Transcriptomic Changes of Drought-Tolerant and Sensitive Banana Cultivars Exposed to Drought Stress.

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Abstract

In banana, drought responsive gene expression profiles of drought-tolerant and sensitive genotypes remain largely unexplored. In this research, the transcriptome of drought-tolerant banana cultivar (Saba, ABB genome) and sensitive cultivar (Grand Naine, AAA genome) was monitored using mRNA-Seq under control and drought stress condition. A total of 162.36 million reads from tolerant and 126.58 million reads from sensitive libraries were produced and mapped onto the *Musa acuminata* genome sequence and assembled into 23,096 and 23,079 unigenes. Differential gene expression between two conditions (control and drought) showed that at least 2268 and 2963 statistically significant, functionally known, non-redundant differentially expressed genes (DEGs) from tolerant and sensitive libraries. Drought has up-regulated 991 and 1378 DEGs and down-regulated 1104 and 1585 DEGs respectively in tolerant and sensitive libraries. Among DEGs, 15.9% are coding for transcription factors (TFs) comprising 46 families and 9.5% of DEGs are constituted by protein kinases from 82 families. Most enriched DEGs are mainly involved in protein modifications, lipid metabolism, alkaloid biosynthesis, carbohydrate degradation, glycan metabolism, and biosynthesis of amino acid, cofactor, nucleotide-sugar, hormone, terpenoids and other secondary metabolites. Several, specific genotype-dependent gene expression pattern was observed for drought stress in both cultivars. A subset of 9 DEGs was confirmed using quantitative reverse transcription-PCR. These results will provide necessary information for developing drought-resilient banana plants.

KEYWORDS:

Hsf; RNA seq; WRKY57; banana transcriptome; drought tolerance; mRNA degradation; osmo-protectants; wax synthase