



SUNLIBB

Sustainable Liquid Biofuels from Biomass Biorefining

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ENERGY

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Deliverable 2.4

“Transcript profiles for the different stages of secondary cell wall development in Miscanthus generated”

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Workpackage: **2**

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Dissemination Level: **PU**

D2.4 Transcript profiles for the different stages of secondary cell wall development in miscanthus generated (month 18)

In order to uncover key genes involved in the synthesis and modification of the different components of the cell wall, an initial experiment was set up using three independent accessions showing contrasting accumulation of cellulose, lignin and hemicellulose in the cell walls (see D2.2). Gene expression of 6 cell wall genes was investigated: *MsCOMT* – caffeic acid O-methyltransferase, *MsPAL* – phenylalanine ammonia lyase, *MsLAC* – laccase, *Ms4CL* – 4-coumarate:coenzyme A ligase, *MsCAD* – cinnamyl alcohol dehydrogenase and *MsCESA* – Cellulose Synthase; these are shown in Figures 1, 2 and 3.

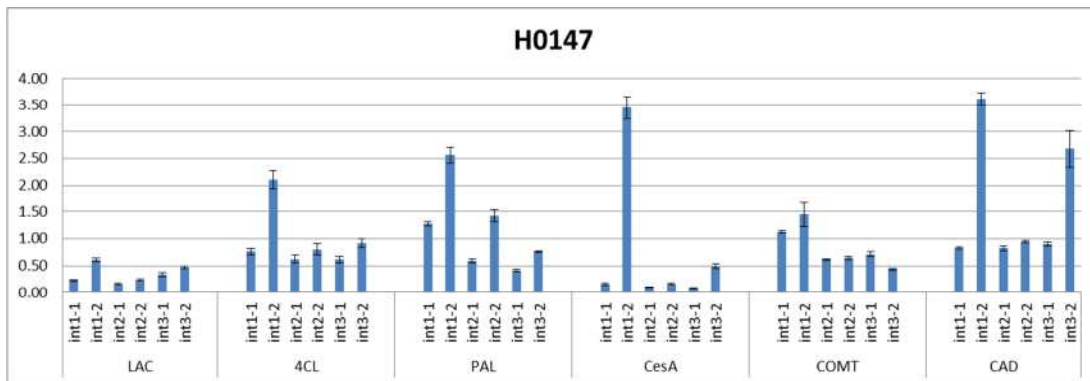


Figure 1. Expression profile of Miscanthus genotype H0147 for three internodes sections, from the shoot apical meristem to the ground tissues. The expression of the following genes involved in the lignin pathway were analysed: *LAC*, *4CL*, *PAL*, *CesA*, *COMT* and *CAD*. Each internode fraction was divided in two pieces, meaning the first digit referred to the highest fragment, and the second digit the upper (1) or lower (2) fraction of the internode.

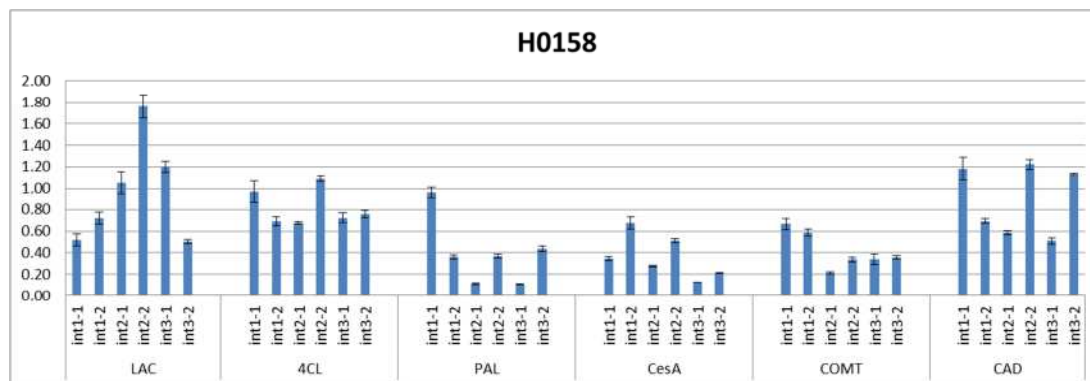


Figure 2. Expression profile of Miscanthus genotype H0158 for three internodes sections, from the shoot apical meristem to the ground tissues. The expression of the following genes involved in the lignin pathway were analysed: *LAC*, *4CL*, *PAL*, *CesA*, *COMT* and *CAD*. Each internode fraction was divided in two pieces, meaning the first digit referred to the highest fragment, and the second digit the upper (1) or lower (2) fraction of the internode.

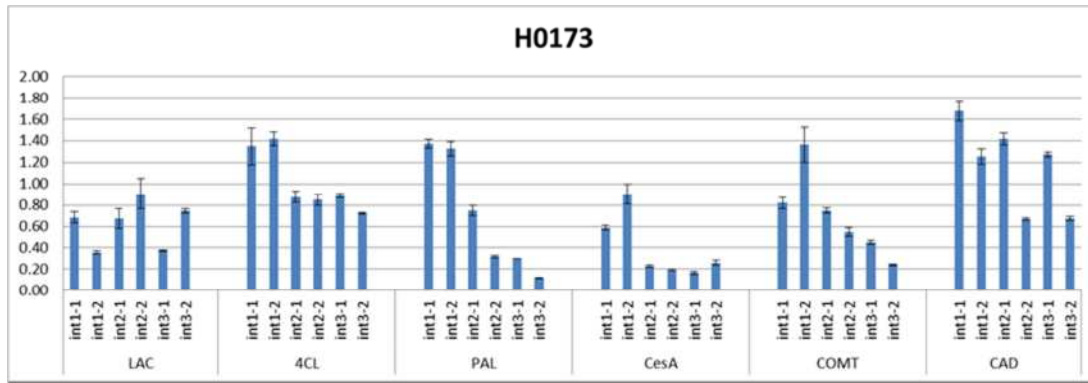


Figure 3. Expression profile of Miscanthus genotype H0173 for three internodes sections, from the shoot apical meristem to the ground tissues. The expression of the following genes involved in the lignin pathway were analysed: *LAC*, *4CL*, *PAL*, *Cesa*, *COMT* and *CAD*. Each internode fraction was divided in two pieces, meaning the first digit referred to the highest fragment, and the second digit the upper (1) or lower (2) fraction of the internode.

This initial experiment helped P13 in the design of a larger and more complete analysis, focusing not only on different internodes, but as well taking into account different developmental stages (see deliverable 2.2). An orthology database has been developed by P13, to identify key cell wall biosynthetic genes using information from other C4 plants. Using this tool more genes have been identified and tested on a broader selection (see deliverable 4.1 for list of identified lignin genes in Miscanthus). Expression analyses are currently being correlated to biochemical composition on internode fragments for a set of lignin and hemicellulose genes. These results are an addition to the promised deliverables and will be completed at the beginning of 2015.