

## ***IN-SILICO* ANALYSIS OF TWO SEQUENCES FROM SUGARCANE SUBTRACTIVE LIBRARY**

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Sugarcane is a crop that is largely cultivated in several countries including Brazil, which is responsible for 25% of world production and its biomass used for sugar and ethanol production. The flowering switch in the apical meristem has a dramatic effect as it reduce production up to 60%. 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 subtrative library using total RNA from apical meristems induced or not induced. Then, it was used the BD Clontech PCRselect cDNAsubtraction 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 using an e-value equal or higher than  $e^{-15}$ . The data obtained correspond to two clones (C01 and C02) presented in this library. The C01 had homology to ATP synthase, and an identity of 87% sugarcane x maize; and 91% sugarcane x rice. The C02 had a homology to the elongation factor alpha-1. The identity found was of 94% sugarcane x maize, 91% sugarcane x rice and 88% sugarcane x *Arabidopsis* and it was found a conserved domain for elongation factor alpha-1. The *in silico* analysis suggested that at least the clone C02 may be involved to the flowering switch in sugarcane.

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