



Abstract

Control of Sugar and Fibre: Insights from Sugarcane Transcriptome Analyses †

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Abstract: Sucrose and fibre in sugarcane share a very dynamic relationship depending largely upon the genetic makeup of the genotypes and growth environment. To investigate the molecular basis of carbon flux into sucrose and fibre that makes the genotypes high sugared or high fibred, or dual purposed, an extensive transcriptomics study was undertaken using a set of sugarcane genotypes differing in sugar and fibre contents. Differential gene expression analyses were performed using 50 transcriptomes revealing a complex network of transcripts associated with growth, defence, vacuole, sucrose and fibre. Rather than merely being a storage sugar of the culms, sucrose might play a significant regulatory role in controlling the expression of several thousand genes including those related to fibre. The high sugar genotypes were not always low in fibre and the fibre might to an extent provide structural framework for maintaining high sugar levels as seen by the high expression of fibre related genes. The study suggests that there could exist certain threshold levels of sugar or fibre contents beyond which an inverse relation would occur. In addition, analysis of the transcriptomes resulted in the identification of a new isoform of sucrose synthase genes, SuSy 7 that was not reported earlier. With the availability of a monoploid reference genome, there is a need for in-depth transcriptome studies to understand and identify finer details of genes, and their transcripts in entirety and regulatory elements of sugarcane genome which is challenging the current capabilities of sequencing technologies unlike any other plant genomes sequenced thus far.

Keywords: sugar; sucrose synthase; sugarcane fibre; differential gene expression



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