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*Mycorrhiza* session: [Abstract for a poster](#)

## **Stress and host driven responses of Glomeromycota- and Mucoromycotina-arbuscular mycorrhizal fungi co-colonizing durum wheat in a field experiment**

Kerbiriou E., E. Guillot, D. Dezette, M. Scellier, A. Houdaer, E. Taschen

Eco&Sols, Institut Agro, Univ Montpellier, CIRAD, INRAE, IRD, F-34060 Montpellier, France

Arbuscular mycorrhizal fungi (AMF) are well-known root symbionts and were long time all classified into the Glomeromycota phylum (Schüssler et al., 2001). Some fine endophytes known to form arbuscular structures were recently reclassified as members of the Mucoromycotina (Spatafora et al., 2016). The only formally described species, *Glomus tenue*, was assigned to a new genus, the *Planticonsortium* (Walker et al., 2018). Both Glomeromycota-AMF (G-AMF) and Mucoromycotina-AMF (M-AMF) were observed in the famous fossils of the Devonian period (Field et al., 2018) and are present from the very beginning of land colonization by plants. Since then, G-AMF and M-AMF have evolved with many plant lineages. Due to the difficulty of microscopic distinction, the paucity of taxonomic descriptions and very recent possibility of molecular characterization, there is much less knowledge on the ecological functioning of M-AMF than of G-AMF. But there is a recent resurgence of interest. Their response to environmental conditions were studied in Australia, showing a strong preference for cultivated ecosystems (Albornoz et al., 2021). In a field study in Southern France, we observed both M-AMF and G-AMF colonizing durum wheat roots, sometimes in close proximity in neighboring root cortex cells. While G-AMF colonization rates were not affected by the combined nitrogen and water stress, M-AMF were significantly more abundant in the no-stress treatment. G-AMF colonization rates depended on the durum wheat variety (11 varieties) and root trait morphology. None of these host-dependent factors significantly affected the abundance of M-AMF; this may suggest different regulation mechanisms for these fungal symbioses.

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