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The production of eucalyptus in Brazil, driven by advances in forestry technology, has achieved satisfactory rates at a worldwide level in recent years. The combination of conventional improvement techniques with modern biotechnology was essential to reach this benefit. Among the molecular tools necessary to ensure further biotechnological progress in Eucalyptus, the identification and characterization of organ/tissue-specific promoters is a priority. Recovery of highly active promoter sequences, especially those leading to tissuespecific expression, is of great interest to manage the perceived risks associated with transgene technology, and to restrict transgene expression to selected parts of the plant. In this context, an EST showing root-specific expression was recently identified by our group from in silico searches in the Brazilian Eucalyptus EST Database (FORESTs). In this study, the expected expression pattern of the mentioned EST was validated by RT-PCR. Subsequently, the DNA regions immediately upstream to the validated EST were amplified using a genome walking technique and fragments of $1.35 \mathrm{~kb}, 2.9 \mathrm{~kb}$ and 3.0 kb were obtained. These fragments were cloned into the pGEM-Teasy vector and sequenced. Among them, the fragment of smaller size ( 1.35 kb ) was completely sequenced and its upstream (5') orientation to the corresponding EST confirmed by PCR using genomic DNA. This fragment was inserted into the binary vector pCambia$1381 z$ in order to direct the expression of a GUS reporter gene. This expression cassette was inserted into the Agrobacterium tumefaciens for transformation of tobacco plants aiming functional analysis.

Key Words: Eucalyptus, gene expression, promoters, tissue-specificity

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