



**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