

Sustainable intensification influences soil quality, biota, and productivity in cereal-based agroecosystems



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ABSTRACT

Monotonous rice-wheat cropping system with conventional management practices have resulted in declining soil quality and biota in addition to low input factor productivity and farmer's profitability in western Indo-Gangetic plains (IGP) of India. Conservation agriculture (CA) based sustainable intensification (SI) is required to improve the soil quality while improving the productivity and profitability. A field experiment was conducted to evaluate the effects of CA based management practices such as zero tillage (ZT), direct seeding of rice (DSR), crop diversification, residue recycling and legume integration for SI in comparison to conventional management on soil quality and biota in cereal (rice and maize) based cropping systems. Fourteen treatments were included in which four treatments (T₁–T₄) with rice–wheat and two treatments (T₁₁–T₁₂) with maize-wheat system were based on conventional management, while six treatments (T₅–T₁₀) with rice–wheat and two (T₁₃–T₁₄) with maize-wheat were based on CA management practices. Conservation agriculture based SI of maize-wheat-mungbean (T₁₄) recorded lower soil bulk density (1.33 Mg m⁻³). Soil organic carbon (OC) was increased by 83% and 72% with CA based rice-wheat-mungbean (T₁₀) and maize-wheat-mungbean (T₁₄) system, respectively and it was at par with T₉ and T₁₂ compared to farmer's practice (T₁) (4.6 g kg⁻¹). Mean microbial biomass carbon (MBC) and microbial biomass nitrogen (MBN) were 213% and 293% higher with T₁₄ over T₁ (646 and 201 μg g⁻¹ dry soil), respectively. However, T₁₀ recorded 117% and 171% higher MBC and MBN, respectively compared to T₁. Dehydrogenase activity (DHA) and alkaline phosphatase activity (APA) were improved by 210% and 49% under T₁₄; 140% and 42% under T₁₀ compared to T₁ (180 μg TPF g⁻¹ soil 24 h⁻¹ and 144 μg p-nitrophenol g⁻¹ h⁻¹), respectively. Mean number of bacteria, fungi and actinomycetes were increased by 28%, 68%, 98% respectively, under T₁₄ relative to T₁, and at par with T₁₂ and T₁₀. Most abundant micro-arthropod group belonged to *Collembola* followed by *Acari* and *Protura*, irrespective of treatments. Higher soil quality index (SQI) was observed in T₁₀ (0.82), followed by T₁₄ and T₆ treatment (0.76). Sustainable intensification of rice and maize based systems (T₁₀ and T₁₄) recorded 39% higher system yield compared to T₁ (11.12 Mg ha⁻¹). CA-based sustainable intensification of rice/maize systems improved soil quality and biota, hence resulted higher system yield in alluvial soils of IGP. Conservation agriculture based SI of maize-wheat-mungbean system was found to be the best alternative option than rice-wheat system to achieve sustainable productivity while improving the soil quality index (35%) and conservation of natural resources.

1. Introduction

Rice-Wheat cropping system is the cornerstone of India's food security and is most widely prevalent not only in India but in entire South

Asia. This cropping system occupies about 13.5 million hectares in the Indo-Gangetic Plains (IGP), of which 10 million hectares are in India, 2.2 million hectares in Pakistan, 0.8 million hectares in Bangladesh and 0.5 million hectares in Nepal (Mahajan and Gupta, 2009). During

Abbreviations: APA, Alkaline phosphatase activity; BD, Bulk density; CA, Conservation agriculture; CT, conventional tillage; DHA, Dehydrogenase activity; EC, Electrical conductivity; EMI, Eco-Morphological Index; IGP, Indo-Gangetic Plains; MBC, Microbial biomass carbon; MBN, Microbial biomass nitrogen; MDS, Minimum data set; OC, Organic carbon; QBS, Biological soil quality; ZT, Zero tillage

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“Green Revolution” in mid-sixties, good quality inputs such as quality seed, chemical fertilizers and assured irrigation facilities remarkably enhanced the productivity of this system. However, nowadays conventional tillage (CT) based practices have proved to be insufficient in meeting the challenges of enhanced and sustained productivity and halting the natural resource degradation. Besides this, global warming also warrants the need to change conventional practices to reduce greenhouse gas emissions (You et al., 2005) from rice-wheat system.

Indiscriminate use of ground water exploitation for irrigation purposes mainly for growing rice made the situation worse in western IGP (Punjab, Haryana and western Uttar Pradesh). Conservation agriculture (CA) with proven principles of minimum soil disturbance, rational surface cover with efficient crop rotation has been introduced with the aim of conserving natural resources (soil, water and energy) (Sharma et al., 2015). More recently, maize has been introduced in lieu of Crop Diversification Program of Government of India in western IGP to replace 5% of rice area due to its lesser (only 10–15% of rice) water requirement, equal production potential and minimum support prices (MSP). The positive effects of CA-based options resulted in higher crop yields, water saving, labour use and soil health improvement in cereal based systems (Gathala et al., 2013; Jat et al., 2015). In addition, system intensification through integration of short duration mungbean (*Vigna radiata*) may provide an opportunity to increase the farmer's profit (Kumar et al., 2018).

Adoption of practices that minimize soil impacts is fundamental to agricultural sustainability as soil environment is affected by returning of plant residues which affect soil structure, temperature, moisture and aeration, which, in turn, affect soil quality and biota. Soil biota directly and indirectly impacts soil ecosystem services that can affect its productivity (Barrios, 2007). The magnitude of microbial biomasses like carbon, nitrogen, phosphorus and enzymatic activities reflects biological health of soils which governs soil productivity (Hussain et al., 2009; Kawabiah et al., 2003). Microbes play an important role in the transformation of organic matter, nutrient cycling, and energy flow (Six et al., 2004; Wardle and Giller, 1996) which significantly impact the sustainability of the system. Microbial activities have been used to measure the influence of soil management practices on soil quality (Kabiri et al., 2016). In soil not only microbes but meso and macrofauna also play an important role in the determination of soil quality (Baretta et al., 2014). Microarthropods are considered important soil biotic component that helps in increasing organic matter availability for microbes through decomposition of crop residues or organic materials present in soil (Petersen and Luxton, 1982). Amount and quality of organic input like green manuring and crop rotation have shown the impact on the population densities of microarthropods (Frampton and van den Brink, 2002).

There is lot of literature available on productivity, profitability and resource use efficiency under CA and CT based cereal systems of western IGP (Kumar et al., 2018; Singh et al., 2016). Many studies had conducted on improvement in soil properties (Bhattacharyya et al., 2015) and nutrient availability (Jat et al., 2017). Hardly there were any study on a series of CA-based cropping system treatments and their influence on soil biological parameters and SQI. Recently in another experiment Choudhary et al. (2018) studied the effect of different CA-based rice-wheat and maize-wheat cropping systems on improvement in soil quality index and observed the higher efficiency of CA-based maize-wheat system in soil quality improvement over rice-wheat system. However, paucity of literature is available on layering of CT vs CA based sustainable intensification management practices on soil quality and soil biota in cereal systems. We hypothesize that CA-based rice-wheat and maize-wheat system with mungbean integration would result improved soil quality index and productivity over others. Among these two systems, maize-wheat-mungbean would lead to higher SQI than rice-wheat-mungbean. Therefore this present study was, undertaken i) to assess the soil quality and soil biota using varied indicators under a series of CA and CT based crop management practices and also

ii) to analyse their influence on the system yield. Through linear contrast analysis, we identified different combinations of systems and studied their interaction effect on individual soil properties.

2. Materials and methods

2.1. Study site

In 2012, a field experiment was set up at Taraori, Karnal, India (Lat. 29°48'N and Long. 76°55'E) in farmer's participatory mode on sustainable intensification of cereal systems by International Maize and Wheat Improvement Centre (CIMMYT). Semi-arid and sub-tropical climate prevails in the experimental area with hot, dry to wet summers (May–October) and cool, dry winters (November–April). The average annual temperature and rainfall are 24 °C and 670 mm, respectively of which 75–80% is received normally during southwest monsoon (July to September). Temperature (maximum and minimum) and rainfall of the study period are presented in supplementary figure (Fig. S1). Soil texture was clay loam (sand 32.08%, silt 29.64%, clay 38.28%) having a soil pH and EC of 7.94 and 0.44 dS m⁻¹ in 1:2 suspension of soil water, respectively. The soil is Typic Ustocret. Soil organic carbon content was 0.47 ± 0.04%. The experimental soil was low in available nitrogen (146.8 kg ha⁻¹), medium in available phosphorus (15.0 kg ha⁻¹) and potassium (242 kg ha⁻¹).

2.2. Treatments and experimental design

Experiment was arranged in randomized block design with fourteen treatment combinations (T₁–T₁₄) varied in crop sequence, tillage, establishment method, residue management, mungbean integration and other management practices. Treatments were based on conventional and conservation agriculture management systems of rice and maize based cropping systems of western IGP. The treatments were designed on different drivers of agricultural changes adopted by the farmers of western IGP. Each plot size was 20 m × 5.4 m. A description of treatment details are presented in Table 1.

2.3. Recycling of crop residues

Entire above ground residues of wheat and rice were removed or retained as per the treatment description given in Table 1. All the residues from T₁, T₂, T₅ and T₆ (rice-wheat system), and T₁₁ (maize-wheat system) were removed. Full residue (100%) of rice, anchored residue of wheat (33%) and maize (50%) were retained or incorporated as per the description given in Table 1 in the remaining treatments. Higher amount of crop residues were retained in T₁₀ (30.95 t ha⁻¹) followed by T₁₄ (29.75 t ha⁻¹), T₁₂ (28.59 t ha⁻¹) and T₄ (26.50 t ha⁻¹) over 3 years.

2.4. Soil sampling and analysis

Soil samples were collected from surface layer (0–10 cm) of all three replicates of each treatment from five locations by auger (with 5 cm diameter) after the harvesting of wheat crop (April) in 2015. Within replicate, a composite sample was prepared. A part of the soil samples were dried in shade, ground and passed through 2-mm sieve and analysed for different soil physico-chemical properties viz., pH, electrical conductivity (EC), organic carbon (OC) and available N, P, K. Fresh soil samples were passed through 2-mm sieve and analysed for different soil biological properties viz., microbial biomass carbon (MBC), microbial biomass nitrogen (MBN), microbial count, dehydrogenase activity (DHA), alkaline phosphatase activity (APA). Soil pH and electrical conductivity (EC) in soil: water ratio of 1:2 was determined by following Jackson (1973). Soil bulk density (BD) was measured by core sampler method (Blake and Hartge, 1986). The oxidizable organic carbon (OC) was determined using wet oxidation method (Walkley and

Table 1
Description of treatment details.

Symbol	Treatment notations	Cropping system	Tillage and crop establishment	Residue management	Residue recycled (t/ha)
T ₁	CTR-CTW (FP)	Rice-wheat-fallow	Rice: Two disc harrow, two cross harrow for puddling (wet tillage) followed by planking. Rice was manually transplanted Wheat: Two passes of harrow, three passes of cultivator followed by planking. wheat seed was broadcasted before last ploughing Same as in T ₁	Residue removed	NA
T ₂	CTR-CTW (RDF)	Rice-wheat-fallow	Same as in T ₁	Same as in T ₁	NA
T ₃	CTR-CTW-CTMb (Mb R _t)	Rice-wheat-mungbean	Same as in T ₁ and one pass of harrow and two pass of cultivator in mungbean	Mungbean residue was incorporated before puddling of rice	5.52
T ₄	CTR-CTW (RW R _t)	Rice-wheat-fallow	Same as in T ₁	100% rice and 33%wheat residue was incorporated	26.50
T ₅	ZTDSR-ZTW (FP)	Rice-wheat-fallow	Zero till DSR (direct seeded rice) and wheat was planted using seed-cum-fertilizer drill	Residue removed	NA
T ₆	ZTDSR-ZTW (RDF)	Rice-wheat-fallow	Same as in T ₅	Same as in T ₅	NA
T ₇	ZTDSR-ZTW-ZTMb (Mb R _r)	Rice-wheat-mungbean	Same as in T ₅ and relay mungbean	Mungbean residue was retained on soil surface	4.56
T ₈	ZTDSR-ZTW (R R _r)	Rice-wheat-fallow	Sowing of both the crops using turbo happy seeder	100% rice residue was retained on soil surface	18.39
T ₉	ZTDSR-ZTW (RW R _r)	Rice-wheat-fallow	Same as in T ₈	100% rice and 33% wheat residue was retained on soil surface	24.53
T ₁₀	ZTDSR-ZTW-ZTMb (RWMbR _r)	Rice-wheat-mungbean	Same as in T ₈ and relay mungbean	100% rice, 33% wheat and 100% mungbean residue retained on soil surface	30.95
T ₁₁	CTM-CTW (FP)	Maize-wheat-fallow	Maize: Two passes of harrow, two passes of cultivator followed by planking. Maize was sown using seed-cum-fertilizer drill Wheat: Two passes of harrow, three passes of cultivator followed by planking. wheat seed was broadcasted before last ploughing Same as in T ₁₁ and one pass of harrow and one pass of cultivator in mungbean	Residue removed	NA
T ₁₂	CTM-CTW-CTMb (MWMbR _r)	Maize-wheat-mungbean	Same as in T ₁₁ and one pass of harrow and one pass of cultivator in mungbean	50% maize, 33% wheat and 100% mungbean residue was incorporated	28.59
T ₁₃	ZTM-ZTW (MW R _r)	Maize-wheat-fallow	ZT maize and wheat. Crops were sown on permanent beds using bed planter	50% maize and 33% wheat residue was retained	24.48
T ₁₄	ZTM-ZTW-ZTMb (MWMbR _r)	Maize-wheat-mungbean	Same as in T ₁₃ and relay mungbean	50% maize, 33% wheat and 100% mungbean residue was retained	29.75

Where: R-rice; W-wheat; M-maize; Mb-mungbean; CT-conventional till; ZT-zero-till; FP-farmers practice; RDF-recommended dose of fertilizer; R_t-residue incorporated; R_r-residue retained, NA-not applicable.

Black, 1934). MBC and MBN were estimated by chloroform fumigation method (Vance et al., 1987) while method of Dick et al. (1996) was followed for estimation of APA and DHA. Soil available nitrogen (N) (Subbiah and Asija, 1956), phosphorus (P) (Olsen et al., 1954) and potassium (K) (Jackson, 1973) were also determined.

Bacteria, fungi and actinomycetes count of soil sample were done on Nutrient Agar media (NA), streptomycin (30 µg/ml) supplemented Rose Bengal Agar (RBA) Media, and Actinomycetes Isolation Agar (AIA) supplemented with nalidixic acid (50 µg/ml), respectively. Data from triplicate readings were expressed as colony forming units (CFU) g⁻¹ dry weight of soil.

2.5. Extraction and assessment of microarthropod diversity

For the extraction of microarthropods two undisturbed blocks of soil sample (10 × 5 × 10 cm³) were taken to laboratory. The sieve was placed on a Berlese–Tullgren funnel for extraction (Parisi et al., 2005), with lamps (60 W) being placed 25 cm above from the sample to dry it and to drive out the microarthropods. The soil core was carefully placed on the mesh above the funnel, before inserting a bottle filled with approximately 30 ml of preservative liquid (75% ethanol: glycerol 2:1) beneath the funnel (Fig. 1). The extraction system was kept free from vibrations and other disturbance. After 7 days, extracts were collected in test tubes (30 ml) for biological determination. Extracted specimens were observed under a stereomicroscope at low magnification (range 5–100×) in the same preservative liquid.

Diversity of soil microarthropod was calculated for each treatment (14 treatments). Shannon diversity indices (H' , Eq. (1)), evenness indices (E_H , Eq. (2)) and richness (S) were calculated following techniques reported by Bernard and Schmitt (2005). The Eqs. (1) and (2) are as follows:

$$H' = - \sum P_i (\ln P_i) \quad (1)$$

$$E_H = H' / \ln S \quad (2)$$

In the above equation $P_i = n_i/N$; n_i = the abundance of i -th species;



Fig. 1. Berlese-Tullgren funnels for micro-arthropods extraction. Each system contains a plastic funnel over which the wire mesh is placed and a collecting vessel below the funnel which contains a liquid preservative.

and N = the total abundance; S = total number of species present in the community or the species richness. Value of evenness ranged from 0 to 1, with 0 indicates completely uneven distribution and 1 being complete evenness.

2.6. Biological soil quality (QBS)

For calculation of QBS index each group of arthropod was given a score from 1 to 20 based on Eco-Morphological Index (EMI). Deep soil dwelling arthropods (eu-edaphic) obtain a score of 20; intermediate soil dwellers (hemi-edaphic) obtain the score proportionate to their degree of specialization; and surface dwellers (epi-edaphic) get an EMI of 1. If more than one eco-morphological form were present in the same treatment, higher EMI was treated as final score, i.e. – most adapted microarthropod determines the EMI of that treatment. QBS score was calculated simply by adding all EMIs of all microarthropod groups present in that treatment.

2.7. Crop and system grain yield

Crops were harvested manually from randomly selected 4 × 2.7 m² quadrat from 2 places within each plot for grain yields. Maize yield was converted to rice equivalent yield (REY) to compare the treatments using Eq. (4). To express the overall impact of treatments system productivity was calculated on wheat equivalent yield (WEY) basis for rice, maize and mungbean grain yield. Grain yield of crops were recorded at 14% moisture basis. System productivity (Mg ha⁻¹) was computed using Eq. (5) of WEY.

$$\text{REY (Mg ha}^{-1}\text{)} = \left\{ \frac{\text{Maize yield (Mg ha}^{-1}\text{)} \times \text{MSP of Maize (INR Mg ha}^{-1}\text{)}}{\text{MSP of Rice (INR Mg ha}^{-1}\text{)}} \right\} \quad (4)$$

$$\text{WEY (Mg ha}^{-1}\text{)} = \left\{ \frac{\text{Rice/Maize/Mungbean yield (Mg ha}^{-1}\text{)} \times \text{MSP of Rice/Maize/Mungbean (INR Mg ha}^{-1}\text{)}}{\text{MSP of Wheat (INR Mg ha}^{-1}\text{)}} \right\} \quad (5)$$

Where, MSP is the Minimum Support Price; INR is the India National Rupee.

2.8. Linear contrast combinations

From 14 treatments we identified 2 groups namely systems and residue. From first group we identified 4 combinations of systems namely R-W-F v/s R-W-Mb, R-W-F v/s M-W-F, R-W-Mb v/s M-W-Mb and M-W-F v/s M-W-Mb. In second group we found 2 combinations namely (residue incorporation v/s retention and residue removal v/s retention). All the treatments reside in those 2 groups and 6 combinations (Table 7). We studied interaction effects of those combinations on individual soil properties.

2.9. Soil quality index (SQI)

Soil quality index (SQI) calculation was performed following Choudhary et al. (2018). Wheat yield, rice equivalent yield and system yield are the goal variables on which farmers are mostly interested. The dataset (of 12 attributes) was reduced to a minimum dataset of soil quality indicators through a series of multivariate statistical methods. Standardized principal component analysis (PCA) was performed with those significant variables and reduced the redundancy summing up simple correlation values among the screened variables (Andrews and Carroll, 2001). Validation of MDS was done through multiple regression analysis to test how best they signify goal variables (yield). A non-linear scoring method (Bastida et al., 2006) was used to transform every observation of each MDS indicator by using Eq. (6).

$$y = a / (1 + (X/X_0)^{-b}) \quad (6)$$

Table 2
Soil physico-chemical properties under different CT (conventional tillage) and CA (conservational agriculture) based management practices.

Treatments ^a	pH	EC (dS m ⁻¹)	BD (Mg m ⁻³)	OC (g kg ⁻¹)
T ₁	7.83 ± 0.05b**	0.52 ± 0.01a	1.47 ± 0.01a	4.6 ± 0.06i
T ₂	7.95 ± 0.05ab	0.40 ± 0.01cd	1.46 ± 0.01a	5.2 ± 0.06h
T ₃	8.10 ± 0.06a	0.41 ± 0.02cd	1.42 ± 0.01b	5.8 ± 0.07fg
T ₄	7.90 ± 0.03b	0.44 ± 0.01c	1.41 ± 0.01c	6.6 ± 0.06d
T ₅	7.90 ± 0.07b	0.53 ± 0.01a	1.37 ± 0.01de	5.4 ± 0.06gh
T ₆	7.88 ± 0.02b	0.48 ± 0.01b	1.37 ± 0.01d	6.0 ± 0.12ef
T ₇	7.99 ± 0.01a	0.36 ± 0.01e	1.37 ± 0.01d	6.2 ± 0.06e
T ₈	7.89 ± 0.03b	0.51 ± 0.02a	1.35 ± 0.01ef	7.6 ± 0.06c
T ₉	7.66 ± 0.06c	0.47 ± 0.01b	1.36 ± 0.00de	8.2 ± 0.06ab
T ₁₀	7.64 ± 0.04c	0.54 ± 0.02a	1.35 ± 0.01ef	8.4 ± 0.06a
T ₁₁	7.95 ± 0.06ab	0.42 ± 0.05cd	1.37 ± 0.00d	5.2 ± 0.06h
T ₁₂	7.91 ± 0.05b	0.41 ± 0.01cd	1.37 ± 0.01d	7.8 ± 0.12c
T ₁₃	7.91 ± 0.04b	0.39 ± 0.01cde	1.34 ± 0.01ef	6.5 ± 0.12d
T ₁₄	7.91 ± 0.07b	0.39 ± 0.01e	1.33 ± 0.00f	7.9 ± 0.09abc

EC Electrical conductivity; BD Bulk density; OC Organic carbon.

For all variables n = 3 ± standard error of mean.

* Refer Table 1 for treatment description.

** Means of column followed by the same letters within each column not statistically different (P ≤ 0.05, Duncan's multiple range test).

where a = maximum value reached by the function, in our case, a = 1, X = unknown of the equation, corresponding to the value of the variable in question in every case, X₀ = mean value of each parameter corresponding to the soils of different treatments of the study b is the slope of the equation and was optimized for different selected indicators.

Each variable was standardized to a value between 0 (least favourable) and 1 (most favourable) scoring functions (Andrews et al., 2002). Once transformed, the MDS variables for each observation were weighted by using the PCA results. A certain amount (%) of variation in the total data set was explained by each PC. This percentage, divided by the total percentage of variation explained by all PCs with eigen vectors greater than 1, provided the weighted factor for variables chosen under a given PC. The weighted MDS variables scores for each observation were then summed up using Eq. (7).

$$SQI = \sum_{i=1}^n SW_i S_i \quad (7)$$

Where, S = indicator score, W = the weighing factor obtained from PCA.

Higher index scores were assumed to mean better soil quality or greater performance of soil function.

2.10. Statistical analysis

Data on all variables were subjected to analysis of variance (ANOVA) using SPSS (16.0) software. Separation of means was done using the least significance difference method at P = 0.05 using Duncan multiple range test (DMRT). Simple correlation coefficients and regression equations were also computed along with principal component analysis (PCA) to evaluate relationships between the response variables and screen the performance of the soil and crop management practices using the same statistical package.

3. Results

3.1. Soil physico-chemical properties

Changes in soil physico-chemical properties under different management practices are presented in Table 2. Results showed that pH and electrical conductivity (EC) of the soil varied significantly among the treatments. Soil pH varied from 7.64 to 8.10 and EC from 0.36 to 0.54 dS m⁻¹ irrespective of treatments (Table 2). Higher pH was recorded under T₃ (8.10), and T₇ (7.99) compared to other treatments and

lowest with T₉ (7.66) and T₁₀ (7.64). Lowest EC (0.36 dS m⁻¹) was recorded under T₇ and closely followed by T₁₄ and T₁₃ (0.39 dS m⁻¹). However, higher EC was observed with T₁, T₅, T₈ and T₁₀.

The effect of different crop management practices on soil bulk density (BD) was significant and ranged from 1.33 Mg m⁻³ (T₁₄) to 1.47 Mg m⁻³ (T₁) (Table 2). Soil BD was higher in conventional till rice-wheat system (T₁-T₄) than rest of the treatments. Maize based systems on permanent beds (T₁₃ and T₁₄) had the least soil BD and were similar to T₁₀ and T₈ (Table 2). The highest organic carbon (OC) was observed under T₁₀ (8.4 g kg⁻¹) and lowest (4.6 g kg⁻¹) under farmer's practice (T₁). Higher OC was in order of T₁₀ (8.4 g kg⁻¹) > T₉ (8.2 g kg⁻¹) > T₈ (7.6 g kg⁻¹) > T₁₄ (7.9 g kg⁻¹) > T₁₂ (7.8 g kg⁻¹).

3.2. Microbial properties and soil enzymes

Soil microbial biomass carbon (MBC) and microbial biomass nitrogen (MBN) varied significantly under different management practices. MBC ranged from 646 to 2021 μg g⁻¹ dry soil irrespective of cropping system and management practices (Table 3). Conservation agriculture (CA) based sustainable intensification of maize-wheat-mungbean system (T₁₄) recorded 213 and 293% higher MBC (2021 μg g⁻¹ dry soil) and MBN (789 μg g⁻¹ dry soil) compared to conventional rice-wheat system (T₁) (646 and 201 μg g⁻¹ dry soil), respectively. MBC and MBN under different treatments showed similar trend. The CA based sustainable intensification of rice-wheat-mungbean system (T₁₀) recorded 117 and 171% higher MBC and MBN, respectively compared to T₁. Mungbean integration in maize-wheat system (T₁₂) recorded 66 and 142% higher MBC (1478 μg g⁻¹ dry soil) and MBN (545 μg g⁻¹ dry soil) than without mungbean (T₁₁) treatment (890 and 239 μg g⁻¹ dry soil) (Table 3). Within conventional tillage treatments (T₁ to T₄), T₄ showed higher MBC and MBN values than T₁, T₂ and T₃ treatments.

Sustainable intensification of rice (T₁₀) and maize (T₁₄) based systems on CA principles increased the bacteria, fungi and actinomycetes population by 26%, 61% and 92% and 28%, 68% and 98%, respectively compared to T₁ (bacteria-74.7 CFU × 10⁴g⁻¹ soil, fungi-45.3 CFU × 10²g⁻¹ soil and actinomycetes-35.5 CFU × 10⁴g⁻¹ soil) (Table 3). Similarly higher microbial populations were also observed in maize-wheat-mungbean with residue incorporation (T₁₂).

Results showed that DHA ranged from 180 to 558 μg TPF g⁻¹ soil 24 h⁻¹ irrespective of treatments. Full CA based sustainable intensification of rice (T₁₀) and maize (T₁₄) based systems recorded 140% and 210% higher DHA compared to T₁ (180 μg TPF g⁻¹ soil 24 h⁻¹), respectively (Table 3). Conventionally sown maize-wheat-mungbean with residue incorporation (T₁₂) also showed 107% higher DHA than

Table 3
Soil microbial activities and count under different management practices.

Treatments ^a	MBC ($\mu\text{g g}^{-1}$ dry soil)	MBN ($\mu\text{g g}^{-1}$ dry soil)	DHA ($\mu\text{g TPF g}^{-1}$ soil 24 h ⁻¹)	APA ($\mu\text{g p-nitrophenol g}^{-1}$ h ⁻¹)	Bacteria (CFU $\times 10^4$ g ⁻¹ soil)	Fungi (CFU $\times 10^2$ g ⁻¹ soil)	Actinomycetes (CFU $\times 10^4$ g ⁻¹ soil)
T ₁	646 \pm 10.33i**	201 \pm 1.86g	180 \pm 8.7f	144 \pm 5.4f	74.7 \pm 0.67h**	45.3 \pm 0.88f	35.5 \pm 0.76g
T ₂	804 \pm 3.31h	221 \pm 1.76fg	193 \pm 13.2ef	150 \pm 9.8ef	76.4 \pm 0.87gh	49.7 \pm 1.67ef	37.6 \pm 1.32g
T ₃	981 \pm 19.86fg	269 \pm 13.42f	245 \pm 12.5def	175 \pm 4.5bcdef	82.3 \pm 1.45efg	56.0 \pm 1.73de	47.3 \pm 0.67de
T ₄	1110 \pm 33.61ef	338 \pm 27.68e	256 \pm 17.4def	176 \pm 4.7bcdef	83.2 \pm 1.61def	57.9 \pm 2.19cd	49.0 \pm 0.17cde
T ₅	887 \pm 33.38gh	233 \pm 2.18fg	196 \pm 7.4ef	153 \pm 8.0ef	78.6 \pm 1.33fgh	52.2 \pm 0.00def	40.2 \pm 1.42fg
T ₆	907 \pm 7.58gh	245 \pm 0.57fg	260 \pm 42.7def	163 \pm 1.2cdef	81.7 \pm 0.88efg	55.4 \pm 2.23de	46.3 \pm 0.93def
T ₇	1158 \pm 72.20de	359 \pm 3.35e	263 \pm 18.1def	183 \pm 3.4abcde	85.0 \pm 0.58def	59.3 \pm 0.33cd	50.7 \pm 0.67bcd
T ₈	1177 \pm 31.76de	359 \pm 14.81de	298 \pm 22.2cde	181 \pm 3.6abcde	85.9 \pm 1.67cde	63.7 \pm 1.48c	51.2 \pm 1.01bcd
T ₉	1295 \pm 33.38cd	475 \pm 5.78c	404 \pm 3.5bc	196 \pm 10.4abc	91.3 \pm 0.17abc	72.1 \pm 1.46ab	54.4 \pm 1.45b
T ₁₀	1404 \pm 29.06bc	545 \pm 3.61b	432 \pm 33.6b	204 \pm 5.3ab	94.3 \pm 0.93ab	73.1 \pm 0.07ab	68.0 \pm 1.73a
T ₁₁	890 \pm 21.22gh	239 \pm 10.54 fg	219 \pm 6.0def	157 \pm 0.9def	81.4 \pm 1.47fgh	53.8 \pm 1.86de	44.9 \pm 1.92ef
T ₁₂	1478 \pm 32.84b	579 \pm 6.76b	453 \pm 27.9b	208 \pm 13.2ab	93.9 \pm 1.04ab	73.6 \pm 1.83ab	68.6 \pm 0.67a
T ₁₃	1270 \pm 16.42cd	412 \pm 2.77d	313 \pm 9.1cd	188 \pm 2.0abcd	87.4 \pm 1.01bcd	65.5 \pm 1.17bc	54.2 \pm 1.09bc
T ₁₄	2021 \pm 37.53a	789 \pm 4.48a	558 \pm 16.2a	214 \pm 1.2a	95.5 \pm 1.01a	76.2 \pm 0.17a	70.3 \pm 0.58a

MBC Microbial biomass carbon; MBN Microbial biomass nitrogen; DHA Dehydrogenase activity; APA Alkaline phosphatase activity; CFU colony forming unit.

For all variables n = 3 \pm standard error of mean.

* Refer Table 1 for treatment description.

** Means of column followed by the same letters within each column not statistically different (P \leq 0.05, Duncan's multiple range test).

Table 4
Microarthropods population under different management practices.

Treatments ^a	Collembola	Acari	Protura	Diplura	Araneae	Hymenoptera	Total population	Evenness	Richness	Shannon diversity index (SDI)
T ₁	12.3 \pm 8.4	1.0 \pm 0.6	0.3 \pm 0.3	–	0.7 \pm 0.7	–	17.0e	0.393d	4a	0.237
T ₂	28.0 \pm 12.0	2.7 \pm 2.7	0.3 \pm 0.3	–	–	0.3 \pm 0.0	31.3d	0.293e	4a	0.177
T ₃	42.7 \pm 12.3	4.7 \pm 3.7	1.3 \pm 1.3	–	0.7 \pm 0.7	–	49.3a	0.364de	4a	0.219
T ₄	29.7 \pm 13.1	2.9 \pm 2.2	–	–	0.4 \pm 0.3	–	34.7c	0.306e	3a	0.146
T ₅	35.6 \pm 16.5	4.1 \pm 3.1	–	–	0.3 \pm 0.3	–	40.0b	0.339de	3a	0.265
T ₆	46.5 \pm 24.5	1.5 \pm 0.5	0.5 \pm 0.7	–	–	–	48.5a	0.178f	3a	0.286
T ₇	12.5 \pm 3.7	2.5 \pm 0.3	0.5 \pm 0.0	0.3 \pm 0.3	–	–	16.3e	0.469c	4a	0.085
T ₈	9.7 \pm 5.2	2.5 \pm 0.3	–	–	–	0.4 \pm 0.3	18.7e	0.541bc	3a	0.283
T ₉	11.0 \pm 4.	5.0 \pm 3.0	–	–	–	0.5 \pm 0.5	16.5e	0.672b	3a	0.321ab
T ₁₀	13.5 \pm 10.9	7.0 \pm 3.5	–	–	0.3 \pm 0.3	–	35.9c	0.637b	3a	0.304b
T ₁₁	2.4 \pm 0.3	1.0 \pm 0.6	–	–	–	–	4.0f	0.881a	2a	0.162
T ₁₂	6.2 \pm 1.9	1.8 \pm 1.2	0.0 \pm 0.5	–	–	0.3 \pm 0.3	8.7f	0.600b	3a	0.258
T ₁₃	1.4 \pm 0.3	–	–	0.3 \pm 0.3	0.3 \pm 0.3	–	2.4f	0.789a	3a	0.377a
T ₁₄	4.5 \pm 2.8	1.1 \pm 1.0	–	0.4 \pm 0.3	–	–	6.0f	0.617b	3a	0.294

For all variables n = 3 \pm standard error of mean.

* Refer Table 1 for treatment description.

without residue incorporation and mungbean integration (T₁₁) (219 $\mu\text{g TPF g}^{-1}$ soil 24 h⁻¹). APA followed similar trend as DHA (Table 3), it ranged from 144 to 214 $\mu\text{g p-nitrophenol g}^{-1}$ h⁻¹, lowest and highest being associated with T₁ and T₁₄ treatments, respectively. Among the rice and maize based treatments, highest APA was recorded with T₁₀ (204 $\mu\text{g p-nitrophenol g}^{-1}$ h⁻¹) and T₁₄ (214 $\mu\text{g p-nitrophenol g}^{-1}$ h⁻¹), respectively. CA based sustainable intensification of maize (T₁₄) and rice (T₁₀) based systems showed 49% and 42% higher APA compared to T₁ (144 $\mu\text{g p-nitrophenol g}^{-1}$ h⁻¹), respectively. Conventionally sown maize-wheat-mungbean with residue incorporation (T₁₂) improved APA by 32 and 44% than without mungbean integration and residue incorporation of maize-wheat (T₁₁) (157 $\mu\text{g p-nitrophenol g}^{-1}$ h⁻¹) and conventional till rice-wheat (T₁), respectively.

3.3. Soil microarthropods

Most abundant microarthropod group was *Collembola* followed by *Acari* and *Protura*, irrespective of treatments. Other micro-arthropod groups viz., *Diplura*, *Araneae*, and *Hymenoptera* were also observed in some of the treatments. *Acari* population was higher under T₁₀ (7.0) followed by T₉ (5.0). Evenness was moderate in most of the treatments; and it varied between 0.178 (T₆) to 0.881 (T₁₁). Richness of the treatment varies from 2 to 4, lowest richness was observed in T₁₁ (2). Shannon diversity index varied from 0.085 to 0.377, lowest and highest

were associated with T₇ and T₁₃, respectively (Table 4). The EMI values of different soil microarthropod community are presented at Table 5. Treatment T₇ showed highest QBS value of 70, followed by T₂, T₃, T₁₂, T₆, and T₁₄ which means in these treatments microarthropods were more adapted than others. While lowest (31) QBS value was associated with T₉ treatment.

3.4. Crop grain yield

Rice equivalent yield were recorded higher by 19%, 15%, 14% and 13% under T₁₄, T₇, T₃ and T₁₃, respectively compared to T₁ (6.53 Mg ha⁻¹). Wheat yield was recorded higher with CA based management practices both in rice (T₅–T₁₀) and maize (T₁₃–T₁₄) systems (Table 6). CA based sustainable intensification of maize (T₁₄) and rice (T₁₀) systems recorded 12% and 29% higher wheat yield compared to T₁ (4.77 Mg ha⁻¹), respectively. Among rice based systems, T₃, T₇ and T₁₀ produced similar system yields, however in maize based systems T₁₂ and T₁₄ produced the similar system yields. System yields (wheat equivalents) were improved by 43%, 40%, 39% and 31% under T₇, T₁₄, T₁₀, and T₁₂, respectively compared to T₁ (11.1 Mg ha⁻¹). Maize-wheat-mungbean with residue incorporation (T₁₂) recorded 29% higher system yield compared to conventional maize-wheat system (T₁₁) (11.2 Mg ha⁻¹).

Table 5
Soil microarthropods taxa, associated eco-morphological index (EMI) and QBS (biological soil quality) values.

Microarthropod Taxa	Eco-morphological index (EMI) values													
	T ₁ ^a	T ₂	T ₃	T ₄	T ₅	T ₆	T ₇	T ₈	T ₉	T ₁₀	T ₁₁	T ₁₂	T ₁₃	T ₁₄
Collembola	20	20	20	10	20	20	10	10	6	20	20	20	20	20
Acari	20	20	20	20	20	20	20	20	20	20	20	20	20	20
Protura	10	20	20	0	0	20	20	0	0	0	0	20	0	0
Diplura	0	0	0	0	0	0	20	0	0	0	0	0	20	20
Araneae	5	0	5	5	5	0	0	0	0	5	0	0	5	0
Hymenoptera	0	5	0	0	0	0	0	5	5	0	0	5	0	0
QBS	55	65	65	35	45	60	70	35	31	45	40	65	45	60

* Refer Table 1 for treatment description.

Table 6
Effect of management practices on yield (Mg ha⁻¹) under different cereal based cropping systems.

Treatments ^a	Rice equivalent yield	Wheat yield	System yield (Wheat equivalent)
T ₁	6.53 ^{d**}	4.77 ^d	11.12 ^e
T ₂	7.29 ^{abc}	5.00 ^{cd}	12.09 ^{de}
T ₃	7.44 ^{abc}	4.73 ^d	14.47 ^{abc} (0.78) ^{****}
T ₄	6.91 ^{bcd}	5.02 ^{cd}	11.74 ^{de}
T ₅	6.77 ^{bcd}	5.47 ^{abcd}	12.06 ^{de}
T ₆	7.06 ^{abcd}	5.60 ^{abcd}	13.34 ^{cd} (0.27)
T ₇	7.48 ^{ab}	5.99 ^{abc}	15.92 ^a (0.83)
T ₈	7.18 ^{abcd}	5.99 ^{abc}	12.98 ^{de}
T ₉	6.71 ^{cd}	6.23 ^a	13.65 ^{bcd} (0.28)
T ₁₀	6.94 ^{bcd}	6.14 ^{ab}	15.50 ^{ab} (0.82)
T ₁₁	6.49 ^d (6.91) ^{***}	4.92 ^{cd}	11.23 ^e
T ₁₂	7.11 ^{abcd} (7.56)	5.13 ^{bcd}	14.51 ^{abc} (0.77)
T ₁₃	7.39 ^{abc} (7.86)	5.22 ^{abcd}	12.40 ^{de}
T ₁₄	7.76 ^a (8.25)	5.36 ^{abcd}	15.54 ^{ab} (0.82)

* Refer Table 1 for treatment description.

** Means of column followed by the same letters within each column not statistically different ($P \leq 0.05$, Duncan's multiple range test).

*** In parenthesis actual yield of maize under column rice yield.

**** In parenthesis actual yield of mung bean under column system yield.

Table 7
Linear contrast treatment combinations.

Systems	R-W-F v/s R-W-Mb	T ₁ , T ₂ , T ₄ , T ₅ , T ₆ , T ₈ , T ₉	T ₃ , T ₇ , T ₁₀
	R-W-F v/s M-W-F	T ₁ , T ₂ , T ₄ , T ₅ , T ₆ , T ₈ , T ₉	T ₁₁ , T ₁₃
	R-W-Mb v/s M-W-Mb	T ₃ , T ₇ , T ₁₀	T ₁₂ , T ₁₄
	M-W-F v/s M-W-Mb	T ₁₁ , T ₁₃	T ₁₂ , T ₁₄
Residue	Incorporation v/s retention	T ₃ , T ₄	T ₇ , T ₈ , T ₉ , T ₁₀
	Removal v/s retention	T ₁ , T ₂ , T ₅ , T ₆	T ₇ , T ₈ , T ₉ , T ₁₀

R Rice; W Wheat; F Fellow; Mb Mungbean; M Maize.

3.5. Interactions of linear contrast combinations on individual soil properties

The interaction effect of all the combinations on pH and EC were non-significant except residue incorporation v/s retention which had significant influence on soil pH (Table S1). All the 6 combinations had significant interaction effect on all the soil properties except the combination R-W-F v/s M-W-F and residue incorporation v/s retention had non-significant interaction effect on DHA, APA, fungi and bacteria population and APA, respectively (Table S1).

3.6. Principal component analysis and soil quality index

Principal component analysis was performed for all the parameters analysed. From that three principal components (PCs) were extracted. Highest loadings of the 1st PC (64.3% of total variance) consisted of parameters that describe the microbiological activity (OC, DHA, APA,

MBC, MBN, Bacteria, actinomycetes, fungal population) of soils. The 2nd PC (14.49% of total variance) was characterized by EC and pH with the highest loadings on the PC. The 3rd PC (9.26% of total variation) was described by microarthropod population of the soil.

Three PCs were extracted having eigenvalue of > 0.9 and explained 93.9% of the variance in the data (Table S2). In PC1, DHA, APA, MBC, MBN, OC, bacteria, fungi and actinomycetes population were the highly weighted variables. Correlation matrix was constructed separately among the highly weighted eight variables under PC1 (Table S3). The variable with highest correlation sum assumed to be best represented the PC. In PC1, among the eight variables, fungal population was chosen for the MDS due to its highest correlation sum. In PC2, soil pH was highly weighted variable and retained for MDS. In PC3, micro-arthropod population was the highly weighted variable and kept for MDS. Therefore, the final MDS consisted of fungal population, soil pH and micro-arthropod population. When these three indicators (independent variables) were regressed with yield of wheat, rice equivalent yield and system yield (dependent/goal variables), the coefficient of determinations (R^2) were 0.50, 0.64 and 0.59, respectively (Table S4). All these indicator variables significantly influenced all the three goal variables as revealed from multiple regression analysis.

After formation of MDS, scoring was done for the three variables following a nonlinear equation (Bastida et al., 2006). We used b value of -30.5 for all the MDS indicators soil pH, fungal population and micro-arthropod population to get a sigmoidal curve. After scoring, each score was multiplied by the respective weight as obtained during PCA analysis. Then summation of those values gave an index called SQI (Fig. 2) as mentioned below.

$$\text{SQI} = \text{S(Population of fungi score} \times 0.685) + (\text{pH score} \times 0.154) + (\text{Microarthropod population score} \times 0.099)$$

SQI values of different treatments showed significant variation among them (Fig. 2).

4. Discussion

4.1. Soil physico-chemical properties

Lower pH was associated with T₉ and T₁₀ where higher amount of residues were recycled. Compaction due to puddling and tillage operations might have resulted highest bulk density in conventional till rice-wheat (T₁) (Gathala et al., 2013; Jat et al., 2017). Lower BD in CA based permanent bed maize-wheat with and without mungbean integration (T₁₄ and T₁₃) might be due to loose soil and more pore space created in the beds through modified land configuration by accumulations of organic carbon on the top of raised beds (Govaerts et al., 2006) and in T₈, T₉ and T₁₀ treatments due to huge quantities of residue retention (Table 1) for six crop seasons (Bhattacharyya et al., 2015). Permanent bed planting provides natural opportunity to reduce compaction by confining traffic to the furrow bottom (Govaerts et al., 2006). ZT helps in improving soil aggregation, consequently lower bulk

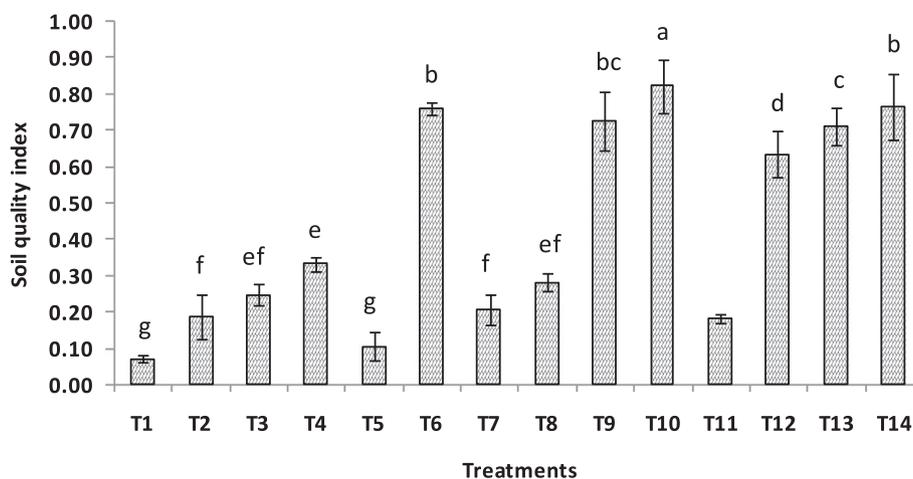


Fig. 2. Soil quality index (SQI) values under different management practices.

density than in conventional tillage in rice-wheat system (Gathala et al., 2011a; Govaerts et al., 2009).

Highest soil OC was observed under T₉ (8.2 g kg⁻¹) and T₁₀ (8.4 g kg⁻¹) which might be due to the retention of higher quantities of crop residues (Paudel et al., 2014). Intensive tillage (puddling/ploughing) practices exposed soils which might facilitates the oxidation of organic matter thereby explaining the lower OC content in farmer's practice. Higher soil OC content in ZT treatments resulted from crop residue retention/recycling (Jat et al., 2017; Mohammad et al., 2012). Moreover, ZT decreases OC decomposition by minimizing breakdown of macro aggregates (Gathala et al., 2011b).

4.2. Microbial properties

The MBC in soil is dominantly dependent on OC input from plant biomass (Campbell et al., 1997). Higher MBC and MBN under T₁₄ (maize-wheat-mungbean on permanent beds) might be due to the addition of huge quantities (29.75 t ha⁻¹) of residues on beds and more pore space in soil provide good aeration to microorganisms. Mungbean integration also might have contributed higher MBC as well as MBN in soil (Masto et al., 2007). Decomposition of crop residues under ZT treatments is slow and thus, there is gradual accumulation of organic matter on soil surface resulting in higher MBC and MBN in upper soil surface. Gajda et al. (2013) reported that in general soil biological activity was enhanced on an average by 15–40% under less disturbing tillage systems than conventional tillage system. Plant roots also play an important role in shaping soil microbial communities by releasing a wide range of compounds that may differ between plant species (Pausch and Kuzyakov, 2017).

Microbial population is influenced by crop rotation, organic matter, tillage practices and amount of crop residues (Table 3). Improved microbial counts under CA based maize-wheat on permanent beds (T₁₃ and T₁₄) than their respective counterparts (T₁₁ and T₁₂) might have been caused, in part, by creation of more favourable microbial microhabitat during construction of the permanent beds. Permanent beds can increase soil aggregate formation and maintain optimal ratios of solid, liquid, and gaseous phase in agricultural soils (Limon-Ortega et al., 2006). Raised bed planting also optimizes water holding capacity and conductivity of soil solutions, increasing bacterial counts relative to flat planting via enhanced aeration/porosity of soil (Patiño-Zúñiga et al., 2009). Whereas within permanent beds, microbial count was higher in T₁₄ compared to T₁₃ might be due to integration of mungbean in T₁₄. Retaining crop residues on the surface (ZT) or residue incorporation (CT) provides a stimulating substrate for microbial growth. Conservation agriculture (CA) practices increases fungal and bacterial population (Helgason et al., 2009). Residue retention induced higher

population counts of total bacteria, fluorescent *Pseudomonas*, and actinomycetes compared to residue removal under ZT and CT (Govaerts et al., 2008). Apart from increases in organic matter, the lack of tillage has also likely contributed to increases in fungal populations because tillage promotes the breakage of hyphae (Drijber et al., 2000).

Highest DHA and APA with CA based SI of rice (T₁₀) and maize (T₁₄) based systems is likely due to production of greater amounts of substrate for microbial growth and production of enzymes by microbes. Higher quantity of residue and roots of previous crops in the surface soil under CA can affect its microbial activity. One of those beneficial effects of CA might be “rhizosphere effect”, which probably contributes significantly for higher enzyme activities when compared with CT systems (Bandick and Dick, 1999). Conservation tillage practices have higher enzyme activities due to higher moisture availability for longer period in the plots rather than the better soil fertilities (Jin et al., 2009). The activity of APA was much greater in cereal-legume rotation because of higher microbial population (Table 3) and affiliation and interaction of phosphate solubilizing microorganisms with mungbean plants (Akmal et al., 2012; Ullah et al., 2013). With the increase of residue layer (as mulch) there is an increase of the supply of readily available substrates, such as carbohydrates, for microorganisms.

4.3. Microarthropod population

Population of *Collembola* was recorded higher under rice-wheat system compared to maize-wheat system irrespective of other variables. However, diversity index was more under maize-wheat cropping system. Residue retention caused increase in total microarthropod population in both the cereal based systems. As surface residues provides food for microarthropods which might help in their growth and multiplication as well as acts as mulch and protects them from soil desiccation during summer (Sapkota et al., 2012; Wardle, 1995). In maize-wheat cropping system, uneven covering of the soil surface with maize residues as compared to rice residues might have caused more soil desiccation of the microarthropods leading to lower population (Choudhary et al., 2018). Higher diversity index of microarthropod groups under CA-based maize-wheat cropping system might be due to higher biomass production (Sapkota et al., 2012) and availability of diverse type of food sources i.e. different types of crop residues (maize, wheat and mungbean) in T₁₄ (Table 1). The age of the experiment is also an important factor. As our experiment is continuing for 3 years only there was not much significant difference in microarthropod population/QBS/richness among the treatments.

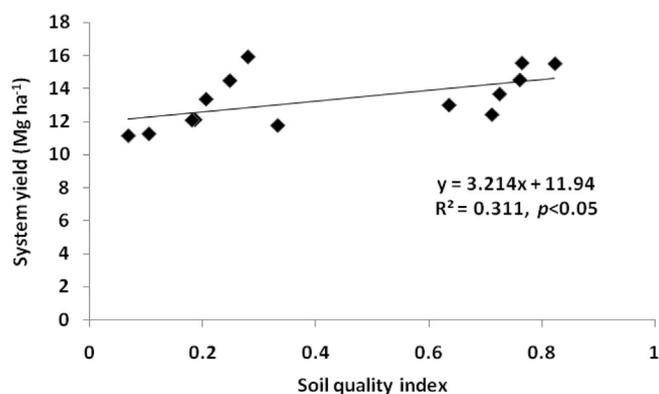


Fig. 3. Relationship between soil quality index (SQI) and system yield.

4.4. Crop grain yield

Result of our study clearly showed the effect of ZT and crop establishment, residue retention/incorporation and legume integration on crops and systems yield. Higher yield with CA based SI of maize-wheat-mungbean (T₁₄) might be due to increased yields of wheat and maize with permanent beds compared to CT (Gathala et al., 2016; Jat et al., 2015). The higher systems yield might be due to the compound effects of many factors like lesser weed infestation (Chauhan et al., 2007), improved soil physical properties (Singh et al., 2016), better water regimes (Govaerts et al., 2009), and improved nutrient availability (Blanco-Canqui and Lal, 2009; Jat et al., 2017);).

4.5. Interaction effect on soil properties

The significant interaction effect of all the 4 system combinations on the soil properties was due to inclusion of mungbean into the crop sequence. As a legume, mungbean not only fixes atmospheric-N but also improves other soil biological properties. The combination R-W-F vs M-W-F had non-significant interaction effect on DHA, APA, fungi and bacteria population which might be due to the common type (cereals) of crops in the rotation. Residue incorporation vs retention had significant interaction effect on soil pH which might be due to the release of organic acids during decomposition of residues. Residue removal vs residue retention also had significant interaction effect on all the soil properties due to decomposition of residues led to addition of organic carbon and other nutrient elements to the soil (Jat et al., 2017) thereby improving the soil quality.

4.6. Soil quality index (SQI)

CA based SI of rice (T₁₀) showed highest SQI value of 0.82 where highest amount of residues (30.95 t ha⁻¹, Table 1) was retained followed by ZTDSR-ZTW (RDF) (T₆) and maize-wheat-mungbean (T₁₄) which were at par (0.76). Higher SQI was also observed in ZTDSR-ZTW (RW Rr) (T₉) (0.73) and ZTM-ZTW (MW Rr) (T₁₃) (0.71) treatment. Higher SQI values indicate the aggregative effect of management practices on soil quality. In all the treatments no-tillage with residue had contributed higher SQI values. Improvement of soil OC, enzymes activity, MBC, MBN as well as microbial population with CA based management practices might have resulted higher SQI values under SI of rice and maize based systems in western IGP. Conventional till rice-wheat system or farmer's practice (T₁) showed lowest SQI value (0.07) due to deterioration or degradative effect of soil properties (Chaudhury et al., 2005; Masto et al., 2007). The SQI values and system yield were regressed and significant positive relation ($p < 0.05$) was observed (Fig. 3).

5. Conclusions

Conservation agriculture (CA) based sustainable intensification of cereal (rice/maize) systems integrated with mungbean improved soil physico-chemical properties and microbial properties. Results showed higher MBC (37%), MBN (51%), DHA (45%) and APA (8.8%) as well as microbial population (5–17%) with CA-based maize-wheat-mungbean system compared to rice-wheat-mungbean system. CA-based maize-wheat-mungbean system recorded ~35% higher soil quality index (SQI) over rice-wheat-mungbean system. The system yield was increased by ~25% with CA-based maize/rice-wheat-mungbean system compared to farmers' practice. Sustainable intensification of cereal based systems showed potential in maintaining systems sustainability in western IGP. CA-based maize-wheat-mungbean proved to be more productive while maintaining the soil quality therefore, needs to be recommended and popularized all across rice-wheat domains in IGP.

Conflict of interest

Authors do not have conflict of interest.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.apsoil.2018.02.027>.

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