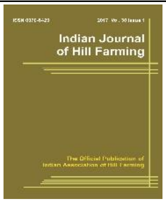
Content list available at http://epubs.icar.org.in, www.kiran.nic.in; ISSN: 0970-6429

Indian Journal of Hill Farming

June 2017, Volume 30, Issue 1, Page 1-6



Role of Crop Residue Management Practices on Microbial Dynamics of Soil – A Mini Review

Richa Rajput[1*] • Kusum Arunachalam[1] • A. Arunachalam[2]

[1]School of Environment and Natural Resources, Doon University, Dehradun 248001, Uttarakhand

[2]Indian Council of Agricultural Research, Krishi Bhawan, New Delhi 110001

ARTICLE INFO

Article history:
Received 3 April 2016
Revision Received 25 September 2016
Accepted 17 January 2017

Key words:
Crop residue, compost, biochar, microbial community shift, soil enzymes

ABSTRACT

The role of microbial species in maintaining the soil fertility is well established. There are various procedures which can be utilized to improve or change the microbial community structure of any soil type by amending it with various soil conditioning treatments. In this mini review changes in microbial community structure have been delineated under different crop residue management practices. Overall, various papers studied reported the synergistic effects on soil nutrient status improvement though there were some papers which quoted no improved results at all. However microbial community structure under different processes is imperative to biogeochemical cycling. Keeping in view the importance of soil microbes, an attempt has been made to identify key researchable areas for better understanding of the functional group in soil metabolism vis-à-vis soil health.

1. Introduction

For an agro-ecosystem, optimal level of soil nutrient status has to be maintained in order to sustain soil productivity. Crop residue mulch is one way to maintain the fertility of the soil on the farm. Nonetheless, the most feasible examples known to manage agricultural waste include farm yard manure, pit composting, making of biochar by pyrolysis and as burnt in shifting agricultural fields. The rate of nutrient release not only depends on the technique followed, but also on the quality of crop residue. Biological nitrogen fixation by leguminous crops and the recycling of the fixed nitrogen when leguminous crop residues are returned to soil can be a significant source of nitrogen to the soil nutrient pool as well as for subsequent plant uptake. Information on the kinetics of decomposition of crop residues and mineralization-immobilization turnover of different quality residues (leguminous and non-leguminous) is required to ascertain the actual amount of crop residues needed to maintain the soil productivity and to ensure environmental protection by minimizing nutrient losses and soil erosion (Strand and Benford 2009).

Another aspect of crop residue management is its effect on the microbial community that regulates soil health. The microbes mineralize organic matter and release essential nutrients into the soil, enabling the biogeochemical process. Thus, even application of different processed decomposed crop residues therefore could affect the diversity and dynamics of microbes present in the soil leading to enhanced or reduced nitrogen and carbon fixation in the crop. All over, the plant-soil-microbe interactions can be visualized as the key-factor of soil fertility management. The inter-dependence of soil, microbial activity, decomposition, detoxification and soil structure formation and their selective impact on soil constraints suggest the manipulation of soil biological processes to improve the soil fertility, but this is often an overlooked management strategy. Despite of well known role of microbes in the soil, not much heed has been paid to the study of their community structure under different crop residue management practices. The present review focuses on the shift in microbial community diversification in various crop residue managing practices and their impact on overall soil nutrient status.

---

*Corresponding author: richa.jan85@gmail.com

2. Conventional crop residue retention and no-retention effect on soil microbial dynamics

Due to the scarcity of alternative organic amendments, the retention of crop residue in fields can be considered key in promoting physical, chemical, and biological attributes of soil health in agricultural systems of developing countries (Marie-Soleil Turmel et al; 2014). In specific, the innumerable benefits of crop residue retention include increase in carbon storage, soil quality, soil organic matter, enhanced nutrient release rate, less soil erosion, organic weed control and other environment and health benefits. Amino sugars are considered as microbial residue biomarkers involved in microbial mediated soil organic matter cycling. For instance, Ding *et al.* (2011) reported 59% increase in amino sugars in no-till plots as compared with conventionally tilled plots. Highlighting the positive effects of no-till that promotes the accumulation of microbial-derived organic matter. It is also evident from the results that microbial community shifted towards fungal dominance under no tillage and the phenomenon was more pronounced within the 0–5 cm layers. When no-till systems were evaluated, the type of crop rotation used had a significant influence on the soil amino sugar content. Significant enrichment of total amino sugars (1042–1317 mg kg^{-1} soil) occurred in the continuous corn monoculture system as compared with the corn–soybean rotation field (943–1112 mg kg^{-1}soil) in the top 0-20 cm soil layers. **(**Xueli Ding *et al.,* 2011).

In 1991, the International Maize and Wheat Improvement Center (CIMMYT) initiated a long-term field experiment at its semi-arid highland experiment station in Mexico (2240 masl; 19.318N, 98.508W; Cumulic Phaeozem) to investigate the long-term effects of tillage/seeding practices, crop rotations, and crop residue management on maize and wheat grown under rain fed conditions. Soil ecological status was evaluated to determine the different soil management practices on soil microbial biomass (substrate-induced respiration (SIR) and chloroform fumigation incubation (CFI)) and micro-flora physiological and catabolic diversity (BIOLOGTM ecoplate well system). SMB-C (CFI, SIR) was significantly and respectively 1.2 and 1.3 times higher for residue retention (average 387 mg C kg1 dry soil and 515 mg C kg1 dry soil, respectively) compared to residue removal. The average well color development (AWCD) obtained by the BIOLOGTM ecoplate essay was implemented to study catabolic capability of soil microbial communities after 15 years of contrasting management practices. While maize and wheat rotation under conventional tillage with residue retention showed a significantly higher overall AWCD value compared to the other treatments, AWCD of maize with zero tillage and residue removal was significantly lower than in the other treatments. It has been further reported that AWCD was significantly higher for residue retention compared to residue removal and for wheat as compared to maize. (Bram Govaerts et al., 2007). In the dry tropical cropland in Tanzania, the potential role of soil microbes has assessed as a temporal N sink–source to conserve the available soil N until later crop growth, which generally requires substantial crop N uptake. The evaluation of the effect of land management [i.e., no input, plant residue application before planting (P plot) with or without fertilizer application, fertilizer application alone, and non-cultivated plots] on the relationship between soil N pool [microbial biomass N (MBN) and inorganic N] and crop N uptake throughout the ∼120-d crop growth period in two consecutive years was studied. The results showed that plant residue application before planting should enhance the role of soil microbes as a temporal N sink–source, leading to the conservation of potentially leachable N until later phase of crop growth, especially in years in which N leaching is relatively severe. (Soh Sugihara *et al.,* 2012)

Different tillage and stubble management practices were compared at two sites in New South Wales, Australia, to determine their effect on soil chemical and microbiological properties and the development of suppression towards *Gaeumannomyces graminis* var. *tritici* (*Ggt*) and *Rhizoctonia solani*. At one site (Harden), the management practices were direct-drilling of crops with stubble retained (DD) and conventional sowing of crops with stubble burnt (CC) for 6 years prior to sampling. At the second site (Cowra), a stubble incorporated (SI) treatment (SI with a single cultivation prior to sowing) was compared with DD and CC treatments and the practices had been in place for 16 years. By comparing the difference in plant growth in γ-irradiated and natural (unsterilised) soil in the presence of added *Ggt* and *Rhizoctonia* inoculum, evidence of suppression towards *Ggt* was observed in soil from both the sites. The suppression was greater in the DD compared to the CC soils. This was associated with higher levels of organic C and total N in the DD compared to the CC soils at Cowra and with higher microbial biomass, CO_2 respiration and populations of fungi (including cellulolytic fungi) in the DD compared to the CC soils at both the sites (Pankhurst *et al.*, 2002). Liang *et al.* (2014) recently studied the soil microbial properties and processes to evaluate the suitability of several legumes cover crops and termination methods for organic transition in south-eastern USA. They collected samples from two newly-established study sites, each containing 12 treatments of three termination methods (disk, flail, and spray) and four cover types (no cover crop, Austrian winter pea, hairy vetch, and crimson clover).

Compared to disking and spraying, flail mowing significantly increased soil microbial biomass C by ∼17%, C mineralization by ∼25%, N mineralization by ∼16%, and nitrification potential by ∼36%, 12 weeks after cover crop termination. Furthermore, the activities of soil enzymes (exoglucanase, β-glucosidase, and β-glucosaminidase) appeared to be more responsive to cover types than to termination methods. Among three cover crops, Austrian winter pea showed the greatest positive effects on nitrification potential, β-glucosidase, and β-glucosaminidase. The ratio of C mineralization to microbial biomass C also differed with cover types, being lowest in Austrian winter pea. Their results indicated that legume species even with small differences in C-to-N ratio and lignin and cellulose contents had varied effects on soil microbial properties and processes. Nitrification potential, representing the function of a small group of soil microbial community, was proved to be sensitive to both legume species and termination methods.

3. Microbial community shifts in soil amended with compost

Soil microbial community structure and crop yield was studied by Carrera *et al.* (2007) in field tomato production systems that compared black polyethylene mulch to hairy vetch mulch and inorganic N to organic N. They reported that fatty acid analysis was used to characterize the total soil microbial community structure, while two substrate utilization assays were used to investigate the community structure of cultivable bacteria and fungi. Crop yield was not significantly increased by hairy vetch cover cropping when compared to black polyethylene mulch, although microbial community structure was significantly affected by cover cropping. Under the black polyethylene mulch, crop yield significantly increased by the highest levels of compost and manure when compared to inorganic fertilizer, but there was no detectable effect on the soil microbial community structure. This study inferred that there is no hard and fast rule to establish the effect of microbial community on crop yield. Therefore, there might be many other factors that play role in enhanced crop productivity.

In a similar study, the impact of five years' applications of different organic and mineral fertilizers on wheat grain yields and soil chemical and microbial characteristics was assessed by Cherif *et al.* (2009). Soils were treated with municipal solid waste compost at rates of 40 (C1) and 80 (C2) Mg ha^{-1}, farmyard manure at a rate of 40 Mg ha^{-1} (M), chemical fertilizers (Cf) and the combinations (C1Cf, C2Cf, MCf). Wheat grain yield was found to be enhanced with all amendments.

Despite polluting effects on soil determined by the treatments, no significant differences between treatments were observed in total bacterial count and soil bacterial community structure, as shown by 16S rRNA gene PCR-denaturing gradient gel electrophoresis banding patterns and 16S rRNA gene Length Heterogeneity-PCR analysis. Similar results were obtained in this study also with different treatments. There was increased wheat grain output, but it cannot be attributed to microbial community structure of the soil amended with the treatments, because no significant shift in the soil microbial structure. The development of communities of three important composting players including actinobacteria, fungi and clostridia was explored during the composting of wheat straw for mushroom production. The results revealed the presence of highly diversified actinobacteria and fungal communities during the composting process. The diversity of the fungal community, however, sharply decreased in the mature compost. Furthermore, an apparent succession of both actinobacteria and fungi with intensive changes in the composition of communities was demonstrated during composting. Notably, cellulolytic actinomycetal and fungal genera represented by *Thermopolyspora*, *Microbispora* and *Humicola* were highly enriched in the mature compost. Analysis of the key cellulolytic genes revealed their prevalence at different composting stages including several novel glycoside hydrolase family 48 exocellulase lineages. The community of cellulolytic microbiota also changed substantially over time. The author suggested that prevalence of the diversified cellulolytic microorganisms holds the great potential of mining novel lignocellulose decomposing enzymes from this specific ecosystem. The study of microbial community during the making of compost also gives a detail insight on the successive microbial community role. It was observed that in mature compost the fungal abundance decreased that is initially the higher rate of decomposition occurs because of fungal species but as the compost started maturing the fugal species exhausted of its substrate. It can therefore be taken as a measure to check the compost maturity index based on microbial community shift (Zhang *et al.,* 2014). The effectiveness of compost supply at several doses (0, 50, 100, and 150 t/ha) to a saline soil was studied using municipal solid waste (MSW) and palm waste (PW) composts. The experiment was carried out in pots under cultivation of *Polypogon monspeliensis* (halophyte forage species) and *Hordeum vulgare* (common forage species) and lasted three months. The investigation focused on some selected soil physico-chemical properties, soil microbial biomass, and ten soil enzymatic activities: Arylsulfatase (ARY), dehydrogenase (DEH), β-glycosidase (β-GLU), protease (PRO), urease (URE), invertase (INV), Fluorescein diacetate hydrolase (FDAH), catalase (CAT), acid and alkaline phosphatases (PHO).

Both amendments improve markedly the saline soil quality. They ameliorate the physico-chemical properties. Soil carbon and nitrogen amounts were also improved and the highest raise (7.5-folds) was noted for carbon. According to the substantial increase of the organic matter, levels of measured microbial biomass and several enzyme activities in saline soil did improved. DEH activity is proposed as a measure of overall microbial activity; it exhibited a significant increase only at dose 2 (100 t/ha). Consequently, one hundred tons of composts per hectare, under which some enzymes exhibited an optimal of activity and metal accumulation can be minimized, appeared an interesting rate for saline soil amendment (Ouni *et al.*, 2013). Microbial communities were so responsive to compost applications than cover crop effects. The measure for community shift on amendment with different treatments in this study was the functional role of microbes (Nair and Ngouajio, 2012).

4. Biochar and compost amendment effect on soil microbial diversity

The role of crop residue management does not hold to only soil nutrient improvement but also in various other conditions such as reducing soil toxicity. As shown in this study which is the first to investigate the *in situ* efficacy of biochar and biochar–compost as Cu immobilizers, reducing Cu uptake by plants and increasing microbial abundance and activity, in a temperate vineyard topsoil (0–10 cm). It is a one year conducted study from Noveber 2011 to November 2012. Treatments with biochar and/or compost initially increased total carbon, with compost and biochar–compost additionally increasing extractable organic carbon in soil. Compost and biochar–compost significantly increased microbial biomass, phospholipid fatty acids (PLFAs), enzyme activities (phosphatase, arylsulfatase) and bacterial taxa abundances (*Actinobacteria*, α-*Proteobacteria*, β *Proteobacteria*, *Firmicutes*, *Gemmatimonadetes*). A high abundance of gram+ *Actinobacteria* in all treatments suggested that they are adapted to heavy metals, likely due to their specific cell membrane structures. Additionally, each treatment was characterized by a specific microbial community composition. Compost and biochar–compost increased the relative abundance of *Firmicutes*, while control and biochar increased *Acidobacteria, Gemmatimonadetes* and *Actinobacteria.* In conclusion, biochar and/or compost were not viable Cu remediation options, but compost and biochar–compost provided ecosystem services by reinforcing the microbial community. The copper tolerant microbes present in the different treatments applied gave a positive remedy for sustainable agriculture where the soil is deteriorated of its nutrients because of excess use of fertilizers. By manipulating the microbial structure of the soil, cultivation of crops can be made possible in degraded soils as well **(**Mackie *et al.*, 2015). In a field experiment, Junhui *et al.* (2013) amended the biochar at the rate of 0, 20 and 40 t ha^{-1} (C0, C1 and C2, respectively) before rice transplantation in a rice paddy from Sichuan, China. Topsoil (0–15 cm) was then collected from the rice paddy while rice harvest to determine soil physico-chemical properties and microbial biomass carbon (MBC) and nitrogen (MBN) as well as selected soil enzyme activities. Based on 16S rRNA and 18S rRNA gene, bacterial and fungal community structure and abundance were characterized using terminal-restriction fragment length polymorphism (T-RFLP) combined with clone library analysis, denaturing gradient gel electrophoresis (DGGE) and quantitative real-time PCR assay (qPCR). Contents of SOC and total N and soil pH were increased but bulk density decreased significantly. While no changes in MBC and MBN, gene copy numbers of bacterial 16S rRNA was shown significantly increased by 28% and 64% and that of fungal 18S rRNA significantly decreased by 35% and 46% under biochar soil amendment (BSA) at 20 and 40 t ha^{-1} respectively over the control. Moreover, there was a significant decrease by 70% in abundance of *Methylophilaceae* and of *Hydrogenophilaceae* with an increase by 45% in *Anaerolineae* abundance under BSA at 40 t ha^{-1} over control. Whereas, using sequencing DGGE bands of fungal 18S rRNA gene, some bands affiliated with *Ascomycota* and *Glomeromycota* were shown inhibited by BSA at rate of 40 t ha^{-1}. Significant increases in activities of dehydrogenase, alkaline phosphatases while decreased β-glucosidase were also observed under BSA. The results here indicated a shift toward a bacterial dominated microbial community in the rice paddy with BSA.

5. Research Gaps and Way Forward

The above review showed a broader picture of impact on overall soil quality by microbial community shifts in the soil as amended with biochar, compost and also by crop residue retention. There are various methods available to maintain soil fertility level and the parameters studied to ascertain it are mainly physic-chemical in nature. The biological parameters are mostly restrained to microbial biomass carbon (MBC), microbial biomass nitrogen (MBN), ATP synthesis and substrate induced respiration. Although these characteristics itself are sufficient to show the actual condition of soil nutrient level, but the core entities i.e. microbial communities because of which these biological processes occur in nature are mainly overlooked.

Molecular level studies are important to understand the processes involved in biogeochemical cycles occurring in order to stimulate the conditioning of soil. Nonetheless, amino sugars can be considered as microbial residue markers to assess the change in microbial community within a ecosystem. Similarly, enzymatic activities such as dehydrogenase, acid phosphatase, catalase, arylsulfatase give an insight of biological activity playing on at functional level. The microbial species involved in these activities are further needed to be identified in order to be able to focus on a particular enzyme for specific purpose. Further studies can be done on microbial cell wall structure to study the microbial shift of communities from the one amended to the non-amended conditions. In general, to study microbial diversity in soils, emphasis is laid on the abundance of a particular species and community structure which does not give much information on the functionality characteristic of the microbes. The need of the hour is therefore to link the microbial community with the function it plays in the biogeochemical cycle which in turn ameliorate the overall condition of soil. Techniques like phospholipid fatty acid, 16S-rRNA, RFLP gives an incomplete information regarding the particular role of a specific microbe therefore to study the functional diversity different techniques are need to be applied along with the study of microbial abundance such as BIOLOGTM ecoplate essay which is used to indicate the differences in the catabolic capability of soil microbial communities. Knowledge of microbial structure can give measures to bring any kind of soil improvement in the agro-ecosystem. The remedial measures for soil toxicity, disease infestation, pollution, leaching can be developed if the potential of microbes present in the soil is fully known. It is also seen that any kind of soil amendment treatment is generally beneficial in nature rather than degrading. Even though there has been results reported where no significant benefit was observed still more studies are required on microbial community level where it can be find out that why in some situations the improvements does not occur at all or no microbial community shift is seen in the treated soils. Also it warrants focus on the sustainable cultivable population of microbes in the soil because much of the biological processes are being performed for vital soil metabolic activities.

References

Carrera LM., Buyer JS., Vinyard B., Abdul-Baki, Sikora A LJ., Teasdale JR (2007), Effects of cover crops, compost, and manure amendments on soil microbial community structure in tomato production systems *Applied Soil Ecology*, 37(3): 247-255.

Chen J., Liu X., Zheng J., Yu X (2013) Biochar soil amendment increased but decreased fungal gene abundance with shifts in community structure in a slightly acid rice paddy from Southwest China, *Applied Soil Ecology* 71: 33-44.

Cherif H., Fathia A., Imene Ouzari H., bdennaceur Hassen A. (2009), Effects of municipal solid waste compost, farmyard manure and chemical fertilizers on wheat growth, soil composition and soil bacterial characteristics under Tunisian arid climate *European Journal of Soil Biology,* 45(2): 138-145.

Cookson WR., Beare MH., Wilson PE. (1998) Effects of prior crop residue management on microbial properties and crop residue decomposition. *Applied Soil Ecology* 7: 179-188.

Ding X., Zhang B., Zhang X., Zhang XP. (2011) Effects of tillage and crop rotation on soil microbial residues in a rainfed agroecosystem of northeast China, *Soil and Tillage Research,* 114(1): 43-49.

Govaerts, B., Mezzalama, M., Unno Y., Deckers J. (2007), Influence of tillage, residue management, and crop rotation on soil microbial biomass and catabolic diversity, *Applied Soil Ecology* 37: 18–30.

Jurado M., Estrella FS., Vargas-Garcia MC., Moreno J. (2014), Evolution of enzymatic activities and carbon fractions throughout composting of plant waste. *Journal of environment management* 133: 355-364.

Khaled D., Alotaibi, Schoenau JJ. (2011) Enzymatic activity and microbial biomass in soil amended with biofuel production byproducts *Applied Soil Ecology,* 48(2): 227-235.

Luo M., Durenkamp., Nobili MD., Lin Q., Devonshire BJ., Brookes PC. (2013) Microbial biomass growth, following incorporation of biochars produced at 350 °C or 700 °C, in a silty-clay loam soil of high and low pH *Soil Biology and Biochemistry,* 57: 513-523 Y.

Mackie KA., Marhan S., Detterich F., Schmidt HP., Kandeler E. (2015) The effects of biochar and compost amendments on copper immobilization and soil microorganisms in a temperate vineyard *Agriculture, Ecosystems & Environment,* 201(1): 58-69.

Marie-Soleil T., Speratti A., Baudron F., Verhulst N., Govaerts B.L., (2014), Crop residue management and soil health: A systems analysis *Agricultural Systems,* 134 (2015): 6-16.

Murugan R., Loges R., Taube F., Joergensen R G (2013) Specific response of fungal and bacterial residues to one-season tillage and repeated slurry application in a permanent grassland soil *Applied Soil Ecology,* 72: 31-40.

Nair A., Ngouajio M. (2012) Soil microbial biomass, functional microbial diversity, and nematode community structure as affected by cover crops and compost in an organic vegetable production system *Applied Soil Ecology,* 58: 45-55.

Ouni Y., Lakhdar A., Scelza R., Scotti R., Abdelly C., Barhoum, Z., Rao MA. (2013), Effects of two composts and two grasses on microbial biomass and biological activity in a salt-affected soil *Ecological Engineering,* 60: 363-369.

Pandey D., Agrawal M., Bohra JS (2014) Effects of conventional tillage and no tillage permutations on extracellular soil enzyme activities and microbial biomass under rice cultivation *Soil and Tillage Research,* 136: 51-60.

Pankhurst CE., McDonald HJ., Hawke BG., Kirkby CA. (2002), Effect of tillage and stubble management on chemical and microbiological properties and the development of suppression towards cereal root disease in soils from two sites in NSW, *Australia, Soil Biology and Biochemistry* 34(6): 833–840.

Schmidt, H.P., Kammann, C., Niggli, C., W.H. M., Evangelou, Kathleen A. Mackie, and S., Abiven (2014), Biochar and biochar-compost as soil amendments to a vineyard soil: Influences on plant growth, nutrient uptake, plant health and grape quality. *Agriculture, Ecosystems & Environment,* 191: 117-123

Singh Y., Sidhu HS. (2014) Management of cereal crop residues for sustainable Rice-Wheat production system in the Indo gangetic plains of India, *National Academy of Science India,* 80(1); 95-114.

Souza RA., Telles TS., Machado W., Hungria M., Filho, JT., Guimarães MF (2012). Effects of sugarcane harvesting with burning on the chemical and microbiological properties of the soil *agriculture, Ecosystems & Environment,* 155: 1-6.

Strand SE., Benford G. (2009) Ocean Sequestration of Crop Residue Carbon: Recycling Fossil Fuel Carbon Back to Deep Sediments, *Environ. Sci. Technol.*, 43(4): 1000–1007.

Sugihara S., Funakawaa S., Kilasara M., Kosaki T. (2012**),** Effect of land management on soil microbial N supply to crop N uptake in a dry tropical cropland in Tanzania, *Agriculture, Ecosystems & Environment,* 146(1): 209-219**.**

Zhang B., He H., Ding X., Zhang X., Zhang X., Yang X., Filley TR. (2012) Soil microbial community dynamics over a maize (*Zea mays* L.) growing season under conventional- and no-tillage practices in a rainfed agroecosystem *Soil and Tillage Research,* 124: 153-160.

Zhang X., Zhong Y., Yang S., Liu W. (2014), Diversity and dynamics of the microbial community on decomposing wheat straw during mushroom compost production. *Bioresource Technology,* 170: 183-195.