Microarray analysis of eucalyptus gene expression

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The Brazilian Research Network on *Eucalyptus* Genome (GENOLYPTUS) has as one of its objectives the identification of estimated 30,000 genes and the determination of their activities in different species of *Eucalyptus*. Based on recent studies using oligonucleotide microarrays to obtain gene expression information, 10 identically-constructed microarrays were ordered to NimbleGen Systems Inc. Each microarray consisted of 380,000 probes (50-mer) covering the GENOLYPTUS collection of 23,000 unique ESTs. Each EST was represented in the array by 6 to 12 non-repetitive probes spanning different regions of the sequence. Total RNA samples were prepared from trunk vascular tissues (xylems) of 4-years old *E. grandis* and *E. globulus* trees planted in the field in close locations (Aracruz Celulose "Barbanegra" Forest Reserve, Barra do Ribeiro, RS, Brazil). Samples were taken from two ramets derived from two clones (8 samples) originally generated from genetically independent matrices. From two ramets of one of the *E. grandis* clones, mature leaves were also taken and RNA was purified. RNA quality and quantity were checked and 20 μg were sent to NimbleGen for microarray hybridizations, washing, scanning and preliminary analysis of the data. Genes were grouped according to their expression profiles in at least 6 independent groups. Genes with most contrasting expressions between *E. grandis* xylem x leaf and between *E. grandis* x *E. globulus* xylems were identified. Real-time RT PCR is going to be conducted to confirm some of the gene expression profiles determined by microarray analysis.

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