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Data Article

Dataset of *Arabidopsis* plants that overexpress *FT* driven by a meristem-specific KNAT1 promoter

L. Duplat-Bermúdez [a], R. Ruiz-Medrano [a], D. Landsman [b], L. Mariño-Ramírez [b], B. Xoconostle-Cázares [a,*]

[a] *Departamento de Biotecnología y Bioingeniería; Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional. Av. IPN 2508 San Pedro Zacatenco, 07360 Mexico City, Mexico*
[b] *Computational Biology Branch, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, United States of America, Bethesda, MD, USA*

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ABSTRACT

In this dataset we integrated figures comparing leaf number and rosette diameter in three *Arabidopsis FT* overexpressor lines (AtFTOE) driven by KNAT1 promoter, "A member of the KNOTTED class of homeodomain proteins encoded by the STM gene of *Arabidopsis*" [5], vs Wild Type (WT) *Arabidopsis* plats. Also, presented in the tables are some transcriptomic data obtained by RNA-seq Illumina HiSeq from rosette leaves of *Arabidopsis* plants of AtFTOE 2.1 line vs WT with accession numbers SRR2094583 and SRR2094587 for AtFTOE replicates 1–3 and AtWT for control replicates 1–2 respectively. Raw data of paired-end sequences are located in the public repository of the National Center for Biotechnology Information of the National Library of Medicine, National Institutes of Health, United States of America, Bethesda, MD, USA as Sequence Read Archive (SRA). Performed analyses of differential expression genes are visualized by Mapman and presented in figures. "Transcriptomic analysis of *Arabidopsis* overexpressing flowering locus T driven by a meristem-specific promoter that induces early flowering" [2], described the interpretation and discussion of the obtained data.

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* Corresponding author.
E-mail address: bxoconos@cinvestav.mx (B. Xoconostle-Cázares).

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Specifications Table

Subject area	Biology
More specific subject area	Plant Sciences
Type of data	Figure; tables
How data was acquired	PCR final point and ddPCR (The QX100 Droplet Digital PCR (ddPCR™ System), direct count of leaves and measurement of rosette diameter with image analysis software (Imagej [http://rsb.info.nih.gov]), RNA-seq by Illumina HiSeq Sequencing,
Data format	Analyzed
Experimental factors	Three lines overexpressing *FT* (AtFTOE) and WT *Arabidopsis* plants
Experimental features	Three lines of AtFTOE and WT *Arabidopsis* plants were grown on hydroponic under controlled conditions at 22 °C in short day (SD) photoperiod (8 h light /16 h dark) up to day 21 and then transferred to inductive conditions of long days (LD) photoperiod (16 h light /8 h dark)
Data source location	Mexico City, Mexico and at the National Center for Biotechnology Information (NCBI)
Data accessibility	Data is available with this article and at NCBI accession numbers SRR2094583 and SRR2094587

Value of the data

- The amplification of transgene by PCR and copy variation number by ddPCR is fundamental to compare independent transgenic events.
- ANOVA and *T*-Student test were employed to assess statistical significance of data ($\alpha = 0.05$) for leaf count and rosette diameter in order to compare three AtFTOE lines and WT.
- Differentially expressed genes in the context of cellular functions are graphically presented by Mapman to understand the integrative changes in the metabolism.
- Raw data from the Illumina HiSeq sequencing are available for further analyses.

1. Data

In this article are presented the data analyses (figures) from leaf count and rosette diameter for three lines AtFTOE (2.1, 3.1 an 4.3) compared with WT *Arabidopsis* plants (Fig. 2A and B respectively). Data corresponding to differential expression (log2 fold change) from AtFTOE 2.1 line vs WT *Arabidopsis* are visualized by Mapman (Fig. 3). Some data corresponding to down-regulated genes are presented in Table 3.

2. Experimental design, materials and methods

2.1. Determination of transgene (FT) and copy variation number in three AtFTOE lines

Transgene *FT* (560 bp) was amplified by PCR from three AtFTOE (2.1,3.1 and 4.3) lines (Fig. 1A). Droplet digital PCR (ddPCR) was employed to determine transgene (*FT*) copy variation number (CVN) (Fig. 1B). As template were used 2.5 ng of genomic DNA previously digested with HindIII. Droplets were generated for PCR reaction with the specific primers AtFT-qPCR (F) (5′-TCCGTTTAATA-GATCAATCAC-3′), FT-qPCR (R) (5′-CCACCATAACCAAAGTATAG-3) and probe TaqMan ddPCRFT [5′FAM]

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