IN SILICO ANALYSIS AND A FUNCTIONAL CHARACTERIZATION OF A TAG GENE FROM SUGARCANE

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The Base Excision Repair (BER) pathway is highly conserved, but in plants is not well known. The 3-methyladenine-DNA-glycosilases (TAG) is associated to alkylated lesions. In the SUCEST data-mining, it was found in sugarcane 5 clusters that had homology to TAG-protein. The aim of this work is by *in silico* analysis does a characterization of this protein in plants and by bacteria complementation verify a possible DNA repair function. The *in silico* results showed that plants have many copies of the TAG-sequences, and all the sequences had the Adenine-glycosilase domain. The bacteria complementation assays were done using the strain AB1157 (wild type) and the double mutant BW535. Both strains have either the empty plasmid or with the scTAGI.1 or scTAGI.5 cDNAs. The strains were grown to an 0,4 OD, centrifuged and ressupended into 0,5M $MgSO_4$. Then, aliquots were exposure to 10mM MMS by 1, 3 or 5 min, diluted at 10^{-4} and spread on LB plates. The bacteria complementation results suggest that the sugarcane sequences might have a DNA repair function, but these results are not conclusive as the standard deviation was high. In order to reduce that, the treatment conditions are being set up (increasing the time and MMS concentration). After this set up, new treatments will be done to verify if these sequences have the DNA repair function.

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