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P0120 Comparative Transcriptome Analysis of Eucalyptus Genotypes That Differ in Carbon Allocation

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The global demand for wood combined with its diversified use requires the generation of trees that sequester and accumulate more carbon, providing differentiated raw material for the production of pulp, paper, charcoal and even cellulosic ethanol. Carbon allocation is the process of translocation of photosynthate from source to sink organs, and though its physiology is well known, the genetic mechanisms involved in its regulation are still poorly understood. Since differences in levels of gene expression may largely explain the observed phenotypic variation in organisms, and there is great variability among species of *Eucalyptus* in relation to the characteristics of biomass production and growth, we decided to perform a comparative analysis of global gene expression of four contrasting *Eucalyptus* genotypes to gain insight into the mechanisms that lead to differences in carbon allocation. Leaf, xylem and root samples from each genotype were used for transcriptome sequencing using Illumina Hi-Seq technology (RNA-seq). After control quality analysis, the reads are being aligned against *Eucapyptus grandis* reference genome (BRASUZ1) using Blat and TopHat softwares. The contigs assembled for each tissue are annotated by similarity search, in databases of non-redundant sequences of nucleotides and proteins, using the AutoFact software. Applications based on in-house scripts in Perl, together with DESeq package (R/BioConductor), are being developed to estimate transcripts abundance and calculate differential expression. We expect to unveil candidate genes that will be further investigated by transgenic over- and down-regulated expression approaches.