IDENTIFICATION OF CANDIDATE GENES ASSOCIATED WITH DROUGHT TOLERANCE IN SORGHUM

Barros, BA[1*]; Carneiro, AA[1]; Carneiro, NP[1]; Magalhães, PC[1]; Alves, MC[1]; Pinto, MO[1]; Noda, RW[1]; Magalhães, JV[1]; Guimarães, CT[1]; Menezes, CB[1]; Tardin, FD[1]; Schaffert, RE[1].
[1]Embrapa Milho e Sorgo, Sete Lagoas, MG, 35701-970.

[*]E-mail: beatriz.barros@embrapa.br

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Sorghum is one of the most adapted cereal to water stress. However, drought stress is still a major factor in reducing production in this crop. The development of sorghum cultivars tolerant to water stress is part of the objectives of the Breeding Program at Embrapa Maize and Sorghum. To optimize this process, it is essential to identify genes in drought tolerant genotypes that respond to changes in soil water. Functional genomic tools have enabled large-scale gene expression studies to an unprecedented speed and accuracy, which may lead to the identification of genes involved in differential responses between genotypes under different stress conditions. The objective of this study was to compare gene expression of a drought tolerant sorghum genotype in the presence and absence of the stress to identify candidate gene association with this phenotype in sorghum. The plant material used was an Embrapa Maize and Sorghum 9910032 sorghum genotype that is drought tolerant. Total RNA was extracted from roots of plants under conditions of normal irrigation (100%) and stressed (50%) with two biological replicates per treatment. The cDNA libraries were constructed and sequenced by the company Eurofins (Alabama, USA). The differential expression analysis was performed using the GeneSifter ® Analysis Edition software (Perkin Elmer). From this analysis, it was possible to identify 662 differentially expressed genes, of which 21 were up-regulated under conditions of water stress. The increase of expression varied between 10 and 65X. The proteins encoded by these genes can be grouped into three functional groups: i) protein that lacks functional annotation ii) protein post-translational modification, and iii) proteins in response to stress. Now, efforts should be used for the functional characterization and validation of candidate genes that could be used to obtain elite sorghum inbred lines tolerant to drought.

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