

## The arbuscular mycorrhizal fungi of *Lotus glaber*.

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We intended to study the composition and structure of arbuscular mycorrhizal (AM) fungal community associated with *Lotus glaber* in sodic soils of the Salado River basin.

Roots were cleared, stained with Trypan blue and the amount of intraradical mycorrhizal structures estimated by the slide method. Spores were identified after isolation by wet sieving and decanting. The chemical analysis of rhizospheric soil was performed.

Spores of eighteen different AM species were detected. *Glomus geosporum*, the most frequently isolated AM fungus, was also the dominant one. Shannon-Wiener diversity index varied between 0.65 and 1.65.

Morphological types of AM fungi associated with *L. glaber* were also studied. At least eight colonization patterns (IP) of AM fungi in roots of *L. glaber* were observed. *Arum*- and *Paris*-types of infection were found in the same plant species. This result supports the idea that the morphology of AM is not solely under plant control, but is also influenced by fungal identity. One IP presumably corresponding to *G. intraradices* and a second one possibly assignable to *G. tenue* were the most commonly found.

Additionally, DNA from the root samples was isolated and intergenic DNA sequences from the AM fungi were amplified through a nested PCR with taxon-specific primers. Problems in cloning and sequencing caused that only two fragments have been successfully sequenced. Sequencing of these clones and the comparisons with the data in the Genbank revealed that the amplified fragments possess a high homology percentage with sequences from *G. intraradices*

Our findings reinforce previous suggestions that *G. geosporum* and *G. intraradices* are well adapted to sodic-saline conditions and would play a role in the resistance of *L. glaber* to these soils.