Abstract

Differential Gene Expression Among Genotypes of the Genus *Saccharum* Contrasting in Biomass Production [†]

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Abstract: The development of biomass crops aims to meet industrial yield demands to become a profitable and sustainable activity. Achieving these goals in an energy crop such as sugarcane relies on breeding for sucrose accumulation, fiber content and tillering capacity. Sucrose storage depends on transport from leaves to culms driven by enzymes involved in sucrose synthesis and hydrolysis. High biomass genotypes often use photosynthesis products to produce lignocellulosic compounds to form the cell wall. To expand the understanding of the pathways related to these traits, we evaluated gene expression of two groups of genotypes contrasting in biomass yield, as well as testing for differences among members within the same group. First visible dewlap leaves were collected from six genotypes of each group to perform RNA-Seq. We found evidence that both groups differ with regard to genomic stress caused by polyploidy, as indicated by the enrichment of genes involved in transposition activity and defense response processes. Although carbon assimilation terms were not enriched, genes annotated with such terms were co-expressed with those coding for members of hormonal pathways. Sucrose phosphate synthase and hydrolytic enzymes coding genes were upregulated in leaves of sucrose-accumulating genotypes, as genes coding for enzymes involved in the biosynthesis of lignin. Compared to other high biomass accessions, the hybrid US85-1008 presented upregulation of photosynthesis-related genes probably due to its sink demand to store sugar in culms. This study expands the knowledge of gene expression in sugarcane leaves, revealing differences between and within phenotypically distinct groups.

Keywords: sugarcane; fiber; sucrose; RNA-Seq; functional genomics

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