Eucalyptus response to nutritional stress based on gene expression analyses: preliminary steps for defining ideotype

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Tackling the question of defining a new eucalyptus ideotype, more efficient to use nutrients, can be done through different strategies. Analysing the genotype by nutritional stress interaction in an adequate experiment is among the most consistent strategies. The recent advances of high-throughput molecular technology has opened up new perspectives, giving an easy access to transcriptome resulting from gene expression Transcriptome data have become relevant to gaining insights into plant biology and provide complementary information to the classical methods based on ecophysiological and growth variables. To address these questions and facilitate the understanding of tree functioning, we implemented a field experiment (Botucatu, SP, Brazil) with three *Eucalyptus grandis* clones facing contrasting nutrient deficiencies (non-limiting fertilisation (NLF) considered as the baseline; NLF - N: N deficiency; NLF - P: P deficiency; NLF - K: K deficiency). Gene expression obtained by RNA-seq technology was the variable analysed to improve our understanding of tree response to the stressing nutritional environments tested. After filtering process, 21698 expressed genes were obtained for leaf and 21443 for xylem. For both tissues, the number of genes differentially expressed between the three clones was very high: around 3500 to 4000 genes down and up regulated. The genes differentially expressed for leaf were only observed for N deficiency treatment. The number of genes up regulated was 116 and 99 genes were down regulated at FDR p value$<$ 0.05. The same pattern was observed for xylem but the number of genes differentially expressed for N deficiency was much higher, 1403 for up and 569 for down, at FDR p value$<$ 0.05. This result based on gene expression was consistent with the first phenotypic observations in our field experiment showing that tree growth from 6 to 18 months after planting was much more affected by N deficiency than by P or K deficiency. The next steps will consist in identifying major genes involved in N deficiency response by using network approach and analysing the co-variation between gene expression and eco-physiological and growth variables.

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