

MYCORRHIZAS AS A TOOL IN MAPPING AGRICULTURAL SOILS

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Abstract

Current agronomic practices are defined by two components: technology and biological dynamics. The response of agroecosystems to applied technologies is visible in the structure and interrelations of the biological component, which defines the actual fertility of soils. In soil-plant-soil biota system, both soil and plant have a rich history in terms of analysis and dynamics. Soil biota is a relatively new component studied, but without an integrated mapping. The response of soil micro-flora and -fauna to technological pressure is found in fertility level, resilience potential, yield stability and conservative status of soil. Mycorrhizas are co-evolutionary symbiotic partners of most cultivated plants. The complex of fungi-roots is defining overall nutrients absorption, plant nutrition and productivity. In this context, development of a mycorrhizal mapping system has a high value represented by an improvement of agronomic technologies. The design of mycorrhizal maps can serve to create a management adapted to the specific conditions of agricultural holdings and to increase productivity.

Key words: *symbiotic status, biological fertility, agroecosystems, technological improvements.*

INTRODUCTION

Agriculture in the 21st century underwent major changes due to the steady increase in feed requirements and the need to increase productivity at the surface unit (Ewert et al., 2005; Long et al., 2014; Quintero-Angel, González-Acevedo, 2018). Current agricultural systems are defined by an integrative management of soil-technological inputs-biological components (Jones et al., 2017). In this type of management has increased the importance of microorganisms for their efficiency in nutrient utilization and transfer processes to plants (Hodobod et al., 2016; Li et al., 2017). The presence of microflora in biogeochemical cycles makes them perfect candidates for plant growth promoting with a rhizospheric and trans-rhizospheric activity (Olivares et al., 2017; Mishra et al., 2018; Techenand Helming, 2017). In addition, the microbial community reduces the pressure of technological inputs and stimulates ecosystem resilience (Müller et al., 2016; Preece, Peñuelas, 2016; van Lenteren et al., 2018).

An intimate contact and the most performant mechanisms are found in symbiotic interactions, with plant benefiting from a

broad-based interface and the highest level of microbial activity (Saleemi et al., 2017; Schlöter et al., 2018). Rhizospheric symbiosis permanently changes the size of populations under the combined influence of cultivated plants and technology (Andreote et al., 2017; Denison et al., 2011; Vimal et al., 2017). The specificity of management induces changes to existing microbial resources in soil, both oriented to reorganize specific feeding niches and to restructure local diversity (Compant et al., 2016; Terrazas et al., 2016).

The efficiency of using native soil resources and technologically applied (i.e., different types of fertilizers) is evolutionarily conditioned in most plants by the presence of mycorrhizal fungi in the rhizosphere (Ehrmann and Ritz, 2014). Intimate contact with plant roots promotes this type of symbionts as evolutionary nutrition regulators, connecting the rhizosphere to a large number of species and maintaining the stability of agroecosystems (Bonfanteand Genre, 2010; Kraigher et al., 2013; Zemunik et al., 2015). Current applications focus on either boosting native communities in the soil or supplementing them with different microbial consortia (French et al., 2017; Martinez et al., 2010; Munyanziza et al.,

1997; Sruthilaxmi et al., 2017; St-Denis et al., 2017). In the first case, long-term studies with a high number of variables are needed: fertilizers, pests, diseases and weeds management combined with different soil management systems. In the second case, it is necessary to follow a large number of inoculation variants to ensure the installation of the most effective symbiotic mechanisms. Both variants require long test periods, high financial resources in order to identify a recipe adapted to each agroecosystem.

The context has created the possibility of developing an effective alternative for stimulating mycorrhizal activity by identifying areas with high symbiotic potential and transferring active rhizosphere into similar agroecosystems. The proposed concept aims to create maps of the efficiency and dependence on mycorrhizal mechanism in agroecosystems, integrating soil type, regional eco-climatic factors, assemblage of native vegetation and microbial communities.

MYCORRHIZAS - MANDATORY MICROBIAL RESOURCES IN AGROECOSYSTEMS

Mycorrhizal symbiotic fungi have evolved to be the regulators of the host plants they interact with. Current estimates have established a 1:5 ratio of mycorrhizal fungi against host plants (Heijden et al., 2015), with a predominance of vesicular-arbuscular fungi (VAM) as symbionts. This ratio is due to the plant's need for complex soil nutritional solutions but which are limited as solubility in parent material (von Tucher et al., 2018; Zhang et al., 2016; Zhu et al., 2018). The potential for the development of extensive hyphal systems in search for nutrients has progressively promoted them as agents to facilitate exchanges within plant communities (Angel et al., 2016; Garcia et al., 2016; Wang et al., 2017). Mycorrhizal hyphae have small diameters, the fungi being able to access the spaces too small for the roots of the plants (Smith and Read, 2008). Plants with thick roots are much more susceptible to association with mycorrhizae than those with thin roots. VAM diversity in agricultural soils depends on the development of the host plant interface, soil type and eco-climatic conditions (Giovannetti,

Avio, 2002; Rúa et al., 2016). The reduced specificity of the host plants, together with the adaptive capacity, makes them potential partners in agricultural crops (Karandashov, Bucher, 2005). However, at local level the specificity of the plants for a small number of species prevails over the high diversity of VAM fungi (Goss et al., 2017; Veresoglou et al., 2012). In agroecosystems, fungi act as regulators of biogeochemical circuits, a service that is visible in the phenomena of plant growth promotion (Barea et al., 2002; Jeffries et al., 2003; Nadeem et al., 2014). Between nutrients, phosphorus transferred from fungi to plants can reach high quantities, and nitrogen can be absorbed in high amounts in the mycelium during this process (Basu et al., 2018). Mobile forms of phosphorus have a high rate of immobilization in soil solution which affects normal plant growth. The phenomenon is countered by mycorrhizas that provide an alternative to transporting phosphorus through the hyphal networks in root of host plants (Cavagnaro et al., 2015).

Translocation of carbon has generally been assessed in forest ecosystems, but new agronomic concepts for returning secondary production to soil will reveal the role of VAM in this biogeochemical circuit. Through their extra-radicular mycelial extension, mycorrhizas contribute to a reduction of nutrient losses, either organic or mineral, while maintaining ecosystem sustainability at a high level (Thornley, Parsons, 2014; Wu et al., 2013).

SOIL - SUBSTRATE FOR MYCORRHIZAL NETWORK DEVELOPMENT

In soil, mycorrhizas stimulate the settlement of new seedlings, release of nutrients from organic matter simultaneous with stabilization of formation and aggregation processes of the particles (Lehmann et al., 2017). Mycorrhizal plants possess an increased resistance to water stress, heavy metal accumulation and soil borne pathogen attack (Latef et al., 2016). Current agronomic practices are reevaluated for taking into account the pressure on soil biological communities and, in particular, the link between mycorrhizal fungi and plant (Buczko et al., 2018). VAM dynamics in soil tends to

produce complex mycelia, creating extensive interconnected networks (Cabral et al., 2016; Hussain et al., 2016). Networks serve as a point of insertion of host plants into the nutrient flow and favor interspecific metabolites exchanges. The regulation of flows to and towards plants is dependent on the number of individuals/surface unit, the transferable carbon capacity to fungal symbionts and the transfer strategy of mycorrhizas (Gu et al., 2016; Sciacca et al., 2013).

Agronomic pressure on soil in food-based ecosystems acts both on the extension of mycorrhizal networks and on potential host plants (Islas et al., 2016). In general, conventional soil cultivation systems severely fragment VAM by reducing the localization of symbiosis only in the host plant's rhizosphere in the first phase of growth (Kabir, 2005). Soil plowing or the frequent movement of soil particles blocks the formation of trans-rhizospheric networks, leading to a nutritional imbalance of cultivated plants (Brito et al., 2012). Shallower no-tillage systems maintain VAM networks and stimulate the installation of a high-functionality symbiotic transfer interface (Verhulst et al., 2010). Thus, the plants grown in successive vegetation cycles always benefit from the extra-radicular systems of the precursor. At the same time, reduced soil tillage maintains propagule function of mycorrhizal mycelium and stimulates the increase in the number of spores present in the upper layer of the soil (Isobe et al., 2008). Soil processing also induces changes in VAM species that colonize crop plants by selecting species adapted to each type of management (Martin et al., 2017; Oehl et al., 2004). The phenomenon of selection is visible in the quality of the symbiotic interface, each species having its own colonization pattern based on spores or mycelial fragments. To this is added the change of host plant from one cycle to the next growing season. In monoculture conditions, the mechanism of selection of species adapted to the rhizosphere type is activated by a certain host but not always the most prolific symbiotic partners (Dharand Pagano, 2016). The cultivation of plants in complex rotations balances the representation of each mycorrhizal species in soil, the symbiotic association being much more efficient (Bakhshandeh et al., 2017). Species that are not associated with the main

crop survive as symbionts in weeds rhizosphere and plants located outside the parcels (Asmelash et al., 2016; Hodge, Fitter, 2013). Selection induced by the principal crop serves as the main source of variation in mycorrhizal community, allowing the restoration of the population of each species over different time periods.

MYCORRHIZAL MAPS - AN AGRONOMIC SCENARIO

Sustainable agronomy requires efficient, high-performance technologies and interdisciplinary integrative approaches (Wang et al., 2009). Soil systems have developed extremely strongly in last decades by adapting existing technologies or innovation (Hagemann, Potthast, 2015, Poppy et al., 2014). But the development of these systems has generally become independent of soil biology, at this time there is a low database of biota dynamics under different management conditions (Baez-Rogelio et al., 2017; Kumar, Gopal, 2015). Reverse site analysis methodology where different soil work systems have been applied can be a base for monitoring and extrapolation of results.

Generally, independent of the pressure of technologies, soil type or native vegetation from agroecosystems, techniques of biological analysis of fauna and flora have been developed (Jones, Bradford, 2001; Lemanceau et al., 2015; Parker, 2010; Zalibekov et al., 214; Wall et al., 2001; Wachira et al., 2014). The efficiency of a particular type of farming system is segmented analyzed, without taking into account the whole range of factors (Culman et al., 2010). Mycorrhizas are symbionts present in any type of agro ecosystem with a high number of host plants. The dynamics of mycorrhizal interaction with plants go from symbiosis to parasitism, in close dependence with ensuring of optimal ecopedological factors. This point to the need for analyzing the current state of mycorrhizal mechanisms in agroecosystems, and to integrate the results into complex databases. The ability to collect mycorrhizal inoculum and transfer to similar agroecosystems can increase the efficiency of soil nutrient cycles and

increase long-term production and sustainability.

The mapping system we propose takes into account biotic and abiotic components with high integrative capacity (Figure 1). The general foundations of the system relate to the monitoring of the current state of agroecosystems with the possibility of completing the historical data on each site.

The type of soil is required to establish potential ecotrophic indices, water dynamics and biogeochemical cycles. The soil demarcation of agricultural crops defines the range of soils that can be cultivated simultaneously with the same plant. Soil technological management induces changes in natural vegetation present in each area, defining the conservation status of the symbiotic rhizosphere. The assessment of native

vegetation allows identification of the rhizospheric similarity between geographically distant agroecosystems. Main crops serve as a base for active rhizosphere sampling and targeted transfer to adapted areas. The active rhizosphere also serves as the base for laboratory testing in order to identify the most effective partnerships with host plants and site-specific bioproduct synthesis. The functionality of mycorrhizal mechanisms, the extension of extra-radicular hyphal networks and the efficiency of symbiotic association define the potential of connecting crop plants to the biological nutrient networks in the soil. Identifying and transferring the best performing mycorrhizal partners increases the economic and biological efficiency of a crop and the agroecosystem stability.

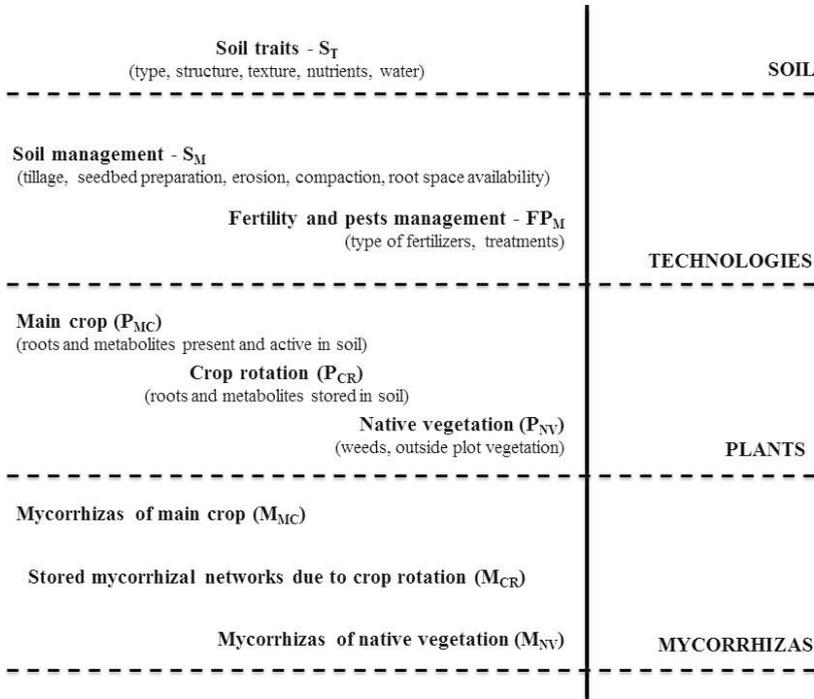


Figure 1. Methodological framework for mycorrhizal maps

The agronomic utility of complex mycorrhizal maps comes from the constant expansion of databases, facilitating access to the best symbiotic resources. The geographic assemblage of similar agroecosystems on complex maps streamlines the targeted transfer processes of mycorrhizal rhizosphere into areas

requiring improvements for these mechanisms. Identifying as many as possible of similar characteristics leads to the obtaining of rhizospheric grafts with high adaptive potential under transfer conditions.

Soil analysis (S_T), technologies (S_M , FP_M) and present and past vegetation (P_{MC} , P_{CR} , P_{NV})

have a historical character, as a basis for assembling inter-plot transfer scenarios. The mycorrhizal potential (M_{MC} , M_{CR} , M_{NV}) indicates the efficiency of the current symbiotic mechanism related to the state of the crop and the associated vegetation. Mycorrhizal testing is done in real time to identify the optimum time for collecting the rhizosphere when the number of propagules is the maximum.

CONCLUSIONS

Future agriculture tends to resize and adapt technologies to soil-plant-microflora complexes. The transfer of active rhizosphere will stimulate the sustainable development of agroecosystems. Mycorrhizal maps serve to streamline plant nutrition processes by identifying the most successful symbiotic partners.

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