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Data in Brief

Gene expression analysis of *Solanum lycopersicum* and *Solanum habrochaites* under drought conditions

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ABSTRACT

Drought is one of the limiting environmental factors that affect crop production worldwide. Understanding the molecular mechanism of drought stress is the key to developing drought tolerant crop. In this experiment we performed expression profiling of tomato plants under water deficit conditions using microarray technology. The data set we generated (available in the NCBI/GEO database under GSE22304) has been analyzed to identify genes that are involved in the regulation of tomato's responses to drought.

Specifications	
Organism/cell line/tissue	Drought stress Leaf tissues of *Solanum lycopersicum*/cultivated and wild type
Sex	N/A
Sequencer or array type	Tomato Micrroarray Gene chip Affymetrix, USA
Data format	Raw and analyzed
Experimental factors	Drought stress treated vs. control leaves
Experimental features	Gene expression profiling for drought resistance mechanism
Consent	Yes
Sample source location	IIVR Varanasi, India-221305

1. Direct link to deposited data

Deposited data can be found here: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22304. (See Fig. 1.)

2. Introduction

Drought is one of the important environmental stresses reducing the yield of cultivated plants [1]. Extent of Drought stress tolerance varies from species to species [2]. Tomato is one of the most widely grown vegetable in the world. It is a warm season perennial crop [3]. Tomato needs enough irrigation based on climatic conditions and soil type [4]. Most of the tomato cultivars are drought sensitive at all stages of plant development, while at the stage of seed germination and early seedling growth being the most sensitive stages [5].

During the process of plant response to drought stress, a large number of genes are activated. The genes include osmo regulatory genes, antioxidant proteins, acquaporins, late embrygenesis abundant (LEA) and different transcription factors. The stress related transcription factors mainly including bZIP, WRKY, MYB, and AP2/EREBP proteins have been proven to play important roles in the regulation of drought tolerance [6,7,8,9].

Changes of gene expression under drought stress leads to a series of physiological and biochemical changes in plants. Photosynthesis, the most important biosynthetic pathways, is significantly affected by water stress, which restricts the normal function of other metabolic pathways. Genome-wide expression profiling in tomato under stress conditions have been performed by various groups to identify key pathways responsible for tolerance and susceptibility mechanisms [10]. In this study drought tolerant and drought susceptible tomato lines were used for expression profiling to gain a deeper understanding of the drought tolerance mechanisms in tomato.

3. Materials and methods

3.1. Plant material

Plant material utilized for these experiments were tomato variety CO-3 and EC-520061 as susceptible and tolerant variety respectively.

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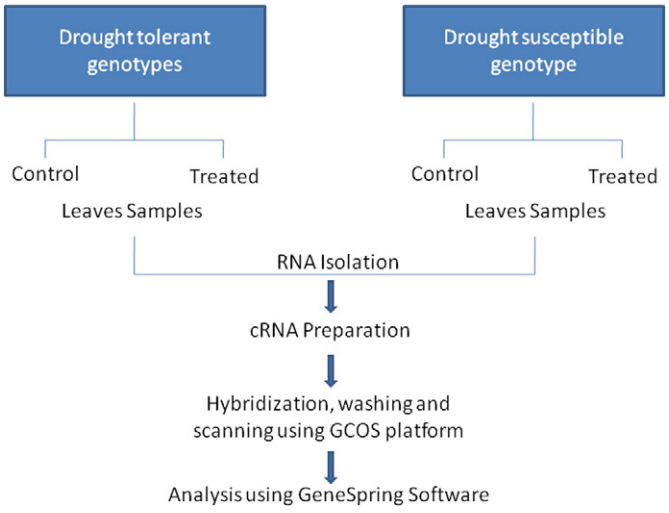

Fig. 1.

The seeds of these varieties were provided by Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh, India. The basis of their selection was their performance against drought stress [6]. The plants were grown in growth chambers under temperature controlled conditions at 25 °C.

3.2. Stress treatment

Tomato seeds were sown in pots filled with a mixture of soil and compost. Germinated seedlings were transplanted in pots (30.0 cm diameter and 30.0 cm height) and maintained at 25 °C under optimal conditions in a glass house with regular watering. Drought stress treatment was initiated two weeks after transplanting the plants. Stress was imposed by withholding water for 14 days and controlled plants were watered regularly. After treatment, the leaves were taken in three biological replications from drought-treated and control plants, frozen in liquid nitrogen, and stored at −80 °C for further analysis.

3.3. Total RNA extraction and quality control

Total RNA was extracted using TRI reagent (Ambion) following the manufacturer's protocol. To remove genomic DNA, the total RNA was treated with RNase-free DNase (RQ1; Promega, USA). Quantity and quality of total RNA were accessed by ND-1000 Nanodrop spectrometer (Nanodrop Technologies, USA) and on 2% denatured agarose gel. DNA free RNA was used for microarray and qRT PCR experiments.

3.4. Microarray experiment

The Affymetrix Gene Chip array was used for gene expression analysis in tomato. The Affymetrix GeneChip Tomato Genome Array contains 10,038 probe sets, representing about 4600 unigenes. Microarray experiment was performed following the manufacturer's protocol (Affymetrix, USA). The expression data were normalized globally before data analysis. The data were analyzed using GeneSpring 12.1 GX software (Agilent Technologies). Signal intensities were recorded for all the 10,038 probe sets. The data has been deposited at NCBI (http://www.ncbi.nlm.nih.gov), with accession number GSE22304. Signal intensities were normalized using Robust Multiarray Average (RMA) algorithm [11]. The Principal Component Analysis (PCA) in GeneSpring GX 12.1 established that the three biological replicates were located close to one another. The high correlation coefficient was observed among the three replicated samples, indicating less genetic background noise. To correct the variability in the normalized expression values, the probe sets with a coefficient of variation ˂50% were retained, and the rest was discarded.

3.5. Functional annotation of the differentially expressed probe sets

The tables of significant transcripts were generated at p values ˂0.05 and fold change value ˃2.0. For the annotation of transcripts an annotated probe file was referred which was generated at Cornell University, USA (ted.bti.cornell.edu/TFGD/array/Affy_probe_annotation.xls) and NCBI website. Among those significantly differentially expressed transcripts, we selected the transcripts which had their function as regulation of transcription. Screening of transcription factor from microarray data. The Tomato transcription factors analyzed in this experiment were described in the transcription factor database. According to the annotation of Affymetrix genome microarray, we screened for TF genes that were differentially induced or repressed after drought stress in CO-3 and EC-520061 with a fold change (FC) of ˃2.0 and a p-value of ˂0.05. The results were shown as a Venn diagram (http://bioinformatics.psb.ugent.be/webtools/Venn/ website). Further probe filtering for TF genes that were significantly induced by drought stress or constitutively expressed in the tolerant cultivar EC-520061 was performed with the fold-change tool in Genespring GX 12.1.

Conflict of interest

The authors have no conflicts of interest.

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