CLONING OF PROMOTER REGIONS FROM ScMUTM2 GENE FROM SUGARCANE

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The oxidative damage has been associated to different diseases. In order to correct lesion, the cell has different mechanism to prevent it. One pathway is the Base Excision DNA repair. The MUTM/FPG protein is a DNA glycosylase in order to correct oxidative damage. In the sugarcane genome it was found two possible genes that had homology to this protein: scMUTM1 and scMUTM2. The aim of this work is to characterize the role of these genes in plants by cloning the promoter regions. In order to do this, it was used the PCR walking approach. Three libraries were constructed by digesting the DNA genomic with *EcoRV*, *PvuII*, or *SmaI*, then ligating with adaptors. These libraries were diluted and PCR reactions were done using one specific primer for the gene adaptor. The fragments obtained were cloned into pGEMT-easy (Promega), sequenced and analyzed. The results obtained showed that the fragment cloned for scMUTM2 correspond probably to a promoter region. Using the program PlantCARE (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/) is possible to identify the regulatory regions TATA-box and CAAT-box at the positions -14 and –37, and regulatory regions that response to light, gibberellin and abscisic acid hormones. The presence of these regions suggests that this gene scMUTM2 might have other function besides DNA repair. It will be important to characterize the promoter function using a reporter gene.

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