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Decomposition and soil biological quality under pulse-maize sequence

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Abstract

A trial was conducted in order to assess the undecomposed crop residues left after decomposition of pulses and some soil microbiological properties. A split plot design replicated thrice with three pulses and fallow was conducted during *kharif* 2017 and 2018 at Agricultural College Farm, Bapatla. Greengram and blackgram had lower values of undecomposed matter left after decomposition while soil microbial population were higher with cowpea incorporated plots during the experimental period of two years.

Keywords: Undecomposed crop residue and Soil microbial population

Introduction

Crop residues decomposition plays a decisive role in carbon cycling in terrestrial ecosystems. The content of soil organic matter in agro ecological systems would largely depend on farmer's practices particularly on crop rotations and crop residue management. Knowledge of crop residue decomposition becomes important for a sustainable management of agricultural ecosystem. Residue decomposition and release of nutrients depend on residue quality, environmental conditions and decomposing microbial communities. On the other hand, soil microbial biomass is considered to be the most important indicator of soil quality which is very much sensitive and can respond quickly to any changes in soil management. Therefore in order to assess the decomposition pattern and changes in soil microbial population a field study was conducted with three different pulses along with fallow and residue management.

Material and Methods

The study was conducted in Agricultural College Farm, Bapatla during *kharif* 2017 and 2018 in Northern block. The texture of soil was clay loam, medium in organic carbon content, low in available nitrogen, medium in phosphorus and high in potassium content with slightly alkaline condition. The experiment was conducted in split plot design with three pulses and fallow as main plots and three residue management practices as sub plots which are replicated thrice. Main plots include P₁- cowpea, P₂-blackgram, P₃-greengram and P₄-fallow while subplots include R₁- residue retained, R₂-residue incorporated and R₃-residue removed.

Determination of undecomposed crop residue

The litter bag method (Anderson and Ingram, 1993) was used to measure the decomposition of cowpea, blackgram and greengram residues. Nylon bags of 20 cm x 20 cm with 1mm thickness containing 50 g of plant sample were used to determine biomass breakdown of mulched or incorporated plant residues. The bags were buried 15 cm deep in the residue incorporated treatment and left on surface for the residue retained treatments on the same day as when the residue management were imposed. The litter bags were removed at 10 and 20 days after incorporation to determine the undecomposed residues still remaining. The percent of undecomposed crop residue from each litter bag was calculated by using the formula

$$\frac{\text{Initial weight of sample} - \text{final weight of sample}}{\text{Initial weight of sample}} \times 100$$

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Soil microbial analysis

Soil samples were collected from experimental plots for estimation of bacteria, fungi, *Azotobacter* and *Rhizobia* by using standard serial dilution plate count method. The media used for estimation are Nutrient Agar media for bacteria, Potato Dextrose Agar media for fungi, Asbhy's agar for *Azotobacter* and Yeast Extract Mannitol Agar (YEMA) with congo red for *Rhizobia*. The total bacteria, fungi, *Azotobacter* and *Rhizobia* were expressed as colony forming units per gram of soil (cfu g⁻¹).

Results and Discussion

Undecomposed crop residue percent of *kharif* pulses

The decomposition for different *kharif* pulses along with the weeds in fallow were assessed using litter bags at two different intervals one at 10 days after incorporation and another one at 20 days after incorporation of crop residues. The results over two years inferred that with increase in days of incorporation there was significant decrease in quantity of crop residues which were either incorporated or retained. However, the percentage of undecomposed crop residue during the process of decomposition did not differ with *kharif* pulses as well as with the weeds in the fallow and was found non-significant. However, numerically among the pulses, blackgram and greengram had lower values for

undecomposed matter as compared to cowpea and fallow weeds which imply that crop differ in their decomposition rates which may be attributed to the content of lignin and lignin/nitrogen ratio. Similar findings were in compliance from the experiments of Ibewiro *et al.* (2000) [5], Lupwayi *et al.* (2004) [6], Mwangi *et al.* (2013) [10], Pereira *et al.* (2016) [12] and Paul Anguria *et al.* (2017) [11].

With regard to the crop residue management, retention of residue in plots had higher values for undecomposed crop residues when compared to incorporated plots during two years of the study. Incorporated plots had 43.1 percent and 27.2 percent of undecomposed crop residue for 10 and 20 days after incorporation during the first year of study while it was 49.8 percent and 30.4 percent for 10 and 20 days after incorporation during second year of study (Table 1). The faster decomposition rates for incorporated treatments may be due to availability of more surface area for microbial activity as compared to residue retained plots which may be susceptible to varying environmental conditions than incorporated plots. Incorporation of crop residues resulted in proper mixing with the soil which had resulted in simultaneous decomposition and was in accordance with the research findings of Thonissen *et al.* (2000) [14], Arthur Alfred (2009) [2], Mulvaney *et al.* (2010) [9] and Lynch *et al.* (2016) [7].

Table 1: Undecomposed crop residue (%) of *kharif* pulses at 10 and 20 days after residue retention and incorporation by litter bag method

Treatments	2017		2018	
	Days after incorporation		Days after incorporation	
	10 days	20 days	10 days	20 days
Main plots				
P ₁ -Cowpea	52.7	41.5	31.7	24.7
P ₂ -Blackgram	44.3	33.8	31.7	22.6
P ₃ -Greengram	44.6	32.7	28.3	21.5
P ₄ -Fallow	50.6	39.0	35.6	22.2
SEm±	2.58	1.54	2.09	1.17
CD (p=0.05)	NS	NS	NS	NS
CV%	24.2	18.9	21.1	15.4
Sub-plots				
R ₁ -Residue retained	56.5	41.1	56.8	38.6
R ₂ -Residue incorporated	39.5	32.3	37.9	29.6
R ₃ -Residue removed	0	0	0	0
SEm±	0.65	0.39	0.55	0.29
CD (p=0.05)	1.9	1.2	1.7	0.9
CV%	16.8	20.5	18.3	10.8
Interaction	NS	NS	NS	NS

The interaction for different pulses along with the placement of residues did not influence the percentage of undecomposed crop residue and was non-significant during the experiment of two years.

2. Soil microbial population

The soil microbial biomass *i.e.*, bacteria, fungi, *Azotobacter* and *Rhizobium* resulted an increase in their population with inclusion of pulses in the cropping sequence from both the years of study when compared to the initial microbial counts.

The soil bacteria count at the time of incorporation was higher with cowpea (143.6 x 10⁴g⁻¹ of soil and 191.9 x 10⁴ g⁻¹ of soil) followed by greengram (129.9 x 10⁴ g⁻¹ of soil and 176.7 x 10⁴ g⁻¹ of soil) and blackgram (115.4 x 10⁴ g⁻¹ of soil and 150.0 x 10⁴ g⁻¹ of soil). However, the lower soil bacteria count was recorded with fallow plots (73.6x 10⁴ g⁻¹ of soil and 115.0 x 10⁴ g⁻¹ of soil) during two years of study represented in the Table 2 and 2a. The increase in soil bacteria in all the pulse crops when compared to fallow might be because of

modification of environment of soil by release of organic exudates from the roots of plants there by resulting a change in soil biota composition. Among the pulses, cowpea had higher values which implied that soil bacteria varied with the type of pulse crop, and cowpea due to its spreading habit provided the higher input of drymatter that might have increased the availability of carbon to the soil microorganisms.

With increase in days of incorporation of crop residues (15 days after incorporation) the soil bacterial population was also increased. Among the residue management plots, the higher values for bacteria was obtained with residue incorporated plot (142.0 x 10⁴ g⁻¹ of soil and 195.1x 10⁴ g⁻¹ of soil) followed by residue retained plots (133.7x 10⁴ g⁻¹ of soil and 180.8 x 10⁴ g⁻¹ of soil) while there was decrease in soil bacteria in residue removed plots (101.5 x 10⁴ g⁻¹ of soil and 123.3 x 10⁴ g⁻¹ of soil) over two years. The enhancement in soil microbial population from 1st day of incorporation to 15 days of incorporation might be due to the reason that all the

pulse crops maintained the source of carbon which was released slowly for consumption by the microbes when residues were either retained or incorporated. Even though there was decline in population of soil bacteria in residue removed plots, the decrease was not drastic as the organic

matter that was added during crop growth might have supported the growth of microbes and moreover the dead cells of other microbes also serve as source of carbon to the existing microbes to continue their life cycle for some more period even after removal of crop residues.

Table 2: Soil microbial population at the time of incorporation and 15 days after incorporation of *kharif* pulses during 2017

Treatments	Bacteria (10^4 g ⁻¹ of soil)		Fungi (10^3 g ⁻¹ of soil)		Azotobacter (10^4 g ⁻¹ of soil)		Rhizobium (10^4 g ⁻¹ of soil)	
	Days after incorporation		Days after incorporation		Days after incorporation		Days after incorporation	
	At the time of incorporation	15 days	At the time of incorporation	15 days	At the time of incorporation	15 days	At the time of incorporation	15 days
Main plots								
P ₁ -Cowpea	143.6	164.4	12.4	14.0	10.8	11.4	35.5	17.2
P ₂ -Blackgram	115.4	121.6	13.5	12.4	8.6	9.7	24.9	17.0
P ₃ -Greengram	129.9	136.9	10.3	13.5	10.8	11.2	26.5	16.9
P ₄ -Fallow	73.6	80.0	13.6	12.7	6.9	9.6	7.6	7.8
SEm _±	4.74	5.57	0.48	0.22	0.16	0.28	0.87	0.82
CD (p=0.05)	16.4	19.3	1.7	0.8	0.6	0.9	3.1	2.9
CV%	12.3	13.2	11.8	5.3	5.4	8.1	11.2	16.9
Sub-plots								
R ₁ -Residue retained	126.9	133.7	11.0	17.1	9.3	10.6	23.1	14.8
R ₂ -Residue incorporated	112.3	142.0	14.0	11.7	9.5	10.5	23.7	14.7
R ₃ -Residue removed	107.6	101.5	12.3	10.5	9.2	10.2	23.9	14.6
SEm _±	6.93	1.39	0.12	0.05	0.04	0.07	0.22	0.21
CD (p=0.05)	NS	4.2	NS	0.2	NS	NS	NS	NS
CV%	17.9	16.2	22.3	6.7	10.9	9.7	15.1	14.9
Interaction	NS	NS	NS	NS	NS	NS	NS	NS
Initial value before experiment	56	-	6.6	-	4.6	-	6.6	-

Table 2a: Soil microbial population at the time of incorporation and 15 days after incorporation of *kharif* pulses during 2018

Treatments	Bacteria (10^4 g ⁻¹ of soil)		Fungi (10^3 g ⁻¹ of soil)		Azotobacter (10^4 g ⁻¹ of soil)		Rhizobium (10^4 g ⁻¹ of soil)	
	Days after incorporation		Days after incorporation		Days after incorporation		Days after incorporation	
	At the time of incorporation	15 days	At the time of incorporation	15 days	At the time of incorporation	15 days	At the time of incorporation	15 days
Main plots								
P ₁ -Cowpea	191.9	212.9	14.3	15.0	13.4	14.2	41.6	18.6
P ₂ -Blackgram	150.0	154.7	11.8	13.2	11.9	13.7	24.6	14.8
P ₃ -Greengram	176.7	187.3	13.6	14.3	12.4	13.9	27	16.9
P ₄ -Fallow	115.0	110.8	10.3	12.9	8.3	9.5	7.8	6.7
SEm _±	4.61	6.59	0.60	0.51	0.67	0.76	1.97	0.88
CD (p=0.05)	15.9	22.8	2.1	NS	2.4	2.6	6.9	3.1
CV%	8.8	11.9	14.5	11.1	17.7	17.7	23.4	18.6
Sub-plots								
R ₁ -Residue retained	159.2	180.8	11.6	18.2	11.7	12.9	25.1	14.1
R ₂ -Residue incorporated	158.1	195.1	13.5	12.4	11.4	12.9	25.1	14.4
R ₃ -Residue removed	157.5	123.3	12.3	10.9	11.4	12.7	25.4	14.3
SEm _±	1.15	1.64	0.15	0.12	0.16	0.19	0.49	0.22
CD (p=0.05)	NS	4.9	NS	0.4	NS	NS	NS	NS
CV%	18.3	18.3	23.5	25.2	16.3	10.7	19.9	23.0
Interaction	NS	NS	NS	NS	NS	NS	NS	NS
Initial value before experiment	78	-	8.7	-	11.2	-	5.7	-

During first year of study, the total fungal count was higher for fallow (13.6×10^3 g⁻¹ of soil) followed by blackgram and cowpea at the time of incorporation while greengram had lower total fungal count of 10.3×10^3 g⁻¹ of soil.

However, 15 days after incorporation of crop residues during study of two years the higher total fungal count was observed for cowpea (14.0×10^3 g⁻¹ of soil and 15.0×10^3 g⁻¹ of soil), respectively. The total fungal count for greengram during 2017-18, was 13.5×10^3 g⁻¹ of soil for 15 days after incorporation and during 2018-19 the count was 13.6×10^3 g⁻¹ of soil and 14.3×10^3 g⁻¹ of soil at initial day of incorporation and 15 days after incorporation, respectively followed by blackgram (13.5×10^3 g⁻¹ of soil and 12.4×10^3 g⁻¹ of soil and 11.8×10^3 g⁻¹ of soil and 13.2×10^3 g⁻¹ of soil). The lower values were obtained with fallow for 15 days after

incorporation for the experimented two years. The changes in fungal counts might be because of the change in soil management by addition of crop residues either through incorporation or retention (Table 2 and 2a).

With advancement in days of incorporation (15 days of incorporation) the residue retained plots (17.1×10^3 g⁻¹ of soil and 18.2×10^3 g⁻¹ of soil) recorded the higher values of total fungal counts for the experimented two years followed by residue incorporated plots (11.7×10^3 g⁻¹ of soil and 12.4×10^3 g⁻¹ of soil) while residue removed plots had fungal count of 10.5×10^3 g⁻¹ of soil and 10.9×10^3 g⁻¹ of soil, respectively during both the years of study. The increased fungal count in the plots where residue were retained might be due to reduced disturbances in the soil surface which might have encouraged the establishment and activity of fungal population for

development and maintenance of hyphal networks of fungi. Fungal population are mostly responsible for the decomposition of surface placed residues and there by affecting the nutrient cycling processes (Yadvinder Singh *et al.*, 2005^[16] and Madhu Choudhary *et al.*, 2018)^[8].

The total soil *Azotobacter* was increased in cowpea plots during both the years of study followed by greengram and blackgram and the lower values were with fallow (Table 2 and 2a). 15 days after incorporation could not influence significant changes in the count of *Azotobacter* as these soil organisms are mostly involved in nitrogen fixation and not involved in any decomposition of soil organic matter.

Rhizobia which are known for biological fixation of nitrogen in association with legumes had shown increased values during both the years of the experimentation due to inclusion of pulses in the crop sequence when compared to fallow plots. The higher values were with cowpea ($35.5 \times 10^4 \text{ g}^{-1}$ of soil and $41.6 \times 10^4 \text{ g}^{-1}$ of soil) over two years of study (Table 2 and 2a). The lower values were with fallow due to lack of legumes for association. With increase in advancement of incorporation (15 days of incorporation) the soil *Rhizobium* count decreased due to removal of pulse crops.

The research findings of many researchers observed an enhancement in soil microbial biomass with inclusion of legumes in sequence and incorporation of their residues in soil which might have provided continuous carbon for the development of soil microbes as inferred by Roldan *et al.* (2003)^[13], Venkateswarlu *et al.* (2007)^[15], Fosu *et al.* (2007)^[4], Awanish Kumar *et al.* (2017)^[3], Amresh Chaudhary *et al.* (2017)^[1] and Zuber *et al.* (2018)^[17].

Conclusions

Based on the results it can be concluded that decomposition of crop residues depend upon the biochemical composition of crops and placement of crop residues. The inclusion of pulses in crop sequence lead to increase in soil microbial population when compared to initial values and the fungal colonies were higher with residue retention while bacterial count were more with incorporation of residues there by affecting the decomposition of crop residues and subsequent mineralisation and release of nutrients.

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