

Functional Characterization a New Cotton Promoter

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The cotton (*Gossypium hirsutum*) crop is one of the most important and social economic crops in Brazil. The cotton plant is damaged by several insect species that cause important economic damages. Among these insects, the cotton boll weevil (*Anthonomus grandis*), which is one of the most important cotton insect in Brazil, is very inefficient and difficult of controlling by conventional insecticides because of its endophytic behavior, feeding on the floral buds and bolls. The use of these insecticides accounts for up to 25% of the total controlling cost. Therefore, the utilization of molecular strategies applied to the development of insect resistant transgenic plants has been very successful in many countries. However, besides the search for new insecticidal molecules is necessary to identify and isolate promoters for drive the gene expression specifically to locals, where the target insects feed on. With that, the objective of this work was to isolate new regulatory sequence able to drive the expression of exogenous proteins to the cotton flower bud. A new promoter, named UceA, from *G. hirsutum* plants, was isolated through TAIL-PCR technique. The UceA sequence was subcloned into pCAMBIA vectors, fused with the GUS reporter gene and *Arabidopsis thaliana* plants were transformed. The transformed plants were analyzed by histochemistry assays to check the spatial and time expression capacity from different plant parts. Fluorimetric assays were done to quantify the different levels of expression. The results showed that the new isolated promoter was able of regulating the gene GUS expression and the protein expression levels were similar or better than the known 35sd promoter, mainly in the floral bud tissue. Our data indicate that this new promoter represent great potential to be used for generate cotton genetically modified plants.

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