

Mycorrhizas as tripartite associations

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More than 450 Mya certain Early Devonian plants established an intimate association with filamentous fungi that have been identified, on the basis of morphological features detectable in the fossils, as the ancestors of today's mycorrhizal fungi (Bonfante and Genre 2008). Hypogeous plant organs, mostly roots, are in fact the preferred niche for soil fungi, which live in the rhizosphere as saprotrophs or are directly associated with photosynthetic plants as mycorrhizal symbionts. The latter represent a vital component in plant ecosystems: They are widely distributed in natural and agricultural environments and are present in more than 80% of land plants, liverworts, ferns, woody gymnosperms and angiosperms, and grasses (Parniske, 2008). For efficient nutrient uptake, most land plants need to be associated with mycorrhizal fungi that supply minerals, increasing their productivity and conferring resistance to stress. The exploitation of these symbioses in natural and agronomic environments is of high environmental and economic value.

In recent years soil bacteria have garnered attention in the context of plant-fungal symbioses, as many bacterial populations have been found to be loosely or tightly associated with mycorrhizal fungi, most likely playing a role in mycorrhizal function. They seem therefore to represent the third component of mycorrhizas (Bonfante and Anca, 2009). J. Garbaye (1994) opened this field with the widely acknowledged term helper bacteria, which defined those bacteria that support mycorrhizal establishment; but now new knowledge and insight have been added, leading to a new scenario. There is increasing evidence that bacteria-fungi interactions are more widespread than expected and that their dynamics may be crucial in ecosystems (Leveau, Preston, 2008). The presentation will focus on bacteria which are tightly associated to arbuscular mycorrhizal fungi, since they thrive inside the fungal cytoplasm. These endobacteria are currently distinguished in two morphotypes. The first is coccoid in shape and has been called "bacterium-like organism" (BLO). An inventory of diverse AMF lineages have demonstrated a widespread occurrence of BLOs, which on the basis of their 16S rDNA resulted to be located inside the Mollicutes, whose members are usually lacking cell walls and show symbiotic/ parasitic lifestyles (Naumann et al, 2010). The other bacterial type is restricted to a phylogenetically relatively young AMF family (*Gigasporaceae*), is rod-shaped, vertically transmitted, *Burkholderia*-related and described as an uncultured taxon, *Candidatus Glomeribacter gigasporarum* (Lumini et al, 2006). A genome sequencing project faced through a combination of Sanger sequencing and 454 technology is revealing a small genome (1.6-1.8 Mb) characterized by peculiarities, like genes putatively involved in vitamin B12 pathways. A fungal line cured from these endobacteria demonstrated that they confer an ecologically relevant fitness to their fungal host, while a proteomic analysis confirmed the presence of stress-related proteins in the cured line (Salvioli et al, 2010). In conclusion current findings demonstrate that endobacteria represent ancient and heritable components of AM fungi, representing therefore the third component of some AM mycorrhizas.

Acknowledgements. Research was funded by the Project Converging technologies, BioBITS, CIPE 2007.

References

- Bonfante, P., Anca, I.A. (2009). Plants, mycorrhizal fungi, and bacteria: a network of interactions. *Annual Review of Microbiology* 63 363-383
- Bonfante P, Genre A. 2008. Plants and arbuscular mycorrhizal fungi: an evolutionary-developmental

perspective. *Trends Plant Sci.* 13:492–98

Garbaye J. 1994. Helper bacteria: a new dimension to the mycorrhizal symbiosis. *New Phytol.* 128:197–210

Leveau JH, Preston GM. 2008. Bacterial mycophagy: definition and diagnosis of a unique bacterial-fungal interaction. *New Phytol.* 177:859–76

Lumini E, Ghignone S, Bianciotto V, Bonfante P. 2006. Endobacteria or bacterial endosymbionts? To be or not to be. *New Phytol.* 170:205–8

Naumann, M., Schüssler, A., Bonfante, P. (2010). The obligate endobacteria of arbuscular mycorrhizal fungi are ancient heritable components related to the Mollicutes. *ISME Journal* 4(7) 862–871. ISSN:1751-7362

Parniske, M. Arbuscular mycorrhiza: the mother of plant root endosymbioses. *Nat. Rev. Microbiol.* 6, 763-775 (2008)

Salvioli, A., Chiapello, M., Fontaine, J., Hadj-Sahraoui, A.L., Grandmougin-Ferjani, A., Lanfranco, L., Bonfante, P. (2010). Endobacteria affect the metabolic profile of their host *Gigaspora margarita*, an arbuscular mycorrhizal fungus. *Environmental Microbiology* **12**(8) 2083-2095.