

Dataset description

Overview

This dataset contains transcriptome data from four stages of carpel development in two eudicot species: *Eschscholzia californica* and *Solanum lycopersicum*. These data enable the identification of co-expressed gene modules, potential transcriptional regulators, and conserved or divergent expression dynamics across species. This resource aims to contribute toward a broader understanding of the regulatory networks shaping carpel development across eudicots.

File Structure and Annotation

Files are provided in “.tsv” format for each species:

Data1, “*Eschscholzia californica*_LMD_Carpel.TPM.tsv”

Data2, “*Solanum lycopersicum*_Carpel.TPM.tsv”

Row name = gene IDs

Columns = biological replicates (**Data1**, three replicates per stage at four stages, 12 columns in total, **Data2**, four replicates per stage at four stages, 16 columns in total)

Column names follow this format: Species_CarpelStage_Replicate

Examples:

SlCarpel1r1: *S. lycopersicum*, Carpel Stage 1, Replicate 1

EcCarpel2r3: *E. californica*, Carpel Stage 2, Replicate 3

Sampling strategy

The table provides the information about the correlation between the four developmental stages in this study and previously described somewhere else. The header row is the stages we define in the data.

	Stage 1: carpel initiation	Stage 2: elongation of carpel walls	Stage 3: during meiosis	Stage 4: after meiosis	Source
<i>E. californica</i>	0.39–0.65 mm BD: carpel initiation	1.65–2.25 mm BD: microsporangia initiate	2.3–2.8 mm BD: male meiosis	3.5–5.5 mm BD: female meiosis	Becker et al. (2005)

<i>S. lycopersicum</i>	~0.6 mm BL: Carpel initiation	0.8-1.5 mm BL: Carpel wall elongation	2-3.5 mm BL: Pre-meiosis	4-6 mm BL: Post-meiosis	Brukhin et al. (2003)
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* BD Bud Diameter, BL Bud Length

Library Preparation and Sequencing

All RNA samples were pre-amplified using Nugen Ovation® RNA-Seq System (PART NO. 7102) (NuGEN Technologies, San Carlos, California, United States) suitable for an input of 500 pg–100 ng of RNA and the cDNA generated was used for library preparation. Amplification and cDNA generation was conducted according to the manufacturer's instructions. Library preparation was done with the Illumina Nextera XT kit (Illumina Inc., San Diego, California, USA) suitable for 1 ng DNA. The cDNA was measured before the preparation with Qubit and normalized to 0.2 ng/μl. 5 μl of dilution was used for the library preparation. Libraries were prepared according to the manufacturer's instructions. Generated libraries were sequenced with Illumina HiSeq 4000. 9 samples were sequenced per lane generating approximately 33 million reads per sample. Paired-end sequencing was used for each sample with read length of approximately 76 bp.

Transcript Quantification

Raw reads were processed using CLC Genomics Workbench v11.0.1. The analysis workflow included quality control, adapter trimming, read mapping, and transcript quantification. TPM (Transcripts Per Million) values were computed directly within CLC using its default RNA-seq analysis parameters.

References

- Becker A, Gleissberg S, Smyth DR. Floral and Vegetative Morphogenesis in California Poppy (*Eschscholzia californica* Cham.). *Int J Plant Sci.* 166:537–55 (2005).
- Brukhin, V., Hernould, M., Gonzalez, N. et al. Flower development schedule in tomato *Lycopersicon esculentum* cv. sweet cherry. *Sex Plant Reprod.* 15, 311–320 (2003).
- Kivivirta, K., Herbert, D., Lange, M. et al. A protocol for laser microdissection (LMD) followed by transcriptome analysis of plant reproductive tissue in phylogenetically distant angiosperms. *Plant Methods* 15, 151 (2019).