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Understanding cell wall re-modelling during the symbiotic interaction between the ectomycorrhizal fungus *Tuber melanosporum* and *Corylus avellana*

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It has been reported that the symbiotic ectomycorrhizal fungi have a small set of genes coding for secreted enzymes putatively involved in the degradation of plant cell wall polysaccharides [1, 2]. Within the context of the *Tuber melanosporum* genome sequencing project, genes coding for putative plant cell wall degrading enzymes (CDWEs) have been identified and manually annotated; several of them were found to be up-regulated during the symbiosis, suggesting a role in plant cell wall degradation and facilitation of the fungal progression through the pectin-rich middle lamella, when the fungus develops inside plant tissues. Gene expression data (microarray, RNAseq, qRT-PCR) on *T. melanosporum* and *Corylus avellana* ectomycorrhizae (ECM) have shown that two fungal putative endoglucanases (*TmelCMC3* and *TmelEG*), a pectate lyase B (*TmelPLB*), a GH28 polygalacturonase (*TmelPGN1*) and a rhamnogalacturonase (*TmelRghA*) were up-regulated. qRT-PCR experiments have demonstrated that, in agreement with the RNAseq data, a gene encoding a rhamnogalacturonan acetylesterase (*TmelRgaE*) is also highly up-regulated in ECM, although the array data did not indicate any up-regulation. In addition, we have employed glycan microarray technology [3] to analyse the impact of fungal colonization on plant cell wall composition in the ectomycorrhizae, compared with uncolonized halzenut roots. Preliminary data suggest that cell walls are affected by the presence of the fungus and the observed changes are consistent with gene expression data, which have shown an up-regulation of enzymes involved in pectin degradation. To support glycoarray data, *in situ* immunolabelling experiments are ongoing by using monoclonal antibodies with specificity for plant cell-wall components.

[1] F. Martin et al. (2008) Nature, **452**, 88-92; [2] F. Martin et al. (2010) Nature, **464**, 1033-1038; [3] I. Moller et al. (2007) Plant J., **50**, 1118-1128.

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Genome-wide characterisation of mechanical stress responsive miRNAs from xylem tissues of different poplar genotypes

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miRNAs are small non-coding RNAs 20-24 nucleotides in length that can direct the cleavage or inhibit the translation of target gene transcripts. Since their discovery, miRNAs have been involved in various biological processes but our knowledge for their involvement in regulating wood formation is still scarce. In poplar, tension wood formation in response to gravitropic stimuli is largely used as a model system to study wood formation [1]. Up to now, *Populus* mechanical stress miRNAs have been identified from a single genotype, *Populus* cv Nisqually-1, the clone used for the *Populus* genome sequencing [2]. In order to discover new miRNAs and/or genotype specific expressed miRNAs, the content in small RNAs from tension wood (TW) and opposite wood (OW) tissues have been characterized using next-generation sequencing. 1708 distinct putative miRNAs sequences were identified from 12 sequenced libraries (3 poplar genotypes, TW/OW, 2 biological replicates). Only 95 miRNAs correspond to previously characterized mature miRNAs and a few of newly identified sequences are only detected from some genotypes. Some conserved as well as newly identified miRNAs present tissue-specific and/or genotype-specific expression patterns. These results together with prediction of gene targets may help us to infer transcriptional networks associated with regulation of wood formation. This work was supported by the ANR project “TreeForJoules” ANR-10-KBBE-0007.

[1] G. Pilate *et al.* (2004) New Phytol., **164**, 63-72 ; [2] S.F. Lu *et al.* (2005) Plant Cell, **17** (8), 2186-2203.