Data in Brief

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

Iqmal Asyraf Ilias, Othman Babul Airianah, Syarul Nataqain Baharum, Hoe-Han Goh

**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.

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).

1. Direct link to deposited data

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

---

* Corresponding author.

E-mail address: gohhh@ukm.edu.my (H.-H. Goh).

http://dx.doi.org/10.1016/j.gdata.2017.05.002

Received 4 April 2017; Received in revised form 26 April 2017; Accepted 2 May 2017

Available online 03 May 2017

2213-5960/ © 2017 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/BY-NC-ND/4.0/).
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 Reidow tool [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.

Acknowledgements

This research was funded by Fundamental Research Grant Scheme (FRGS/1/2013/ST04/UKM/02/1) from the Ministry of Higher Education, Malaysia.

References

[1] H.-H. Goh, J. Sloan, C. Doeza-Fornell, A. Fleming, Inducible repression of multiple expansin genes leads to growth suppression during leaf development, Plant Physiol. 159 (2012) 1759–1770.
[2] S. Zenoni, L. Reale, G.B. Tornielli, L. Lanfaloni, A. Porceddu, A. Moretti, A. Zamboni, A. Speghini, F. Ferranti, M. Pezzotti, Downregulation of the Petunia hybrida alpha-expansin gene PhEXP1 reduces the amount of crystalline cellulose in cell walls and leads to phenotypic changes in petal limbs, Plant Cell 16 (2004) 295–308.
[3] P. Moll, M. Ante, A. Seitz, T. Reda, QuantSeq 3′ mRNA sequencing for RNA quantification, Nat. Methods 11 (2014).
[4] B. Langmead, S.L. Salzberg, Fast gapped-read alignment with bowtie 2, Nat. Methods 9 (2012) 357–359.
[5] V. Liao, G.K. Smyth, W. Shi, featureCounts: an efficient general purpose program for assigning sequence reads to genomic features, Bioinformatics 30 (2014) 923–930.