

Title: Diversity of endophytic fungi in *Glycine max*

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Abstract

Endophytic fungi are microorganisms that live within plant tissues without causing disease during part of their life cycle. With the isolation and identification of these fungi, new species are being discovered, and ecological relationships with their hosts have also been studied. In *Glycine max*, limited studies have investigated the isolation and distribution of endophytic fungi throughout leaves and roots. The distribution of these fungi in various plant organs differs in diversity and abundance, even when analyzed using molecular techniques that can evaluate fungal communities in different parts of the plants, such as DGGE (denaturing gradient gel electrophoresis). Our results show there is greater species richness of culturable endophytic filamentous fungi in the leaves *G. max* as compared to roots. Additionally, the leaves had high values for diversity indices i.e. Simpsons, Shannon and Equitability. Conversely, Dominance index was higher in roots as compared to leaves. The fungi *Ampelomyces* sp., *Cladosporium cladosporioides*, *Colletotrichum gloeosporioides*, *Diaporthe helianthi*, *Guignardia mangiferae* and *Phoma* sp. were more frequently isolated from the leaves, whereas the fungi *Fusarium oxysporum*, *Fusarium solani* and *Fusarium* sp. were prevalent in the roots. However, by evaluating the two communities by DGGE, we concluded that the species richness was higher in the roots than in the leaves. UPGMA analysis showed consistent clustering of isolates; however, the fungus *Leptospora rubella*, which belongs to the order Dothideales, was grouped with species of the order Pleosporales. The presence of endophytic *Fusarium* species in *G. max* roots is unsurprising, since *Fusarium* spp. isolates have been previously described as endophyte in other reports. However, it remains to be determined whether the *G. max* *Fusarium* endophytes are latent pathogens or non-pathogenic forms that benefit the plant. This study provides a broader knowledge of the distribution of the fungal community in *G. max* leaves and roots, and identifies the genetic relationships among the isolated species.

Keywords: DGGE, fungal community, ITS, clustering analysis, phytopathogenic fungi.

Financing: CAPES, CNPQ and FAPEMIG