

***IN SILICO* ANALYSIS OF FLOWERING GENES IN SUGARCANE**

Silva, F.L.; Furtado, C.M.; Bertolim, R.B.; Agnez-Lima, L.; Medeiros, S.R.B.;
Scortecci, K.C.

LBMG laboratory, Depto de Biologia Celular e Genética, DBG, UFRN.

The transition of shoot apical meristem from vegetative growth to flowering is the major developmental switch in the plant life cycle. The switch to flowering in sugarcane has a dramatic effect reducing up to 60% in sugar or ethanol production. The aim of this work is characterized some genes that may be associated to flowering in sugarcane. In order to do this, it was done a subtractive library using total RNA from apical meristems induced or not induced. Then, it was used the BD Clontech PCRselect cDNA subtraction kit (Clontech), cloned into pGEMT-easy (Promega) and then transformed into *E. coli* DH10B cells. The clones obtained were sequenced. The *in silico* analysis were done against the NCBI, TIGR database. The data obtained correspond to three clones. The seq1 had homology to the MAP65 protein with conserved functional domain. In rice it was found 3 copies (e-value $1.9e^{-147}$, $9.9e^{-57}$), and 3 copies in maize (e-value $2.7e^{-123}$, $5.5e^{-14}$). The seq7 had homology to a protein that has a RING Finger domain which may be associated to the photoperiodic pathway. It was found only one copy of this protein in sugarcane, rice and maize. For seq8, it was found the SEC14p domain (e-value $1e^{-19}$). This domain is involved in the transfer of phosphatidylinositol/phosphatidylcholine phospholipids in eukaryotic cells, in *A. thaliana* is transcribed only in flowers. The *in silico* analysis suggested that the clones obtained in the subtractive library may be involved to the flowering process in sugarcane.

Supported by: CNPq

Key words: flowering, subtractive library, sugarcane