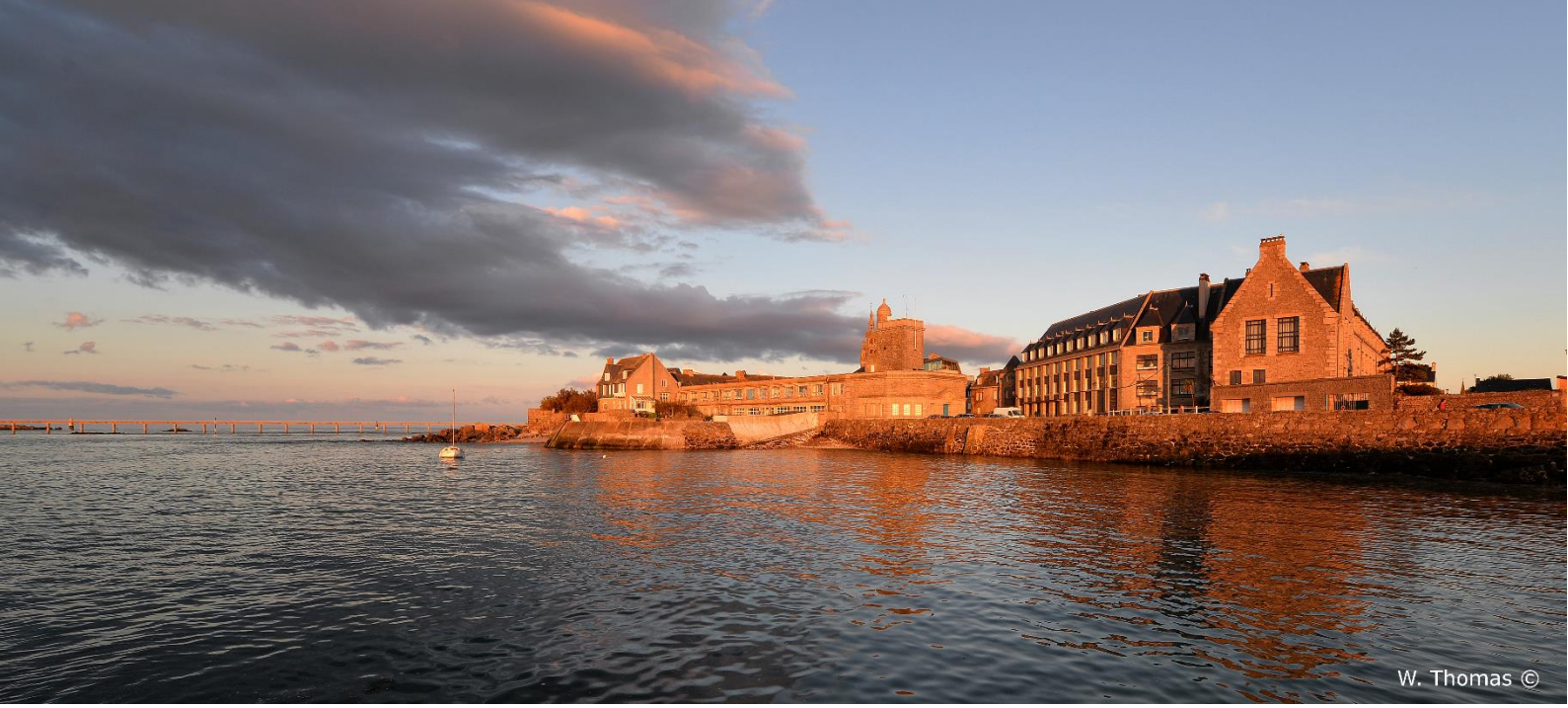
Fiber-and ray-specific transcriptomics in poplar wood: what can we learn for the building of secondary cell walls?

Annabelle Déjardin, Clément Cuello, Françoise Laurans, Marie-Claude Lesage-Descauses, Odile Rogier, Véronique Laine-Prade, Nathalie Boizot, Jean-Charles Gaudin, Gilles Pilate



12èmes journées du Réseau Français des Parois

14-16 mai 2019

Station Biologique de Roscoff

Réseau Français des Parois

CNRS • SORBONNE UNIVERSITÉ
Station Biologique de Roscoff
1872

P7

Fiber-and ray-specific transcriptomics in poplar wood: what can we learn for the building of secondary cell walls?

Annabelle Déjardin[1,#], Clément Cuello[1], Françoise Laurans[1], Marie-Claude Lesage-Descauses[1], Odile Rogier[1], Véronique Laine-Prade[1], Nathalie Boizot[1], Jean-Charles Gaudin[1], Gilles Pilate[1]
[1] *UMR BioForA, INRA, ONF, F-45075 Orléans Cedex 2, France*
E-mail: annabelle.dejardin@inra.fr

Wood - or secondary xylem - is a complex biological tissue, ensuring three major functions for trees: (1) long-distance transport of water, (2) mechanical support, and (3) storage of temporary reserves. In angiosperm trees, distinct cell types fulfill these functions: fibers and vessels are involved respectively in mechanical support and water conduction, while parenchyma rays radially transfer assimilates and store starch or lipids. Wood is therefore a complex patchwork of cells and its structure is made of the three-dimensional assembly of the cell walls of dead fibers and vessels, interconnected with still living parenchyma rays. Secondary cell walls (SCW) vary according to cell types, developmental stages and environmental conditions. For example, in response to mechanical constraints, angiosperm trees produce tension wood, whose fibers exhibit a thick gelatinous extra-layer, named G-layer, consisting mainly of cellulose and non-cellulosic polysaccharides with almost no lignin (Guedes et al., 2017). By contrast, opposite wood located on the opposite side of the trunk is totally deprived of fibers with G-layers. This great complexity hinders the study of the molecular mechanisms of SCW deposition, but recent development of cell-specific approaches alleviates this problem.

Here, we report an integrative approach combining wood cell microtranscriptomics with SCW microphenotyping on poplar wood samples. This study aims to establish cell-specific gene networks involved in SCW formation. Fiber and ray specific-transcriptomes were obtained using laser capture microdissection on cross-sections of 3 types of poplar wood - tension, opposite and normal wood (717-1B4 genotype, Populus tremula x Populus alba). Differential expression analysis was performed using DESeq2 (v1.20.0, Love et al., 2014). Preliminary analyses revealed the differences between ray and fiber transcriptomes : about 1200 genes were upregulated in normal wood fibers in comparison to rays, with 500 genes being specific of fibers. Transcriptomic differences were detected when comparing the 3 types of wood. In parallel, we have developed a non-destructive microphenotyping method based on ATR-FTIR imaging (see abstract Cuello et al.). Combining microtranscriptomics and SCW microphenotyping will give a comprehensive picture of secondary cell wall formation in poplar fibers and rays.

This work was funded by 'StressInTrees' project (French National Research Agency, ANR-12-BS09-0004) and by 'OPeNSPeNU' project (Région Centre Val de Loire, APR-IR #2016-00108472). The authors acknowledge the OV-Cytology/Imaging platform, INRA Versailles.