The Pharma Innovation Journal 2022; SP-11(1): 1089-1094

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; SP-11(1): 1089-1094

www.thepharmajournal.com
Received: 28-11-2021
Accepted: 30-12-2021

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Effect of incorporation of korra (*Setaria italica*) crop residue along with microbial consortia on soil enzyme activities, microbial population, growth and yield of chickpea (*Cicer aretinum*)

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Abstract
A field experiment was conducted on clay soils of Agricultural Research Station, Amaravathi, Guntur during *rabi* 2017-18 and 2018-19 to find out the influence of crop residues on soil biological activity, growth and yield of chickpea under rainfed agro-climatic condition of Krishna zone. The korra crop residue was incorporated in soil 45 days before sowing of chickpea either alone or in combination with microbial consortia and starter dose of N and P fertilizers as decomposition accelerators. The enzyme activities and microbial populations assayed at different crop growth stages of chickpea were significantly increased by the application of crop residue along with microbial consortia. The dry matter accumulation at different stages and grain yield of chickpea were significantly influenced by the treatments. Among the treatments, the highest dry matter accumulation and grain yield of were recorded with 100 per cent RDF(20:50:0:40) and was at par with the treatment $T_{7,}$ which received crop residue @1.5 t ha^{-1} + Microbial consortium@2 kg t^{-1}+ urea 3 kg t^{-1} + SSP 15 kg t^{-1} of residue incorporated to chickpea during both the years of the experimentation.

Keywords: crop residue, microbial consortium, enzyme activities, microbial population, yield

Introduction
The widespread use of combine harvesters makes crop residues to largely remain in the field and interfere with tillage operations for the next crop. Farmers are forced to take away crop residue from field or burn it in order to take next immediate crop but they often prefer to burn the residues. In addition to environmental pollution, burning results in large losses of organic carbon and plant nutrients. Crop residues offer a sustainable, ecologically sound alternative for meeting nutrient requirement of crops. The time required for decomposition of crop residue in field conditions is usually varying as the non crop period is less between *kharif* and *rabi*. Immobilization of nutrients occurs due to incorporation of crop residue having wider C:N ratio. In rainfed ecosystem of Andhra Pradesh, korra–chickpea cropping system is gaining popularity and occupying substantial area. Utilization of crop residues for the succeeding crop in a cropping system is an alternative organic source of nutrients for sustaining soil health. The information on influence of korra crop residue in sustaining soil health is meager. Keeping this in view, the present study was conducted using korra crop residue, microbial consortium and inorganic fertilizers in chickpea crop.

Materials and Methods
Field experiments were conducted for two consecutive years to study the effect of korra crop residue incorporation along with decomposing microbial consortia and fertilizers on succeeding chickpea, during 2017-18 and 2018-19 in two different locations at Agricultural Research Station, Amaravathi. During *rabi*, 2017-18 and 2018-19, the experiment was laid out with eight treatments in RBD with three replications using the residue obtained from korra grown in *kharif* season. The biomass of korra obtained during *kharif* including stubbles were removed from field, chopped into 3 to 4 cm pieces and incorporated with rotovator to a depth of 15 cm of the soil in the field after quantification except in T_1 (control) and T_8 (RDF) treatments. Microbial Consortium consisting of decompo A and B was applied @2 kg t^{-1} of crop residue either alone or in combination with urea and single super phosphate as per the treatments.

Treatments
T1: Absolute control (No Crop residue)
T2: Crop residue @1.5 t ha^{-1} alone
T3: T2+ Microbial Consortium @2kg t^{-1} of residue
T4: T2 + urea 1.5 kg+ SSP 7.5 kg t^{-1} of residue
T5: T2 + urea 3.0 kg+ SSP 15 kg t^{-1} of residue
T6:T3 + urea 1.5 kg+ SSP 7.5 kg t^{-1} of residue
T7: T3 + urea 3.0 kg+ SSP 15 kg t^{-1} of residue
T8: RDF

Microbial consortium consists of decompo. A (fungal consortium of *Pleurotous ostreatous*, *Phanerochaete chrysosporium*, yeast &*Trichoderma*), decompo. B (bacterial consortium of *Bacillus sp*, *Lactobacillus* sp & *Pseudomonas sp*) developed at Agricultural Research Station, Amaravathi. The soil of experimental field used in both the seasons was clayey in texture, slightly alkaline in reaction, non saline, low in organic carbon and available N, medium in P_2O_5 and K_2O, sufficient in micronutrients. The soil samples collected at the time of sowing, flowering and at harvest of chick pea were assayed for enzyme activity and microbial population by following standard methods of AOAC and the initial activities are presented in Table 1.

Table 1: Initial soil properties

Soil property	2017-18	2018-19
pH	8.1	8.1
Electrical c0nductivity(dSm^{-1})	0.23	0.24
Organic carbon (%)	0.21	0.22
Urease activity(µg NH_4^+-Ng^{-1} soil h^{-1})	12.2	13.2
Dehydrogenase activity(µg TPF g^{-1}soil d^{-1})	40.0	38.0
Alkaline phosphatase activity(µg p-nitrophenol g^{-1} soil h^{-1})	80.2	76.2
Cellulase activity(µg g^{-1} soil d^{-1})	30.0	31.0
Bacteria (CFU g^{-1} soil)	8 x 10^6	7x 10^6
Fungi (CFU g^{-1} soil)	14 x 10^4	18 x 10^4
Actinobacteria (CFU g^{-1} soil)	13 x 10^5	19 x 10^5

Results and Discussion
Enzyme activity
The urease activity (Table 2) was significantly influenced by the treatments and the activity increased up to flowering and then declined at harvest during both the years of study. At sowing, treatment T_7 recorded the highest urease activity and was significantly superior to T_1, T_2 and T_8 while, at par with all other treatments. The enzyme activity at flowering stage was maximum in treatment received RDF and this was found to be comparable with T_3, T_6 and T_7 (crop residue along with microbial consortium and starter dose of N and P fertilizers) while significantly superior to others. Similar results were obtained during *rabi*, 2018-19. The mineralization of applied crop residue in the early stages of crop growth might have provided sufficient nutrients for proliferation of microbes and their activities in terms of soil enzymes. Comparable increase in urease activity was reported by Wu *et al*. (2021) [11]. At harvest the effect of treatments was non-significant.
The maximum dehydrogenase activity at all stages in both the seasons was obtained in treatment T_7 (crop residue along with microbial consortium and starter dose of N and P fertilizers) which was significantly superior to all except T_1 and T_8 in both seasons at sowing and flowering while T_1,T_2 and T_8 at harvest.
Among the treatments, the treatment T_7 which received crop residue inoculated with microbial consortium and starter dose of N and P fertilizer recorded significantly highest dehydrogenase activity while T_1 (absolute control) recorded lowest activity at all stages of crop growth during both the years of study. The treatment T_7 had improved the dehydrogenase activity over initial by 72.5 and 77.18 per cent at sowing (45 DAI) during 2017-18 and 2018-19, respectively which gradually decline when the crop attained maturity. The higher dehydrogenase activity might be due to greater availability of carbon and nutrients for microbial metabolism. Singh *et al*. (2018) [8] earlier reported similar significant improvement in enzyme activity in residue retained plots.
The alkaline phosphatase activity (Table 3) was significantly influenced by the treatments at sowing and flowering while, it was non significant at harvest of chickpea in both the years. The activity was improved at sowing (45 days after imposition of treatments) when compared to the initial activity (before imposition of treatments) in all the treatments and reached to maximum at flowering and then decreased at harvest. Among the treatments, the treatment T_3, which received crop residue and microbial consortium recorded significantly highest activity while, T_1 (absolute control) recorded the lowest activity during the year 2017-18 while T_6 which received crop residue and microbial consortium along with starter dose of N and P fertilizers recorded significantly highest activity during the year 2018-19 at sowing and flowering. At flowering (90 days after incorporation), a per cent increase in alkaline phosphatase activity of 47.96 over initial was recorded in T_3 during 2017-18 and 58.79 per cent in T_6 over initial during 2018-19. The improvement in phosphatase activity was observed even in T_1 at active crop growth stage which might be due to extraction of phosphatases by plant roots and soil organisms. The increase in activity might be attributed to stimulation of microbial activity due to enhanced resource availability. Vazquez (2000) [9] reported that the treatments with decreased phosphorus cause an overall increase in phosphatase activity in soils.
The influence of crop residue on enzyme activity was evident from the increased activity of alkaline phosphatase observed in all the treatments which received crop residue and microbial consortium along with N and P fertilizers over initial and control. Significantly higher activity of alkaline phosphatase with crop residue inoculated with microbial consortia might be due to enhanced microbial activity and diversity of phosphate solubilising bacteria. The results are in agreement with those of Wei *et al*. (2015) [10] and Zhao *et al*. (2009) [12], who also found that incorporation of crop residues increased the phosphatase, urease and invertase enzyme activity.

The cellulase activity (Table 3) was significantly influenced by the treatments and it was increased with advancement of crop growth during both the years. Among the treatments the treatment T_7, which received crop residue inoculated with microbial consortium and starter dose of N and P fertilizer recorded significantly highest cellulase activity while T_1 (absolute control) recorded the lowest activity followed by T_8 (RDF) at all stages of crop growth during both the years of study. The lowest activity in T_1 and T_8 might be due to non addition of carbon source for accumulation of cellulose in soil. The treatment T_7 had improved the cellulase activity over initial by 60.0, 66.6 and 78.9 per cent 49.45.00, 58.0 and 67.7 per cent at sowing (45 DAI), at flowering (90 DAI) and at harvest (135DAI), respectively during 2017-18 and 2018-19.Further it was observed that higher activity of cellulase was recorded in the treatments which received crop residues relative to other treatments. The treatment T_7 was on par with T_3 toT_6. The higher activity in crop residue applied treatments might be due to incorporation of cellulose into soils in the form of plant residue or synthesized by microorganisms in soils. Metabolism of all the components is integrated and interdependent, involving enzyme systems consisting of several enzymes with different catalytic activities acting together (Coughlan and Mayer (1992) [3]. The results were corroborated with the findings of Nagaraju *et al.* (2009) [6]. The improved cellulase activity promote the biodegradation of cellulose in straw and thus providing carbon as a nutrient and energy source for microorganisms. Thus, cellulase in soils is related to soil fertility and nutrient cycling.

Table 2: Effect of incorporation of korra residue on urease activity and dehydrogenase activity of soil at different crop growth stages of chickpea

Treatment details	Urease activity (µg NH_4^+ g^{-1}soil h^{-1})						Dehydrogenase activity (µg TPF g^{-1}soil d^{-1})					
	2017-18			2018-19			2017-18			2018-19		
	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (90DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (90DAI)
T_1: Absolute control	20.67	21.33	15.33	20.33	19.67	15.33	41.00	48.00	32.00	43.67	45.00	30.00
T_2: Crop residue@1.5 t ha^{-1}	22.00	21.67	17.33	21.00	21.50	16.00	57.00	53.00	34.00	57.67	52.00	32.00
T_3: T_2+MC@2 kg t^{-1} of residue	26.00	26.40	19.33	25.00	26.00	18.67	65.00	62.33	36.33	64.00	56.33	38.00
T_4: T_2+Urea 1.5kg+SSP 7.5 kg t^{-1} of residue	23.50	22.67	18.17	24.33	22.00	16.33	59.00	55.67	34.33	58.67	53.67	33.00
T_5: T_2+ Urea 3.0 kg+SSP 15 kg t^{-1} of residue	24.33	23.50	18.33	25.33	23.00	17.67	60.00	56.33	35.33	59.33	55.67	35.00
T_6: T_3+ Urea 1.5 kg+SSP 7.5 kg t^{-1} of residue	26.00	26.67	20.67	25.00	26.67	19.00	66.00	62.00	38.67	65.00	63.00	39.00
T_7: T_3+ Urea 3 kg+SSP 15 kg t^{-1} of residue	27.00	28.00	21.00	26.00	27.67	19.67	69.00	63.33	40.67	67.33	64.00	40.00
T_8: RDF(20:50:0:40)	20.33	30.00	17.00	21.00	29.67	15.67	41.33	54.00	33.00	43.00	51.00	31.00
SE(m)+	1.39	1.19	1.17	1.50	1.93	1.08	3.40	4.04	1.75	3.45	2.91	2.11
CD(0.05)	4.21	3.61	NS	4.54	5.85	NS	10.32	12.25	5.30	10.46	8.83	6.40
CV (%)	10.14	8.27	11.05	10.99	13.60	10.81	10.60	11.65	8.53	10.89	8.51	10.52

*DAI-Days after incorporation

Table 3: Effect of incorporation of korra residue on alkaline phosphatase and cellulase activity of soil at different crop growth stages of chickpea

Treatment details	Alkaline phosphatase activity((µg p-nitrophenol g^{-1} soil h^{-1})						Cellulase activity(µg g^{-1} soil d^{-1})					
	2017-18			2018-19			2017-18			2018-19		
	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (90DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (90DAI)
T_1: Absolute control	76.67	90.00	70.33	85.67	88.00	70.33	33.10	34.33	36.00	32.00	33.00	35.00
T_2: Crop residue@1.5 t ha^{-1}	80.00	99.33	79.33	88.67	96.33	73.83	38.00	39.00	41.00	36.00	37.00	39.33
T_3: T_2+MC@2 kg t^{-1} of residue	97.33	118.67	91.67	100.67	105.33	75.83	45.00	48.33	52.00	44.33	47.33	48.00
T_4: T_2+Urea 1.5kg+SSP 7.5 kg t^{-1} of residue	78.00	96.00	77.67	92.00	98.00	73.33	39.33	40.00	42.00	37.00	39.00	41.00
T_5: T_2+ Urea 3.0 kg+SSP 15 kg t^{-1} of residue	77.33	92.00	75.67	95.33	96.00	74.83	40.00	41.33	42.33	38.00	40.00	42.00
T_6: T_3+ Urea 1.5 kg+SSP 7.5 kg t^{-1} of residue	94.00	116.00	85.33	109.67	121.00	75.17	46.00	49.00	51.00	45.00	48.67	50.00
T_7: T_3+ Urea 3 kg+SSP 15 kg t^{-1} of residue	93.00	112.00	83.00	105.33	119.00	75.67	48.00	50.00	53.67	46.33	49.00	52.00
T_8: RDF(20:50:0:40)	76.67	79.00	69.00	91.67	90.33	72.67	34.00	36.33	39.00	33.00	34.33	35.00
SE(m)+	4.87	5.97	6.57	5.67	5.96	4.79	2.42	3.08	2.71	2.39	2.57	2.62
CD(0.05)	14.78	18.09	NS	17.19	18.07	NS	7.34	9.34	8.20	7.24	7.78	7.95
CV (%)	10.04	10.30	14.40	10.08	10.22	11.24	10.37	12.62	10.44	10.61	10.79	10.62

Microbial population

There was a significant improvement in the population of bacteria, fungi and actinobacteria (table 4) with the incorporation of preceding korra crop residue in chickpea at different stages of crop growth over the initial population. The bacterial population was maximum at flowering in all the treatments during both the years of study. Among the treatments significantly the highest population was recorded in T_7 treatment which received crop residue @1.5 t ha^{-1} and urea 3 kg t^{-1} +SSP 15 kg t^{-1} of residue along with microbial consortia (51 x 10^6 and 49 x 10^6 CFU g^{-1} soil, respectively during 2017-18 and 2018-19) at flowering and it is on par

with T_3 and T_6 which received crop residue along with microbial consortia consisting of *Bacillus sp*, *Lactobacillus* sp & *Pseudomonas sp.* with inorganic fertilizers. Significantly the lowest population was recorded in absolute control (T_1) (18x 10^6 and 15x 10^6 CFU g^{-1} soil respectively during 2017-18 & 2018-19 followed by T_8 which received only inorganic fertilization.

The abundance of bacterial population with crop residue incorporation along with microbial consortia might be due to changes in biochemical composition *viz*., OC, lignin, N, and hemicelluloses levels during biodegradation of incorporated residue. Addition of organic amendments in the form of crop residue enhances the microbial activity which in turn directly associated with and stimulates the indigenous soil microbial population. Moreover, improving the physical properties of soil could also make the soil environment more favourable for microbial life.

Among the treatments, significantly the highest fungal population was recorded in T_7 treatment which received crop residue @1.5 t ha^{-1} and urea 3 kg+ SSP 15 kg t^{-1} of residue along with microbial consortia (48x 10^4 and 50x 10^4 CFU g^{-1} soil during 2017-18 & 2018-19 respectively) at flowering and it was on par with T_3 and T_6 which received crop residue along with microbial consortia and microbial consortia plus inorganic fertilizers. Significantly the lowest population was recorded in case of in absolute control (T_1) (22x 10^4 and 21x 10^4 CFU g^{-1} soil) during 2017-18 and 2018-19, respectively followed by T_8, which received only inorganic fertilization. The improvement in fungal population in T_7 (crop residue@1.5 t ha^{-1} and urea 3 kg t^{-1} +SSP 15 kg t^{-1} of residue along with microbial consortia) over control (T_1) and RDF (T_8) were 54.1 and 50.0 per cent during 2017-18 and 58 and 44 per cent during 2018-19, respectively at flowering. Improvement in fungal activity in soil at different stages of crop growth might be due to incorporation of korra residue having wider C: N ratio and also inoculation of residue with fungi consisting of *Pleurotous ostreatous*, *Phanerochaete chrysosporium*, yeast and *Trichoderma.*

The actinobacterial population was increased with the stages of crop growth and maximum activity was observed at harvest in all the treatments during both the years of study. As the decaying of incorporated crop residue extended shifts occurred in the bacterial groups and the population of actinobacteria were dominant at the end of decaying process. Among the treatments significantly the highest population was recorded in T_7 treatment, which received crop residue@1.5 t ha^{-1} and urea 3 kg t^{-1} +SSP 15 kg t^{-1} of residue along with microbial consortia (38x 10^5 and 40x 10^5 CFU g^{-1} soil during 2017-18 and 2018-19 respectively at harvest) and it was on par with T_3 and T_6 which received crop residue along with microbial consortia plus inorganic fertilization. Cui *et al*. (2005) [4] and Zhong *et al.* (2020) [13] earlier reported higher microbial diversity and activity in residue retention systems with wheat straw.

Dry matter and grain yield

The dry matter production (Table 5) was significantly influenced by the treatments during both the years of experimentation. Significantly, the highest dry matter was recorded in treatment T_8 at flowering (553 and 568 kg ha^{-1} during 2017-18) and at harvest (1196 and 1182 kg ha^{-1} during 2017-18) and it was at par with T_7 at both stages during both the years. However, the treatment T_7 was on par with T_6 and T_3. The lowest dry matter was obtained in treatment T_1 (Absolute control) at flowering (400 and 407 kg ha^{-1}) and at harvest (620 and 637 kg ha^{-1}) in the both the years studied, respectively. The grain yield (Table 5) was significantly influenced by the treatments during both the years of study. The grain yield ranged from 560 to 1097 kg ha^{-1} and from 546 to 1058 kg ha^{-1}. Significantly the highest grain yield of 1097 and 1058 kg ha^{-1} in first and second years, respectively was recorded in treatment T_8 (RDF) and the lowest was recorded in T_1 (560 and 546 kg ha^{-1} during 2017-18 and 2018-19, respectively). The treatments from T_3 to T_7, which received crop residue either with microbial consortia or microbial consortia along with supplemental dose of N and P fertilizers recorded higher yields as the additional materials might have favored the mineralization process and released secondary and micronutrients along with major nutrients throughout the growth period. Incorporation of crop residue along with microbial consortium starter dose of N and P fertilization might have improved the soil health and consequently higher uptake of available nutrients from the soil and increased the yield components, morphological and physiological characteristics which ultimately attributed to increased grain yield. The results are corroborated with the findings of Abbasi *et al*. (2009) [1], Jayadeva *et al.* (2010) [5] and Pandiaraj *et al.* (2018) [7] who reported better performance of crops in residue retained plots, wheat residue incorporation and incorporation of legume residues, respectively.

Table 4: Effect of incorporation of korra residue on total micro flora of soil at different crop growth stages of chickpea

Treatment details	Total micro flora																	
	Bacteria ($\times10^6$ CFU g^{-1} soil)						Fungi ($\times10^4$ CFU g^{-1} soil)						Actinobacteria ($\times10^5$ CFU g^{-1} soil)					
	2017-18			2018-19			2017-18			2018-19			2017-18			2018-19		
	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)	Sowing (45DAI)	Flowering (90DAI)	Harvest (135DAI)
T_1: Absolute control	14	18	13	13	15	9	18	22	12	19	21	12	21	22	23	19	20	21
T_2: Crop residue@1.5 t ha^{-1}	26	28	12	30	38	12	24	29	15	24	29	13	24	25	28	25	24	26
T_3: T_2+MC@2 kg t^{-1} of residue	43	48	15	35	44	16	33	42	26	32	48	19	26	29	32	26	32	33
T_4: T_2+Urea 1.5kg+SSP 7.5 kg t^{-1} of residue	28	30	14	25	30	14	25	34	21	23	35	14	25	27	30	28	33	35
T_5: T_2+ Urea 3.0 kg+SSP 15 kg t^{-1} of residue	30	34	13	26	32	15	31	36	20	30	37	16	26	28	31	29	34	36
T_6: T_3+ Urea 1.5 kg+SSP 7.5 kg t^{-1} of residue	45	49	17	40	47	15	38	45	29	33	49	20	28	31	34	27	35	39
T_7: T_3+ Urea 3 kg+SSP 15 kg t^{-1} of residue	49	51	18	41	49	17	40	48	30	38	50	22	29	34	38	30	36	40
T_8: RDF(20:50:0:40)	17	19	14	16	17	10	20	24	14	20	28	12	22	23	24	20	21	23
SE(m)±	2.18	2.62	1.09	1.99	2.19	1.15	2.44	2.06	1.41	2.19	2.51	1.35	2.26	1.66	1.98	2.12	1.95	1.88
CD(0.05)	6.60	7.95	3.32	6.03	6.63	3.48	7.39	6.25	4.29	6.64	7.60	4.09	6.85	5.05	6.00	6.43	5.90	5.71
CV (%)	11.92	13.22	13.07	12.19	11.10	14.78	14.82	10.21	15.31	13.98	11.73	14.58	15.57	10.55	11.42	14.41	11.23	10.24

Table 5: Effect of incorporation of korra crop residue on yield of succeeding chick pea

Treatment details	2017-18			2018-19		
	Dry matter (kg ha^{-1})		Grain yield (kg ha^{-1})	Dry matter (kg ha^{-1})		Grain yield (kg ha^{-1})
	Flowering	Harvest		Flowering	Harvest	
T_1: Absolute control	400	620	560	407	637	546
T_2: Crop residue@1.5 t ha^{-1}	410	740	680	423	760	663
T_3: T_2+MC@2 kg t^{-1} of residue	464	957	860	469	934	877
T_4: T_2+Urea 1.5kg+SSP 7.5 kg t^{-1} of residue	411	783	708	457	778	690
T_5: T_2+ Urea 3.0 kg +SSP 15 kg t^{-1} of residue	412	807	720	480	800	701
T_6: T_3+ Urea 1.5 kg +SSP 7.5 kg t^{-1} of residue	470	1017	883	490	973	887
T_7: T_3+ Urea 3 kg +SSP 15 kg t^{-1} of residue	495	1063	963	511	1093	967
T_8: RDF(20:50:0:40)	553	1196	1097	568	1182	1058
SE(m)±	22.08	52.45	48.14	25.08	53.45	42.64
CD(0.05)	66.94	159.01	145.93	76.03	162.03	129.28
CV (%)	8.47	10.12	10.31	9.13	10.35	9.20

Conclusion

The enzyme activities and microbial population were higher in residue treated plots along with microbial consortium. Better soil biological activity even at harvest in residue treated soils compared to no residue treated soils as well as initial values indicated a positive influence of organics in sustaining soil health and in turn improving the productivity.

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