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Data in Brief

Transcriptomic data of *Arabidopsis thaliana* hypocotyl upon suppression of expansin genes

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ABSTRACT

Expansin is a cell wall loosening protein without hydrolytic activity, which allows cell expansion by influencing cell wall extensibility. Previous studies showed that the suppression of expansin genes (*EXPA1*, *EXPA3*, *EXPA5* and *EXPA10*) resulted in defective organ growth and altered cell wall chemical composition [1,2]. However, the molecular mechanism on how the suppression of non-enzymatic expansin expression can result in widespread effects on plant cell wall and organ growth is still unclear. In this study, we performed transcriptomic analysis on the hypocotyls of previously reported transgenic *Arabidopsis* line [1] to investigate the effects of expansin gene suppression on the global gene expression pattern, particularly on the cell wall related genes.

Specifications	
Organism/cell line/tissue	*Arabidopsis thaliana* etiolated hypocotyl tissue
Sex	Not applicable
Sequencer or array type	Illumina HiSeq 2500 system
Data format	Raw (FASTQ) sequences
Experimental factors	RNA used for library preparation and sequencing was isolated from transgenic etiolated Arabidopsis hypocotyls with inducible suppression of targeted endogenous expansin genes on day 3 and day 5 after sowing
Experimental features	RNA-seq data was obtained from 3′ mRNA sequencing to estimate gene abundance in count per million (CPM) represent the expression level of each transcripts
Consent	Not applicable
Sample source location	Bangi, Malaysia (Transgenic seeds were obtained from Fleming lab, Department of Animal and Plant Sciences, University of Sheffield)

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/sra/SRP076440.

2. Value of the data

- This is the first transcriptome data of Arabidopsis hypocotyl upon expansin gene suppression.
- The present dataset is valuable for the identification of the genes which response to expansin gene suppression.
- This information will be useful for better understanding on the relationship between expansin genes and other cell wall related genes, as well as for studying the regulatory and molecular feedback mechanism upon the perturbation of a cell wall loosening factor [1,2].

3. Data

Data reported here describes the sequencing results (Table 1) obtained from the control and dex-treated *pOpON:amREXP* Arabidopsis hypocotyls harvested on day 3 and day 5; each set with three biological replicates. This transcriptomic dataset was generated by QuantSeq 3′ mRNA sequencing [3]. A total of twelve raw sequence data were deposited into NCBI SRA database and can be accessed with the accession number SRP076440 (http://www.ncbi.nlm.nih.gov/sra/SRP076440).

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Table 1
Statistics on *Arabidopsis* hypocotyl QuantSeq sequencing.

Treatment	Day	Samples	Accession no.	Total reads	No. of reads mapped	% reads mapped
Control	3	a3o3_19	SRX1837983	7,509,396	4,281,517	57.0
		a3o3_24	SRX1837984	6,746,469	3,878,238	57.5
		a3o3_28	SRX1837987	6,212,651	4,044,870	65.1
	5	a3o5_11	SRX1837988	5,944,751	3,554,862	59.8
		a3o5_15	SRX1837989	7,746,511	4,630,272	59.8
		a3o5_7	SRX1837990	6,146,498	2,562,293	41.7
Dex-treated	3	a3x3_20	SRX1837991	7,291,149	3,839,633	52.7
		a3x3_25	SRX1837992	6,175,917	3,290,287	53.3
		a3x3_29	SRX1837993	6,884,806	4,620,247	67.1
	5	a3x5_12	SRX1837994	6,546,270	3,830,054	58.5
		a3x5_16	SRX1837985	6,677,956	3,794,879	56.8
		a3x5_8	SRX1837986	6,173,617	3,201,258	51.9

4. Experimental design, materials, and methods

4.1. Plant materials and treatments

This study utilised previously reported transgenic Arabidopsis line *pOpON::amiREXP* containing a dex-inducible transactivating system which allowed the induced suppression of endogenous expansin genes, namely *EXPA1*, *EXPA3*, *EXPA5 and EXPA10* [1]. Seed sowing, growing media and conditions followed as previously described [1], but in the dark with petri dishes double wrapped in aluminium foil and placed vertically. For induction, growth media were supplemented with 10 μM of dexamethasone (dex). Control media were supplemented with an equivalent concentration of solvent DMSO (0.1% v/v). Etiolated hypocotyls samples were harvested on day 3 and day 5 after seed sowing. A total of 100 hypocotyls were pooled as one biological replicate. Three biological replicates were sampled for each treatment at each time point, totalling twelve samples.

4.2. RNA extraction, library construction and sequencing

RNA from pools of 100 hypocotyls was extracted using TRIzol (Invitrogen) according to manufacturer's instruction. RNA purity and integrity was measured using the ND-1000 Nanodrop spectrophotometer (Thermo Fisher Scientific Inc., USA) and Agilent 2100 bioanalyzer (Agilent Technologies, USA), respectively. RNA samples were cleaned using DNAse I kit according to the Rapid out removal DNA kit instruction (Thermoscientific) and converted into cDNA by using QuantSeq 3′ mRNA-Seq Reverse (REV) Library Prep Kit (Lexogen) according to manufacturer's instruction to generate compatible library for Illumina sequencing. cDNA libraries were assessed using TapeStation (Agilent Technologies, USA) before 100 bp single end sequencing using Illumina HiSeq 2500 system at Australian Genome Research Facility (AGRF) based on standard protocols.

4.3. Transcriptome analysis

Raw sequencing reads (FASTQ) were processed individually to checked for per base sequence quality and screened for the presence of any Illumina adaptor/overrepresented sequences and cross-species contamination through the AGRF quality control (QC) pipeline as per Lexogen QuantSeq data analysis workflow (https://www.lexogen.com/quantseq-data-analysis/). To quantify transcript abundance, the processed reads (FASTA) were mapped to Arabidopsis genome reference (TAIR10-release-30 ftp://ftp.ensemblgenomes.org/pub/plants/release-30/fasta/arabidopsis_thaliana/dna/). The mapping was performed using bowtie2 [4] with stringent “end-to-end” alignment and all other parameters were set to default values according to recommended data analysis workflow by Lexogen. The counts of reads mapping to each known gene were summarised in CPM (count per million) values using the TAIR10 gene annotation with the featureCounts utility of the subread package [5]. This transcript abundance dataset can be utilised to study the genome-wide changes in gene expression during etiolated hypocotyl development from day 3 to day 5, and to identify differentially expressed genes which are affected by the suppression of expansin genes (*EXPA1*, *EXPA3*, *EXPA5* and *EXPA10*).

Conflict of interest

The authors declare there is no conflict of interest on any work in this paper.

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