Long Term Resource Conservation Technologies Sustained Yield, Microbial Activities and Soil Physico-chemical Properties in Rice-green Gram Cropping System

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Abstract

Purpose

Microbial communities in rhizospheric soil play a significant role in sustaining the soil quality and also recognized as key ecological indicators to assess the soil health.

Methods

We studied the long-term effects of resource conservation technologies on functional microbial diversity and their interactions with soil biochemical properties and enzymatic activities in tropical rice-green gram cropping system. The experiment included conventional practice (CC), brown manuring (BM), green manuring (GM), wet direct drum sowing (WDS), zero tillage (ZT), green manuring-customized leaf colour chart based-N application (GM-CLCC N) and biochar (BC) treatments.

Results

The result revealed that microbial biomass nitrogen (N), carbon (C) and phosphorus (P) in GM practice increased by 23.3, 37.7 and 35.1%, respectively over CC. The Shannon index and McIntosh index were higher by 86.9% and 29.2% in GM as compared to conventional practice and significantly correlated with microbial biomass (C & P) and soil microbial populations whereas, Shannon index was positively correlated with the microbial biomass (C, N & P) and soil enzyme activities. Principal component analysis showed a significant separate cluster among the treatments amended with and without biomass addition.

Conclusions

Moreover, dominance of carbon utilizing microbes in biomass amended treatments indicated that these could supply good amount of labile carbon sources on real time basis for microbial activity. Which may protect the stable carbon fraction in soil, hence could support higher build-up of carbon in long run and could offer sustainable yield under rice-green gram soil.

Introduction

The relationships of soil microorganisms and ecosystems are highly complex. The soil biota are essential for several ecosystem functions including nutrient-cycling, biomass decomposition, soil organic matter (SOM) restoration and maintenance of plant health (Zhang et al., 2012; Dossou-Yovo et al., 2016; Dash et al., 2017; Kumar et al., 2017). However, microbial population structure and their function in soils were influenced by several environmental factors (Kibblewhite et al., 2008) and the addition of different soil amendments (Benbi et al., 2016) , which could alter the soil characteristics (Li et al., 2011; Shahid et al., 2017). Soil microbes also interact directly with soil environment as well as their extracellular enzyme activities that play a vital role in decomposition process for nutrients (carbon, nitrogen, phosphorous and sulphur) availability (Hartmann et al., 2006). These indicators suit for assessing soil microbial activities which improve the soil fertility resulting crop growth productivity (Acosta-martínez et al., 2011; Min et al., 2016).

Different resource conservation technologies (RCTs) are now being popular due to concerns about soil fertility deterioration as a consequences of exhaustive tillage practices (Ladha et al., 2003). Resource conservation practices like zero tillage; biomass retention etc. have minimized soil erosion, enhanced nutrient conservation and fetched low economic input (Lal, 2004). The researchers are also assessing the economic turn outs different nutrient management practices and tillage operations under RCTs to understand the behaviour of soil biochemical properties. However, such nutrient management in resource conservation practices affect soil microbial diversities both structural and functional and thereby influence the soil biochemical properties (Cookson et al., 2007).

Applications of chemicals and fertilizers affect the soil biota and their functions (Anderson, 2003; Weber et al., 2008; Su et al., 2015; Kumar et al., 2017; Shahid et al., 2017). The direct effects include shift in soil pH and heavy metals accumulation which negatively impacted the soil microbiota (Zhang et al., 2012; Turner et al., 2013; Chen et al., 2016). The indirect effects through stimulation of the soil microbiota activity and of crop growth due to higher residues inputs and rhizo-depositions to soil (Su et al., 2015; Tang et al., 2016). Studies conducted under different climatic regimes have shown that the extracellular enzymatic activities respond towards minimum modifications in the environmental conditions and organic and mineral fertilization management practices, tillage operations and applications of pesticides and herbicides (Tejada et al., 2008; E. Liu et al., 2014; Jacobsen and Hjelmsø, 2014; Wezel et al., 2014). The β -glucosidase is an important soil quality indicator used to evaluate the impacts of different cultural practices on physicochemical properties and organic matter stabilization in soil (García-Gil et al., 2000; Badiane et al., 2001). Other enzymes like dehydrogenase, fluorescein di-acetate, urease, cellulase etc. are also good indicators of soil fertility (Wanjiru et al., 2015; Tautges et al., 2016).

Long-term resource conservation practices are valuable for residue management and evaluation the residual effects of tillage on soil microbial diversities (both structural and functional) (Lienhard et al., 2013; Pandey et al., 2014). Long-term application of soil amendments (both inorganic and organic) affect the soil microbial communities in different agro-ecosystems (Zhong and Cai, 2007; Baudoin et al., 2009; Wanjiru et al., 2015). Profiling of different carbon source utilization by groups of soil microbes under different fertilization treatments can be significantly generated by using Biolog eco- plates (Kumar et al., 2017). Some researchers reported that measurement of soil microbial diversity through Biolog alone is not a valid method (Zhou et al., 2008; Tan et al., 2013), however, it gives the indication towards functional microbial diversity.

Rice-green gram system is a widely practiced cropping system in India (Raja et al., 2015; Shahid et al., 2017) however, information on long-term effect of resource conservation practices involving different sources of organic matter and methods of incorporation into the soil in rice-green gram cropping system are lacking. Further, the effect of rice-green gram system on soil fertility due to temporal shifts of functional microbial diversity in rhizospheric soil is also limited. Hence, the objectives of the study were formulated to find out the effects of resource conservation technologies on (i) soil chemical and biological

properties, and changes of functional diversity of soil microbial communities and (ii) to study the relationship among microbial biomass (C, N & P), and soil enzymes in rice-green gram system.

Materials And Methods

Experimental setup

The study area of the long-term resource conservation technology was situated at ICAR-National Rice Research Institute (NRRI), Cuttack (20° 44' N, 85° 94' E) and continuously practiced for five years. The climate of this area has sub-humid tropical. The annual mean precipitation is around 1500 mm; occurred during the month of June-September and the minimum and maximum mean annual temperatures were 22.5 °C and 39.2 °C, respectively. The soils of the experimental field were classified as 'Aeric Endoaquept' having a sandy clay loam texture (17% silt, 30% clay and 56% sand). Some of the initial characteristics of the surface soil (0–15 cm) were as follows: pH was 6.6 (using soil: water suspension, 1:2.5); electrical conductivity (EC) 0.49 dS m⁻¹; bulk density 1.40 Mg m⁻³; total organic C 6.7 g Kg⁻¹; available P 22.8 mg Kg⁻¹; and available K 265 mg Kg⁻¹; respectively.

The study was conducted during dry season of 2016-17 in the long-term experiment of resource conservation technologies which has been initiated in 2012. There were total seven (7) treatments and arranged in a completely randomized block design (CRBD). The treatments were conventional practice (CC), brown manuring (BM), green manuring (GM), wet direct drum sowing (WDS), zero tillage (ZT), green manuring + CLCC-N (GM-CLCC N) and biochar (BC) application, which were replicated thrice (experimental details are given in Table 1). Rice-rice system was followed for initial two years (2012-2014) and then rice-green gram system for three years (2014-17). In our experiment, rice and green gram; varieties were Pooja and Samrat, respectively. The line × plant spacing was 20 × 15 cm in rice and 30 × 10 cm in green gram. The recommended dose of fertilizer (RDF) for N: P₂O₅: K₂O were at the rate of 80: 40: 40 kg ha⁻¹ for

Table 1 Treatment details of the resource conservation experiment

Treatments	Practice Followed	
	Wet Season	Dry Season (Green gram)
Conventional Control (CC)	Manual wet direct sowing + Manual weeding + 100% RDF + Manual harvesting	Conventional tillage + Line sowing + Manual weeding
Brown Manuring (BM)	Dry direct sowing + Inter cropping <i>Sesbania aculeata</i> and knocking down of by 2,4-D at 25 days after sowing + 75% N + mechanical weeding + mechanical harvesting	Conventional tillage + Line sowing + Manual weeding
Green Manuring (GM)	Dry direct sowing + Inter cropping <i>Sesbania aculeata</i> and incorporation through cono-weeder at 25 days after sowing + 75% N + mechanical weeding + mechanical harvesting	Conventional tillage + Line sowing + Manual weeding
Wet Drum Seeding (WDS)	Wet direct sowing by drum seeder + mechanical weeding + 100% RDF + Mechanical harvesting	Conventional tillage + Line sowing + Manual weeding
Zero Tillage (ZT)	Zero tilled dry direct sowing + Residue retention (20 cm above the ground) + 75% N+ Chemical weeding + Manual harvesting	Zero tillage + Line sowing+ chemical weeding
Green Manuring-CLCC-N (GM-CLCC-N)	Paired row dry direct sowing rice with seed drill with one row <i>Sesbania aculeata</i> intercropping and incorporation at 25 days through cono-weeder) + 75% N+ customized leaf colour chart based N management + mechanical weeding + Mechanical harvesting	Conventional tillage + Line sowing + Manual weeding
Biochar (BC)	Wet direct sowing by drum seeder + biochar (5 t/ ha) + 100% RDF + mechanical weeding + Mechanical harvesting	Conventional tillage + Line sowing + Manual weeding

wet-season rice and 20: 40: 20 kg ha⁻¹ for dry-season green gram, respectively. The nitrogen (N) was given as neem coated urea in three splits, i.e. half (50%) at basal and rest (25%) each at two top dressings to rice. However, the entire N fertilizer was applied in green gram as basal dose. The single superphosphate (SSP) and muriate of potash (KCl) was applied as phosphorus and potassium fertilizer, respectively only as basal dose. Under green and brown manuring treatments, 25% less of nitrogen fertilizer was given in the wet season of rice. At the rate of 25 kg ha⁻¹, *Sesbania aculeata* was sown for both the treatments. The 25 days old *Sesbania aculeata* were knocked down in green manuring treatments by using cono-weeder; however, in brown manuring treatment, *Sesbania* was killed with the help of 2, 4-D. The real time N-management was done with the help of customized leaf colour chart (CLCC). In biochar treatment at the beginning of the experiment, rice husk biochar was applied at 5 t ha⁻¹. The biochar was prepared by the process of pyrolysis at high temperature (300°C) for 6 h. During wet season, check-basin irrigation method was followed and irrigation was given at every 3 to 5 days of interval to maintain water level up to 5±2 cm, whereas, irrigation was applied only at flowering stage of green gram in the dry-season. Apart from this, for weeds, insects and diseases control the standard recommended protocol were followed.

Soil sample collection and analyses

The soil samples were collected during dry season of 2016-17 after harvesting of the crop (green gram) at four places randomly from each treatment at 0-15 cm depth by using sample probe. The soil collected was mixed thoroughly and homogenize properly to prepare the composite soil for all the treatments separately. One set of fresh soil samples which was used for biochemical as well as microbial analysis were kept at 4 °C in refrigerator, and rest portion of the soil soil was air dried in shade for 7 days and then processed, through 2 mm sieve and stored in seal container for further analysis.

Soil physico-chemical properties

Soil pH (soil: water::1: 2.5) and electrical conductivity (EC) were analysed in soil with water suspension and soil saturation extract, respectively by using standard methods. Total organic carbon was estimated by potassium dichromate ($K_2Cr_2O_7$) along with sulphuric acid (H_2SO_4) and 85% o-phosphoric acid (H_3PO_4) digestion mixture with a ratio of 3:2 by wet digestion method in a digestion block set for 2h at 120 °C temperature (Snyder and Trofymow, 1984). Available nitrogen (AN) (Hati et al., 2008), available phosphorus (AP) (Bray R.H and Kurtz L.T, 1945) and available potassium (AK) (Hati et al., 2007) were analysed using standard methods.

Biological properties of soil

Soil microbial biomass carbon (MBC) was estimated by using chloroform fumigation-extraction method in which, one set of soil sample was fumigated in vacuum desiccator while other was kept un-fumigated (Witt et al., 2000). Microbial biomass nitrogen (MBN) was analysed following the method of Ross, 1990. Dehydrogenase (DHA) activity was estimated by the formation of 2,3,5-triphenylformazan (TPF) as a result of the reduction of 2, 3, 5-triphenyltetrazolium chloride (TTC) (Casida et al., 1964). Fluorescein di-acetate (FDA) hydrolysis and β -glucosidase activities were measured by following the method of Adam and Duncan, 2001 and Eivazi and Tabatabai, 1988, respectively. Urease activity was estimated by following the method of P. Bhattacharyya et al., 2012. The C and N mineralization were determined by incubating the soil samples for one month. After incubation the C mineralization (C_{min}) was estimated followed by alkali traps method (Mohanty et al., 2013). However, for N mineralization (N_{min}), the mineral N (both NH_4 -N and NO_3 -N) was determined by extraction with 2 M KCl of the incubated soil samples (Abera et al., 2012). Finally, the net N and C mineralization were estimated and the cumulative N_{min} and C_{min} were determined. The aerobic heterotrophic bacterial, fungal and actinomycetes populations were enumerated by adopting the procedure of (Kumar et al., 2017).

Soil microbial community and functional diversity

Soil microbial activity and diversity in the rhizospheric soil was investigated by using Biolog plates (Biolog Inc., CA, USA). Biolog plate consists of 96 wells consisted of one control along with 31 different carbon sources with three replications each. Equivalent to 10 g dry weight of fresh soil sample was taken in a 250 ml conical flask, then 100 ml of distilled water was added and put it in a shaker for 30 minutes at 250 rpm. Then the soil suspension was diluted to 10^{-3} and 150 μ L of this final suspension was inoculated in a Biolog plate and incubated at 25 °C. After incubation of 0, 24, 48, 72, 96 and 120 h, carbon utilization by the microbial community by taking the absorbance of each well at 590 nm. The data were recorded using Microlog 4.01 and to assess total microbial activity the average well color development (AWCD) of the all carbon sources was measured as:

$$AWCD = [\Sigma(C - R)]/31] \dots\dots\dots (i)$$

Where, C and R refer to the optical density (OD) value of the reaction wells and control well, respectively (Li et al., 2012). The AWCD reflects the overall utilization of different carbon sources by the soil microbial community (Choi and Dobbs, 1999).

Functional diversity analysis by utilizing different carbon sources

The McIntosh (U) and Shannon-Weaver (H) indices were estimated from absorbance of the Biolog eco-plates that express the functional microbial diversity of soil. The Shannon-Weaver index is sensitive to the species richness of the microbial diversity and it is calculated by the formula:

$$H = -\sum p_i \ln p_i \dots\dots\dots (ii)$$

" p_i refers to the ratio of relative absorbance (C-R) of i^{th} well to the sum of relative OD values of all the wells.

Similarly, McIntosh index is the measurements of species evenness of the microbial community and it was quantified by using following formula.

$$U = \sqrt{\sum (n_i)^2} \dots\dots\dots (iii)$$

n_i , refers to the relative OD for each of the carbon source wells by subtracting the OD value of control well (Guanghua et al., 2008; An et al., 2014).

Relative yield

Relative yield was calculated from mean seasonal rice and rice equivalent (green gram) yields, which was expressed as $Mg\ ha^{-1}$.

Rice equivalent yield (REY):

The equivalent yield was estimated in kharif crop (rice) by using the equation.

$$REY = \frac{Yield\ of\ green\ gram \times MSP\ of\ green\ gram}{MSP\ of\ rice} \dots\dots\dots (iv)$$

Where, MSP= minimum support price.

Statistical analysis

Analysis of variance (ANOVA) of individual character and means were compared with DMRT at significant level ($p \leq 0.05$) was done by online software version OP STAT. The microbial biomass and activities were analysed by using the coordinate of the points obtained by the principal component analysis (PCA) method in two ways ANOVA. The OD values taken from the Biolog eco-plates of 31 different carbon sources utilization were used to perform the analysis. Multi-element vectors describing the metabolism of microbial communities were obtained from the PCA analysis. The six major carbon classes were made by using 31 kind of different C sources, then the AWCD values of six major classes of carbon sources were normalized in Microsoft excels and analysed by ANOVA and PCA using the SAS (9.2) software.

Results

Relative yield

Relative yield of the experiment was found in the range of 4.19-4.95 Mg ha⁻¹ and it was significantly more under green manuring (GM; 4.95 Mg ha⁻¹) and lowest under biochar (BC) treatment (4.19 Mg ha⁻¹) (Fig. 1).

Soil physico-chemical and biological activities

Soil physico-chemical as well as biological properties were influenced by different resource conservation practices. The pH of the soils in different treatments ranged from 6.6 to 6.8 and was found to be non-significant. Electrical conductance (EC) was varied from 0.46 to 0.48 dS m⁻¹ among the treatments. Total organic carbon was ranged from 6.8 to 8.7 g Kg⁻¹ and was significantly higher under zero tillage practice compared to others. Highest available N content was also recorded under green manuring (326.1 kg ha⁻¹), followed by biochar and brown manuring treatments. Similarly, highest available phosphorous (P) and potassium (K) contents were recorded under green manuring, followed by zero tillage and brown manuring treatments.

Microbial biomass carbon was in the range of 157.1 µg g⁻¹ in control to 252.3 µg g⁻¹ in green manuring treatments, whereas, MBN and MBP in the resultant soils were ranged from 24.5 µg g⁻¹ to 31.9 µg g⁻¹ and 12.8 µg g⁻¹ to 19.7 µg g⁻¹, respectively. The MBC, MBN and MBP were significantly more in green manuring amended plots compared to other treatments, however, significantly lower value of these parameters was found in control treatment. The activity of cellulase was varied in the range of 0.31 to 0.98 µg glucose g⁻¹ d⁻¹. The C_{min} and N_{min} were significantly more in plots treated with green manure than other treatments (Table 2). The content of dehydrogenase activity (DHA), fluorescein di-acetate activity (FDA), β-glucosidase activity, urease activity was found significantly higher in all resource conservation treatments as compared to control, while the highest activity was observed in green manuring treatment (Table 3). Similarly, cellulase, invertase and xylanase activities of soil were also significantly higher under all resource conservation treatments as compared to control, however, the higher activity was observed in zero tillage treatment (Table 3). Among different conservation treatments, the population of aerobic heterotrophic bacteria, fungi and actinomycetes were varied from 6.78 to 6.92 log CFU g⁻¹, 4.55 to 4.75 log CFU g⁻¹, 4.47 to 4.72 log CFU g⁻¹, respectively (Table 3). And the, green manuring treatment recorded the significantly ($p \leq 0.05$) higher population of these microbes.

Table 2 Soil physico-chemical properties under different resource conservation practices.

Treatment	pH	EC	TOC	AN	AP	AK	MBC	MBN	MBP	C _{min}	N _{min}
		(ds m ⁻¹)	(g kg ⁻¹)	(kg ha ⁻¹)	(kg ha ⁻¹)	(kg ha ⁻¹)	(µg C g ⁻¹)	(µg N g ⁻¹)	(µg P g ⁻¹)	(µg C g ⁻¹)	(µg N g ⁻¹)
CC	6.6 ^{ns}	0.46 ^a	6.8 ^f	238.3 ^e	25.6 ^b	175.5 ^b	157.1 ^d	24.5 ^d	12.8 ^e	891.8 ^b	98.3d
BM	6.7 ^{ns}	0.48 ^a	7.5 ^d	301.1 ^b	31.9 ^a	218.4 ^a	222.2 ^b	29.5 ^b	17.3 ^b	926.8 ^a	117.6b
GM	6.8 ^{ns}	0.49 ^a	8.4 ^b	326.1 ^a	34.9 ^a	238.9 ^a	252.3 ^a	31.9 ^a	19.7 ^a	935.2 ^a	123.1a
WDS	6.6 ^{ns}	0.48 ^a	6.9 ^e	250.1 ^d	25.3 ^b	173.6 ^b	168.0 ^d	24.2 ^d	13.8 ^d	820.4 ^c	84.5e
ZT	6.8 ^{ns}	0.49 ^a	8.7 ^a	275.1 ^c	33.5 ^a	229.6 ^a	190.2 ^c	27.0 ^c	15.6 ^c	800.8 ^d	76.0f
G M-CLCC-N	6.7 ^{ns}	0.47 ^a	8.1 ^c	292.7 ^b	33.0 ^a	225.9 ^a	213.0 ^b	31.1 ^a	16.9 ^b	896.0 ^b	105.7c
BC	6.7 ^{ns}	0.46 ^a	7.4 ^d	322.0 ^a	26.2 ^b	179.2 ^b	241.6 ^a	25.8 ^{cd}	14.1 ^{cd}	830.2 ^c	93.5d

† Different characters in a single column indicate significant difference between the treatments at $p \leq 0.05$.

[CC: conventional control; BM: brown manuring; GM: green manuring; WDS: wet drum seeding; ZT: zero tillage; GM-CLCC-N: green manuring-customized leaf color Chart based Nitrogen; BC: biochar; EC: electrical conductance; TOC: total organic carbon; AN, AP, AK: available nitrogen, phosphorus and potassium; MBC: microbial biomass carbon; MBN: microbial biomass nitrogen; MBP: microbial biomass phosphorus; C_{min}: carbon mineralization; N_{min}: nitrogen mineralization]

Table 3 Soil Biological properties under different resource conservation practices.

Treatment	DHA	FDA	β -glucosidase	Urease	Cellulase	Invertase	Xylanase	Heterotrophs	Fungus	Actinomycetes
	($\mu\text{g g}^{-1} \text{d}^{-1}$)	($\mu\text{g g}^{-1} \text{d}^{-1}$)	($\mu\text{g g}^{-1} \text{d}^{-1}$)	($\mu\text{g g}^{-1} \text{d}^{-1}$)	($\mu\text{g g}^{-1} \text{d}^{-1}$)	($\mu\text{g g}^{-1} \text{d}^{-1}$)	($\mu\text{g g}^{-1} \text{d}^{-1}$)	(Log cfu g ⁻¹)	(Log cfu g ⁻¹)	(Log cfu g ⁻¹)
CC	226.8 ^f	83.1 ^e	49.8 ^e	149.0 ^e	0.31 ^g	1.73 ^d	1.17 ^d	6.78 ^d	4.52 ^{cd}	4.47 ^c
BM	294.6 ^c	93.0 ^c	55.2 ^c	163.1 ^c	0.63 ^d	2.17 ^c	1.50 ^c	6.83b ^c	4.59 ^b	4.55 ^{bc}
GM	371.5 ^a	109.1 ^a	64.0 ^a	186.2 ^a	0.89 ^b	2.40 ^a	1.67 ^b	6.92 ^a	4.75 ^a	4.72 ^a
WDS	254.7 ^e	87.6 ^d	52.2 ^d	155.1 ^d	0.39 ^f	1.83 ^d	1.23 ^d	6.79 ^c	4.54 ^d	4.49 ^{bc}
ZT	275.8 ^d	78.1 ^f	47.0 ^f	141.5 ^f	0.98 ^a	2.50 ^a	1.80 ^a	6.84 ^b	4.63 ^b	4.59 ^b
G M-CLCC-N	314.2 ^b	102.3 ^b	60.3 ^b	176.6 ^b	0.84 ^c	2.37 ^b	1.67 ^b	6.90 ^a	4.72 ^a	4.69 ^a
BC	258.6 ^e	90.0 ^d	53.7 ^{cd}	159.0 ^d	0.56 ^e	2.07 ^c	1.43 ^c	6.82 ^{bc}	4.59 ^b	4.54 ^{bc}

† Different characters in a single column indicate significant difference between the treatments at $p \leq 0.05$.

[CC: conventional control; BM: brown manuring; GM: green manuring; WDS: wet drum seeding; ZT: zero tillage; GM-CLCC-N: green manuring-customized leaf color Chart based Nitrogen; BC: biochar; DHA: dehydrogenase activity; FDA: fluorescein di-acetate activity]

Average well color development by using Biolog eco-plates

Average well color development showed differences in the metabolic reaction rate of microbial communities among resource conservation treatments. The development of colour based an average utilization of carbon sources using Biolog eco-plates usually showed an S-shaped pattern in relation to time during the 120h incubation-period (Fig. 2). For the duration of incubation, different sources of carbon mineralization by microbes were significantly higher in green manuring (GM) than other treatments irrespective of the duration of incubation. The AWCD values in control (CC) were the lowest while under green manuring; the values were found to be highest in all the incubation periods (Fig. 2).

The rate of change in microbial metabolic activities was observed maximum at 48 h of incubation and in the order of GM > BM > ZT > WDS > GM + CLCC-N > CC > BC. After 48 h, the metabolic activities of all the treatments were reduced significantly, while, the rate of microbial activities were enhanced in all treatments up to 96 h of incubation and then decreased gradually (Fig. 3).

The AWCD value observed at 72 h of incubation was also higher (26.6%) in green manuring treatment than others. The Shannon index has shown a significantly higher values in GM by 86.9% as compared to the control treatment and the lowest was recorded under WDS treatment. The McIntosh index determined from the 72 h incubation period of Biolog® data was also higher in GM by 29.2% than that of control. The AWCD, Shannon index and McIntosh indices indicated a significantly higher microbial activity under GM compared to the RCTs and control (Table 4).

Table 4 The average well colour development (AWCD) and diversity indices of microbial communities (based on 72 h data from biolog analysis) of the soil under resource conservation.

Treatment	AWCD	Shannon Index	McIntosh index
CC	0.88 ^c	0.35 ^e	5.62 ^e
BM	1.10 ^{ab}	1.64 ^c	7.28 ^b
GM	1.20 ^a	2.70 ^a	7.94 ^a
WDS	0.89 ^c	0.58 ^e	6.29 ^d
ZT	1.01 ^b	1.29 ^d	6.95 ^c
G M-CLCC-N	1.17 ^{ab}	2.23 ^b	7.80 ^a
BC	0.95 ^b	1.21 ^d	6.94 ^c

† Different characters in a single column indicate significant difference between the treatments at $p \leq 0.05$.

[CC: conventional control; BM: brown manuring; GM: green manuring; WDS: wet drum seeding; ZT: zero tillage; GM-CLCC-N: green manuring-customized leaf color Chart based Nitrogen; BC: biochar; AWCD: average well color development]

Utilization of six major carbon substrates under different resource conservation practices

Use of six major carbon sources such as carboxylic acids (CA), carbohydrates (CB), phenolic compounds (PC), amino acids (AA), polymers (PO), and amines (AM) showed large variations under different resource conservation treatments. Carboxylic acids (CA), carbohydrates (CB) and amino acids (AA) utilization

was higher in green manuring (GM) followed by GM-CLCC-N treatment and lowest in control. However, relative stable C compounds like, amines (AM), phenolic compounds (PC) and polymers (PO) utilization were found higher in control treatment followed by WDS, ZT and BC (Fig. 4).

The amines and amino acid utilizing microbes were dominant in all the treatments under resource conservation (Fig. 4). The consumption of carbohydrates and carboxylic acids were found to be highest in CC and BM, respectively, whereas BM showed the highest consumption of amines and GM towards amino acids. However, there was no significant difference among all the treatments in the consumption of phenolic compounds and polymers (Fig. 4).

Principal component coupled with biplot analysis

Biplot analysis of seven treatments showed different spatial distribution on the coordinate axis. The corresponding projective points indicate that the BM, GM-CLCC-N treatment plots were in one quadrant and showed significantly utilization of amines (AM). Similarly, GM, ZT in another quadrant which gives strong response to amino acids (AA). Biochar detached from all the treatments, occupied a separate quadrant and gives strong response to carboxylic acids (CA).

WDS and CC inhabited in same quadrant, which showed significant utilization of carbohydrates (CB), phenolic compounds (PC) and polymers (PO) (Fig. 5 A). Similarly, biplot analysis of six major groups of specific kinds of carbon sources, such as carboxylic acid; amino acids; amines; carbohydrates, phenolic compounds and polymers were laid at the 1st, 2nd, 3rd and 4th quadrant, respectively (Fig. 5 A).

PCA was applied to the dataset consisting of seven treatments (BM, BC, CC, GM, GM-CLCC N, WDS and ZT) in three replications having a total of thirty parameters. As shown in Fig. 5 B. PCA explained a total variance of 65% with PC1 contributing to 51.7% and PC2 contributing to 13.3% respectively. The seven treatments has been found to aggregate into definite clusters displayed as elliptical circles over the ordination planes, with the larger symbols in centre of each ellipse representing the mean of three replications. In the first (+/+) quadrant GM-CLCC N and GM treatments are found, in the second (+/-) quadrant ZT treatment is found, in the third quadrant (-/-) BC is found along with WDS treatment and in the fourth quadrant (-/+) CC is found with WDS but having less interaction as compared to BC. The first dimension PC1 could explain the variances of four treatments with GM showing maximum variances followed by CC, WDS and GM-CLCCN. Similarly, the second dimension PC2 could explain the maximum variances of only one treatment ZT. The other two treatments BM and BC had less contribution on overall variances represented by PCA. Contribution (coefficient values given in parenthesis) of the parameters were higher in DHA (0.915), A (0.912), F (0.910), MBN (0.905), H (0.903), MBP (0.886). As shown in the PCA ordination biplot, it could be inferred these highly correlated parameters to be chiefly associated with GM and GM-CLCC N. The parameters CL (0.849), IN (0.815), XY (0.812), MI (0.808), TOC (0.799), AP (0.783), PC (0.741), PO (0.739), AWCD (0.733), AK (0.726) variances was found to be attributed the ZT treatment. MBC (0.723), AN (0.715), FDA (0.723), BG (0.704), UR (0.703) demonstrated lesser variances and from the ordination biplot could be attributed to GM and GM-CLCCN treatments. The treatments CB (-0.405), AA (-0.606) and SI (-0.648) showed negative correlation with GM and GM-CLCC N treatments, however was positively correlated with CC treatment followed by WDS. In the second dimension PC2, the components NM (0.730) and CM (0.72b) showed the highest contribution which can be attributed to GM and GM-CLCC N treatments. The parameters CA (0.450), EC (0.396) were found to have very low correlation coefficient in first dimension PC1, whose contribution increased in third dimension (0.730). However, only the first two dimensions were taken for analysis.

Principal component coupled with biplot analysis

Biplot analysis of seven treatments showed different spatial distribution on the coordinate axis. The corresponding projective points indicate that the BM, GM-CLCC-N treatment plots were in one quadrant and showed significantly utilization of amines (AM). Similarly, GM, ZT in another quadrant which gives strong response to amino acids (AA). Biochar detached from all the treatments, occupied a separate quadrant and gives strong response to carboxylic acids (CA).

WDS and CC inhabited in same quadrant, which showed significant utilization of carbohydrates (CB), phenolic compounds (PC) and polymers (PO) (Fig. 5 A). Similarly, biplot analysis of six major groups of specific kinds of carbon sources, such as carboxylic acid; amino acids; amines; carbohydrates, phenolic compounds and polymers were laid at the 1st, 2nd, 3rd and 4th quadrant, respectively (Fig. 5 A).

PCA was applied to the dataset consisting of seven treatments (BM, BC, CC, GM, GM-CLCC N, WDS and ZT) in three replications having a total of thirty parameters. As shown in Fig. 5 B. PCA explained a total variance of 65% with PC1 contributing to 51.7% and PC2 contributing to 13.3% respectively. The seven treatments has been found to aggregate into definite clusters displayed as elliptical circles over the ordination planes, with the larger symbols in centre of each ellipse representing the mean of three replications. In the first (+/+) quadrant GM-CLCC N and GM treatments are found, in the second (+/-) quadrant ZT treatment is found, in the third quadrant (-/-) BC is found along with WDS treatment and in the fourth quadrant (-/+) CC is found with WDS but having less interaction as compared to BC. The first dimension PC1 could explain the variances of four treatments with GM showing maximum variances followed by CC, WDS and GM-CLCCN. Similarly, the second dimension PC2 could explain the maximum variances of only one treatment ZT. The other two treatments BM and BC had less contribution on overall variances represented by PCA. Contribution (coefficient values given in parenthesis) of the parameters were higher in DHA (0.915), A (0.912), F (0.910), MBN (0.905), H (0.903), MBP (0.886). As shown in the PCA ordination biplot, it could be inferred these highly correlated parameters to be chiefly associated with GM and GM-CLCC N. The parameters CL (0.849), IN (0.815), XY (0.812), MI (0.808), TOC (0.799), AP (0.783), PC (0.741), PO (0.739), AWCD (0.733), AK (0.726) variances was found to be attributed the ZT treatment. MBC (0.723), AN (0.715), FDA (0.723), BG (0.704), UR (0.703) demonstrated lesser variances and from the ordination biplot could be attributed to GM and GM-CLCCN treatments. The treatments CB (-0.405), AA (-0.606) and SI (-0.648) showed negative correlation with GM and GM-CLCC N treatments, however was positively correlated with CC treatment followed by WDS. In the second dimension PC2, the components NM (0.730) and CM (0.72b) showed the highest contribution which can be attributed to GM and GM-CLCC N treatments. The parameters CA (0.450), EC (0.396) were found to have very low correlation coefficient in first dimension PC1, whose contribution increased in third dimension (0.730). However, only the first two dimensions were taken for analysis.

Discussion

Impact of resource conservation on soil physical properties

In the present study, higher pH was recorded under green manuring and zero tillage treatments, as compared to other treatments. Addition of *Sesbania* and rice residues increased the soil pH and thereby reduces the exchangeable acidity (Opala et al., 2012). Exogenous application of manure might buffer the soil acidity which changed the soil pH to a slightly higher value by defusing some free H⁺ ions (Kumar et al., 2017). Chemical fertilizers have acidifying effects that decrease in soil pH of conventional practice (Hati et al., 2008).

Impact of resource conservation on soil carbon and nitrogen fractions

Total organic carbon (TOC) was recorded higher in organic amendment treatments (GM, BM, ZT and BC) compared to CC. Combined application of inorganic fertilizer and manure enhanced the TOC under paddy soil environment (Mohanty et al., 2013; Dossou-Yovo et al., 2016; Kumar et al., 2017).

Our findings also showed that resource conservation practices have higher microbial biomass carbon (MBC) content compared to CC (Table 2). Balanced nutrient inputs and supplemented by resource conservation practices play a crucial role for enhancement of soil organic carbon (SOC) and MBC (Cookson et al., 2007; Balachandar et al., 2014). The higher content of MBC in green manuring treatment might be due to presence of higher shoot and root biomass turn-

Table 5 Correlation matrix analysis with different variables of microbial indicators under resource conservation practices.

	MBC	MBN	MBP	DHA	FDA	BGL	URE	CEL	INV	XYL	HET	FUN	ACT
MBC	1.00												
MBN	0.710 ^{ns}	1.00											
MBP	0.724 ^{ns}	0.948 ^{**}	1.00										
DHA	0.736 ^{ns}	0.929 ^{**}	0.974 ^{**}	1.00									
FDA	0.590 ^{ns}	0.792 [*]	0.659 ^{ns}	0.727 ^{ns}	1.00								
BGL	0.591 ^{ns}	0.794 [*]	0.662 ^{ns}	0.729 ^{ns}	1.000 ^{**}	1.00							
URE	0.590 ^{ns}	0.793 [*]	0.661 ^{ns}	0.728 ^{ns}	1.000 ^{**}	1.000 ^{**}	1.00						
CEL	0.543 ^{ns}	0.760 [*]	0.729 ^{ns}	0.720 ^{ns}	0.401 ^{ns}	0.402 ^{ns}	0.399 ^{ns}	1.00					
INV	0.569 ^{ns}	0.752 ^{ns}	0.733 ^{ns}	0.709 ^{ns}	0.367 ^{ns}	0.368 ^{ns}	0.365 ^{ns}	0.996 ^{**}	1.00				
XYL	0.554 ^{ns}	0.718 ^{ns}	0.710 ^{ns}	0.684 ^{ns}	0.308 ^{ns}	0.308 ^{ns}	0.306 ^{ns}	0.992 ^{**}	0.998 ^{**}	1.00			
HET	0.686 ^{ns}	0.916 ^{**}	0.867 [*]	0.926 ^{**}	0.763 [*]	0.764 [*]	0.763 [*]	0.842 [*]	0.814 [*]	0.787 [*]	1.00		
FUN	0.691 ^{ns}	0.915 ^{**}	0.872 [*]	0.927 ^{**}	0.745 ^{ns}	0.746 ^{ns}	0.745 ^{ns}	0.858 [*]	0.832 [*]	0.807 [*]	0.999 ^{**}	1.00	
ACT	0.680 ^{ns}	0.914 ^{**}	0.872 [*]	0.925 ^{**}	0.738 ^{ns}	0.739 ^{ns}	0.737 ^{ns}	0.866 [*]	0.840 [*]	0.815 [*]	0.999 ^{**}	1.000 ^{**}	1.00
AWCD	0.786 [*]	0.801 [*]	0.907 ^{**}	0.872 [*]	0.430 ^{ns}	0.432 ^{ns}	0.429 ^{ns}	0.807 [*]	0.833 [*]	0.827 [*]	0.773 [*]	0.790 [*]	0.792 [*]
RAWCD	-0.219 ^{ns}	-0.782 [*]	-0.803 [*]	-0.731 ^{ns}	-0.513 ^{ns}	-0.514 ^{ns}	-0.513 ^{ns}	-0.627 ^{ns}	-0.619 ^{ns}	-0.589 ^{ns}	-0.646 ^{ns}	-0.650 ^{ns}	-0.661 ^{ns}
SNI	0.848 [*]	0.798 [*]	0.853 [*]	0.858 [*]	0.584 ^{ns}	0.585 ^{ns}	0.581 ^{ns}	0.802 [*]	0.818 [*]	0.800 [*]	0.816 [*]	0.830 [*]	0.829 [*]
MCI	0.830 [*]	0.925 ^{**}	0.901 ^{**}	0.907 ^{**}	0.754 ^{ns}	0.755 [*]	0.753 ^{ns}	0.833 [*]	0.835 [*]	0.804 [*]	0.915 ^{**}	0.921 ^{**}	0.920 ^{**}
RY	0.767 [*]	0.938 ^{**}	0.995 ^{**}	0.961 ^{**}	0.646 ^{ns}	0.648 ^{ns}	0.647 ^{ns}	0.696 ^{ns}	0.706 ^{ns}	0.684 ^{ns}	0.837 [*]	0.842 [*]	0.841 [*]

† ns: non-significant at $p \leq 0.05$ or $p \leq 0.01$. ** Correlation is significant at $p \leq 0.01$. * Correlation is significant at $p \leq 0.05$.

[DHA: dehydrogenase activity; FDA: fluorescein di-acetate activity; β -glu: β -glucosidase; URE: urease activity; CEL: cellulase activity; INV: invertase activity; XYL: xylanase activity; HET: heterotrophs; FUN: fungus; ACT: actinomycetes; AWCD: average well color development; RAWCD: rate of average well color development; SNI: Shannon index; MCI: McIntosh index; RY: relative yield]

Table 6 Stepwise regression analysis with different variables of microbial indicators under different resource conservation practices.

Dependents	Variable related	R ²	Significant level (p)
MBC	MBN, MBP, DHA, FDA, β -Glucosidase, Urease, Heterotrophs, Fungus, Actinomycetes, Cmin, Nmin, AWCD, Shannon index, McIntosh Index	0.999	≤ 0.000
MBN	MBC, FDA, β -Glucosidase, Urease, Cmin, Nmin, Shannon index	0.996	≤ 0.000
MBP	Cellulase, Invertase, Xylanase, Cmin, Nmin, AWCD, McIntosh Index, TOC, MBC, MBN, Ntot, AN, AP, AK	0.949	≤ 0.000
Heterotrophs	Cmin, Nmin, AWCD, Shannon index, MBC, MBN, MBP, DHA, FDA, β -Glucosidase, Urease, Cellulase, Invertase	0.998	≤ 0.000
Actinomycetes	MBC, MBN, MBP, DHA, FDA, β -Glucosidase, Urease, Cellulase, Invertase, Xylanase, Heterotrophs, Fungus, Actinomycetes, Cmin, Nmin, TOC, Ntot, AN, AP, AK, AWCD, McIntosh Index	0.998	≤ 0.001
Fungus	Cmin, Nmin, Shannon index, MBC, AN, Heterotrophs	0.998	≤ 0.000
AWCD	McIntosh Index, TOC, MBC, Ntot, AP, AK, MBP, DHA, Cellulase, Invertase, Xylanase, Heterotrophs, Fungus	0.996	≤ 0.000
Shannon index	MBC, MBN, MBP, DHA, FDA, β -Glucosidase, Urease, Cellulase, Invertase, Xylanase, Heterotrophs, Fungus, Actinomycetes	0.972	≤ 0.002
McIntosh Index	TOC, MBC, Ntot, AN, MBP, DHA, β -Glucosidase, Urease, Cellulase, Invertase, Xylanase, Heterotrophs, Fungus, Actinomycetes	0.887	≤ 0.002

[DHA: dehydrogenase activity; FDA: fluorescein di-acetate activity; β -glu: β -glucosidase; URE: urease activity; CEL: cellulase activity; INV: invertase activity; XYL: xylanase activity; HET: heterotrophs; FUN: fungus; ACT: actinomycetes; AWCD: average well color development; RAWCD: rate of average well color development; SNI: Shannon index; MCI: McIntosh index; RY: relative yield]

over (Mandal et al., 2007; Liu et al., 2013; Shahid et al., 2017), which significantly increases carbon input (Manna et al., 2005; Lal, 2015). Soil microbial biomass carbon also controls nutrient cycling soil organic matter decomposition, thereby plays a vital role in sustaining soil health. Green manuring and rice residue provide a potent source of C nutrients that facilitates the growth of soil microorganism.

Our findings also showed that resource conservation practices have higher microbial biomass carbon (MBC) content compared to CC (Table 2). Balanced nutrient inputs and supplemented by resource conservation practices play a crucial role for enhancement of soil organic carbon (SOC) and MBC (Cookson et al., 2007; Balachandar et al., 2014). The higher content of MBC in green manuring treatment might be due to presence of higher shoot and root biomass turnover (Mandal et al., 2007; Liu et al., 2013; Shahid et al., 2017), which significantly increases carbon input (Manna et al., 2005; Lal, 2015). Soil microbial biomass carbon also controls nutrient cycling soil organic matter decomposition, thereby plays a vital role in sustaining soil health. Green manuring and rice residue provide a potent source of C nutrients that facilitates the growth of soil microorganism.

Resource conservation treatments enhances mineralization rate (C and N), by enhancing microbial growth and thereby enhanced the decomposition of crop residues (roots and stubbles) in the soil (Muhammad et al., 2014). Incorporation of green manuring and brown manuring, adoption of zero tillage improve soil aggregation and aggregate associate carbon, thereby facilitating SOC build up (Gupta et al., 2014; M.-Y. Liu et al., 2014; Shahid et al., 2017).

The green manuring provided a simple form of organic C to sustaining the microbial growth and have potential for maintaining higher level of MBC (Mandal et al., 2007). Microbial biomass (C, N and P) increased significantly with the addition of leguminous residue has low C:N ratio as compared to crop residue has reach high C:N ratios (Weber et al., 2008; Yu et al., 2015).

Impact of resource conservation on Soil enzymatic activities

Compared to rice residue, green manuring can easily decomposed by the soil microorganisms to produce simple sugar compounds, which enhances soil enzyme activities (Bhattacharyya et al., 2012). Dehydrogenase activity mostly depends on the soil microbial respiration, highest activities of which occurred under green manuring treatment also recording highest microbial population. Higher C, N substrate level (Bhattacharyya et al., 2013b) and microbial population (Kumar et al., 2017) in green manuring plots, might have promoted the soil enzymatic activities. More organic matter in amended soil contributes more C source for microorganisms resulting in higher C-mineralization and enzymatic activities (Tian et al., 2016).

Effect of resource conservation technology on microbial population

The population of total aerobic heterotrophic bacteria (AHB), fungi, and actinomycetes were significantly higher in resource conservation practices than that of control, which publicized that some specific individual nutrients (Ramirez-Villanueva et al., 2015) present in RCTs treatments might have increased total soil microbial populations. Long-term resource conservation practices in rice soil enhance fungal and bacterial populations due to favourable substrate base (Six et al., 2006). Organic amendments provide necessary C, N and energy for microbial growth and reproduction (Huang et al., 2010). Organic manure applications significantly changes bacteria, actinomycetes and fungi population in soils as compared to the soils treated with mineral fertilizer (Dong et al., 2014).

Effect of resource conservation technology on microbial diversity

Several investigations use to find out the functional diversity of soil-microbes in rhizosphere using Biolog® eco-plates (Xu and Ge, 2015). The variation in the microbial community functions due to their different metabolic activities were indicated according to optical density (OD) values (colour change) at every reaction holes that utilizes 31 kind of different C-sources (Calbrix et al., 2005). The sigmoid curves of AWCD were found in all the treatments except control in all the incubation period (i.e. 0–120 h), almost resembles the S-arch of bacterial growth (Guanghua et al., 2008), which indicated that the richness of microbial communities (Zhong and Cai, 2007) in those treatments, however, the conventional control treatment having linear curve indicated the low microbial richness (Guanghua et al., 2008).

In the present study, the increasing average well color development (AWCD) values under the different treatments was in the order of GM > GM-CLCC-N > BM > ZT > BC > WDS > CC. The highest rate of AWCD observed in green manuring and the lowest was under CC could be due to increased soil microbial biomass (C, N and P) in GM that enriched the biomass addition and microbial activities (Gu et al., 2009). Combined application of most diverse resources of organic + mineral fertilizers could greatly increase in microbial biomass and their activity which enhances nutrient availability in soils (Chang et al., 2016). It was also recommended that adjustment of the appropriate proportion of specific organic amendments such as farmyard manure, green manure, rice straw, etc. can enhance the fertility through shifting of microbial community in rice soil under different fertilization practices (Wanjiru et al., 2015).

The higher metabolic activities of active microbial communities utilizing the C-substrates within 48 h, resulted the decrease in the rate of AWCD after 48 h of incubation in different resource conservation treatments. Since, the metabolic activity was reduced under all the treatments after 72 h; hence the analysis of soil microbial functional diversity was done at this particular time. Significantly higher AWCD in green manuring treatment compared to other treatments indicated that addition of biomass (green manure, rice residue, biochar) played crucial role in microbial dynamics and also shifting the soil microbial community structure. Shannon index of green manuring treated plots was significantly higher ($p \leq 0.05$) which implied that the species richness and evenness of soil microbial communities in that particular treatment might be different from other treatments. The increasing order of Shannon index in GM, GM+CLCC-N and BM indicated that soil microbial communities were affected by biomass addition which accounts for rapid increase in microbial population (Baldrian et al., 2012) rather than their diversity (Guanghua et al., 2008; Moharana et al., 2012; Nayak et al., 2012). Resource conservation treatments could enhance the accumulation of organic which altered the pattern of potential carbon utilization and increased the Shannon, McIntosh and AWCD indices values (Chinnadurai et al., 2014). The biplot analysis (Fig. 5A) indicated the separation of RCT treatments (biomass added) from WDS and conventional control (chemical fertilizer) treatment which supported that treatments receiving green manuring, brown manuring, rice residue and biochar could have a greater influence on microbial functional diversity than conventional control.

It has been observed that the utilization of six major carbon groups by microbial communities within and between different treatments showed a unique pattern. Consumption of carbohydrates, amino acids and carboxylic acid were higher with application of green manuring and brown manuring, which indicates that microorganisms present in that treatments were more active towards easily decomposable carbon sources than other treatments. Addition of *Lupin* green manure (organic N source) resulted in significantly higher microbial biomass and activity as compared to control soils (Preethi et al., 2013). Kumar et al. (2017) reported that at the early stages, microbial communities utilized simple sugars as major substrates, whereas complex C-substrates were utilized at later stages, which indicated that shifting of the microbial community based on presence and/or absence of available nutrients. However, microbes utilize complex C substrates (phenolic compounds, amines, polymers) more in control due to less microbial activities (An et al., 2014). Variation in Biolog patterns was mainly due to applications of different biomass and could be explained by the second quadrant and third quadrant of principal components (PCs). The present study revealed that resource conservation (chemical fertilizer + organic matter) practices significantly enhanced the soil biological-activity which promoted the microorganisms to utilise the different C sources.

Correlation and Stepwise regression of microbial indicators

Highly significant positive correlations existed among MBC with soil enzymatic activities and microbial populations, which suggested that MBC content, increased simultaneously to give rise to enzymatic activities and microbial population in the soil. The enzyme activities were highly correlated with C/N fractions; microbial populations, Shannon index and McIntosh index because their activities were increased considerable by increasing addition of labile N and C source (Bhattacharyya et al., 2013a; Zhu et al., 2014; Chaudhary et al., 2017).

The AWCD, Shannon index and McIntosh were highly correlated with microbial biomass (C, N & P), enzymatic activities and microbial populations, whereas, they were not correlated with each other except AWCD (Table 4). Shannon index provides information about the spread/distribution of C source utilization by microbes and affected more by species richness (Zhang et al., 2014; Guo et al., 2016; Tautges et al., 2016). Our study suggested that the decreased in Shannon index was due to dominance of common species of microorganisms as well as MBC, MBN and MBP which were increased along with the increasing C_{min} in the green manuring treated soil.

Conclusions

This study demonstrated the Biolog based technique to differentiate the functional soil microbial diversities under different resource conservation practices. The present study is implying that microbial community present in biomass amended treatments (GM, GM-CLCC N, BM) utilize available or simple form of carbons for their growth (carbohydrates, amino acids and carboxylic acid), whereas microorganisms prevalent in the treatments of chemical fertilizers alone preferably utilize stable C compounds (phenolic compounds, amines, polymers) due to unavailability of labile C sources. It indicates that biomass amended treatments (GM, GM-CLCC N, BM) could supply good amount of labile C sources on real time basis for microbial activity that may protect the stable C fraction in soil, hence could support higher build-up of C in long run. Therefore, various resource conservation practices that enhance the microbial biomass, enzymatic activities and diversity at the same time maintaining or enhancing the yield need to be adopted suiting to the local condition.

Declarations

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Conflict of Interest

The authors declare that they have no conflict of interest.

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Figures

Figure 1
Relative yield (Mg ha⁻¹) under different resource conservation practices [Here, CC: conventional control; BM: brown manuring; GM: green manuring; WDS: wet drum seeding; ZT: zero tillage; GM-CLCC-N: green manuring- CLCC-N; BC: biochar]

Figure 2
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Changes in average well colour development (AWCD) over time of the soil under different resource conservation practices. Mean value with standard deviation bars, n = 3. [Here, CC: conventional control; BM: brown manuring; GM: green manuring; WDS: wet drum seeding; ZT: zero tillage; GM-CLCC-N: green manuring-CLCC-N; BC: biochar]

Figure 3
Variation of average well colour development (AWCD) for five consecutive days of the soil under resource conservation. Mean value with standard deviation bars, n = 3. [Here, CC: conventional control; BM: brown manuring; GM: green manuring; WDS: wet drum seeding; ZT: zero tillage; GM-CLCC-N: green manuring-CLCC-N; BC: biochar]

Figure 4

Heat map (A) of microbial consumption of six major groups of carbon sources of soil under different resource conservation with cluster dendrogram (B). [Here, CC: conventional control; BM: brown manuring; GM: green manuring; WDS: wet drum seeding; ZT: zero tillage; GM-CLCC-N: green manuring- CLCC-N; BC: biochar and AA: Amino acids; AM: Amines; CB: Carbohydrates; CA: Carboxylic acids; PO: Polymers; PC: Phenolics compounds.]