## Identification of genes differential expressed in shoot apical meristems in sugarcane

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Sugarcane is an important tropical crop that is used for sugar and biofuel production. Flower induction in this crop leads to stopping vegetative growth, consequently reducing yield. The identification of genes and reproductive developmental pathways involved in environmental signal perception and transduction will produce tools to improved genotypes that are more suitable for different climatic regions. Here, we report the analysis of subtractive libraries produced with contrasting genotypes to flowering induction (non- vs. early-flowering) grown under equatorial conditions. Differentially expressed transcripts were sequenced and analyzed against a sugarcane-database. Sequences related to cell cycle were approximately 2% reaching 10%; signal transduction was high 25%, transcription factors were 4% to 8%. Also noteworthy, unknown sequences participated with from 14% up to 29%. Transcripts with homology to genes such as the scPP1, scPPO, scSHAGGY and scCYP51 were chosen for confirmation via qPCR in a year-round time-course analysis. The results obtained suggest a role as a flowering promoter for ScCYP51. On the other hand, for ScSHAGGY, ScPP1 and ScPPO the data propose a role as an inhibitor of flowering. Furthermore, overexpression construct in sense and anti-sense were done for scSHAGGY cDNA and Nicotiana tobacco plants were transformed. Transgenic plants with 35::scSHAGGY/sense didn't show any development change when compared to wild-type. The only modification observed was an increase in stigma. The expression analysis from keyflowering genes will be done in order to better understand the potential role of scSHAGGY. The results presented here contribute to a better understand of the identification and potential role of these cDNAs in sugarcane.

Supported by: CNPq (Brazil)

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