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**Title:** Genomic and transcriptomic analysis of *Laccaria bicolor* CAZome reveals insights into polysaccharides remodelling during symbiosis establishment  
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**Abstract:** Ectomycorrhizal fungi, living in soil forests, are required microorganisms to sustain tree growth and productivity. The establishment of mutualistic interaction with roots to form ectomycorrhiza (ECM) is not well known at the molecular level. In particular, how fungal and plant cell walls are rearranged to establish a fully functional ectomycorrhiza is poorly understood. Nevertheless, it is likely that Carbohydrate Active enZymes (CAZyme) produced by the fungus participate in this process. Genome-wide transcriptome profiling during ECM development was used to examine how the CAZome of *Laccaria bicolor* is regulated during symbiosis establishment. CAZymes active on fungal cell wall were upregulated during ECM development in particular after 4 weeks of contact when the hyphae are surrounding the root cells and start to colonize the apoplast. We demonstrated that one expansin-like protein, whose expression is specific to symbiotic tissues, localizes within fungal cell wall. Whereas *L. bicolor* genome contained a constricted repertoire of CAZymes active on cellulose and hemicellulose, these CAZymes were expressed during the first steps of root cells colonization. *L. bicolor* retained the ability to use homogalacturonan, a pectin-derived substrate, as carbon source. CAZymes likely involved in pectin hydrolysis were mainly expressed at the stage of a fully mature ECM.

All together, our data suggest an active remodelling of fungal cell wall with a possible involvement of expansin during ECM development. By contrast, a soft remodelling of the plant cell wall likely occurs through the loosening of the cellulose microfibrils by AA9 or GH12 CAZymes and middle lamella smooth remodelling through pectin (homogalacturonan) hydrolysis likely by GH28, GH12 CAZymes. (C) 2014 Elsevier Inc. All rights reserved.

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