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Research Article

Long-term Effects of Tillage, Crop Residue and Crop Rotations on Soil Microbial Parameters under the Wheat (*Triticum aestivum*) Based Cropping Systems in Semi-Arid Northern India

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ABSTRACT

A long-term study (2004–2010) was conducted at Research Farm of ICAR-IARI, New Delhi, to evaluate the effects of tillage, residue management and crop rotations on soil microbial parameters in wheat (Triticum aestivum) based cropping systems. The results revealed that soil under maize–wheat and pigeonpea–wheat rotations showed the highest fluorescein diacetate (FDA) activity. Cotton–wheat cropping system consistently supported the lowest FDA and dehydrogenase (DHA) activity at both stages. The soils under ZT with and without residue had higher soil organic carbon (SOC), SMBC, FDA, DHA and urease than CT. The ZT soils with and without residue showed increased values of organic C (24%, 23.9%), FDA (400%, 97.7%), dehydrogenase (31.4%, 38.2%), urease (28.2%, 28.3%) compared to CT at the germination stage. At this stage, addition of crop residues in ZT enhanced dehydrogenase activity (54.7%), FDA (6.50%), alkaline phosphatases (4%), urease (4.80%), SOC (8.71%) and SMBC (13.4%) but reduced glomalin content. The acid phosphatase activity was reduced by 9.11% under ZT. Microbial population and diversity, and productivity of soil could be maintained or improved with zero tillage and crop residue recycling. Thus, in wheat based cropping systems, ZT with and without addition of crop residues is a viable option for improving the soil microbial properties.

Keywords: *Crop residues, Cropping systems, Enzymes, Soil microbial parameters, Tillage.*

INTRODUCTION

Semi-arid sub-tropical soils are characterized by low organic carbon and poor soil fertility. In the Indo-Gangetic plains (IGPs) of South Asia, crop residues generated are either removed or burnt in the field itself causing loss of valuable resource and environment pollution.

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Therefore, resource–management strategies involving modified tillage combined with crop rotation and residue recycling are receiving attention. Tillage and residue–management practices result in alterations in soil physico-chemical properties, which leading to changes in soil microbial activities (Zablotowicz et al., 2007). Adoption of zero tillage system results in an increase in organic matter content, soil microbial biomass and activity, (Singh et al., 2011). A large fraction of soil nutrients are organically- bound **(**Franzluebbers & Stuedemann 2008), and the mineralization of the soil organic matter by microbial enzymes contributes to nutrient cycling in the soil (Marinari et al., 2000). Assessment of microbial activity through FDA hydrolysis provides a general measure of organic matter turnover in soil. It is considered as a soil quality indicator as about 90% of the energy in the soil environment flows through microbial decomposers (Green et al., 2006).

Soil-enzyme activities have the potential to provide biological assessment of soils because of their relationship to microbial activity, ease of measurement and sensitivity to soil management (Dick, 1994). Further, the biologically active fractions of soil organic carbon, such as microbial biomass C are found to be more sensitive to changes in soil quality brought about by cover cropping. β-glucosidase has a critical role in releasing low molecular weight sugars that are important as energy sources for microorganisms, an important component of soil P cycling that provides an indicator of a soil's capacity to mineralize P (Dick et al., 1996). Plant growth promoting bacteria such as free-living N_2 fixers, phosphate-solubilizing bacteria, and fluorescent *Pseudomonas* are sensitive to management practices (Govaerts et al., 2007). Their assay provides a broad-spectrum indicator of soil biological activity. Keeping above facts in mind the objective of the study was to determine the effect of tillage and crop-residue management on soil microbial parameters a wheat-based cropping system followed in semi-arid sub-tropical soils of North India.

MATERIALS AND METHODS

2.1. Experimental site

A field experiment was conducted for 6 consecutive years from 2004-2010 at Experimental Farm of ICAR-Indian Agricultural Research Institute, New Delhi is situated at 28° 38' N, 77° 12' E and 228.6 m above mean sea level. The Farm has semi-arid and sub-tropical climate with hot and dry summer and severe cold winter. On the basis of 30 years data, the mean maximum temperature, minimum temperature and rainfall are 32.1, 17.3°C and 788 mm respectively. The 84% of the annual rainfall is received from June to September (monsoon) and 12% from November to March. The Farm represents Indo-Gangatic plains and belongs to Mehrauli seriese of order Inceptisols. The soil have sandy loam in texture, alkaline in reaction and free from salinity, low SOC, available nitrogen and medium available phosphorus and high available potassium (Table 1).

2.2 Treatment details

The field experiment was conducted from 2004-2010 involving pigeonpea, groundnut, maize, soybean and cotton in *Kharif* season followed by wheat crop (November–April) during winter season. All the crops were grown in a fixed layout with the following treatments: zero tillage with residue (ZT+R), zero tillage without residue (ZT–R), conventional tillage with residue (CT+R) and conventional tillage without residue (CT–R). The experiment was laid out in a split-plot design, with cropping systems in main plot, and tillage residue management in subplots, with 3 replications. The residues of the previous crop were applied @ 3 t ha^{-1} for maize and cotton and 2 t ha^{-1} for pigeonpea, soybean and groundnut before sowing of wheat in the respective plots. The nutrient compositions of different crop residues have given in Table 2. Recommended doses of N: P: K fertilizer were applied to each crop *i.e.* 120:26:33, 25:26:33, 25:26:33, 120:26:33, 20:26:33 and 160:35:66 kg/ha for wheat, pigeonpea, groundnut, maize, soybean and cotton respectively. The half dose of N and

full dose of P and K were applied basal in wheat, maize and cotton, whereas the remaining N was top-dressed as per requirement of crop. For the other crops, entire fertilizer was applied basal. Urea, diammonium phosphate and muriate of potash were used as source of N, P and K respectively. The weeds were killed by application of paraquat @ 1 kg ha^{-1} in ZT plots before sowing. Later, during the crop-growth period, weeds were controlled by manual weeding. Other operations were carried out as per the recommendation.

2.3 Soil sampling and analysis

The composite soil samples (10 random samples from each plot mixed together) were taken at 30 cm soil depth with help of tube auger at time of sowing and maturity. Moist soil was sieved (2 mm mesh size), homogenized and stored at 4^{o}C. Microbial analysis was done using fresh soil samples, and the results were expressed on dry-weight basis.

2.4 Soil biological analysis

Soil microbial activity expressed as fluorescein diacetate hydrolysis (FDA) was determined (Green et al., 2006). Triphenyl-tetrazolium chloride (TTC)-dehydrogenase activity was used to estimate respiratory activity for viable microorganisms (Casida, 1964). Alkaline phosphomonoesterase (EC 3.1.3.1) and acid phosphomonoesterase (EC 3.1. 3.2) activities were determined by the *p*-nitrophenol release from analog substrate methods (Tabatabai, 1994). β-glucosidase activity was determined as per Eivazi and Tabatabai (1988). Soil urease (EC 3.5.1.5, 37 ^{o}C) activity was assayed by the method of Tabatabai (1994). Total glomalin (T-GRSP) was estimated as per Wright and Upadhyaya (1996), and the protein content was expressed as µg g^{-1} dry weight soil. Soil microbial biomass carbon (SMBC) was estimated following chloroform-fumigation extraction method (Vance, 1987). The soil respiration was measured by alkali-entrapment method (Stotzky, 1965), and the metabolic quotient was calculated as respiratory activity in relation to microbial biomass (Anderson & Domsch, 1989). Soil organic carbon (SOC) was determined by wet oxidation method (Walkley & Black, 1934). The pH was determined in soil water (1:2.5) suspension at 25°C using glass electrode pH meter after equilibrating for 30 minutes (Jackson, 1973). The microbial metabolic quotient (qCO_2) was calculated as the amount of CO_2-C produced per unit MBC. All values for enzymatic activities were reported on dry-soil basis. After drying of soil at 105 °C for 24 hrs, soil-moisture content was determined.

Enumeration of plant growth promoting rhizobacteria, viz. *Azotobacter*, fluorescent *pseudomonas* and phosphate-solubilizing bacteria was undertaken using serial dilution plating method in sterile phosphate-buffered saline (PBS, 10 mM K_2HPO_4–KH_2PO_4, 0.14 M NaCl, pH 7.2) on selective medium, *viz.* plating on (Jensen, 1954), King's B agar medium (King et al., 1954) supplemented with 80 mg g^{-1} of cycloheximide to suppress fungal growth (Araujo et al., 1996) and Pikovskaya's medium (Pikovskaya, 1948). Plates were incubated at 27^{o}C for 3 days, after which, bacterial colony forming units (CFUs) were enumerated. Confirmation of the fluorescent pseudomonas was on the basis of fluorescent pigment production ability, detected by exposing bacterial colonies to ultraviolet light (< 260 nm wavelength) for 1–2 sec.

2.5 Statistical analysis

The data were analyzed using Analysis of Variance (ANOVA) technique for split-plot design using MSTAT-C (Version 1.41, Crop and Soil Department, Michigan State University). The treatment means were compared at $P \leq 0.05$ level of probability using student t-test and working out LSD values.

RESULTS

3.1. FDA Analysis

A significant decline in the FDA activity was observed from sowing to maturity of wheat in all cropping systems under tillage and residue-management systems. The cropping systems exerted a differential influence on the soil-

microbial activity at both stages as revealed by the FDA activity. At sowing, soil under maize and pigeonpea showed the highest FDA activities. While, under soybean and cotton the activity was the lowest (Table 3). The FDA hydrolysis followed the order maize–wheat = pigeonpea–wheat > groundnut–wheat > soybean–wheat = cotton–wheat. At maturity, the order was soybean–wheat > maize–wheat = groundnut–wheat = cotton–wheat > pigeonpea–wheat. On the other hand, higher FDA hydrolysis activity at sowing was recorded under ZT over CT not so at maturity. Under CT, the residue addition improved the FDA activity by 168 % and 62% at sowing and maturity, respectively. However, under ZT, the effect of residue addition was not pronounced at sowing.

3.2. Dehydrogenase activity

The DHA in soil samples varied significant by tillage and residue management in different crop sequences (Table 3). The highest and the lowest DHA was recorded in groundnut–wheat and cotton–wheat sequence at sowing and maturity, respectively. The decending order of DHA at sowing and maturity was groundnut–wheat>soybean–wheat> pigeonpea–wheat > cotton–wheat > maize–wheat. Addition of crop residues significantly stimulated the DHA at sowing and maturity. The ZT+R supported the maximum DHA followed by CT+R, ZT–R and CT–R.

3.3 Phosphatase activity

Acid phosphatase (ACP) and alkaline phosphatase (ALP) activities were significantly influenced by the cropping system, tillage and residue management (Table 3). At sowing, the highest ACP and ALP activity was recorded in groundnut–wheat and pigeonpea–wheat sequence. Interestingly, the lowest ALP activity was recorded under groundnut–wheat sequence. The rhizosphere of pigeonpea–wheat, and soybean–wheat registered lower ACP at sowing. Crop residues increased ACP activity by 19.9% under CT but reduced by 9.11% under ZT at sowing. At maturity the residue increased ACP activity by 15.5% under CT and 10.5% under ZT. Residue addition also stimulated the ALP activity the effect being more pronounced under CT than ZT. There was a marginal increase in ALP under ZT with residue both at sowing and maturity.

3.4 Urease and ß-glucosidase

The urease activity in soil at wheat maturity was the highest than maize and the lowest after cotton (Table 4). At sowing ZT–R activity of urease was 28.3% higher than CT–R. A similar increase was obtained under ZT+R compared with CT+R. ß-glucosidase showed sharp decline from sowing to maturity in cotton and soybean. Further, maize, pigeonpea and groundnut were registerd the highest identical ß-glucosidase enzyme activity at sowing. Tillage and residue management had no effect on ß-glucosidase at sowing but at maturity, a positive stimulation under ZT (258%), and CT (34.8%) was observed on the residue application.

3.5 Glomalin content

Total extractable glomalin (TEG) content in the soil ranged from 2,497–2,923 μg g^{-1}soil at sowing and 3,710–4,292 μg g^{-1} soil at maturity (Table 4). The TEG was identical after maize, pigeonpea and cotton, and were significantly higher than after soybean and groundnut. Addition of crop residues improved the TEG significantly under CT, while under ZT, the addition of crop residue resulted in a decrease of TEG by 7.12 and 8.71% at the germination and maturity stages respectively.

3.6 Plant growth-promoting rhizobacteria (PGPR)

The population of *Azotobacter* was the highest in soybean–wheat cropping system at the germination stage, but towards maturity, all the cropping systems recorded an identical population level (Table 5). Application of crop residues led to a decline in population under CT during germination stage, whereas a significant stimulation in the population of *Azotobacter* was recorded by application of crop residues under ZT during both the stages of soil sampling.

3.7 Phosphate-solubilizing bacteria (PSB)

The significant differences were recorded among different cropping systems for PSB. The PSB counts ranged from 6.13 to 7.04 log cfu ml^{-1} in the different cropping systems. The highest PSB count was recorded under maize-wheat and the lowest under soybean–wheat system at post-germination. However, the tillage and residue management did not exert effect on PSB populations.

3.8 Fluorescent Pseudomonads

Fluorescent Pseudomonas (FP) is known to exert biocontrol action against soil and root–borne phytopathogens through release of anti-microbials and siderophores. The FP activity at sowing was identical higher in pigeonpea and groundnut and lowest in maize. Crop-specific effect was absent at maturity due to the diminished and chemically altered root exudates. The abundance of FP was noted under ZT than CT and residue addition.

3.9 Soil respiration (SR)

In absence of crop–residues CT and ZT were identical in terms of CO_2 evolution at sowing, but at maturity ZT–R was significantly higher (18.7%) than CT–R. The residue resulted in a significant decline in SR activity at sowing of wheat possibly due to the immobilization of microbial biomass. The soil under CT–R and ZT–R evolved 42.2 and 12.0% more CO_2 evolution than CT+R and ZT+R, respectively. The treatment CT+R recorded 29.9% decrease in CO_2 evolution at sowing and 15.3% increase of at maturity over CT–R.

3.10 Soil microbial biomass carbon (SMBC)

The SMBC content was in order: pigeonpea–wheat > maize–wheat > soybean–wheat > cotton–wheat > groundnut-wheat (Table 6). The ZT soils consistently supported higher SMBC content than CT soils at germination (30.7%) and maturity (11.7%) stages of wheat crop. In the present study, SMBC in ZT with or without residue at germination and maturity stages of wheat was higher by 22.1%, 30.7% and 15.1%, 11.9%, respectively, than the corresponding CT treatments. Similar trend was observed in organic carbon content of soil with ZT having 23.9% higher content than CT soils. A highly significant interaction was observed between tillage, residue addition and crop rotations. The increase in SMBC following residue application was more pronounced (21.4%) in CT at germination, which declined (0.42%) at maturity. Residue addition was relatively less effective in ZT as an enhancement (13.4%) in SMBC content was recorded over ZT–R and a marginal stimulation was recorded at maturity.

3.11 Metabolic quotient of soil micro-biota

A pronounced difference in the metabolic quotient was also seen among the different cropping systems at both sampling stages (Table 6). Input of crop residues significantly reduced the metabolic quotient in the 2 tillage systems at the germination stage, but at the maturity, only ZT confirmed to this trend, which was minor. However, in CT plots receiving residue showed a pronounced gain in metabolic quotient. These differences may be due to accessibility to C substrates by microorganisms, changes in the metabolic rates and changes in microbial community composition. The soil under ZT+R and CT+R also may have a greater amount of larger aggregates, which protect microorganisms from adverse conditions. This has potentially important implications on climate change because less C is emitted from the soils receiving crop residues and more can be stored as soil organic matter. The elevated qCO_2 values detected in the crop residue amended conventional tilled soil at the harvest stage indicate less efficient microbial utilization of C. This indicates that the high qCO_2 values are due to more available C for micro-biota of the r-strategy ecotype would thrive under such conditions. These respire more C per unit of degradable C than K strategies which are adapted to more complex C-utilization patterns.

DISCUSSIONS

Continuous rice–wheat (RW) cropping in an area of 13.5 million ha with intensive tillage has resulted in over–exploitation of resources, and decline of the factor productivity, loss of soil fertility and biodiversity, decline of resource–use efficiency etc. in the Indo-Gangetic plains (IGPs) of South Asia. This has led to unsustainability of agriculture in the region. Replacement of rice with less–water requiring crops such as soybean, pigeonpea, cotton, groundnut, maize etc. in rice–wheat system and identification of efficient strategies for tillage management could result in sustainable agriculture in IGP. Besides, replacement of a cereal–cereal system with a legume–cereal system may prove beneficial for long-term sustainability of the system. Thus, the paper focuses on the development and evaluation of sustainable management practices for crop production in semi-arid subtropical Indo-Gangetic plains. For a sustainable production system, soil with high levels of biological diversity and activity, internal nutrient cycling, and resilience to disturbance is a prerequisite. Tillage alters soil physical structure exposing more organic matter to microbial attack, while no-tillage practices stimulate the formation and stabilization of macro-aggregates (Behera & Sharma, 2011). This is an important mechanism for protection and maintenance of SOM. Crop rotations involving diverse crop sequences are beneficial in terms of maintenance and improvement of soil quality. Soil management involving no-tillage and crop rotations are important practices, which can reduce soil erosion, conserve organic matter and water, and stimulate microbial activity (Zhang et al., 2012).

4.1. Crop Rotation

There was an effect of crops on the PGPB abundance, total microbial biomass, and microbial activity. The identity of crop species also influenced microorganisms, with overall higher soil microbial biomass under pigeonpea–wheat crop rotation. Therefore, the observed response of microorganisms could be derived from plant specific differences in rhizodeposition or root architecture since they can affect the ratio of C_{mic}/C_{org} (Anderson & Domsch, 1989; & Insam et al., 1989). The SOC content varied among crop rotations with the highest SOC values recorded in groundnut –wheat and the lowest in pigeonpea–wheat. These results confirm the findings of Sombrero and de Benitos (2010) on the effect that nature of crop contributes to soil surface carbon storage. In general, crop rotation had positive effect on microbial parameters or SOM and this observation is in disagreement with those of Hungaria et al. (2009).

4.2. Crop–residue addition

In the present study, crop–residue addition resulted in significantly higher levels of soil microbal activity and biomass C than without crop residue in both ZT and CT. Residue incorporation had a pronounced effect on soil microbial activity as revealed by the FDA in CT at the two physiological stages of wheat but had an significant impact on FDA in ZT. This could be explained on the basis of difference in the SOC levels in CT–R and ZT-R treatments. A significant gain in the FDA, dehydrogenase, acid and alkaline phosphatase, urease, TEG, soil organic carbon content was recorded under CT+R over CT–R at both stages of soil sampling. Zablotowicz et al. (2007) also reported similar observations in the CT, with a ryegrass cover crop. A continuous, uniform supply of C from crop residues serves as an energy source for microorganisms, improves the abundance of the microbial populations (Govaerts et al., 2008), and stimulate their activity (Martens et al., 1992). The impact of residue retention on SMBC was highly pronounced in CT, but relatively less effective in ZT at germination stage. This may be due to differences in the organic C content in the corresponding treatments. In the present study, significant gain in the soil organic carbon content following the addition of crop residue recorded, colloborates with confirm the

observation of Sombrero and Benito (2010). Influence of crop physiological stage was also apparent on the response of SMBC to residue retention.

Residue retention promotes the microbial abundance compared to residue removal Govaerts et al. (2007) and Navarro-Noya et al. (2013). The positive effect could be related to improved aggregate formation, leading to an increase in water and nutrient retention. This, in turn, increased the microbial biomass, and the stability and production of enzymes in soils.

4.3 Soil enzymes

Zero-till soils showed consistently higher values of FDA, DHA, urease and ALP compared to CT at sowing. The beneficial effect was done to higher SOC under ZT, which led to significantly higher enzyme activities compared with CT. Various workers have indicated that ZT and/or cover crop systems can alter enzymatic activity (Bandick & Dick, 1999), microbial biomass and microbial community structure (Singh et al., 2011). The ACP declined from sowing to maturity but then was not the case with ALP activity. This is because major fraction of soil ACP are derived from plant roots, and as the crop reaches maturity, the roots becomes physiologically less active. The CT+R significantly improved the soil ACP and ALP activity over the CT–R due to higher substrate availability for the microflora. Zero tillage was found to support higher FDA hydrolysis in comparison to CT only at sowing, while at maturity, the CT supported higher FDA than ZT. These results indicate that a cropping system which includes residue application can increase overall biomass and micro-flora more effectively. The increase in DHA activity following residue incorporation ranged from 63.4 - 113.8% under CT, and 54.7-122.6% under ZT from sowing to maturity. Assays of soil enzymes, revealed that residue incorporation supported the highest level of soil biological activity, the exception being FDA, urease and glucosidase activity at sowing under ZT. The lack of stimulation of the enzyme activity in ZT+R may be explained to a substrate concentration exceeding the optimum levels required for the maximum enzyme activity. The ZT supported significantly higher soil urease activity than CT due to higher substrate availability in ZT soils. Residue incorporation did not alter the urease and glucosidase enzyme activity at sowing due to immobilization of N and C. However, residue addition exerted beneficial effect at maturity of wheat Dick (1997) showed that amidase and urease activity decreased with increasing application of the end–product of the enzymatic reaction.

Phospho-monoesterases catalyse the mineralization of soil organic P. Plant roots and microorganisms selectively release P from organic matter through the production of ester-hydrolysing enzymes. An increase in the level of phosphatases reflects increased need of P and/or greater availability of organic substrate. The CT+R significantly improved the ACP and ALP activity over CT–R, indicating the beneficial response of the residue. The initial effect of residue on ACP under ZT may be due to possible feedback inhibition of enzyme by the excessive phosphate ions. Phosphatases are adaptive enzymes, and regulated by the amount of available P. At maturity, the ACP was significantly higher under ZT than CT, irrespective of residue application. Hence, this system can be advantageous under limited P conditions.

Rainy season crops of maize, pigeonpea and groundnut followed by wheat supported identical ß-glucosidase enzyme activity at sowing. The soils under cotton–wheat sequence showed the highest ß-glucosidase activity. This indicates that there are qualities unique to each crop that influences activity of specific enzymes. The rhizosphere of legumes shows increased enzyme activity. Tillage and residue management had insignificant effect on the activity of ß-glucosidase at sowing.

The residue stimulated the activity under ZT by 258%, whereas it was only 35% under CT. Under Dornbush et al. (2007) reported that β-glucosidase activity varied with environmental conditions and soil organic C substrate. Some cellulase complex enzymes respond to organic matter additions, while others are of a more constitutive nature, responding more to soil moisture and temperature (Dick, 1997). In this experiment, soil moisture was not limiting and the differences in β-glucosidase activity responded to changes in C availability of the system. Glycosidases are involved in C cycling by catalyzing decomposition and releasing energy from polysaccharides (Tabatabai, 1994). Crop residues supply labile C and P to soil, which can stimulate soil microbial biomass, enzyme activities (Ebhin Masto et al., 2006) and CO_2 evolution (Singh et al., 2011).

Removal of crop residue resulted in a decline in soil microbial biomass over corresponding treatments retaining crop residue at both stages. Zero tillage maintained a higher SMB than CT as per report by Salinas–Garcia et al. (2002). Residue retention on the surface soil causes less fluctuation in moisture and temperature (Dahiya et al., 2007) and better soil aggregation (Six et al., 2000). By retaining residue, the OC accumulates in the topsoil and microbial substrates of different quality and quantity are provided. This affects the dynamics of soil C and nutrient cycling, inducing higher SMB. Generally, SMBC increases with amount and quality of organic C and total N, which are known effects of crop–residue application (Chu et al., 2007). In the present study, the magnitude of stimulation of SMB following residue addition under ZT declined towards crop maturity, whereas under CT, significant impact of residue addition was noted. The negative effect of residue removal was less accentuated under CT at maturity, possibly due to altered soil physical and chemical properties. In crop rotations under ZT, the residues from several different crops in preceding years result in a greater diversity of substrates than in tilled soils where litter does not accumulate. The mixing action of tillage disperses patches of crop residues and soil microorganisms into a relatively uniform mixture. Our study was in subtropical setting where soils remain warm for a long or part of the year, which facilitates high rates of decomposition and mineralization, reducing the potential to build-up organic matter. The results indicate that the turnover of C and N in the microbial communities was rapid (Hungaria et al., 2009).

4.4 Dehydrogenase activity

A comparison of tillage methods revealed that ZT favoured soil microbial activity as assayed by DHA over CT, irrespective of residue application. Sharma et al. (2011) attributed the greater DHA under ZT to enhanced sequestering of soil C. The high DHA under ZT could be owing to its higher bulk density and compaction, which decreased air-filled macroporosity, resulting in deficient aeration and consequently low redox conditions of the soil. Riffaldi et al. (2002) reported negative correlation between DHA and soil aeration. Unlike FDA, the stimulation of DHA by residue addition was observed from sowing to maturity due to degradation of residues and accompanying physico-chemical changes in the soil. Further, occurrence of higher fungal population (Doran, 1980), which rapidly colonize and degrade the crop residues, led to release of easily assimilizable C favouring microbial dehydrogenases. The observed differential stimulation of microbial population under different crops may be attributed to chemical composition of the root exudates, which exert a significant influence on soil micro–flora (Singh & Mukerji, 2006). Thus, above–ground plant species regulate quantity and quality of C resources, resulting in different microbial assemblages in agro-ecosystems (Ladygina & Hedlund, 2010). These differences in the rhizodeposition accounted for the observed varieties in soil enzymes, MBC, glomalin and SOC.

Total extractable glomalin was identical in wheat following maize, pigeonpea and cotton, but significantly higher than following soybean and groundnut. The differences in the TEG as influenced by the plant species highlight the possibility of a linkage between the species composition and soil C storage (Rillig et al., 2002). The inclusion of different crop species in rotation with wheat contributed differently to glomalin production, which is responsible for soil aggregation and C sequestration. The TEG was significantly higher under ZT–R than CT confirming the findings of Helgason et al. (2010), due to negative effect of tillage on AM fungal mycelia (Castillo et al., 2006). Tillage abrades the mycelial network due to mechanical breakdown of macro-aggregates (Curaqueo et al., 2011) and consequently the production of glomalin (Borie et al., 2006). Incorporation of crop residues stimulated TEG content of soil under CT (Ngosong et al., 2010). Residue retention under ZT significantly reduced the TEG due to accumulation of soil organic matter above a threshold. Borie et al. (2006), reported higher glomalin concentrations under ZT and reduced tillage in comparison to CT with stubble. Soil compaction as encountered under the ZT may also adversely affect the AMF population. Moreover, glycoprotein and glomalin production are fungus controlled (not constitutive), and responsive to environmental factors (Rillig & Steinberg, 2002). Soil glomalin concentration was positively correlated with the occurrence of AMF (Rillig et al., 2004) and inorganic C, pH, and total C. Nutrient-rich soils are unfavorable for AMF population. This indicates that the AMF population is not favoured beyond a certain threshold level of SOM. Higher values of TEG were recorded at maturity in comparison to the sowing. The observed gain in the 2 fractions of glomalin from sowing to maturity can be explained on the basis that the glycoprotein is derived from the hyphae of AMF which are symbiotically associated with the plant roots. As the plant grows the increase in plant photosynthates in the roots resulting in proliferation of AMF hyphae and synthesis of higher amounts of glycoprotein.

Application of crop residue had positive influence on SOC and SMBC. Soil C storage and CO_2 emission responded differently to the tillage system. The initial lowering effect of residue under CO_2 emissions at sowing was absent at the maturity. Where as a reverse trend was noticed in CT. As the wheat crop proceeded towards maturity, the easily mineralizable C substrate was depleted and the treatments CT+R, ZT+R and ZT–R showed level of CO_2 emission which was significantly higher than CT–R. This led to the lowest SOC and SMBC in the soil under CT-R. Soil respiration is related to C availability in the biomass, and the greater amount of CO_2-C is generated at the upper layer of ZT soil than CT soil because of greater population and activity of soil microorganisms (Gajda & Przewoka, 2012). In our study, the SMBC at maturity of wheat was in order ZT+R> ZT-R > CT+R = CT–R, and the SOC content was in order: ZT+R > ZT–R > CT+R = CT–R. This variation can be explained on the basis of the lack of stratification of C in the soil profile under CT conditions. The impact of the residue addition was not visible as (ZT–R), (ZT+R) and CT+R were at par for CO_2 release, and significantly higher than CT–R. The low value of CO_2 emission under CT–R at maturity was due to the low SOC and SMBC. The CO_2 evolution increased from sowing to maturity of wheat due to increase in ambient temperature. A moisture has been reported by several researchers (Allison, 2005; Curie l yuste et al., 2007; & Dorodnikov et al., 2009). Groundnut–wheat recorded the lowest soil respiration and the corresponding value of the SMBC was also low. Incorporation of crop residues significantly improved SOC and reduced CO_2 emission and thus contributed to soil C sequestration in different crop rotations.

Table 1: Physico-chemical characteristics of initial soil of the experimental site

Sl. No.	Soil characteristics	0-15 cm	15-30 cm	Method followed
1.	Mechanical composition (%)			
	Sand % (2.0-0.05 mm)	55.6	55.4	
	Silt % (0.05-0.002 mm)	26	26	Bouyoucos (1962)
	Clay % (0.002 mm)	18.4	18.6	
	Texture	Sandy loam	Sandy loam	
2.	pH (1:2.5)	7.5	7.9	Jackson (1973)
3.	EC (1:2.5) (dSm^{-1})	0.35	0.31	Jackson (1980)
4.	Soil CEC [C mol (P^{+}) kg^{-1}]	10.4	9.8	Jackson (1980)
5.	Soil organic carbon (%)	0.48	0.32	Walkley and Black (1934)
6.	Available soil N (kg ha^{-1})	194	178	Subbiah and Asija (1956)
7.	Available soil P (kg ha^{-1})	9.9	5.5	Olsen *et al.* (1954),
8.	Total soil P (kg ha^{-1})	1407	824	Walker and Adams (1958)
9.	Inorganic soil P (kg ha^{-1})	870	580	Walker and Adams (1958)
10.	Organic soil P (kg ha^{-1})	537	244	Walker and Adams (1958)
11.	Available soil K (kg ha^{-1})	186	147	Hanway and Heidel (1952)
12.	Available soil S (kg ha^{-1})	16.8	39.2	Chesnin and Yien (1950)
13.	Available soil micronutrients (µg/g)			
	Mn	7.19	3.95	Lindsay and Norvell (1978)
	Fe	1.80	1.70	
	Zn	0.83	0.36	
	Cu	0.50	0.31	

Table 2: Chemical composition of different crop residues used in the field experiment

Crop residues	Nutrient content (%)						
	C	N	P	K	S	C:N	C:P
Wheat	44	0.51	0.07	1.48	0.21	86	628
Pigeonpea	42	1.26	0.09	0.41	0.26	33	466
Groundnut	41	1.92	0.20	0.83	0.25	21	205
Maize	43	0.81	0.13	0.88	0.22	53	330
Soybean	39	1.27	0.25	0.66	0.27	31	156
Cotton	42	0.50	0.21	1.67	0.24	84	200

Table 3: Soil biological parameters in wheat at germination and maturity stage as influenced by cropping systems,tillage and residue management after 5th cropping cycle

Treatment	FDA (mg kg^{-1} soil h^{-1})		Dehydrogenase (µg TPF g^{-1} soil 24 h^{-1})		Acid-phosphatase (µg PNP g^{-1} h^{-1})		Alkali-phosphatase (µg PNP g^{-1} h^{-1})	
Cropping systems	Germination	Maturity	Germination	Maturity	Germination	Maturity	Germination	Maturity
Maize	1.40	0.405	8.8	4.27	291.2	122.5	252.3	276.0
Pigeonpea	1.38	0.297	12.0	2.22	251.9	128.0	301.9	296.4
Soybean	0.92	0.743	15.7	4.05	251.5	127.4	265.0	295.4
Groundnut	1.05	0.398	25.4	7.96	304.4	100.2	245.2	269.5
Cotton	0.84	0.380	10.4	1.34	268.2	147.5	271.3	274.5
SEm±	0.036	0.013	0.25	0.283	2.84	1.67	1.17	1.92
CD (P=0.05)	0.118	0.043	0.81	0.922	9.25	5.45	3.79	6.25
Tillage and residue management								
CT–R	0.32	0.458	9.4	2.26	250.4	103.5	251.9	263.0
CT+R	0.86	0.741	15.3	4.84	300.4	119.6	309.9	272.6
ZT–R	1.60	0.289	13.0	2.72	284.4	131.8	248.3	296.0
ZT+R	1.70	0.290	20.1	6.06	258.6	145.6	258.4	297.8
SEm±	0.039	0.014	0.24	0.263	1.71	1.53	1.13	2.05
CD (P=0.05)	0.113	0.040	0.69	0.759	4.92	4.41	3.27	5.92

Table 4: Soil biological parameters in wheat at germination and maturity stage as influenced by cropping systems, tillage and residue management after 5th cropping cycle

Treatment	Urease (µg PNP g^{-1} h^{-1})		B- Glucosidase (µg PNP g^{-1} h^{-1})		Total extractable Glomalin content (µg g^{-1} soil)		pH	
Cropping systems	Germination	Maturity	Germination	Maturity	Germination	Maturity	Germination	Maturity
Maize	1300	1312	72.0	4.32	2832	4156	7.30	7.77
Pigeonpea	1339	1137	75.5	5.14	2868	4283	7.28	7.85
Soybean	1299	1166	77.2	3.48	2497	3710	7.38	7.63
Groundnut	1360	1117	73.8	4.42	2569	3743	7.20	7.57
Cotton	1287	1103	78.3	9.49	2868	4153	7.23	7.73
SEm±	31.66	2.565	1.28	0.75	16.83	3.9	0.084	0.115
CD (P=0.05)	NS	8.364	4.17	2.45	55.00	12.8	NS	NS
Tillage and residue management								
CT–R	1167	1068	75.0	4.24	2535	3822	7.28	7.75
CT+R	1141	1101	76.6	5.71	2734	4003	7.28	7.76
ZT–R	1497	1220	76.5	2.52	2924	4292	7.36	7.47
ZT+R	1463	1279	73.4	9.02	2716	3919	7.18	7.84
SEm±	20.57	2.069	1.34	0.435	21. 97	4.3	0.055	0.073
CD (P=0.05)	59.38	5.973	NS	1.255	63.44	12.35	NS	NS

Table 5: Plant growth promoting bacterial groups in wheat at germination and maturity stage as influenced by cropping systems, tillage and residue management after 5th cropping cycle

Treatment	*Azotobacter* (log cfu g^{-1}dry weight of soil)		Phosphate solubilizing bacteria (log cfu g^{-1} dry weight of soil)		Fluorescent pseudomonas (log cfu g^{-1} dry weight of soil)	
Preceding crops	Germination	Maturity	Germination	Maturity	Germination	Maturity
Maize	3.96	3.89	6.62	6.94	5.60	7.75
Pigeonpea	3.80	3.80	6.38	6.85	6.67	7.78
Soybean	4.04	3.71	6.08	7.01	6.17	7.473
Groundnut	3.48	3.38	6.45	6.57	6.62	7.47
Cotton	3.26	3.74	6.44	6.25	6.31	7.75
SEm±	0.070	0.180	0.075	0.087	0.099	0.164
CD (P=0.05)	0.227	0.588	0.245	0.284	0.322	NS
Tillage and residue management						
CT–R	3.92	3.69	6.41	6.78	6.74	6.86
CT+R	3.48	3.78	6.13	6.73	6.90	7.19
ZT–R	3.40	3.42	6.58	6.63	5.74	7.56
ZT+R	4.04	3.92	6.45	6.75	5.72	8. 97
SEm±	0.095	0.091	0.135	0.09	0.132	0.095
CD (P=0.05)	0.275	0.262	NS	0.259	0.382	0.274

Table 6: Soil biological parameters in wheat at germination and maturity stage as influenced by cropping systems, tillage and residue management after 5th cropping cycle

Treatment	Organic C (%)	Microbial C biomass (µg g^{-1} dry weight of soil)		Soil respiration (mg CO_2 1000 g^{-1} soil $week^{-1}$)		Metabolic quotient (q CO_2) (µg CO_2-C µg^{-1} biomass C h^{-1} x10^{-3})	
Preceding crops	Maturity	Germination	Maturity	Germination	Maturity	Germination	Maturity
Maize	0.54	553.3	432.9	16.2	22.0	1.74	3.02
Pigeonpea	0.51	667.9	532.5	17.8	25.5	1.58	2.85
Soybean	0.52	508.6	425.4	17.7	22.1	2.07	3.09
Groundnut	0.59	454.8	333.6	15.2	24.0	1.99	4.20
Cotton	0.54	491.3	457.2	18.2	25.1	2.20	3.27
SEm±	0.050	1.01	0.95	0.55	0.25		
CD (P=0.05)	0.163	2.90	3.08	1.79	0.81		
Tillage and residue management							
CT–R	0.46	427.9	426.7	19.4	20.9	2.70	2.91
CT+R	0.50	519.4	428.5	13.6	24.1	1.56	3.35
ZT–R	0.57	559.2	477.0	18.5	24.8	1.96	3.09
ZT+R	0.62	634.1	493.0	16.5	25.1	1.54	3.03
SEm±	0.032	1.05	0.60	0.35	0.47		
CD (P=0.05)	0.094	3.05	1.74	1.02	1.36		

CONCLUSION

Conservation agriculture-land involving new tillage with retention of crop residues proved to be an effective management practice improving soil microbial parameters in wheat-based cropping system. Further, residue retention is not beneficial for improving the glomalin content in conventional tillage, thereby it is an option to improve soil fertility and helps in carbon sequestration in semi–arid subtropical soils, under zero till wheat–based cropping systems.

REFERENCES

Allison, S. D. (2005). Cheaters, diffusion and nutrients constrain decomposition by microbial enzymes in spatially structured environments. *Ecology Letters*, *8*, 626–635.

Anderson, T. H., & Domsch, K. H. (1989). Ratios of microbial biomass carbon to total organic carbon in arable soils. *Soil Biology and Biochemistry*, *21*, 471–479.

Araújo, M. A. V., Mendonça–Hagler, L. C., Hagler, A. N., & Elsas, J. D. (1996). Selection of rhizosphere–competent Pseudomonas strains as biocontrol agents in tropical soils. *World Journal of Microbiology & Biotechnology*, *12*, 589–593.

Bandick, A. K., & Dick, R. P. (1999). Field management effects on soil enzyme activities. *Soil Biology and Biochemistry*, *31*, 1471–1479.

Barnes, R. J., Baxter, S. J., & Lark, R. M. (2007). Spatial covariation of Azotobacter abundance and soil properties: A case study using the wavelet transform. *Soil Biology and Biochemistry*, *39*, 295–310.

Behera, U. K., & Sharma, A. R. (2011). Effect of conservation tillage on performance of greengram– mustard–cowpea cropping system. *Journal of Soil and Water Conservation*, *10*, 233–236.

Borges, C. D., Corá, J. E., Barbosa, J. C., & Nahas, E. (2012). Soil microbiological attributes under summer/winter crops rotation in a no–tillage system. *Archives of Agronomy and Soil Science*, *59*, 1471–1485.

Borie, F., Rubio, R., Rouanet, J. L., Morales, A., Borie, G., & Rojas, C. (2006). Effects of tillage systems on soil characteristics, glomalin and mycorrhizal propagules in a Chilean Ultisol. *Soil and Tillage Research*, *88*, 253–261.

Bouyoucos, G. J. (1962). Hydrometer method for making particle size analysis of soils. *Journal of Agronomy*, *54*, 464.

Casida, L. E. (Jr.) (1964). Soil dehydrogenase activity. *Soil Science*, *98*, 371–376.

Castillo, C. G., Rubio, R., Rouanet, J. L., & Borie, F. (2006). Early effects of tillage and crop rotation on arbuscular mycorrhizal fungal propagules in an Ultisol. *Biology and Fertility of Soils*, *43*, 83–92.

Ceja–Navarro, J. A., Rivera–Orduna, F. N., Patino–Zuniga, L., Vila–Sanjurjo, A., Crossa, J., Govaerts, B., & Dendooven, L. (2010). Phylogenetic and multivariate analyses to determine the effects of different tillage and residue management practices on soil bacterial communities. *Applied and environmental microbiology*, *76*, 3685–3691.

Chesnin, L., & Yien, C. H. (1950). Turbidimetric determination of available sulphates. *Soil Science Society of America, Proceedings*, *14*, 149–151.

Chu, H., Lin, X., Fujii, T., Morimoto, S., Yagi, K., Hu, J., & Zhang, J. (2007). Soil microbial biomass, dehydrogenase activity, bacterial community structure in response to long–term fertilizer management. *Soil Biology and Biochemistry*, *39*, 2971–2976.

Crecchio, C., Curci, M., Mininni, R., Ricciuti, P., & Ruggiero, P. (2001). Short–term effects of municipal solid waste compost amendments on soil carbon and nitrogen content, some enzyme activities and genetic diversity. *Biology and Fertility of Soils*, *34*, 311–318.

Curaqueo, G., Barea, J. M., Acevedo, E., Rubio, R., Cornejo, P., & Borie, F. (2011). Effects of different tillage system on arbuscular mycorrhizal fungal propagules and physical properties in a Mediterranean agroecosystem in central Chile. *Soil and Tillage Research*, *113*, 11–18.

Curiel Yuste, J., Baldocchi, D. D., Gershenson, A., Goldstein, A., Misson, L., & Wong, S. (2007).

Microbial soil respiration and its dependency on carbon inputs, soil temperature and moisture. *Global change biology. Bioenergy*, *13*, 2018–2035.

Dahiya, R., Ingwersen, J., & Streck, T. (2007). The effect of mulching and tillage on the water and temperature regimes of a loess soil: Experimental findings and modeling. *Soil and Tillage Research*, *96*, 52–63.

Dhillion, S. (1997). Fallow age influences microbial functional abilities, soil properties and plant functional groups. (in): *Microbial Communities* pp. 140–148. Insam, H., & Rangger, A., (Eds). Springer, Berlin Heidelberg.

Díaz–Raviña, M., Acea, M. J., & Carballas, T. (1995). Seasonal changes in microbial biomass and nutrient flush in forest soils. *Biology and Fertility of Soils*, *19*, 220–226.

Dick, R. P. (1994). Soil enzyme activities as indicator of soil quality. (in) *Defining Soil Quality for a sustainable Environment*, pp. 107–124. Doran, J. W., Coleman, D. C., Bezdicek, D. F., & Stewart, B. A. (Eds.) SSSA Special publication No. 35, Madison, WI.

Dick, R. P. (1997). Soil enzyme activities as integrative indicators of soil health. (in) *Biological Indicators of Soil Health* pp. 121–156. Pankhurst, C. E., Doube, B. M., & Gupta, V. V. S. R. (Eds.), CAB international, Oxford, UK.

Dick, R. P., Breakwell, D. P., & Turco, R. F. (1996). Soil enzyme activities and biodiversity measurements as integrative microbiological indicators. Methods for Assessing Soil Quality, (in) Doran, J. W., & Jones, A. J. (Eds.), *Soil Science Society of America Journal* pp. 247–271.

Dick, W. A. (1984). Influence of long–term tillage and crop rotation combinations on soil enzyme activities1. *Soil Science Society of America Journal*, *48*, 569–574.

Doran, J. W. (1980). Soil microbial and biochemical changes associated with reduced tillage. *Soil Science Society of America Journal*, *44*, 765–771.

Dornbush, M. E. (2007) Grasses, litter, and their interaction affect microbial biomass and soil enzyme activity. *Soil Biology and Biochemistry*, *39*, 2241–2249.

Dorodnikov, M., Blagodatskaya, E., Blagodatsky, S., Marhan, S., Fangmeier, A., & Kuzyakov, Y. (2009). Stimulation of microbial extracellular enzyme activities by elevated CO_2 depends on soil aggregate size. *Global change biology. Bioenergy*, *15*, 1603–1614.

Ebhin Masto, R., Chhonkar, P. K., Singh, D., & Patra, A. K. (2006). Changes in soil biological and biochemical characteristics in a long–term field trial on a sub–tropical inceptisol. *Soil Biology and Biochemistry*, *38*, 1577–1582.

Eivazi, F., & Tabatabai, M. A. (1988). Glucosidases and galactosidases in soils. *Soil Biology and Biochemistry*, *20*, 601–606.

Eivazi, F., & Tabatabai, M. A. (1990). Factors affecting glucosidase and galactosidase activities in soils. *Soil Biology and Biochemistry*, *22*, 891–897.

Ekenler, M., & Tabatabai, M. A. (2003). Tillage and residue management effects on β–glucosaminidase activity in soils. *Soil Biology and Biochemistry*, *35*, 871–874.

Feng, Y., Motta, A. C., Reeves, D. W., Burmester, C. H., Van Santen, E., & Osborne, J. A. (2003). Soil microbial communities under conventional–till and no–till continuous cotton systems. *Soil Biology and Biochemistry*, *35*, 1693–1703.

Fontaine, S., & Barot, S. (2005). Size and functional diversity of microbe populations control plant persistence and long–term soil carbon

accumulation. *Ecology Letters*, *8*, 1075–1087.

Franchini, J. C., Crispino, C. C., Souza, R. A., Torres, E., & Hungria, M. (2007). Microbiological parameters as indicators of soil quality under various soil management and crop rotation systems in southern Brazil. *Soil and Tillage Research*, *92*, 18–29.

Franzluebbers, A. J., Hons, F. M., & Zuberer, D. A. (1995). Tillage and crop effects on seasonal dynamics of soil CO_2 evolution, water content, temperature, and bulk density. *Applied Soil Ecology*, *2*, 95–109.

Franzluebbers, A. J., & Stuedemann, J. A. (2008). Early response of soil organic fractions to tillage and integrated crop–livestock production. *Soil Science Society of America Journal*, *72*, 613–625.

Gajda, A., & Przewłoka, B. (2012). Soil biological activity as affected by tillage intensity. *International Agrophysics*, p. 15.

Gomez, K. A., & Gomez, A. A. (1985). Statistical Procedures for Agricultural Research. John Wiley & Sons Inc., New York.

Govaerts, B., Mezzalama, M., Sayre, K. D., Crossa, J., Lichter, K., Troch, V., Vanherck, K., De Corte, P., & Deckers, J. (2008). Long–term consequences of tillage, residue management, and crop rotation on selected soil micro–flora groups in the subtropical highlands. *Applied Soil Ecology*, *38*, 197–210.

Govaerts, B., Mezzalama, M., Unno, Y., Sayre, K. D., Luna–Guido, M., Vanherck, K., Dendooven, L., & Deckers, J. (2007). Influence of tillage, residue management, and crop rotation on soil microbial biomass and catabolic diversity. *Applied Soil Ecology*, *37*, 18–30.

Green, V. S., Stott, D. E., & Diack, M. (2006). Assay for fluoresce in diacetate hydrolytic activity: Optimization for soil samples. *Soil Biology and Biochemistry*, *38*, 693–701.

Haddad, M. J., & Sarkar, D. (2003). Glomalin, a newly discovered component of soil organic matter: Part II—Relationship with soil properties. *Environmental Geosciences*, *10*, 99–106.

Hallett, P., Feeney, D., Bengough, A. G., Rillig, M., Scrimgeour, C., & Young, I. (2009). Disentangling the impact of AM fungi versus roots on soil structure and water transport. *Plant Soil*, *314*, 183–196.

Hanway, J. J., & Heidal, H. (1952). Soil analysis methods as used in Iowa state college soil testing laboratory. *Iowa Agriculture*, *57*, 1–31.

Helgason, B. L., Walley, F. L., & Germida, J. J. (2010). No–till soil management increases microbial biomass and alters community profiles in soil aggregates. *Applied Soil Ecology*, *46*, 390–397.

Hernanz, J. L., López, R., Navarrete, L., & Sánchez–Girón, V. (2002). Long–term effects of tillage systems and rotations on soil structural stability and organic carbon stratification in semiarid central Spain *Soil and Tillage Research*, *66*, 129–141.

Hungaria, M., Franchini, J. C., Brandão–Junior, O., Kaschuk, G., & Souza, R. A. (2009). Soil microbial activity and crop sustainability in a long–term experiment with three soil–tillage and two crop–rotation systems. *Applied Soil Ecology*, *42*, 288–296.

Insam, H. (1990). Are the soil microbial biomass and basal respiration governed by the climatic regime? *Soil Biology and Biochemistry*, *22*, 525–532.

Insam, H., Parkinson, D., & Domsch, K. H. (1989). Influence of macroclimate on soil microbial biomass. *Soil Biology and Biochemistry*, *21*, 211–221.

Jackson, M. L. (1973). Soil Chemical Analysis. Prentice Hall of India Pvt. Ltd., New Delhi.

Jackson, M. L. (1980). Soil Chemical Analysis. Prentice Hall of India Pvt. Ltd., New Delhi, India.

Jensen, H. L. (1954). The Azotobacteriaceae. *Bacteriological Reviews*, *18*, 195–214.

King, E. O., Ward, M. K., & Raney, D. E. (1954). Two simple media for the demonstration of pyocyanin and fluorescin. *Journal of Laboratory and Clinical Medicine*, *44*, 301–307.

Kirchner, M. J., Wollum, A. G., & King, L. D. (1993). Soil microbial populations and activities in reduced chemical input agroecosystems. *Soil Science Society of America Journal*, *57*, 1289–1295.

Kowalchuk, G. A., Buma, D., de Boer, W., Klinkhamer, P. L., & van Veen, J. (2002) Effects of above–ground plant species composition and diversity on the diversity of soil–borne microorganisms. *Antonie Van Leeuwenhoek*, *81*, 509–520.

Ladd, J. N. (1978). Origin and range of enzymes in soil. (in) *Soil Enzymes*, pp. 51–96. Burns, R.G. (Ed.). Academic Press, London.

Ladd, J. N., Amato, M., Zhou, L. K., & Schultz, J. E. (1994). Differential effects of rotation, plant residue and nitrogen fertilizer on microbial biomass and organic matter in an Australian alfisol. *Soil Biology and Biochemistry*, *26*, 821–831.

Ladygina, N., & Hedlund, K. (2010). Plant species influence microbial diversity and carbon allocation in the rhizosphere. *Soil Biology and Biochemistry*, *42*, 162–168.

Lindsay, W. L., & Norvell, W. A. (1978). Development of DTPA soil test for Zinc, Iron, manganese and copper. *Soil Science Society of America Journal*, *42*, 421–428.

Lupwayi, N. Z., Rice, W. A., & Clayton, G. W. (1998). Soil microbial diversity and community structure under wheat as influenced by tillage and crop rotation. *Soil Biology and Biochemistry*, *30*, 1733–1741.

Madejón, E., Moreno, F., Murillo, J. M., & Pelegrín, F. (2007). Soil biochemical response to long–term conservation tillage under semi–arid Mediterranean conditions. *Soil and Tillage Research*, *94*, 346–352.

Marinari, S., Masciandaro, G., Ceccanti, B., & Grego, S. (2000). Influence of organic and mineral fertilisers on soil biological and physical properties. *Bioresource Technology*, *72*, 9–17.

Martens, D. A., Johanson, J. B., & Frankenberger, W. T. J. (1992). Production and persistence of soil enzymes with repeated addition of organic residues. *Soil Science*, *153*, 53–61.

Nannipieri, P., Grego, S., & Ceccanti, B. (1990). Ecological significance of the biological activity in soils. (in), *Soil Biochemistry* pp. 293–355. Bollag, J. M., & Stotzky, G., (Eds.) Marcel Dekker, New York,

Navarro–Noya, Y. E., Gómez–Acata, S., Montoya–Ciriaco, N., Rojas–Valdez, A., Suárez–Arriaga, M. C., Valenzuela–Encinas, C., Jiménez–Bueno, N., Verhulst, N., Govaerts, B., & Dendooven, L. (2013). Relative impacts of tillage, residue management and crop–rotation on soil bacterial communities in a semi–arid agroecosystem. *Soil Biology and Biochemistry*, *65*, 86–95.

Ngosong, C., Jarosch, M., Raupp, J., Neumann, E., & Ruess, L. (2010). The impact of farming practice on soil microorganisms and arbuscular mycorrhizal fungi: Crop type versus long–term mineral and organic fertilization. *Applied Soil Ecology*, *46*, 134–142.

Olsen, S. R., Cole, C. V., Watanabe, F. S., & Dean, L. A. (1954). Estimation of available phosphorus in soils by extracting with sodium bicarbonate. USDA Circular No. 939.

Patiño–Zúñiga, L., Ceja–Navarro, J. A., Govaerts, B., Luna–Guido, M., Sayre,

K. D., & Dendooven, L. (2009). The effect of different tillage and residue management practices on soil characteristics, inorganic N dynamics and emissions of N_2O, CO_2 and CH_4 in the central highlands of Mexico: a laboratory study. *Plant and Soil*, *314*, 231–241.

Pikovskaya, R. I. (1948). Mobilization of phosphorus in soil in connection with vital activity of some microbial species. *Microbiologiya*, *17*, 362–370.

Pikul, J. L., Chilom, G., Rice, J., Eynard, A., Schumacher, T. E., Nichols, K., Johnson, J. M. F., Wright, S., Caesar, T., & Ellsbury, M. (2009). Organic matter and water stability of field aggregates affected by tillage in South Dakota. *Soil Science Society of America Journal*, *73*, 197–206.

Riffaldi, R., Saviozzi, A., Levi–Minzi, R., & Cardelli, R. (2002). Biochemical properties of a Mediterranean soil as affected by long–term crop management systems. *Soil and Tillage Research*, *67*, 109–114.

Rillig, M., Wright, S., Nichols, K., Schmidt, W., & Torn, M. (2001). Large contribution of arbuscular mycorrhizal fungi to soil carbon pools in tropical forest soils. *Plant and Soil*, *233*, 167–177.

Rillig, M. C. (2004). Arbuscular mycorrhizae, glomalin, and soil aggregation. *Canadian Journal of Soil Science*, *84*, 355–363.

Rillig, M. C., & Mummey, D. L. (2006). Mycorrhizas and soil structure. *New Phytologist*, *171*, 41–53.

Rillig, M. C., & Steinberg, P. D. (2002). Glomalin production by an arbuscular mycorrhizal fungus: a mechanism of habitat modification? *Soil Biology and Biochemistry*, *34*, 1371–1374.

Rillig, M. C., Wright, S. F., Kimball, B. A., Pinter, P. J., Wall, G. W., Ottman, M. J., & Leavitt, S. W. (2001). Elevated carbon dioxide and irrigation effects on water stable aggregates in a Sorghum field: a possible role for arbuscular mycorrhizal fungi. *Global Change Biology*, *7*, 333–337.

Rillig, M. C., Wright, S. F., Shaw, M. R., & Field, C. B. (2002). Artificial climate warming positively affects arbuscular mycorrhizae but decreases soil aggregate water stability in an annual grassland. *Oikos*, *97*, 52–58.

Roldán, A., Salinas–García, J. R., Alguacil, M. M., Díaz, E., & Caravaca, F. (2005). Soil enzyme activities suggest advantages of conservation tillage practices in sorghum cultivation under subtropical conditions. *Geoderma*, *129*, 178–185.

Salinas–García, J. R., Velázquez–García, J. D. J., Gallardo–Valdez, M., Díaz–Mederos, P., Caballero–Hernández, F., Tapia–Vargas, L. M., & Rosales–Robles, E. (2002). Tillage effects on microbial biomass and nutrient distribution in soils under rain–fed corn production in central–western Mexico. *Soil and Tillage Research*, *66*, 143–152.

Sharma, P., Singh, G., & Singh, R. P. (2011). Conservation tillage, optimal water and organic nutrient supply enhance soil microbial activities during wheat (Triticum aestivum L.) cultivation. *Brazilian Journal of Microbiology*, *42*, 531–542.

Singh, G., Kumar, D., Marwaha, T. S., Singh, A. K., & Srinivasmurthy, K. (2011). Conservation tillage and integrated nitrogen management stimulates soil microbial properties under varying water regimes in maize–wheat cropping system in northern India. *Archives of agronomy and soil science*, *57*, 507–521.

Singh, G., & Mukerji, K. (2006). Root exudates as determinant of rhizospheric microbial biodiversity, (in): *Microbial Activity in the Rhizoshere* pp. 39–53. Mukerji, K. G., Manoharachary, C., &Singh, J., (Eds.). Springer Berlin Heidelberg.

Six, J., Conant, R. T., Paul, E. A., & Paustian, K. (2002). Stabilization mechanisms of soil organic matter: Implications for C–saturation of soils. *Plant and Soil*, *241*, 155–176.

Six, J., Elliott, E. T., & Paustian, K. (2000). Soil macroaggregate turnover and microaggregate formation: a mechanism for C sequestration under no–tillage agriculture. *Soil Biology and Biochemistry*, *32*, 2099–2103.

Sombrero, A., & De Benito, A. (2010). Carbon accumulation in soil. Ten–year study of conservation tillage and crop rotation in a semi–arid area of Castile–Leon, Spain. *Soil and Tillage Research*, *107*, 64–70.

Stotzky, G. (1965). Microbial respiration. (in): *Methods of Soil Analysis. Part 2. Chemical and Microbiological Properties* pp. 1550–1572.

Subbiah, B. V., & Asija, G. L. (1956). A rapid procedure for the estimation of available Nitrogen in soil. *Current Science*, *25*, 259–260.

Tabatabai, M. A. (1994). Soil Enzymes, (in): Bottomley, P. S., Angle, J. S., & Weaver, R.W., (Eds.), Methods of Soil Analysis: Part 2—Microbiological and Biochemical Properties. *Soil Science Society of America Journal* pp. 775–833.

Tabatabai, M. A., & Bremner, J. M. (1969). Use of p–nitrophenyl phosphate for assay of soil phosphatase activity. *Soil Biology and Biochemistry*, *1*, 301–307.

Vance, E. D., Brookes, P. C., & Jenkinson, D. S. (1987). Microbial biomass measurements in forest soils: The use of the chloroform fumigation–incubation method in strongly acid soils. *Soil Biology and Biochemistry*, *19*, 697–702.

Walker, T. W., & Adams, A. F. R. (1958). Indices in soil organic matter. *Soil Science*, *85*, 307–318.

Walkley, A., & Black, I. A. (1934). An examination of Degtjareff method for determining soil organic matter and a proposed modification of the chromic acid titration method. *Soil Science*, *37*, 29–38.

Wang, Q., Bai, Y., Gao, H., He, J., Chen, H., Chesney, R. C., Kuhn, N. J., & Li, H. (2008). Soil chemical properties and microbial biomass after 16 years of no–tillage farming on the Loess Plateau, China. *Geoderma*, *144*, 502–508.

Watanabe, F. S., & Olsen, S. R. (1965). Test of an ascorbic acid method for determining phosphorus in water and $NaHCO_3$ extracts from soil. *Soil Science Society of America Journal*, *29*, 677–678.

Wright, S. F., & Upadhyaya, A. (1996). Extraction of an abundant and unusual protein from soil and comparison with hyphal protein of arbuscular mycorrhizal fungi. *Soil Science*, *161*, 575–586.

Zablotowicz, R., Locke, M., & Gaston, L. (2007). Tillage and cover effects on soil microbial properties and fluometuron degradation. *Biology and Fertility of Soils*, *44*, 27–35.

Zhang, S., Li, Q., Zhang, X., Wei, K., Chen, L., & Liang, W. (2012). Effects of conservation tillage on soil aggregation and aggregate binding agents in black soil of Northeast China. *Soil and Tillage Research*, *124*, 196–202.