Soil Biology & Biochemistry 40 (2008) 2811–2818

Contents lists available at ScienceDirect

Soil Biology & Biochemistry

journal homepage: www.elsevier.com/locate/soilbio

Changes in the biodiversity of microbial populations in tropical soils under different fallow treatments

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ARTICLE INFO

Article history:
Received 14 August 2007
Received in revised form 4 July 2008
Accepted 4 August 2008
Available online 4 September 2008

Keywords:
Biodiversity
Fallow management
Proteobacteria
Phospholipid fatty acid analysis

ABSTRACT

Favorable cropping systems that promote residue retention would normally lead to increased soil carbon storage. Experiments were conducted to test the hypothesis that soil carbon of different fallow management practices influences more the microbial biomass carbon and activity than the microbial community structure. Also, the distribution of the major microbial grouping in soil is influenced by how much carbon is sequestered in soil.

Soils were sampled from the Kpeve Agricultural Experimental Station (KAES) in the Volta Region in Ghana. The treatments involved T1 – maize followed by fallow elephant grass that is burnt before planting, T3 – maize followed by pigeon pea fallow, T4 – maize followed by bare fallow, T7 – fertilized maize followed by elephant grass fallow, FR – forest reserve (unmanaged native vegetation).

As the soil sequestered carbon, there was a corresponding increase in the microbial biomass carbon. The treatment effects were significantly different ($p < 0.007$).

Correlation between biomass carbon and soil organic carbon was significant ($r = 0.63^*$).

Treatments with the least amount of carbon sequestered showed the least microbial activity. Significant relationship existed between dehydrogenase activity and the soil organic carbon ($r = 0.683^*$). The phospholipid fatty acid (PLFA) analysis was used to assess the effect of different soil management practices on biodiversity of soil organisms. Differences in carbon sequestered in the treatments affected the percentage PLFA compositions of the various treatments, thus affecting the distribution.

The amount of carbon sequestered in soil significantly influenced the proteobacteria ($p < 0.001$) and actinomycetes populations ($p < 0.028$). Thus, soils with high carbon storage showed high proteobacteria population and vice versa but the actinomycete population showed no particular trend with soil carbon. Diversity of the microbial community as assessed by the Shannon–Weiner Diversity Index showed no significant differences in treatments even though T4 had the highest diversity and FR the least diversity. The terminal Restriction Fragment Length Polymorphism on the soil DNA samples showed that the bacterial species' richness was greatest in T1 and T4. The most dominant bacterial groups were found in T1 and FR. Evenness was greatest in T7. We conclude from this study that the different fallow management practices influence the microbial biomass carbon and microbial activity. Secondly, the distribution of the major microbial grouping in soil is influenced by carbon stored in soil.

1. Introduction

Soil carbon sequestration is proposed as one of the major ways of capturing atmospheric carbon for safekeeping, thus reducing the ever-increasing atmospheric carbon load. Carbon is primarily stored in soil as soil organic matter (SOM). The majority of the accumulation of soil organic carbon due to additional carbon inputs is preferentially sequestered in microaggregates or within small macroaggregates (Kong et al., 2005). Carbon stored can remain in soils for millennia or be quickly released back into the atmosphere depending on soil management and cropping system. The use of cover crops in soil management plays an important role in sequestering carbon in soil and also increases the total microbial biomass by shifting the microbial community structure towards fungal dominated community, thereby enhancing the accumulation of microbial derived organic matter (Six et al., 2006). Also, growing leguminous cover crops enhance biodiversity, through the quality of residue input and soil organic pool (Singh et al., 1998; Fullen and Auerswal, 1998).

A healthy soil is comprised of highly diverse soil biota. The latter is made up of representations of many groups of organisms

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doi:10.1016/j.soilbio.2008.08.010

including, for example, bacteria, algae, fungi, worms, termites, ants, insect larvae and others, even larger animals.

Ecosystems with high biodiversity generally sequester more carbon in the soil than those with reduced biodiversity (Lal and Akinremi, 1983). This is partly due to the activity of the soil biota that produces organic polymers stabilizing aggregates.

Several studies have been carried out (Halvorson et al., 2002; Machado et al., 2006; Al-Kaisi et al., 2005) and others ongoing to evaluate the effect of cropping systems and fallow management on soil carbon storage. Experiments conducted at the Kpeve Agricultural Experimental Station in Ghana investigated soil carbon stocks under varying fallow management systems including: fertilized maize–natural bush (elephant grass) rotation, maize–mucuna rotation, maize–pigeon pea rotation and maize–bare fallow rotation (Adiku et al., 2003). Observations indicated total failure of the maize plant in the maize–bare fallow rotation three years after the commencement of the study while soil carbon reduced to more than half of its original value.

Since microorganisms are the main contributors in the conversion of residues into soil carbon and the release of CO_2 back to the atmosphere during residue decomposition and soil carbon mineralization, it would be appropriate to conceive that soil and cropping system management would not only affect the microbial populations but also their diversity and subsequent soil carbon storage. Indeed, in the light of the observations from Adiku et al. (2003), a number of questions can be raised, such as "how has the low sequestered carbon affected the microbial community in the bare fallow plot compared to other treatments?" "Is the biodiversity in the bare fallow plot different from other plots?" We hypothesize that carbon stored in soils of different fallow management practices affects more the microbial biomass carbon and activity than the microbial community structure and that the distribution of the major microbial groups in soil is influenced by how much carbon is sequestered in soil.

The aims of this study were to:

1. determine the type of relationship that exists between the carbon stored in soil and microbial biomass carbon and activity,
2. ascertain the extent to which soil of different carbon levels (through different fallow management practices) affects the bacterial diversity in soil, and
3. assess the effects of different soil management practices on biodiversity of microorganisms in soils.

2. Material and methods

2.1. Soil sampling

Soil was sampled immediately after maize harvest at Kpeve in the Volta Region. The soil is classified as Haplic Lixisols. It is a highly weathered sandy loam with appreciable gravel content and has little structure especially when the organic carbon content is depleted. The soil pH in water is slightly acid (6.38–6.73) and the soil organic carbon ranged from 0.80 to 1.67% in the various treatments (Table 1). The pH of soil in 1 M KCl ranged from 5.29 to 5.64 (Table 1).

Table 1
Some physical and chemical characteristics of soils sampled

Treatments (%)	$pH_{(water)}$	$pH_{(KCl)}$	Soil organic carbon
T1	6.73	5.56	1.29
T3	6.53	5.52	1.54
T4	6.53	5.29	0.80
T7	6.38	5.53	1.67
FR	6.68	5.64	1.34

Five different fallow management treatments were used:

1. Maize, following the native practice of fallow where elephant grass is burnt and no fertilizer is added to the maize – T1
2. Maize following pigeon pea fallow – T3
3. Maize planted on land, which before was always kept bare (bare fallow) – T4
4. Fertilized maize following native elephant grass fallow – T7
5. Not farmed native land – FR (control)

The plot size for each treatment was 10 m by 12 m and these were laid in a 'randomized block complete design' with four replicates on the experimental field.

The above experiment had been ongoing for three years before soil sampling was done.

No plots were tilled, and at planting times the local farmers' practice was followed to dig holes in soil for seeding. Ploughing was only done at the initial preparation of the experimental plots in the first year.

Soil was sampled with sterilized soil corer to a depth of 18.5 cm. No samples were taken from the border zones of each plot of 0.5 m around that plot. Ten sub samples were collected from the various parts of the plot (e.g. T1R1, Treatment 1 replicate 1) excluding the border rows. These sub samples were composited to represent the plot. Similarly, all the other treatments such as T1R2, T1R3, and T1R4 were sampled and pooled separately. All samples were then cooled on ice and transported to the Soil Science Laboratory of the University of Ghana. The soil was sieved through a 2 mm sieve while cross contaminations were avoided by thoroughly washing and drying before tackling each sample. Fresh soil samples were used for enzyme activity measurements and microbial biomass determination. Some of these samples were immediately stored at $-20\,^{\circ}C$ and later used for phospholipid fatty acid and soil DNA analyses. The phospholipid fatty acid analysis (PLFA) was performed in collaboration with Microbial Insight at Rockford, Tennessee, USA and the terminal Restriction Length Polymorphism (t-RFLP) in collaboration with the Center for Microbial Ecology at Michigan State University, East Lansing, USA.

The microbial community of the various treatments was described by using the PLFA signatures for the following: eukaryotes, general representing the normal saturates, actinomycetes, anaerobic metal reducers (anaerobic M. red), proteobacteria, and terminally branched saturated (tet. br. sat) representative of mostly the Gram-positive bacteria. The eukaryote of the microbial community are represented by fungi, protozoa, algae, and the diatoms (18:2ω6, 18:3ω3, 20:4ω6 and 20:5ω3), whilst the fungal biomass was represented by the following signatures18:1ω9, 18:2ω6 and 18:3ω3 (Vestal and White, 1989).

The PLFA stress signatures used in analyzing Gram-negative bacterial community were, cy17:0/16:1ω7c, cy19:0/18:1ω7c, and cy17:0/16:1ω7c + cy19:0/18:1ω7c. To assess the membrane fluidity of the microbial community, the following ratios, 16:0/18:0, a15:0/a17:0, i17:0/a17:0, i15:0/a15:0 were used.

Soil moisture content was determined by drying a known quantity of soil in a $105\,^{\circ}C$ oven over night for 24 h.

The approximate water holding capacity for the soil sample was also estimated by averaging the calculated water contents (pw's) of several similar samples that have been saturated and then drained to field capacity over filter paper in a 100% humidity environment for 24 h.

2.2. Microbial biomass determination

Microbial biomass carbon was determined for the soil sample according to the method of Jenkinson and Powlson (1976). The CO_2-C evolved at room temperature ($28\,^{\circ}C$) over 0–10 days from both