Symbiosis in the -*OMICS* era: a glance into the arbuscular mycorrhizal symbiosis

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-*OMICS* technologies, providing the description of whole genomes, transcriptomes, proteomes, have offered novel and powerful tools to decipher the evolution and the functioning of biological systems.

The arbuscular mycorrhizal (AM) symbiosis displays a multifunctional nature providing several benefits to the host plants from an improved mineral nutrition to protection against biotic and abiotic stresses (Pozo & Azcon-Aguilar 2007; Aroca et al. 2008). The molecular mechanisms at the basis of these effects are largely unknown. In the last years -*OMICS* approaches have been applied to shed light on the events that accompany the formation of arbuscular mycorrhizas where extensive cellular reorganizations and physiological and metabolic changes occur on both the plant and the fungal side.

Transcriptomic studies, mainly based on microarray technologies, have been carried out on several host plants (Gomez et al. 2009; Guether et al. 2009 and references therein). We focused our attention on *Solanum lycopersicum* (tomato) plants and used the TOM2 microarray platform (about 12,000 genes) to show that the colonization by an AM fungus triggers considerable local (root) and systemic (shoot) alterations in the transcript profiles. Novel genes, which are candidates to partecipate in aspects of arbuscule development and/or functioning, have been identified on the basis of their expression pattern associated to arbuscule-containing cells (Fiorilli et al. 2009). The same microarray platform was used to investigate, at the molecular level, the impact of the AM symbiosis on the infection by the Tomato Spotted Wilt Virus, an important pathogen of tomato.

OMICS-data are much more limited for the AM fungal partner. As members of the international consortium of a genome project devoted to an AM fungus (Martin et al. 2008) we are currently investigating gene expression profiles of fungal structures developing inside the root taking advantage of the laser microdissection approach (Balestrini et al. 2007) with the aim to identify fungal genetic determinants of a functional symbiosis.

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