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In silico analysis and evaluation of drought responsive genes in pigeonpea by comparing with the cDNA libraries of soybean leaf

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Drought is one of the major abiotic stress conditions limiting the crop productivity all over the world. Pigeonpea (*Cajanus cajan* (L.) Millspaugh) is a drought tolerant pulse crop, grown mainly in semi-arid regions and India ranks first in its production. Presently less genomic resources are available on pigeonpea for drought related studies at molecular level. On the contrary, significant amount of genomic information are in the domain for a closely related leguminous crop soybean (*Glycine max* L.). Here, we have reported an *in silico* analysis for the identification of differentially expressed genes (DEGs) and their signaling pathways due to drought stress. The soybean cDNA libraries of drought stressed and unstressed leaf tissues were downloaded from unigene database of NCBI. Five unstressed libraries were independently analyzed and compared to one drought stressed library. Expressed sequence tag (EST) counts per unigene were used for *in silico* expression analysis by online IDEG6 web statistical tool. From IDEG6, we obtained 34, 30, l1, 13 and 7 DEGs respectively by comparing independently between normal and drought library. Among these, 52 non redundant DEGs were subjected to BLAST analysis for similarity search using BioEdit local blast tool (E-values 1.0E-50) against total ESTs, genomic survey sequences (GSS) and nucleotide sequences of pigeonpea downloaded from NCBI. Out of 52 DEGs, 4 up-regulated and 30 down-regulated genes showed blast hits against pigeonpea sequences and, their relation to drought response was confirmed by comparing with the previous studies. The pathways for 34 genes were assigned based on Kyoto Encyclopedia of Genes and Genomes (KEGG), indicating 25 genes involved in 11 pathways. Photosynthesis and light harvesting proteins showed more reduction in drought stress condition. This study reveals that the genes expressed due to drought stress and the pathways triggered in soybean were similar with the pigeonpea and hence, it can be extrapolated for further biochemical analysis.