

Regulatory elements of carbon metabolism in sugarcane

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Abstract

The increase in the access to renewable energy sources contributes to the global efforts to reduce greenhouse gas emissions. Among these sources, we highlight the cellulosic bioethanol technology, which is generated from plant parts, mainly sugarcane. Knowledge of the components of secondary cell wall metabolism regulation networks will allow the construction of biotechnological tools for the development of energy cane, which has more fiber and biomass, by changing the carbon partition of sugar to biomass. Synthetic promoters are a potential tool for the creation of technology that can be applied in the production of transgenic plants with the desired biomass characteristics or by the use of gene editing methodologies such as CRISPR-CAS. Thus, the characterization of the architecture of the promoters of the target genes involved in the carbon metabolism regulatory networks is essential to provide tools for transgene technology and gene editing. In the present work, a gene from the sugarcane SP80-3280 genome involved in the starch and sucrose metabolic pathway was selected for the initial testing of the analysis methodologies. An important aspect of motif discovery is the delimitation of the sequences that will be used to search for motifs. This delimitation was based on the location of the transcription start site, which was determined by three different approaches. Only one of these approaches yielded positive results for the detection of representative motifs. Based on that, it was possible to identify six potential transcription factor binding sites for this gene. The next steps involve the comparison of these detected motifs to the ones already described in the literature, as well as applying the methodology to a great number of genes at the same time.

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