Agriculture, Ecosystems and Environment 263 (2018) 7–17

Contents lists available at ScienceDirect

Agriculture, Ecosystems and Environment

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

Organic management and cover crop species steer soil microbial community structure and functionality along with soil organic matter properties

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ARTICLE INFO

Keywords:
Aromaticity
Dissolved organic matter
Legacy effects
MicroResp™
PLFA/NLFA
Water repellency

ABSTRACT

It is well recognized that organic soil management stimulates bacterial biomass and activity and that including cover crops in the rotation increases soil organic matter (SOM). Yet, to date the relative impact of different cover crop species and organic vs. non-organic soil management on soil bacteria and fungi and on SOM quantity and quality remains to be tested. We used a long-term (10 years) full-factorial field experiment to test the combined effects of organic vs. conventional soil management with different cover crop species (oat or rye) and the legacy effects of seven soil health treatments (SHTs: treatments with compost, chitin, marigold, grass–clover, biofumigation or anaerobic soil disinfestation (ASD), and fallow as control) on microbial community biomass, structure and catabolic activity and on SOM quantity and quality (dissolved organic carbon (DOC), aromaticity and water repellency).

Microbial community traits were assessed using PLFA/NLFA analyses and multi-substrate induced respiration. We found that organic soil management enhanced total microbial biomass by increasing bacterial, saprotrophic and arbuscular mycorrhizal fungal biomass; and increased total microbial catabolic activity, associated with maintaining high microbial efficiency (low qCO_2). Effects of organic management were amplified by oat as cover crop, which enhanced the abundance of saprotrophic fungi resulting in a higher fungal:bacterial ratio. Total SOM concentration was similar among treatments, however the most easily accessible fraction, i.e. DOC, was higher in organic compared to conventional soils. Also, the aromaticity of the DOC was lower in organic than in conventional systems, which was associated with lower water repellency. There was a legacy effect of SHTs on fungal:bacterial ratio in that chitin and marigold showed higher fungal:bacterial ratio compared to compost, biofumigation and ASD even 6 years after the last application.

We conclude that organic soil management enhances the abundance of all microbial groups and their total catabolic activity, associated with a higher concentration and lower aromaticity of dissolved organic matter. These effects can be enlarged by the growth of specific cover crops and the application of certain soil health treatments.

1. Introduction

Decades of intensive agriculture have diminished soil organic matter (SOM) content, thereby reducing fertility and biodiversity of arable lands (Moore et al., 2004; Gardi et al., 2013). Consequently, important soil ecosystem services such as nutrient cycling, water regulation, carbon (C) storage and functional biodiversity are in many cases impaired. Microbial communities are crucial to maintain soil functioning since they are the main decomposers of fresh organic matter, which drives biogeochemical nutrient cycling (Swift et al., 1979; Hättenschwiler et al., 2005). The effects of organic management on microbial communities is well documented, at least with respect to the increase of bacterial abundance and enzyme activities (Lori et al., 2017). However the combined effect of soil management with cover crops on microbial and SOM traits and the legacy effects of organic amendments are largely unknown and warrant further investigation in order to understand management impacts on SOM and soil functioning (Lori et al., 2017). This study integrates the long-term effect of agricultural practices (conventional vs. organic and two different cover crop species) and the legacy effects of seven soil health treatments

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https://doi.org/10.1016/j.agee.2018.04.018
Received 2 January 2018; Received in revised form 20 April 2018; Accepted 23 April 2018

(SHT) based on the addition of organic amendments, on the composition and functionality of the soil microbial community and on SOM properties. The main aim of this study is to elucidate the effect of agricultural practices on microbial community and SOM traits that impact on C cycling in agro-ecosystems.

Usually, in organic agriculture large amounts of C are incorporated into the soil via organic fertilizers that replace mineral fertilizers, and which are known to increase SOM content (Lal, 2009). Recently it was shown that the increase of SOC stocks in organic versus conventional agriculture (Gattinger et al., 2012) is strongly dependent on (cover) crop residue decomposability traits (e.g. leaf C:N) (García-Palacios et al., in press). These traits differ among plant species, even for plant species belonging to the same plant family, but they can also be modified via soil feedbacks, for example the addition of N based fertilizers can increase leaf N concentrations and decrease leaf C:N ratio. This implies that growth of different cover crop species can alter SOM quantity, quality and accumulation rate. Besides the beneficial effects of cover cropping to enhance SOM content, cover crops can also increase microbial biomass and activity and induce changes in microbial community structure (Buyer et al., 2010). These shifts are likely dependent on cover crop chemical traits and plant-soil biotic interactions. For instance, leguminous plant species associated with N-fixing rhizobacteria produce low C:N residues, and thereby impact on microbial N mineralization activity and soil N availability (Kumar and Goh, 1999). Similarly, previous studies showed that different cover crop species can associate to different fungal communities (Benitez et al., 2016; Detheridge et al., 2016).

The net change in the soil C pool results from the balance between the C input and C losses that are mainly driven by two factors: 1- the input of C in the soil via plant material and other organic amendments and 2- the metabolic capacities of the soil biota (Six et al., 2006; De Deyn, 2013). The first factor, the chemical composition of the OM input, has a strong impact on the rate and efficiency with which the microbes break down the OM and form SOM (Bending et al., 2002), resulting in changes in the composition of the soil microbial community (De Deyn et al., 2008; Wickings et al., 2012). For instance, growth and further incorporation of plant species, such as *Tagetes patula* or *Brassica* spp. can have an impact on soil biota by exuding secondary metabolites with fungicidal and bacterial effect (Korthals et al., 2014). With respect to the second factor, the metabolic capacities of the soil biota, saprotrophic fungi are generally more efficient at decomposing complex SOM than bacteria and need less N per unit C to build their own biomass (Hodge et al., 2000). Thus, higher saprotrophic fungal biomass increases soil C and N retention relative to bacteria (de Vries et al., 2012; De Deyn, 2013) since fungal tissues accumulate more C and are more recalcitrant than bacterial tissues. Furthermore, higher functional diversity of the microbial community will enhance the breakdown of the OM, especially for complex processes such as chitin degradation that requires the functional complementarity of a diverse microbial community that involves bacteria and fungi (Beier and Bertilsson, 2013). Arbuscular mycorrhizal fungi (AMF) also contribute to increase soil C storage due to their extensive mycelium and necromass (Zhu and Michael Miller, 2003), whereas they have limited capacity to decompose OM (Hodge et al., 2001). Overall, from an agro-ecosystem long term perspective, high abundance of soil microbes with high functional diversity will enhance nutrient mineralization (De Ruiter et al., 1993), and fungi particularly (saprotrophic and AMF) will promote SOM stabilization and carbon sequestration.

Despite the impact of OM amendments on soil biotic and abiotic properties is well recognized (Six et al., 2006; Mulder et al., 2013), the legacy effects (i.e. the still measurable effects of an application after a certain timespan) of organic amendments on the development of microbial communities and soil properties are still unknown. A previous study by Lupatini et al. (2017), based on the same farmland as the present study, showed that after 3 years of application of different soil organic amendments there were still shifts in the relative abundance of some bacterial groups. However, Lupatini et al. (2017) did not include fungal communities (saprotrophic and AMF), which, as we discussed above, have key functions for soil C cycling. Besides, regarding the legacy effect of soil management on abiotic soil properties, Lewis et al. (2014) concluded that the impact of different land uses (desert, agrarian and residential lands) on soil organic C can last for several centuries. However, in continuously managed farmlands where C turnover is sped up by soil management, the legacy effect of previous soil management has not yet been studied. Information about the strength of treatments with organic amendments on both biotic and abiotic soil properties is relevant to design management strategies that efficiently promote the build-up of long-lasting soil-based ecosystem services.

The composition and abundance of SOM determine to a large extent soil water regulation (Saxton and Rawls, 2006), which is important in crop production in terms of nutrient and water availability and prevention of leaching. In this study, we focus particularly on soil water repellency (SWR), which, when high, reduces soil water infiltration, and can influence plant germination, productivity and nutrient leaching (Doerr et al., 2000). Moreover, low SWR is indicative of improved soil structure and soil C sequestration (Bachmann et al., 2008). Addition of organic amendments in agricultural lands can have an effect on water repellency because OM decomposition releases hydrophobic molecules that enhance SWR (Doerr et al., 2000) and therefore water drops take longer time to penetrate into the soil. Therefore, it could be expected that addition of complex organic matter could result in enhanced SWR.

In this research, we use the "Vredepeel long-term experiment" that during 10 years had a consistent management regarding conventional/organic management and cover crop treatments to study shifts in soil properties related to C cycling (microbial and SOM traits). Furthermore, we study the legacy effect of seven soil health treatments (SHT: addition of compost, chitin, *T. patula,* grass–clover, biofumigation or anaerobic soil disinfestation, and fallow as control). As microbial traits we characterized the microbial community structure, the relative abundance of the different microbial functional groups (including bacteria, saprotrophic fungi and AMF), and its catabolic profile. As SOM traits we characterized the SOM concentration, the dissolved organic carbon (DOC) and the aromaticity of the DOC. Fig. 1 shows the relationships that we expected among the measured variables. We hypothesized that:

H1. Organic management compared to conventional promotes activity and abundance of bacteria, saprotrophic fungi and AMF (H1a); and different cover crop species from the same plant family (*Grammineae*) result in distinct microbial community structures due to differences in cover crop residue decomposability traits (H1b)

H2. Organic management compared to conventional increases SOM, DOC concentration and aromaticity of the DOC (H2a), while cover crop identity does not affect SOM traits (H2b).

H3. SHTs leave long-term legacy effects on microbial community structure and functionality (H3a) and on SOM quality (H3b).

H4. Soil management effects on SOM feed back to cover crop productivity and chemical composition (H4a), resulting in different cover crop litter traits (H4b).

H5. Soil management effects on SOM feed back to differences in SWR. Particularly, we expect that soils under organic management receive larger amounts of OM resulting in increased SWR.

2. Material and methods

2.1. Study site and experimental design

This study was conducted at Vredepeel long-term experimental farm (The Netherlands: N – 51° 32′ 24.958′́, E – 5° 51′13826′́). The soil type is a Hortic Podzol (FAO, 2015), texture is 1.1% clay, 3.7% silt and