



Category: Plant Genomics

Transcriptomic responses to drought and salt stress in desert tree *Prosopis juliflora*

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Abstract

Abiotic stresses affect crop productivity worldwide. Understanding molecular mechanisms of plant abiotic stress tolerance is important for developing stress tolerant crop plants for sustaining crop productivity in future. *Prosopis juliflora* (Sw) DC (mesquite) is a leguminous tree species tolerant to drought and heavy metal stress. Studies at the whole transcriptome level to understand molecular mechanisms of drought and salinity stress tolerance in *P. juliflora* are not reported yet. Here, we subjected *P. juliflora* seedlings to salt and drought stress and carried out whole transcriptome profiling to identify stress responsive genes and pathways. A total of 0.20 billion clean paired end reads were generated from sequencing of 6 RNAseq libraries. De novo assembly of the clean reads resulted in 234486 unigenes. Four Differentially Expressing Genes (DEG) profiles were generated; 1) Drought responsive DEGs in leaf, 2) Salt responsive DEGs in leaf, 3) Drought responsive DEGs in root and 4) Salt responsive DEGs in root. 6874 genes were found to be differentially expressing at least in one tissue/stress and unique genes with a Gene Ontology (GO) annotation (2932) were further analyzed. Among these, 1339 were found to be upregulated under either salt or drought stress in leaf or root tissue and 1596 were found to be downregulated. Overall, the number of DEGs was greater in the roots than those in the leaves. Drought stress caused more differential gene expression in leaf and root combined than salt stress. In both leaf and root tissues, more genes were downregulated than upregulated under salt stress. However, under drought stress, leaf tissue showed more upregulation than downregulation while in root tissue; more genes were downregulated than upregulated. Our studies identified stress responsive genes commonly and differently regulated under stress/tissue conditions. A high percentage of genes commonly downregulated by drought and salt stress specifically in root tissue were coding for various ribosomal proteins. The study also indicated a possible role for 'centrins' in stress response. Our data will facilitate further molecular studies on stress tolerance of *P. juliflora*. The DEGs from our results are potential candidates for understanding and engineering abiotic stress tolerance in plants.

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