Applied Soil Ecology 98 (2016) 121–131

Contents lists available at ScienceDirect

Applied Soil Ecology

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

Switching between monocot and dicot crops in rotation schemes of Argentinean productive fields results in an increment of arbuscular mycorrhizal fungi diversity

Andrea G. Albarracín Orio[a], Elsa Brücher[a], Daniel A. Ducasse[a,b,*]

[a] Laboratorio de Biología Molecular, Facultad de Ciencias Agropecuarias, Universidad Católica de Córdoba, Av. Armada Argentina 3555, Córdoba 5017, Argentina
[b] Instituto de Patología Vegetal IPAVE-CIAP-INTA, Camino 60 Cuadras Km $5^{1/2}$, Córdoba 5119, Argentina

ARTICLE INFO

Article history:
Received 18 February 2015
Received in revised form 19 September 2015
Accepted 8 October 2015
Available online 27 October 2015

Keywords:
AMF diversity
Monocots
Dicots
Crop rotation

ABSTRACT

Despite the importance of mycorrhizal symbiosis, we understand little how different soil managements affect arbuscular mycorrhizal fungi (AMF) communities. Crop rotation is recommended in sustainable agriculture because of its benefits in soil fertility improvement and positive effect decreasing soil borne diseases incidence and pest abundance. Amplicon sequencing of LSU and SSU rRNA gene fragments was used to analyse AMF diversity in fields from one of the most productive regions in Argentina, which varied in the main class of the plant component included in the crop rotation scheme. The samples encompassed different agricultural settings; one involving only monocot plants in the crop rotation schemes, one including a dicot crop, and the other an alternation and/or a combination of monocot and dicot plant components. We found lower richness and diversity in soils under monocot succession than in a dicot/monocot rotation or consociation. We observed that agricultural management had an influence on beta diversity patterns. Principal coordinate analysis showed that communities from the dicot/monocot rotation or consociation samples clustered together and separated from the monocots samples. These findings suggested that the increment of soil AMF diversity is more dependent on the alternation between monocot and dicot crops than other factors related to the farming systems.

1. Introduction

Arbuscular mycorrhizal fungi (AMF) belonging to the phylum Glomeromycota (Schüßler et al., 2001), together with ectomycorrhizal fungi (EMF) colonize the roots of most land plants, facilitating mineral nutrient uptake from soil in exchange for plant-assimilated carbon (Smith and Read, 2008). AMF are the beneficial microorganisms more often associated to plant roots (Smith and Read, 2008) and represent an important group in ecosystem functioning because of its ubiquity and direct implications in different processes involved in plant-soil interactions. AMF act at different levels, leading to morphological and anatomical changes in host plants such as shoot–root ratio, root tissue structure, chloroplast numbers, lignification enhancement and other effects that are not explicable merely as a simple plant nutrition improvement due to an increased efficiency in nutrient uptake by the root, but to more complex metabolic changes related to the physiological integration of the symbionts (Smith and Smith, 2011).

Different agroecosystems involve a wide range of possibilities in the crops management and therefore the soil. One specific plot could be managed under traditional plowing to no tillage, and from monoculture production to rational crop rotation between species with different root exploration capabilities etc., according to the type of production pursued. It is not surprising that such different agricultural practices could alter AMF communities. Thus, it has been reported that conventional tillage or plowing, breaks and concomitantly reduces the network length of AMF hyphae and root colonization (McGonigle and Miller, 1996). A comparative study showed the effect of conventional tillage and no-till system on the formation of mycorrhizal symbiosis in wheat (Schalamuk et al., 2006). While the effect of tillage with nitrogen (N) fertilization significantly reduced the colonization and the number of infective propagules, no-till practice increased colonization during flowering and grain filling. Soil biodiversity has been recognized as an important component of soil health, potentially enhancing plant

---

* Corresponding author at: Instituto de Patología Vegetal IPAVE-CIAP-INTA, Camino 60 Cuadras Km $5^{1/2}$, Córdoba 5119, Argentina.
E-mail addresses: ducasse.daniel@inta.gob.ar, aaorio@hotmail.com (D.A. Ducasse).

http://dx.doi.org/10.1016/j.apsoil.2015.10.004
0929-1393/

productivity and ecosystem sustainability (Brussaard et al., 2007; van der Heijden et al., 2008). It is worth mentioning that it is being progressively more accepted that some farming managements have a negative impact on the environment, resulting in a reduced biodiversity (Tilman et al., 2002). In general, agroecosystems showed less AMF diversity along with different other sites in which AMF communities have been analysed (Oehl et al., 2003; Öpik et al., 2006), although specific results might depend on the study location. It is still not well understood if one particular land-use treatment leads to AMF communities that are more similar to natural assemblages. (Verbruggen et al., 2010). AMF usually have broad host ranges, although some preferences or functional diversifications between plants and mycorrhizal fungi have been suggested (Goomaral et al., 2003; Helgason et al., 2002; Vandenkoornhuyse et al., 2003). Moreover, it has been proposed that plant communities' composition and productivity might be in some way dependent on AMF diversity (Klironomos et al., 2000; van der Heijden et al., 2008). In agreement to this fact, Burrows and Pfleger (2002) reported that a rise in the number of plant species correlated to AMFs sporulation increment and to the composition of their communities. However, this apparent selection of AMF species by the plant has not been extensively investigated. In mycorrhiza is easy to imagine that partners, plant and AMF, influence one another and consequently changes in the AMF communities composition could influence the plants community. In a complementary view of the same scenario, it would be foreseeable, that changes in the plant communities have an effect on the AMF community. Variations in fungal population have been reported in agricultural soils under different cropping practices (Johnson et al., 1991). Meanwhile, many studies showed that AMF communities are diversified among different plant species (Bever et al., 1996; Sanders and Fitter, 1992; Vandenkoornhuyse et al., 2002, 2003). Thus, it is feasible that plant community could themselves be a determinant of the mycorrhizal fungi community (Goomaral et al., 2003).

It has been demonstrated that diversifying the crops used in a rotation scheme, increases the taxonomic and functional diversity of soil fungal communities (Larkin and Honeycutt, 2006). Crop rotation has an effect on the microbial activity and on the substrate utilization (Larkin et al., 2010). This is a remarkably significant practice in conventional agriculture because contributes to the improvement of soil quality (Anderson, 2005; Varela et al., 2014), and offers a possibility for management of pathogenic soil-borne fungi and weeds (Chave et al., 2014; Dias et al., 2015; Garrison et al., 2014; Schillinger and Paulitz, 2013). Thus, combining different crops such as cereals with canola (Nelson et al., 2012), or legumes (Blackshaw et al., 2010) can result in an increase of productivity by reducing diseases and weeds incidence.

The application of a well-planned crop rotation scheme implies much less synthetic external inputs and consequently, less environmental impact to manage diverse pests (Davis et al., 2012; Karlen et al., 1994). In the case of weeds management, when a dicot crop is followed by a monocot one, the combination of both chemical and mechanical control can be done more properly (Heap, 2014; Leroux et al., 1996).

Despite the fact that AMF are possibly the most important fungi in terrestrial ecosystems, we understand very little about many aspects of their biology partly because of their asexual, obligate symbiotic and subterranean lifestyle. Nevertheless, traditional culture-independent methods have shed light on some aspect of AMF phylogenetic relationships and diversity. The limitation of these methods is that they are low throughput that renders many taxa undetectable. The massively parallel pyrosequencing enables metagenomic and metagenetic analyses in a way that exceeds the capacity of traditional Sanger sequencing-based approaches by several orders of magnitude (Margulies et al., 2005; Sogin et al., 2006). Pyrosequencing offers great promise in the high-throughput identification of hundreds of samples at a reasonable cost and time consumption (Margulies et al., 2005; Roesch et al., 2007; Sogin et al., 2006). The most frequently used markers are the nuclear ribosomal RNA genes, especially the small subunit rRNA (SSU) (Helgason et al., 1999; Lee et al., 2008; Wubet et al., 2006) and the internal transcribed spacer rRNA region (ITS) including the 5.8S rRNA (Hempel et al., 2007; Sýkorová et al., 2007; Wubet et al.,

Table 1
General characteristics, soil chemical properties and descriptions of the agricultural treatments and crop rotations schemes.

Treatments	Agricultural managements	Crop rotation schemes						Soil characteristics		
		Year 1	Year 2	Year 3	Year 4	Year 5	Year 6	pH	OC (%)[a]	EP (ppm)[b]
Monocots	RG3	*Allium cepa* Tillage	*Allium cepa*	*Lolium perenne* No-till	*Lolium perenne*	*Lolium perenne*	*Allium cepa* Tillage	7.8	1.6	48.4
	Agropyron	*Thinopyrum ponticum* No-till	*Thinopyrum ponticum*	*Thinopyrum ponticum*	*Thinopyrum ponticum*	*Thinopyrum ponticum*	*Allium cepa* Tillage	8.0	1.8	40.2
	GM	*Setaria italica* Tillage	*Allium cepa*	*Setaria italica*	*Allium cepa*	*Setaria italica*	*Allium cepa*	7.9	1.0	43.9
Monocot/dicot alternation	Grain	*Helianthus annuus* Tillage	*Triticum aestivum*	*Helianthus annuus*	*Triticum aestivum*	*Helianthus annuus*	*Allium cepa*	8.0	1.7	39.2
	RM	*Helianthus annuus* Tillage	*Triticum aestivum* No-till	*Medicago sativa*–*Thinopyrum ponticum*	*Medicago sativa*–*Thinopyrum ponticum*	*Medicago sativa*–*Thinopyrum ponticum*	*Allium cepa* Tillage	7.7	2.3	18.8
	Alfa3	*Medicago sativa* No-till	*Medicago sativa* Tillage	*Medicago sativa*	*Allium cepa*	*Allium cepa*	*Allium cepa*	7.7	2.1	23.9
Dicots	Alfa5	*Medicago sativa* No-till	*Medicago sativa*	*Medicago sativa*	*Medicago sativa*	*Medicago sativa*	*Allium cepa* Tillage	7.7	2.1	19.9

[a] OC, percentage of organic content in the soil samples as determined by the Walkley and Black method.

[b] EP, extractable phosphorous in the soil samples.