scMUTM/FPG DNA GLICOSYLASE FROM SUGARCANE: A HOMOLOG TO THE BACTERIA PROTEIN

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The Base Excision DNA repair (BER) is one the pathways that the organism have to correct oxidative damage. It was found three clusters in sugarcane (scMUTM1, scMUTM2, scMUT4) that had homology to MutM/Fpg bacteria protein. The aim of this work was to clone the promoter region as well as to analyze if the N-terminal region is important for catalytic activity. The cloning the promoter was done by PCR walking. The promoter region obtained was for scMUTM2. It was found the CAAT-box and TATA-box regions and other regulatory regions for light, gibereline and abisicacid hormones response. The N-terminal protein characterization was done by PCR. It was generated two deletions for scMUTM1 and scMUTM4. The preliminary complementation assays showed that both proteins with deletions of N-terminal region are able to complement the double mutant CC104*mutMmutY* in similar way of the full-length protein. This result suggests that the six amino acid highly conserved localized at the N-terminal region probably may be not so important for the catalytic activity in the sugarcane DNA glycosylase. The expression pattern was also analyzed by semi-quantitative RT-PCR. The results showed the expression pattern between these cDNAs are tissue-specific and might respond to different factors. Now, it is important to characterize the importance of these cDNA in plants.

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