Mycorrhizal diversity of glomaceae family from sorghum rhizosphere in cerrado soil with different aluminum saturation

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Introduction

Phosphorus (P) is an essential nutrient and it is frequently limiting macronutrient for plant growth, especially in acid soils. In many agricultural systems in which high application of P to the soil is necessary to ensure plant productivity, the recovery of applied P by crop plants is very low, because in the soil more than 80% of the P becomes immobile and unavailable for plant uptake due to adsorption, precipitation, or conversion to the organic form (Raij, 1991; Holford, 1997). On the other hand, microbial associations, including mycorrhizal symbioses, are alternatives of low cost important for phosphorus supply. Arbuscular mycorrhizas (AM) are likely a primitive state for all vascular plants, and the glomalean fungi that produce them form symbiotic associations with most terrestrial plants (Smith & Read, 1997; Brundrett, 2002). Plants benefit from these associations by improved nutrient acquisition and protection from other biotic and abiotic factors less well defined (Schachtman et al., 1998). However, plant and soil factors can influence the benefits provided by mycorrhizal fungi to plants. Little information currently exists on species diversity in communities of arbuscular mycorrhizal fungi (AMF) associated with sorghum plant. Recently, progress has occurred in the study of plant-microorganisms interactions mainly because of the introduction of new molecular techniques such as polymerase chain reaction (PCR) (Smalla et al., 1993) and denaturing gradient gel electrophoresis (DGGE) (Muyzer and Smalla, 1998). The aim of this work was to characterize the genetic diversity of arbuscular mycorrhizas colonizing sorghum rhizosphere in cerrado affected by genotypes and aluminum saturation.

Materials and Methods

Rhizosphere soil were collected from two sorghum cultivars (G1-tolerant and G2-sensible) growing in cerrado soil, with three levels of aluminum saturation (0, low; 30 intermediary and 50%, high) and sieved through a 2-mm sieve. For non-rhizosphere control, soil without roots was used. Soil samples of 500 mg were used for total DNA extraction using BIO 101 Kit protocols, following the manufacturer's recommendations. The small subunit (SSU) ribosomal RNA gene were amplified from a total soil DNA extract based on nested PCR using fungal universal primers (NS5 and ITS4) and ITS/Glomaceae specific primers attached with the sequence clamp, GLOM1310 and ITS2 (Redecker, 2000). PCR products were loaded by electrophoresis in a 6% polyacrilamide gel composed of denaturing gradients between 45 and 70% of urea-formamide gels (DGGE) and run for 16h in a BIO-RAD Dcode System, VA, USA. A routine silver staining protocol was used for detection of DNA and the gels were documented with digital camera before analysis.

Results and Discussion

Based on DGGE patterns, the dates allow the comparison of variation in the AM fungal community composition among plants genotypes, between presence and absence of plants and between levels of aluminum saturation. As expected, diversity (measured here as the number of amplicons) was higher on roots than in non-rhizosphere soil. There was a strong shift in the mycorrhizal communities due to Al in the non-rhizosphere soil samples and in the rhizosphere soil of the sensible genotype, with reduced diversity. But, an apparent paradoxical increase in AMF richness was noted with tolerant genotype. There was high diversity AMF at high Al level, perhaps

reflecting association with sorghum adaptation to Al stress. Similarly, the cluster analysis identified two principal groups. Group I with samples of soil free of roots, and group II, with samples of rhizosphere, suggesting two different communities. The subgroups observed – two in the group I and three in the group II, show the influence aluminum saturation and genotypes in the composition of the studied fungi, respectively. The high diversity and variation detected due to analyzed factors implies that the AM fungal types are ecologically distinct and thus may have the potential to influence adaptation of sorghum cultivars to acid soil.

Conclusions

The diversity in communities of arbuscular mycorrhizal fungi of Glomaceae family in cerrado soil is stimulated by sorghum plants and reduced by aluminum toxicity.

The arbuscular mycorrhizal community composition of Glomaceae family in cerrado soil depends of sorghum genotype.

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