

RESEARCH PAPER

Microbial population in soil as influenced by organic and inorganic fertilizers under different cropping systems

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Studies were undertaken to evaluate the impact of application of organic and inorganic on soil microbial population under different cropping systems such as soybean-pigeonpea and sorghum-pigeonpea. After these two cycles, the soil microbial properties were significantly influenced due to various combinations of manurial treatments. The population of bacteria, fungi and actinomycetes decreased in higher proportion in control followed by farmer's practice, however, highest population of microbes was observed in the treatment receiving FYM. Fertilizer application alone showed relatively less increase in population of microbes. However, application of organics in the form of FYM, glyricidia, vermi-compost, plant and weed residues, bio-fertilizers, neem seed cake, press mud etc. helped to increase bacteria, actinomycetes, fungi and total microbes after these two cycles of cropping systems.

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INTRODUCTION

The organic material in the combination with fertilizers enhance the biological activities and in turn increase the kinetics of CO₂ evaluation, Judicious use of organic manure and fertilizers is, thus, essential to maintain soil flora for sustainable agricultural. In this present investigation, few aspect of soil biology is assessed in the presence of organic and inorganic under different cropping system such as soybean-pigeonpea and sorghum-pigeonpea.

RESEARCH METHODOLOGY

The experiment involving two cropping system were such as soybean (JS-335)-pigeonpea (BSMR-853) and sorghum (CSH-9) – pigeonpea. (BSMR-853) conducted at organic farming and Dry land Agricultural Research Farm at Vasantrao Naik Marathwada Agricultural

University, Parbhani. The field experiment were conducted for successive two years from 2003-2004 and 2004-2005. The initial soil had pH 7.80, EC 0.3 dSm⁻¹, organic carbon 4.2 g kg⁻¹, CaCO₃ 84.0 g kg⁻¹ and available N,P,K 174.52, 14.29,203.83 g kg⁻¹, respectively. The manurial treatments comprised of inorganic and organics sources such as FYM, glyricidia, vermicompost, plant and weed residues, neem seed cake, press mud, bio-fertilizers, RDF etc. which were replicated thrice in a Randomized Block Design. Soil microbial analyses were periodically carried out as per the methods given by Dhingra and Sinclair (1993).The treatment details of experiment given below as :

Treatment details :*Cropping system* :C₁ Soybean + pigeonpea (4:2)C₂ Sorghum + pigeonpea (4:2)

Fertility levels :

Treatment codes	Treatment details
T ₁	50% RDF + FYM@ 2.5t ha ⁻¹
T ₂	<i>Glyricidia</i> @ 6 t ha ⁻¹
T ₃	FYM @ 5 t ha ⁻¹
T ₄	Vermicompost @ 1 t ha ⁻¹
T ₅	Plant and weed residues (<i>in situ</i>)
T ₆	Pressmud cake @ 3 t ha ⁻¹
T ₇	Neem seed cake @ 1t ha ⁻¹
T ₈	Biofertilizer (<i>Rhizobium</i> and <i>Azotobacter</i>)
T ₉	Recommended dose of fertilizer, NPK (30:60:30)
T ₁₀	Control (No manures or fertilizers)

RESEARCH FINDINGS AND ANALYSIS

The data on bacterial population, fungal population, actinomycetes population as influenced by different manurial practices during 2003-04 and 2004-05 at both the stage of crop growth *i.e.* at flowering and harvesting stages are presented in Tables 1 to 3.

During 2003-04, at flowering and harvesting stages of soybean the beneficial bacterial population ranged from 27.67 (T₁₀) to 44.00 x 10⁵cell g⁻¹ (T₅) with a mean value of 37.57 x 10⁵ cell g⁻¹ and from 17.00 (T₁₀) to 23.33 x 10⁵ cell g⁻¹ (T₅) with a mean value of 20.27 x 10⁵cell g⁻¹, respectively. However, at flowering and harvesting stages of pigeonpea it ranged between 29.00 (T₁₀) to 44.67 x

10⁵cell g⁻¹ (T₅) with a mean value of 38.337 and from 17.33 (T₁₀) to 22.67 x 10⁵cell g⁻¹ (T₅) with a mean value of 19.80 x 10⁵cell g⁻¹, respectively.

But during 2004-05, at flowering and harvesting stages of sorghum crop, the bacterial population ranged from 29.67 (T₁₀) to 47.00 x 10⁵cell g⁻¹ (T₃) with a mean value of 40.37 x 10⁵cell g⁻¹ and from 17.00 (T₁₀) to 23.33 x 10⁵cell g⁻¹ (T₃) with a mean value of 20.56 x 10⁵cell g⁻¹, respectively. Whereas, at flowering and harvesting stages of pigeonpea the bacterial population ranged between 29.00 (T₁₀) to 44.00 x 10⁵cell g⁻¹ (T₃) with a mean value of 39.70 and from 16.33 (T₁₀) to 22.33 x 10⁵cell g⁻¹ (T₃) with a mean value of 20.33 x 10⁵cell g⁻¹, respectively.

During 2003-04 at flowering and harvesting stages of soybean, the fungal population ranged from 4.33 (T₁₀) to 6.93 x 10⁵cell g⁻¹ (T₅) with a mean value of 6.13 x 10⁵cell g⁻¹ and from 2.16 (T₁₀) to 3.90 x 10⁵cell g⁻¹ (T₅) with a mean value of 3.29 x 10⁵cell g⁻¹, respectively. However, at flowering and harvesting stages of pigeonpea, the population ranged between 4.83 (T₁₀) to 7.50 x 10⁵ cell g⁻¹ (T₅) with a mean value of 6.62 x 10⁵cell g⁻¹ and from 2.43 (T₁₀) to 3.77 x 10⁵cell g⁻¹ (T₅) with a mean value of 3.35 x 10⁵cell g⁻¹, respectively.

But during 2004-05, at flowering and harvesting stages of sorghum, crop fungal population ranged from 4.47 (T₁₀) to 7.67 x 10⁵cell g⁻¹ (T₃) with a mean value of 6.62 x 10⁵cell g⁻¹ and from 2.33 (T₁₀) to 3.80 x 10⁵cell

Treatments	2003-04				2004-05			
	Soybean		Pigeonpea		Sorghum		Pigeonpea	
	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage
T ₁	38.67	20.67	40.00	20.33	41.33	20.33	41.00	21.00
T ₂	38.67	21.67	39.67	19.33	41.00	20.67	40.67	20.33
T ₃	44.00	23.33	44.67	22.67	47.00	23.33	44.00	22.33
T ₄	40.33	21.67	43.00	21.67	43.00	22.00	42.33	21.33
T ₅	41.67	22.33	42.33	21.33	43.67	22.00	43.67	21.67
T ₆	36.67	19.33	36.67	19.00	42.00	21.33	40.00	20.33
T ₇	36.33	18.67	37.67	18.67	40.67	20.00	41.00	21.00
T ₈	40.67	20.33	40.00	19.67	42.33	21.57	42.00	21.33
T ₉	31.00	17.67	30.67	18.00	33.00	17.33	33.33	17.67
T ₁₀	27.67	17.00	29.00	17.33	29.67	17.00	29.00	16.33
Mean	37.57	20.27	38.37	19.80	40.37	20.56	39.70	20.33
S.E.±	0.84	0.50	0.61	0.40	0.73	0.47	0.78	0.37
C.D. (P=0.05)	2.48	1.49	1.80	1.18	2.17	1.38	2.31	1.09
Initial	22.00	15.00	25.00	15.33	26.00	15.20	24.00	15.50

g^{-1} (T_3) with a mean value of $3.33 \times 10^5 \text{ cell } g^{-1}$, respectively. Whereas, at flowering and harvesting stages of pigeonpea, the population ranged between 4.27 (T_{10}) to $7.43 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $6.51 \times 10^5 \text{ cell } g^{-1}$ and from 2.17 (T_{10}) to 3.73 (T_3) $\times 10^5 \text{ cell } g^{-1}$ with a mean value of $3.28 \times 10^5 \text{ cell } g^{-1}$, respectively.

During 2003-04, at flowering and harvesting stages of soybean, the actinomycetes population ranged from 9.00 (T_{10}) to $20.67 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $15.43 \times 10^5 \text{ cell } g^{-1}$ and from 5.00 (T_{10}) to $10.33 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $7.67 \times 10^5 \text{ cell } g^{-1}$, respectively. However, at flowering and harvesting stages of pigeonpea, the population ranged between 14.67 (T_{10}) to $21.67 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $18.63 \times 10^5 \text{ cell } g^{-1}$ and from 6.67 (T_{10}) to $11.00 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $9.33 \times 10^5 \text{ cell } g^{-1}$, respectively.

Actinomycetes population during 2004-05, at flowering and harvesting stages of sorghum crop ranged from 9.33 (T_{10}) to $21.00 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $17.37 \times 10^5 \text{ cell } g^{-1}$ and from 5.33 (T_{10}) to $10.33 \times 10^5 \text{ cell } g^{-1}$ (T_3) with mean value of $8.80 \times 10^5 \text{ cell } g^{-1}$, respectively. Whereas, at flowering and harvesting stages of pigeonpea, it ranged between 10.67 (T_{10}) to $21.67 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $17.93 \times 10^5 \text{ cell } g^{-1}$ and from 5.33 (T_{10}) to $11.00 \times 10^5 \text{ cell } g^{-1}$ (T_3) with a mean value of $9.10 \times 10^5 \text{ cell } g^{-1}$, respectively.

The bacterial population differs greatly due to application of organic and inorganic nutrients sources

under both cropping systems. The difference in bacterial population under various cropping systems could be attributed to differences in chemistry and biology of root rhizospheres of the respective crops. The bacterial population also differed with the stage of crop growth as well. Generally higher bacterial population was observed at flowering stage than at harvesting stage. This could be attributed to higher degree of plant metabolism activities at flowering stage, thereby, secreting higher amount of root exudates which acts as substrates to microbial population. Hence, in general, higher degree of bacterial population was observed at flowering stage than that at harvesting stage.

The data on bacterial population as influenced by organic and inorganic nutrient sources were found significant. Highest bacterial population was recorded with the treatment T_3 *i.e.* FYM @ 5 t ha^{-1} followed by T_5, T_8, T_4, T_1 and T_2 . These treatments provided sufficient organic matter which act as a substrate and sources of food for bacteria. Inorganic treatment such as T_9 recorded lower bacterial count as compared to organic sources. The lower bacterial population in inorganic treatment as in the case of T_9 could be attributed to lack of sufficient organic substrate. The role of organic matter for bacterial growth was reported by Sharma *et al.* (1987).

Mishra *et al.* (1991) found that the microbial population increased with increasing application of FYM upto 20 t ha^{-1} . Biomass was more in treatment receiving

Table 2 : Fungal population ($X \times 10^5 \text{ cells } g^{-1}$) as influenced by various organic and inorganic sources of nutrients

Treatments	2003-04				2004-05			
	Soybean		Pigeonpea		Sorghum		Pigeonpea	
	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage
T_1	6.43	3.43	6.83	3.57	7.17	3.67	7.00	3.50
T_2	6.87	3.60	7.16	3.60	7.27	3.70	7.23	3.63
T_3	6.93	3.90	7.50	3.77	7.67	3.80	7.43	3.73
T_4	6.90	3.87	7.00	3.50	6.73	3.37	7.07	3.53
T_5	6.60	3.60	7.27	3.73	7.00	3.50	6.93	3.57
T_6	6.70	3.73	7.23	3.60	7.33	3.70	7.17	3.60
T_7	6.33	3.33	6.70	3.37	6.60	3.30	6.77	3.40
T_8	5.40	2.87	6.27	3.23	6.63	3.33	6.47	3.23
T_9	4.77	2.43	5.40	2.70	5.53	2.67	4.77	2.47
T_{10}	4.33	2.16	4.83	2.43	4.47	2.23	4.27	2.17
Mean	6.13	3.29	6.62	3.35	6.62	3.33	6.51	3.28
S.E. \pm	0.10	0.11	0.17	0.07	0.14	0.07	0.12	0.07
C.D. (P=0.05)	0.28	0.33	0.51	0.21	0.42	0.20	0.36	0.21
Initial	4.00	2.00	5.00	3.10	4.00	2.10	4.20	2.10

FYM. In the study on effect of FYM which serve as a source of carbon and nutrients. Biomass recorded were bacteria from 6 to 95 x 10³ cell g⁻¹ of soil.

Hasnabade (1992) reported that the highest microbial population *viz.*, a bacteria, actinomycetes and fungi was registered in 50 % NPK + 50 % through FYM. Radha and Mallesh (1992) studied the use of chemical fertilizer and vermicompost as organic fertilizer applied to the summer crop of paddy. Vermicompost application enhanced the bacterial population *i.e.* 5.21 x 10³ cell g⁻¹ of the soil in experimental plot than control plot *i.e.* 3 x 10³ cell g⁻¹.

Chowksey (1994) reported a decline in the count of bacteria and actinomycetes with inorganic fertilizer application. The count of all the microbes was sustainably increased when inorganic was combined with organic. Suresh *et al.* (1995) reported that the application of green leaf manure (*Glyricidia speciosa*) resulted in the highest total bacterial population (42 x 10⁶ g⁻¹ soil) than with the other treatments in rice.

Manna and Hazra (1996) reported that FYM application @ 4 t ha⁻¹ increased microbial biomass in soybean -wheat cropping system. Manna and Hazra (1996) found that higher size of microbial biomass and soil respiration were recorded in the treatment 5 t ha⁻¹ cow dung slurry +50 kg P₂O₅+*Azotobacter chroococcum*.

Thakur *et al.* (1998) reported that the microbial population in the soil *viz.*, bacteria, fungi, actinomycetes

etc. were found maximum with the combined use of chemical fertilizer and organic manure (5t FYM ha⁻¹) and Shendria Sanjivani (37 kg ha⁻¹) in cotton, Sharma *et al.* (1998) reported that the microbial population was almost doubled with the balanced and integrated use of chemical fertilizers and organics than with imbalanced use of chemical fertilizers and treatments involving the use of 100 per cent NPK.

Manna and Ganguly (2001) also reported that incorporation of FYM increased the soil microbial biomass than the chemical fertilizer. Tompe and More (1996) found that the application of 15 t ha⁻¹ of PMC resulted in the highest bacteria, fungi and *Azotobacter* population whereas the recommended dose of fertilizers recorded highest actinomycetes population at all the stages of sunflower.

Patil and Varade (1998) pointed out that the available nitrogen was significantly and positively correlated with total bacterial and actinomycetes population under organic and inorganic treatment in sorghum grown on vertisol.

Fungi population was influenced by different manurial treatments and cropping systems (Table 1). The data on fungal population influenced by various cropping systems were found significant. The treatment T₃ *i.e.* FYM found maximum fungal population as compared to other cropping systems. The beneficial effect of crop residue addition to soil on increased microbial population was also reported by Tiwari *et al.* (2001).

Treatments	2003-04				2004-05			
	Soybean		Pigeonpea		Sorghum		Pigeonpea	
	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage	Flowering stage	Harvesting stage
T ₁	15.67	7.33	19.67	10.00	18.33	9.67	18.00	9.00
T ₂	12.33	5.67	20.67	10.67	19.00	9.33	21.00	10.67
T ₃	20.67	10.33	21.67	11.00	21.00	10.33	21.67	11.00
T ₄	15.67	7.67	17.67	9.00	19.00	9.33	18.67	9.33
T ₅	16.00	8.00	16.33	8.00	17.00	8.33	17.33	9.00
T ₆	15.33	8.00	17.67	9.00	17.67	8.67	17.67	9.16
T ₇	17.00	8.67	20.00	10.00	18.00	9.67	18.33	9.07
T ₈	16.67	8.33	18.00	9.00	17.00	8.67	17.33	8.93
T ₉	16.00	7.67	20.00	10.00	17.33	8.67	18.67	9.50
T ₁₀	9.00	5.00	14.67	6.67	9.33	5.33	10.67	5.33
Mean	15.43	7.67	18.63	9.33	17.37	8.80	17.93	9.10
S.E.±	0.81	0.44	1.17	0.57	0.96	0.47	0.71	0.45
C.D. (P=0.05)	2.41	1.30	3.48	1.70	2.84	1.39	2.11	1.33
Initial	8.00	4.5	14.00	6.00	9.10	5.00	10.00	5.10

The results showed maximum fungal population with treatment T₃ *i.e.* FYM @ 5 t ha⁻¹ and was almost at par with T₂, T₄, T₆ and significant higher over other treatment. Badole and More (2000) also reported that application of FYM reported in higher fungal population as compared to other organic as well as inorganic sources. Among the organic sources, performances of FYM which stimulates fungal growth were of higher order, which is mainly attributed to dead food material available from FYM. Suistova and Diuvelikawkah (1992) also reported that application of 50 t FYM ha⁻¹ promoted the bacterial, actinomycetes and fungal population in soil.

Badole and More (2000) reported that application of FYM resulted in the higher fungal population than the other organic source in cotton-groundnut cropping system.

The results on actinomycetes population showed that the influence of various cropping systems was significant. However, highest actinomycetes population was recorded in the treatment T₃ *i.e.* FYM. Sharma *et al.* (1986) also reported maximum actinomycetes population under legume rotation.

Manna and Ganguly (2001) reported that incorporation of FYM increased the soil microbial biomass than the chemical fertilizer. In soybean-wheat-fallow cropping system, application of FYM @ 8 t ha⁻¹ resulted in the highest soil microbial count than the recommended dose of fertilizers and control treatments.

The data on actinomycetes populations as affected by different manurial practices were also significant. Maximum actinomycetes population was recorded with treatment T₃ *i.e.* FYM @ 5 t ha⁻¹ followed by T₈, T₅ and T₉. The treatment receiving organic matter showed increase in actinomycetes population. Mishra *et al.* (1991) also found that microbial population increased with

increasing application of FYM upto 20 t ha⁻¹ and biomass was more in treatment receiving FYM, which serves as a sources of carbon and nutrients. Selvi *et al.* (2004) reported that amongst the microbes, bacterial population was the highest as compared to fungi and actinomycetes in soil after all crops of cropping sequence. The control showed significantly lower value of microbial count. The higher level of N as well as use of FYM produced favourable influences on soil bacteria.

Thus, it can be concluded from these research findings that application of manures in any organic sources such as FYM, glyricidia, vermi-compost, plant and weed residues, bio-fertilizers, neem seed cake, press mud or in combination with fertilizer such as T₁ enhances soil microbial population. The effect of cropping system on bacterial population was significant. The, maximum bacterial count (22.67 x 10⁵ cell g⁻¹) was recorded in cropping system sorghum + pigeonpea.

Maximum actinomycetes population (11.0 x 10⁴ cell g⁻¹) was recorded soybean + pigeonpea cropping system, but the results are statistically significant. The cropping system *i.e.* soybean + pigeonpea showed highest fungi population (3.63 x 10³ cell g⁻¹) over other cropping system.

Among different manorial treatments T₃ *i.e.* application of FYM @ 5 t ha⁻¹ resulted in maximum bacterial population (22.67 x 10⁵ cell g⁻¹), actinomycetes population (11.0 x 10⁴ cell g⁻¹) and fungi population (3.63 x 10³ cell g⁻¹), it was superior to all other treatments. Inorganic treatments *i.e.* T₉ showed lower microbial population in soil as compared to organic sources.

The manurial treatments apart from providing sources of organic carbon also helped improving soil physical properties thereby built up of soil microbial population.

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