APPLIED SOIL ECOLOGY 40 (2008) 229–239

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Effect of mulching on labile soil organic matter pools, microbial community functional diversity and nitrogen transformations in two hardwood plantations of subtropical Australia

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ARTICLE INFO

Article history:
Received 14 June 2007
Received in revised form
16 April 2008
Accepted 23 April 2008

Keywords:
BIOLOG
Hot water extractable organic matter
Microbial biomass
Shannon's diversity index

ABSTRACT

The aims of this study were to: (1) assess the effects of mulching on labile soil organic matter (SOM) pools (water-soluble organic matter, WSOM; hot water extractable organic matter, HWEOM; microbial biomass, MB; acid hydrolysable organic matter, AHOM), microbial community functional diversity and soil nitrogen (N) transformations and (2) quantify the relationships among labile SOM pools, soil N transformations and microbial community functional diversity. Soil (0–10 cm) was collected from two hardwood plantations in subtropical Australia to which plant residues (1.57 kg m^{-1}, C/N ratio of 80) had previously been applied as mulch for 12 months. Both in southeast Queensland, Australia, one plantation was located in dry area (Pechey, average annual rainfall 851 mm) and the other at Proston, drier by comparison (average annual rainfall 613 mm). At both locations, soil WSOM-carbon (C), HWEOM-C, MB-C, and AHOM-C were significantly higher in the mulch treatment than in the non-mulch treatment. The soil microbial community functional diversity (Shannon's diversity index, H') measured by BIOLOG GN2 micro-plates was significantly greater in the mulch treatment than in the non-mulch treatment. The mulch treatment had significantly higher soil gross N mineralization and gross N immobilization rates than the non-mulch treatment. However, there was no significant difference in soil gross nitrification between the two treatments. Stepwise multiple regressions revealed that HWEOM-C had significant correlation with soil microbial functional diversity and explained more of the variation in microbial functional diversity than any other labile SOM pools. The MB-N explained more of the variations in gross N transformations than other labile SOM pools.

1. Introduction

Mulching is frequently used during the establishment of hardwood plantation in subtropical Australia. The most common practice to mulch soil during establishment of plantations is to chip the existing vegetations using a tractor-driven mulch machine and leave a reasonably homogenous covering by plant materials at the ground through

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0929-1393/$ – see front matter
doi:10.1016/j.apsoil.2008.04.009

which seedlings are planted. When mulch is applied on the surface soil, the evaporation rate decreases, leaving greater moisture and less variation in soil temperature for a longer period of time (Athy et al., 2006). Appropriate moisture and temperature are important for metabolic activity of the soil microbes that recycle and release nutrients that are essential for tree growth. Beside moderating soil moisture and temperature, mulch residue affects the dynamics of soil organic matter (SOM). For example, mulch residues can increase dissolved organic carbon (C) and nitrogen (N) by the decomposition of plant materials and leaching (Chantigny, 2003). Mulching may also help control weeds and therefore decrease the quantity of root exudates (Budelman, 1988), which are important sources of SOM.

SOM is an important ecosystem property, and closely associated with many critical soil chemical, physical and biological processes (Mathers et al., 2000; Chen et al., 2004). The bioavailability of SOM largely depends on intrinsic SOM quality factors and soil biological, chemical and physical characteristics (Oades, 1988). A number of techniques, including chemical, physical and biological fractionations, have been developed to fractionate SOM into labile or rapidly decomposed, and stable or slowly decomposed parts (Mathers et al., 2003; McLauchlan and Hobbie, 2004). Labile pools of SOM are especially important because they control ecosystem productivity in the short term, and could be most affected by soil management practices. For example, the labile C pools extracted by the hot and cold water were determined to degrade rapidly (Jandl and Sollins, 1997) and may be immediate energy sources for microorganisms (Huang and Schoenau, 1996). Although the hot water extracted SOM pool had more intensive signals of carbohydrates, phenols and lignin monomers than cold water extracted SOM (Kalbitz et al., 2000), the turnovers of both hot and cold water extracted SOM pools have been reported as major pathways of nutrient cycling (Curtin et al., 2006). In addition to water, chemical extraction using acid hydrolysis is an important tool to extract labile SOM pools (Xu et al., 1997). The most widely adopted acid hydrolysis process is refluxing soil with 6 mol L^{-1} HCl for 10–24 h (Sollins et al., 1999). The acid hydrolyzed SOM pools have a much shorter mean residence time than the un-hydrolyzed pools (Sollins et al., 1999).

Soil microorganisms are actively involved in soil biochemical processes, including organic matter decomposition, nutrient mineralization and cycling. As an important microbiological parameter, soil microbial diversity has been suggested as a possible indicator of soil quality (Kennedy and Smith, 1995). It has been shown that soil microbial diversity is changed by soil management practices, such as mulching, especially organic mulch with plant residues (Bending et al., 2000). Recent researches have reported that soil microbial community structure and diversity are correlated with the variations of soil total organic-C and soil C/N ratio resulting from organic mulch (Marschner et al., 2003; Cookson et al., 2005). However, few authors have measured the relationships between soil microbial diversity and labile SOM pools. Labile SOM pools have been hypothesized to play a central role in the transport and supply of C and N to microbial populations in the forest soils and thus the regulation of subsequent microbially mediated N transformations (Cookson and Murphy, 2004). Especially, soil hot water extractable C and N have been demonstrated to be sensitive measurements for determining impacts of soil management practices on soil fertility (Ghani et al., 2003). This implied that change in soil microbial diversity might be regulated by C and N availability through labile SOM pools. On the other hand, change in microbial functional diversity and metabolic activity can affect ecosystem process (Garland, 1997). It is suggested that changes in soil N mineralization may be related to changes in functional diversity of soil bacterial community (Calderon et al., 2001). In addition, both microbial biomass and microbial community functional diversity were reported to play a role in plant litter decomposition and carbon cycling in a forest ecosystem (Carney and Matson, 2005). In this study, we hypothesized that (1) soil microbial functional diversity and metabolic activity would be affected by mulching due to the change in quality and quantity of labile SOM pools and (2) the changed soil microbial functional diversity and metabolic activity would, in turn, impact soil N transformations.

Soil microbial functional diversity can be assessed using the BIOLOG system. The technique determines how microbial communities use a variety of C compounds. BIOLOG has been used to evaluate microbial metabolic diversity in both agricultural and forest soils under different management strategies (Garland, 1997; Graham and Haynes, 2005; Grayston and Prescott, 2005; White et al., 2005). In general, these studies used principal component analysis (PCA) or similar types of multivariate statistical analyses for data analysis and showed that various microbial communities produce changed metabolic diversity patterns. Over the years, increased understanding of the BIOLOG assay has demonstrated the reproducibility of BIOLOG profiles and supported the theory that shifts in BIOLOG metabolic diversity patterns are related to shifts in community composition (Schutter and Dick, 2001; Crecchio et al., 2004). It should be acknowledged here that use of BIOLOG assay to assess microbial community functional diversity does not necessarily reflect the *in situ* activity and diversity of the soil microbial community, since the assay is selective for microorganisms capable of growth on the C substrates and may represent only a part of the whole microbial community (Bending et al., 2002). However, BIOLOG technique does provide a rapid and convenient assay for culturable heterotrophic organisms, as shown by other studies that have found that BIOLOG analyses provide sensitive indicators of changes in soil microbial functional diversity due to C substrate input from plant residues (Grayston et al., 1998, 2001; Rogers and Tate, 2001). In addition, BIOLOG studies of native soil microbial communities may provide baseline data for hardwood plantation ecosystems and show the dynamic effect of mulching on the functional diversity of the soil microbial community.

The detailed aims of this study were to investigate (1) the impacts of mulching on the amounts of labile SOM pools, the metabolic profiles and functional diversity of the soil microbial community, and the soil gross N transformations and (2) the correlations among labile SOM pools, soil gross N transformation and soil microbial functional diversity in two hardwood plantations soils of subtropical Australia.