

Identification, isolation and *in silico* characterization of a soybean putative tissue specific promoter

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Cis-acting regulatory elements are short DNA sequences recognized by transcription factors and thus control gene expression. These sequences are located in promoters, which are regions upstream the coding sequence (CDS) of genes. Isolation and characterization of non-constitutive plant promoters is necessary to improve the application of transgenic technology, as they provide a fine-tune control of transgene expression. There are few tissue-specific promoters of soybean isolated so far. Additionally, there is no guarantee that such promoters from heterologous species will direct transgene expression in soybean as predicted. The aim of this work is to isolate and characterize *in silico* the promoter sequence of a preferentially expressed gene in soybean. The transcript, named GCGmRz1 was identified through electronic northern using soybean ESTs databases and its expression patterns were determined with RT-PCR and northern blot assays. Bioinformatics analysis of GCGmRz1 showed a root specific expression, however our previous experimental analysis exhibited a preferential expression in roots and seeds. The CDS of the gene was aligned to the soybean genomic sequence and the 3000 bp upstream of the start codon were used for primers design. The sequence of the larger fragment (1848 bp) amplified with the primers was analyzed with PLACE database to identify promoter's *cis* regulatory elements. Among the 423 putative *cis*-regulatory elements detected, 80 different types of *cis* elements were identified. The most represented classes were DOFCOREZM and GT1CONSENSUS, with 34 motifs each. DOFCOREZM is related with diverse functions, such as tissue specificity, transcription activation or suppression, while GT1CONSENSUS is related with light-regulated transcription factors. The 46 elements involved in root specific and the 33 elements in seed specific expression are heterogeneously distributed throughout the promoter. The analyzed *cis*-acting regulatory elements will be tested in transgenic model plants and in soybean plants, in order to validate the regions responsible for tissue-specific activity, which could be further used for soybean genetic engineering.

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