

Blurred boundaries: lifestyle lessons from ectomycorrhizal fungal genomes

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- Ectomycorrhizal (ECM) fungi form mutualistic relationships with the roots of a wide range of tree species.
- Fungal genome analyses of *L. bicolor* and the recently sequenced *T. melanosporum* were compared so as to reveal the genetic nature of the mutualistic symbiosis between ECM and plants. These comparisons are suggestive of the genetic components involved in the symbiosis.
 - A decreased contingent of plant cell wall-degrading enzymes was found to be a trademark of these fungal genomes, likely forcing the ECM fungi to be more dependent on the plants for photosynthate as a carbon source.
- The genetic sequences also enable transcriptomics studies
 - Transcriptomic evidence suggests that genes encoding mycorrhiza-induced small secreted proteins present in *L. bicolor*, may have a role during the colonization of plant roots by ECM fungi
 - A common core set of symbiosis-induced metabolic transcripts related to nutrient cycling was found, thereby suggesting that provision of nutrients to the plant host is a key factor driving and maintaining symbiosis.

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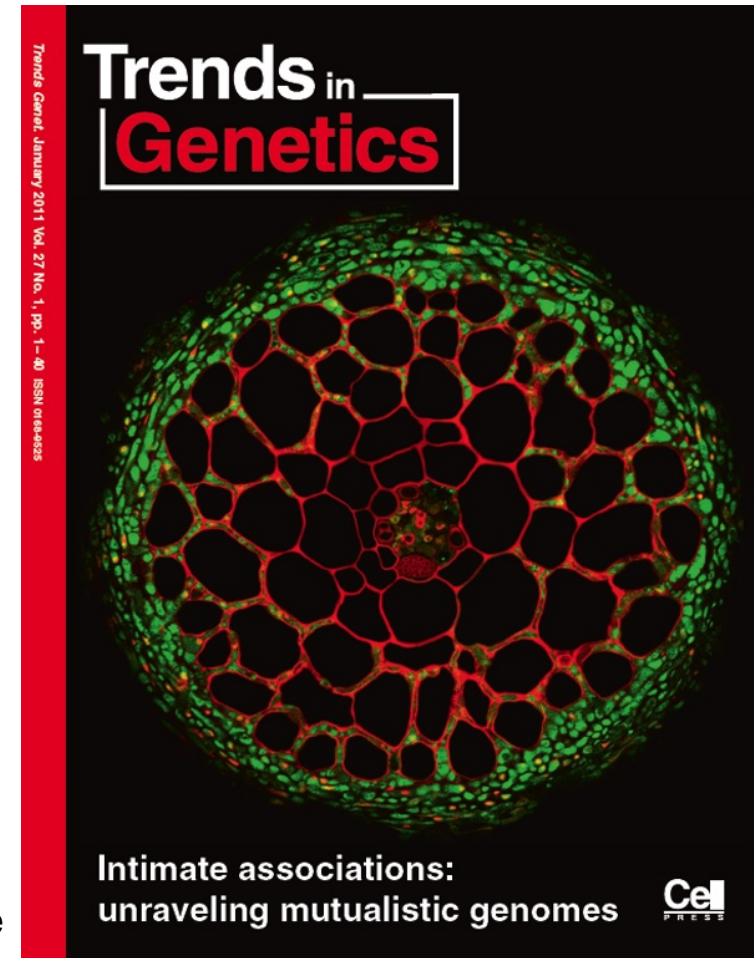


Figure 1. Formation of the Hartig net. The hyphae from the ECM fungus, *L. bicolor* (green), residing within the apoplastic spaces of host *Populus* roots (red) (Trends in Genetics, January 2011, 7(1): 14-22)