NH_4 µg/g/h with a mean value of 29.8 NH_4 µg/g/h during the *kharif* season, the higher value was recorded under T_4 cropping sequence and the lower value was recorded under T_9 cropping sequence. In *rabi* season, the values of urease activity of the soil ranged from 22.9 to 40.6 NH_4 µg/g/h with a mean value of 30.4 NH_4 µg/g/h. The higher value of urease activity present under T_4 cropping sequence and the lower present under T_9 cropping sequence. During summer season values of urease activity of the soil ranged from 16.0 to 31.1 NH_4 µg/g/h with a mean value of 24.5 NH_4 µg/g/h. The highest urease value was recorded in T_4 cropping sequence whereas the lowest value was found in T_2 cropping sequence. The inclusion of green manure crop and legume black gram in the T_4 cropping sequence may have caused the greatest urease activity to be detected. This crop may have fixed more N than in the T_9 crop. This is in line with [13]. The inclusion of readily decomposable organic materials did not hinder abiotic urease's capacity to hydrolyze urea, and thus considerably enhanced the microbiological production of urease by soil microorganisms [14].

Acid phosphatase activity of the soil samples ranged from 21.4 to 27.5 P-NP µg/g/h with a mean value of 25.1 P-NP µg/g/h during the *kharif* season, the higher value was recorded under T_4 cropping sequence and the lower value was recorded under T_2 cropping sequence. In *rabi* season, the values of acid phosphatase activity of the soil ranged from 19.2 to 33.6 NH_4 P-NP µg/g/h with a mean value of 26.3 NH_4 P-NP µg/g/h. The higher value of acid phosphatase activity present under T_4 cropping sequence and the lower present under T_2 cropping sequence. During summer season, values of acid phosphatase activity of the soil ranged from 25.5 NH_4 to 43.6 NH_4 P-NP µg/g/h with a mean value of 33.5 NH_4 P-NP µg/g/h. The highest acid phosphatase activity was recorded in T_4 cropping sequence whereas the lowest value was found in T_9 cropping sequence. Legumes in agricultural rotations may have generated more acid phosphatase enzymes than non-legume crops. Furthermore, compared to legumes and green manure crops, cereals did not require as much P for the symbiotic N fixation process [15] [16].

Table 2. Effect of various cropping sequence on Urease and Phosphatase

Cropping sequence	**Urease (NH_4 µg/g/h)**			**Acid Phosphatase (P-NP µg/g/h)**		
	Kharif	***Rabi***	**Summer**	***Kharif***	***Rabi***	**Summer**
T_1	39.8	40.6	31.1	24.2	30.1	39.3
T_2	19.9	24.0	16.0	21.4	19.2	27.8
T_3	35.3	35.1	29.5	25.6	32.4	41.9
T_4	38.4	38.7	30.2	27.5	33.6	43.6
T_5	32.1	27.5	28.3	26.9	22.5	37.4
T_6	31.7	29.2	26.9	24.7	21.7	36.1
T_7	29.2	30.4	19.7	24.5	29.8	35.5
T_8	28.0	30.8	23.6	26.7	27.3	29.0
T_9	18.6	22.9	18.1	23.9	20.8	25.5
T_{10}	25.6	25.6	21.8	25.1	25.9	27.4
Mean	29.8	30.4	24.5	25.1	26.3	33.5
SEd	0.72	0.61	0.59	0.62	0.63	0.62
CD (0.05)	1.52	1.29	1.24	1.32	1.33	1.31

3.2. Dehydrogenase and Microbial biomass carbon

From table 3, the values of dehydrogenase enzyme of the soil ranged from 21.1 to 33.6 TPF µg/g/day with a mean value of 27.9 NH_4 TPF µg/g/day during the *kharif* season, the higher value was recorded under T_4 cropping sequence and the lower value was recorded under T_8 cropping sequence. In *rabi* season, the values of dehydrogenase in the soil ranged from 42.7 to 137.9 TPF µg/g/day with a mean value of 81.3 TPF µg/g/day. The higher value of dehydrogenase activity present under T_4 cropping sequence and the lower value is present under T_2 cropping sequence. During summer season, values of dehydrogenase value in the soil ranged from 23.2 to 36.4 TPF µg/g/day with a mean value of 29.3 TPF µg/g/day. The highest dehydrogenase activity was recorded in T_4 cropping sequence whereas the lowest value was found in T_{10} cropping sequence. The activity was brought on by the presence of legume and green manure crop in the cropping sequence, which improved organic matter addition and root exudation [17]. *Rabi* season dehydrogenase levels were greater, which may be related to the increased organic matter storage caused by the cooler temperatures and favourable dehydrogenase activity-promoting conditions. Additionally, [18] noted that autumn (wet) had greater dehydrogenase activity than dry season.

In *kharif* season, microbial biomass carbon of the soil samples ranged from 223 to 279 mg kg^{-1} with a mean value of 250 mg kg^{-1}, the higher value was recorded under T_4 cropping sequence and the lower value was recorded under T_2 cropping sequence. In *rabi* season, the values microbial biomass carbon of the soil ranged from 245 to 307 mg kg^{-1} with a mean value of 273 mg kg^{-1}. The higher value of microbial biomass carbon present under T_4 cropping sequence and the lowest present under T_2 cropping sequence. During summer season, values of microbial biomass carbon of the soil ranged from 152 to 269 mg kg^{-1} with a mean value of 213 mg kg^{-1}. The highest microbial biomass carbon was recorded in T_4 cropping sequence whereas the lowest value was found in T_9 cropping sequence. Compared to other fractions of organic matter the turnover rate of soil microbial biomass carbon is rapid and higher due to microbial activity [19]. Cropping sequence had the significance impact on the soil microbial carbon.

Table 3. Effect of various cropping sequences on soil dehydrogenase activity and soil microbial biomass carbon

Cropping sequence	**Dehydrogenase (TPF µg/g/day)**			**Microbial biomass carbon (mg kg^{-1})**		
	Kharif	***Rabi***	**Summer**	***Kharif***	***Rabi***	**Summer**
T_1	23.5	50.8	24.6	237	251	189
T_2	30.4	42.7	34.6	223	245	169
T_3	32.8	112.0	33.1	241	295	254
T_4	33.6	137.0	36.4	279	307	269

T_5	28.3	74.2	32.0	265	287	237
T_6	26.2	92.4	30.1	267	278	234
T_7	29.6	89.3	27.7	259	274	222
T_8	21.1	63.0	26.9	234	256	217
T_9	24.8	44.6	25.3	243	263	152
T_{10}	28.9	106.0	23.2	253	280	195
Mean	27.9	81.3	29.3	250.1	273.6	213.8
SEd	0.59	1.34	0.45	5.15	6.09	5.44
CD (0.05)	1.24	2.83	0.96	10.81	12.79	11.42

3.4. Soil microbial population (Bacteria, fungi and actinomycetes)

From fig. 1, the bacterial population in the soil ranged from 41.1 to 50.1 cfu g^{-1} soil with a mean value of 45 cfu g^{-1} soil during the *kharif* season, the higher value was recorded under T_4 and the lower value was recorded under T_2. In *rabi* season, the values of bacterial population of the soil ranged from 43.4 to 55.6 cfu g^{-1} soil with a mean value of 49 cfu g^{-1}. The higher value of bacterial population is present under T_4 cropping sequence and the lower value present under T_2 cropping sequence**.** During summer season, values of bacterial population of the soil ranged from 39.2 to 48.7 cfu g^{-1} with a mean value of 44.8 cfu g^{-1}. The highest bacterial population was recorded in T_4 cropping sequence whereas the lowest value was found in T_8 cropping sequence. Fungal population of the soil samples ranged from 10.8 to 19.6 cfu g^{-1} with a mean value of 15.1 cfu g^{-1} during the *kharif* season, the higher value was recorded under T_4 cropping sequence and the lower value was recorded under T_2 cropping sequence. In *rabi* season, the values of fungal population of the soil ranged from 12.3 to 23.5 cfu g^{-1} with a mean value of 17.7 cfu g^{-1}. The higher value of fungal population is present under T_4 cropping sequence and the lower value present under T_2 cropping sequence. During summer season, values of fungal population of the soil ranged from 9.2 to 16.1 cfu g^{-1} with a mean value of 12.6 cfu g^{-1}. The highest fungal population was recorded in T_4 cropping sequence whereas the lowest value was found in T_9 cropping sequence. Actinomycetes population of the soil samples ranged from 33.7 to 38.5 cfu g^{-1} with a mean value of 36 cfu g^{-1} during the *kharif* season, the higher value was recorded under T_4 cropping sequence and the lower value was recorded under T_2 cropping sequence. In *rabi* season, the values of actinomycetes population of the soil ranged from 36.9 to 41.2 cfu g^{-1} with a mean value of 39 cfu g^{-1}. The higher value of actinomycetes population present under T_4 cropping sequence and the lower value is present under T_2 cropping sequence. During summer season, values of actinomycetes population of the soil ranged from 31.1 to 35.4 cfu g^{-1} with a mean value of 33.7 cfu g^{-1}. The highest actinomycetes value was recorded in T_4 cropping sequence whereas the lowest value was found in T_9 cropping sequence. In this study, the legume-dominated sequence with green manure crop had a higher microbial population than the cereal-dominated system because the former system was better for the growth and development of the soil microorganisms. This could be because bacteria and the nodules found in the roots of the leguminous crops have a symbiotic interaction. Legumes may also enhance SOC, which is good for the growth of microorganisms, and their roots produce sugar-like compounds that aid in the growth of soil bacteria in the rhizosphere [20] [21]. Legume-based cropping methods boost microbiological and enzymatic activity because they supply high-quality biomass (low C:N ratio) to the soil through active root development and exudation, nodule degeneration and leaf shedding. Different environmental conditions in the root zone are brought about by the legume systems, which have an impact on nutrient uptake and carbon exudation [22].

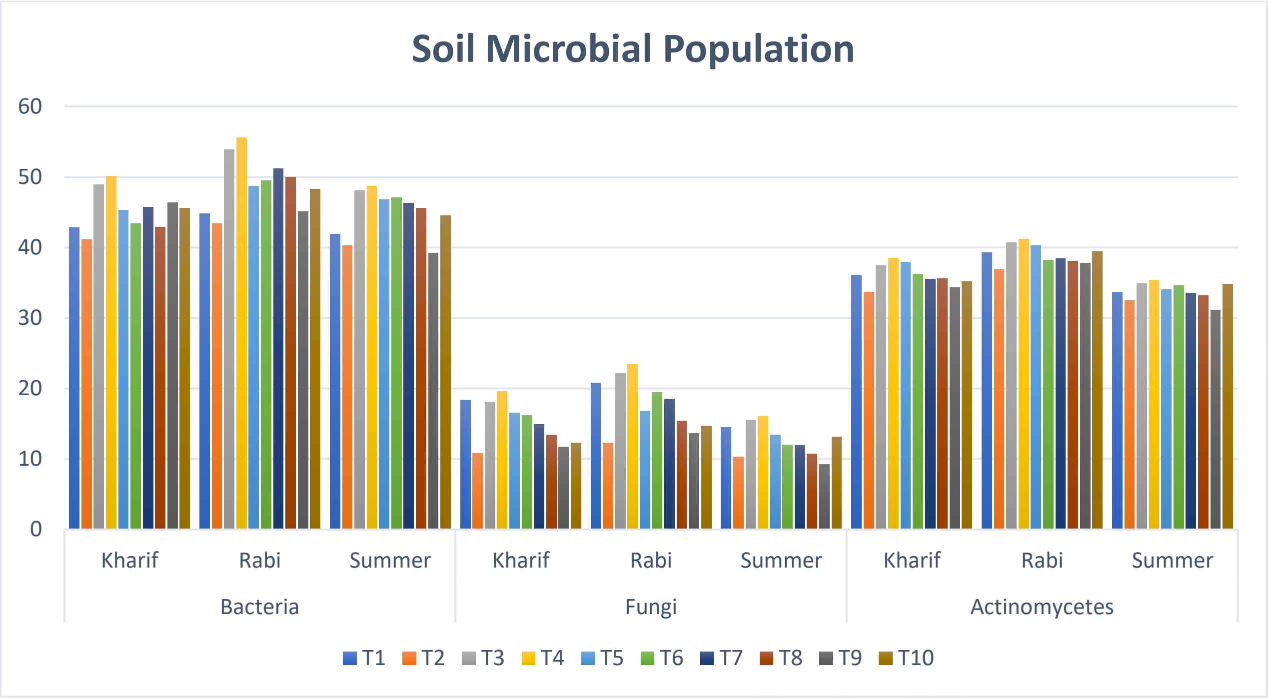

Fig. 1. Effect of various cropping sequences on soil microbial populations (bacteria, fungi and actinomycetes)

4. CONCLUSION

From the investigation, it was observed that the soil biological parameters differ significantly due to the effect of various cropping sequences. It was observed that, most of the parameters show higher values in *rabi* season than *kharif* and summer. Under various cropping sequences taken for research work, sunhemp-rice+dhaincha(10:1)-green gram cropping sequence shows higher fertility status than other cropping sequences as it contains higher biological activity and better soil properties than others due to inclusion of green manure and legume crop. The cropping system rice-rice-sesame sequence shows minimum value in most of the soil biological properties than other cropping sequence.

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