

Possible Role of SEC14 in Sugarcane Flowering Process – An *In silico* Analysis

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INTRODUCTION: Flowering is a term used to define the key processes in understanding several mechanisms with regards to plant development, which includes plant reproduction. Studies have shown that stress conditions may induce early flowering and suggest that SEC14 might play a role in this process. Little is known about sugarcane flowering, therefore, further studies will help to comprehend the role of SEC14 in this process. **OBJECTIVES:** To analyse *in silico* the SEC14 to better understand its importance in sugarcane flowering. **MATERIAL AND METHODS:** An interactome map was produced to show the correlation between SEC14 and similar sequences using GeneMANIA. Furthermore, PlantPAN was used to analyse miRNAs regulation and PlantCare for promoter motifs. In addition, BAR database was used to see the SEC14 expression pattern in tissues. **RESULTS AND DISCUSSION:** The interactome showed that sugarcane SEC14 sequence is involved in biosynthesis of phosphatidylcholine and transport of phosphatidylinositol, which may be related to FT (*FLOWERING LOCUS T*) gene and a possible relation to phosphatidylcholine transport. The miRNAs analysis showed that SEC14 sequence may be regulated by miRNAs. It appears to have a similar regulatory role for grasses and to participate in axillary meristem formation and leaf development for *A.thaliana*. The promoter motifs showed that there's a regulation by photoreceptors PHYA and PHYB, development of female gametophyte and bears a relationship to ABA. The expression pattern of SEC14 was analysed for *O.sativa* and *A.thaliana*, which exhibited more expression in seed and young leaf for rice and petals and first node for *A.thaliana*. The qPCR data in sugarcane, using early and late flowering genotypes, suggested a possible role of SEC14 in flowering. **CONCLUSIONS:** The *in silico* data and qPCR results reinforce the potential role of SEC14 in sugarcane flowering. Considering the aforementioned data, transgenic plants are being developed for functional characterization of this sequence.

Keywords: Flowering; miRNA; Sec14-like protein; *Saccharum*.
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