

Sugarcane Coexpression Meta-network and a Comparative Analysis of Carbohydrate-related Gene Network Across Plant Species

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The molecular mechanisms responsible for the cross talk between proteins involved in carbon biosynthesis, and their different regulatory and signaling pathways in plants still need to be further elucidated to better understand plant growth patterns and biomass production. We are only beginning to produce the detailed gene expression data needed for understanding the network of interactions at a molecular level. In this study we developed ways to apply analyses of gene regulatory network in molecular and genetic data of sugarcane related with carbohydrate biosynthesis, and investigate the diversification of these gene networks among plant species. A large-scale coexpression network was generated by Heuristic Cluster Chiseling Algorithm (HCCA) method using public available expression data from sugarcane, including data of a source-sink relationship experiment. Using this approach, a sugarcane meta-network of coexpressed gene clusters was identified and was composed by 95 clusters with 365 edges, with interconnectivity between the nodes above a threshold of 0.04. This meta-network includes more than 7,000 unigenes of sugarcane. Features of the sucrose-phosphate synthase coexpressed genes cluster (with 109 genes) was investigated in details. Some carbohydrate-related genes were identified in this network, include all three isoforms of invertases, sucrose transporters, many transcription factors and genes that encode proteins that participate of the sucrose biosynthesis pathway. Combined coexpressed gene vicinities for sucrose-phosphate synthase related genes across plant species results in a core of genes that are evolutionary conserved in angiosperms and are therefore grouped in a consensus network. This study brings new knowledge on the diversification of the regulatory network that controls sucrose biosynthesis and allocation in sugarcane. The results should contribute to improve our ability to manipulate the biomass production through classical breeding or transgenic approaches.

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