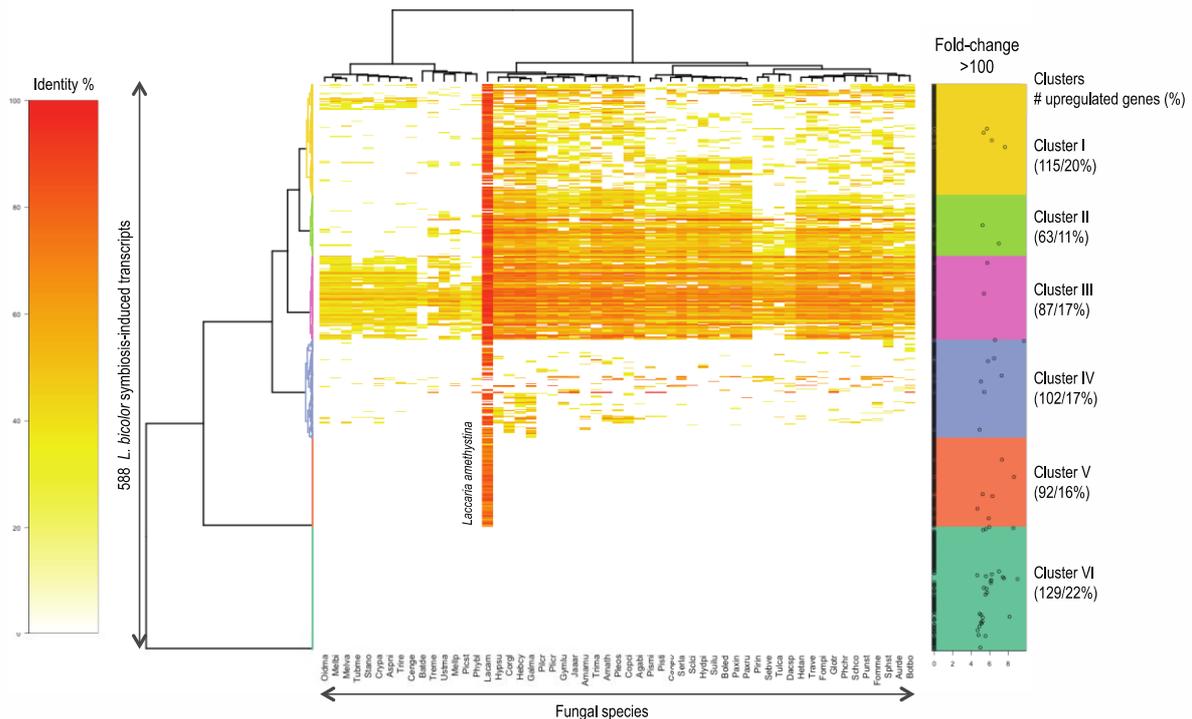


EST



Exploring Symbiotic genomes and Transcriptomes

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Context — Mycorrhizal symbioses are mutualistic associations formed between plant roots and soil-borne fungi, which involve a multitude of plants and fungal species. In exchange for carbon, mycorrhizal fungi provide plants with different resources, including water, nitrogen or phosphorus. Yet the nature and regulation of the genes defining symbiosis still elude us. Mycorrhizal fungi connect plants to soil, plants to plants, microbes to plants, but still, we understand very little about the genetic code driving these connections.

Objectives — We propose to use already available genomes together with transcriptome sequencing (RNA-Seq) to explore symbiosis-related gene networks behind the development and functioning of ectomycorrhizal, ericoid and orchid symbioses. We will compare the transcriptomes of free-living fungi and of plant roots colonised by fungal strains, at the onset of colonisation and once the mycorrhizal structures have been established. We will focus our search to sequence data associated with plant-fungus signaling (effectors), primary metabolism, and degradation metabolism.

Approach — The bioinformatician hired by this project will be in charge of mining the transcriptomic data and to define a workflow for transcriptome analyses. The main missions will be:

- gene expression quantification
- differential expression and coexpression networks analysis
- data visualization tools

Key results —

- By sequencing RNA from free-living mycelia and mycorrhizal roots, we identified genes regulated by symbiosis development in the ECM *Amanita muscaria*, *Hebeloma cylindrosporum*, *Paxillus involutus*, *Piloderma croceum* and *Suillus luteus*, the ERM *Oidiodendron maius* and the ORM *Sebacina vermifera* and *Tulasnella calospora*.
- Of the expressed genes, 1.3–6.0% are up-regulated during symbiosis and 0.2–4.9% are down-regulated by the interaction.
- A large set of symbiosis-up-regulated genes have orthologs in brown- and white-rot fungi, thus suggesting that they are not unique to mycorrhizal symbionts and tend to be associated with essential core metabolic pathways.
- But a subset of the symbiosis-induced genes is restricted to a single ECM species, even in the densely sampled Boletales. Only one-third of the *Laccaria* symbiosis-induced orphan genes have homologs in both *L. bicolor* and *Laccaria amethystina*.
- Genes encoding mycorrhiza-induced small-secreted proteins (MiSSPs) were induced in mycorrhizal roots of all interactions.

Main conclusions including key points of discussion — The analyses of mycorrhizal transcriptomes revealed the involvement of both conserved AND clade-specific genes. Induced are genes without orthology but coding for the same functions, like (often clade-specific) small-secreted proteins, transporters, redox metabolism or carbohydrate active enzymes, suggesting a convergent evolution.

Future perspectives — Of special interest for further functional analyses are mycorrhiza-induced small-secreted proteins (MiSSPs) that have been identified in all interactions studied so far. They are likely used to manipulate their hosts during colonization as it has been shown for *Laccaria bicolor* MiSSP7.

Valorisation —

Annegret Kohler, Alan Kuo, Laszlo G Nagy, Emmanuelle Morin *et al.* (2015) Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. *Nature Genetics*. doi:10.1038/ng.3223