RESEARCH ARTICLE

Expression of Drought Responsive Genes in Pigeonpea and In Silico Comparison with Soybean cDNA Library

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Abstract

Pigeonpea, a drought tolerant, semi-arid pulse crop has been investigated for the expression of differentially expressed genes (DEGs) under drought stress. The cDNA library of soybean leaf tissue retrieved from the Unigene database of the NCBI, were compared for silico expression using IDEGG web statistical tool. A list of 52 non-redundant DEGs consisting of 11 up-regulated and 41 down-regulated was obtained. Among these, more photosynthesis and light harvesting proteins were down-regulated in drought stress conditions. Pathways were assigned based on KEGG database, revealing 32 genes involved in 17 metabolic pathways. Homologous sequences of six up-regulated genes namely, ADF3, APB, ASR, DLP, LTP1, and UGES were then used for quantitative reverse transcription PCR (qRT-PCR) in pigeonpea. The qRT-PCR result revealed the significant up-regulation of dehydrin-like protein (DLP) (5.02 log2 fold) and down-regulation of acid phosphatase class B family protein (APB) (9.43 log2 fold) and non-specific lipid transfer protein 1-like (LTP1) (18.81 log2 fold) in pigeonpea water-stressed leaf sample compared to well-watered leaf samples. No significant difference was observed in the stressed root compared to the stressed pigeonpea leaf sample except that APB showed an up-regulation of 11.35 log2 fold change.

Key words: differentially expressed genes, drought stress, pigeonpea, qRT-PCR

Introduction

Pigeonpea (Cajanus cajan (L.) Millspaugh) belongs to subtribe Cajanina of tribe Phaseoleae under sub-family Papilionoideae of the family Leguminosae (Varshney et al. 2010). It is a semi-arid, drought-tolerant pulse crop grown in a wide variety of soil textures ranging from sandy to heavy clays and usually cultivated under rainfed conditions in hot humid climates (Keller and Ludlow 1993; Saxena et al. 2010). India is the largest producer with a production area of 4.42 million hectares (FAOSTAT 2011). Reports indicate that pigeonpea genes hold promise for engineering crop plants bestowed with tolerance to major abiotic stresses or in multiple abiotic stresses (Priyank et al. 2010; Sekhar et al. 2010). However, genes responsible for the drought resistant characteristics have to be evaluated in detail for the crop improvement. In contrast, detailed cDNA libraries have been studied in soybean (Glycine max L.) a closely related species in the phylogeny of Papilionoideae (Zhu et al. 2005). The reports also indicate that cDNA sequences of pigeonpea showed more homology with soybean sequences because of their phylogenetic relationship (Priyank et al. 2010; Raju et al. 2010). Through in silico comparative study, it is possible to get an insight of the mechanism of drought tolerance in pigeonpea.
Theoretical model of WRKY transcription factor in pigeonpea 
(Cajanus cajan L.)

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ABSTRACT

Pigeonpea (Cajanus cajan (L.) Millspaugh) belongs to subtribe Cajanine of tribe Phaseoleae under sub-family Papilionoideae of family Leguminosae. The genome of pigeonpea has been recently sequenced and available in public domains. The yield of the pigeonpea is affected by several abiotic and biotic stresses. For the improvement of pigeonpea varieties, molecular understanding of these stresses plays a crucial role. Transcriptional regulation is one of the foremost important molecular activities in cell for its growth and development. The WRKY transcription factors (TFs) are the largest family in plants shown to be responsive and involved in abiotic and biotic stress conditions. Though, WRKY transcription factor family proteins were predicted and identified in many plant species, there is no comprehensive study was reported in pigeonpea draft genome. In this study, we identified 97 WRKY domain proteins, where 47 are located on chromosomes and 50 are on scaffolds in pigeonpea genome. Predicted protein CcWRKY28 was modeled using Robetta server. This study provides an overview on CcWRKY TF family and their structural information for transcriptional regulation.

Keywords: Transcription factor, Pigeonpea, CcWRKY, Molecular modeling

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