BMC Genomic Data

DATA NOTE

Open Access

Transcriptomic data of peach varieties with different chilling requirement levels

Weihan Zhang[1,2,3], Yayun Sun[2,4], Haiyan Li[1], Yuepeng Han[2,3,5], Baoxiong Wan[1*] and Liao Liao[2,3*]

Abstract

Objectives Peach is a deciduous tree widely cultivated in temperate and subtropical regions that requires a process of bud endodormancy to produce normal flowering and fruiting. This release requires a certain accumulation of cold, named chilling requirement (CR). CR is genotype dependent and with varies levels among different species and accessions. Thus, we collected the bud transcriptomic data of two peaches with different CR levels and conduct a series standard basic analysis. The peach bud transcriptomic data we gathered provides a valuable dataset for exploring the relationships between gene expression and peach CR levels.

Data description We extracted and sequenced the RNA of different CR peach buds at the same status in three endodormancy stages. Each stages have three biological replicates. A total of 18 RNA-seq libraries were obtained and mapped to the reference genome after quality control. The gene expression level was normalized by two methods (TPM and FPKM). Differentially expressed genes (DEGs) analysis revealed that a total of 2,481 unique genes with an absolute value of log2 fold change (FC) greater than 1.0. Homologous functional annotation of these DEGs were conducted which provided further information for CR potential related genes identified and functional genomics studies.

Keywords Transcriptomic, Peach, Chilling requirement, RNA-seq

Objective

Peach [*Prunus persica* (L.) Batsch] is a representative deciduous fruit tree that is grown worldwide, especially in temperature and subtropical regions. Similar to most deciduous fruit trees, peaches require a certain amount of winter chill, known as chilling requirement (CR), to promote the release of bud endodormancy and ensure subsequent normal flowering and fruiting [1, 2]. High CR can withhold peach buds from initiating growth in response to transient warm temperatures, thereby preventing subsequent frost damage in late winter or early spring, but the inability to obtain sufficient CR in warm climates limits its cultivation areas [3, 4]. Therefore, breeding for CR can be a significant consideration in the development of new cultivars, broadening growing regions, and promoting the use of protected cropping

*Correspondence:
Baoxiong Wan
wan77118@163.com
Liao Liao
liao168000@wbgcas.cn
[1]Guangxi Key Laboratory of Germplasm Innovation and Utilization of Specialty Commercial Crops in North Guangxi, Guangxi Academy of Specialty Crops, Guilin, Guangxi 541004, China
[2]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden of Chinese Academy of Sciences, Wuhan 430074, China
[3]Hubei Hongshan Laboratory, Wuhan 430070, China
[4]University of Chinese Academy of Sciences, Beijing 100049, China
[5]Sino-African Joint Research Center, Chinese Academy of Sciences, Wuhan 430074, China

Table 1 Overview of data files/data sets

Label	Name of data file/data set	File types (file extension)	Data repository and identifier (DOI or accession number)
Data file 1	Gene expression level normalized as TPM	MS Excel file (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.26838976.v1) [22]
Data file 2	Gene expression level normalized as FPKM	MS Excel file (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.26838976.v1) [22]
Data file 3	Gene count matrix	CSV files (.csv)	Figshare (https://doi.org/10.6084/m9.figshare.26838976.v1) [22]
Data file 4	DEGs in S1 between high-CR peach and low-CR peach	CSV files (.csv)	Figshare (https://doi.org/10.6084/m9.figshare.26838976.v1) [22]
Data file 5	DEGs in S2 between high-CR peach and low-CR peach	CSV files (.csv)	Figshare (https://doi.org/10.6084/m9.figshare.26838976.v1) [22]
Data file 6	DEGs in S3 between high-CR peach and low-CR peach	CSV files (.csv)	Figshare (https://doi.org/10.6084/m9.figshare.26838976.v1) [22]
Data file 7	Function annotation of DEGs	MS Excel file (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.26838976.v1) [22]
Data file 8	*Raw sequencing data*	*fastq file (.fastq.gz)*	*NCBI (https://identifiers.org/ncbi/insdc.sra:SRP528936)* [23]

systems, as cultivar adaption to the specific climatic condition of the growing area is essential to ensure peach production. As CR is a heritable quantitative trait [4–8], identifying the genes that relate to CR is the priority task for peach CR breeding [9–14]. We selected a high CR peach variety (ZY4, CR = 700 h) and a low CR peach variety (NG, CR = 200 h) and conducted RNA-seq at different endodormancy release stages, aiming to find or verify candidate genes that control CR at the gene expression level. This first-time public data was previously used only as verification evidence for candidate gene functional experiments conducted in our laboratory, helping us find some candidate genes that control CR in peach. Overall, this dataset is valuable for identifying candidate genes related to CR in peach.

Data description

The peach buds used in this study are collected from the Wuhan Botanical Garden, Chinese Academy of Sciences (Wuhan, China) from October 2022 to February 2023. Samples were collected at three stages, the heavy leaf fall stage (S1) were deemed as endodormancy induction stage, the endodormancy maintenance stage (S2), and the bud slightly sprouting (S3) was deemed as endodormancy release stage. Total RNA isolation was performed using the RNAprep Pure Plant Kit (TianGen, Beijing, China) according to the manufacturer. After adjusting concentration and eliminating any potential genomic DNA contamination during the RNA extractions, the cDNA libraries were constructed according to the MGIEasy Kit (MGI, Wuhan, China). A total of 18 libraries were used for RNA sequencing by MGISEQ-T7 in paired-end sequencing model with a length of 150-bp. Raw sequencing reads quality control was conducted by fastp [15] with default parameters and obtain clean reads. The clean reads were mapped to the reference genome LoveII v2.0a1 [16, 17] using HISAT2 [18] with default parameters. Gene expression levels were normalized as per kilobase million (TPM) and fragments per kilobase of exon per million fragments mapped (FPKM) by StringTie [19]. Differentially expressed genes (DEGs) analysis was performed by DESeq2 [20]. Read counts matrix was obtained from prepDE.py scripts included in StringTie. There are 1,567, 1,645 and 3,930 DEGs in S1, S2 and S3, respectively. A total of 2,481 unique DEGs were identified among three stages. Homologous functional annotation was performed by blastp [21].

Limitations

More samples with different CR levels should be collected and sequenced for transcriptome comparing. If it is possible to determine a more detailed endodormancy period by measuring relevant hormone levels or observing under a microscope, it would be more reasonable to increase the sampling density.

Abbreviations

CR	Chilling Requirement
TPM	Per Kilobase Million
FPKM	Fragments Per Kilobase of exon per Million fragments mapped
FC	Fold Change
DEG	Differentially Expressed Genes

Acknowledgements

We thank the workers in our institute's orchards.

Author contributions

W.Z. and L.L. conceived this project. Y.H. and L.L. collected these samples. Y.S. performed RNA extraction. W.Z. performed data analysis and wrote the manuscript. B.W. and H.L. checked the data and reviewed the manuscript. All authors read and approved the final manuscript.

Funding

This work was supported by the Opening Project of Guangxi Key Laboratory of Germplasm Innovation and Utilization of Specialty Commercial Crops in North Guangxi (GASCKF202406), the Key Special Project of Intergovernmental International Cooperation of the National Key R&D Program of China (2023YFE0125100), and the China Agriculture Research System (CARS-30).

Data availability

The data described in this Data note can be freely and openly accessed on Figshare under https://doi.org/10.6084/m9.figshare.26838976.v1. Please see Table 1 for details and links to the data.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

Received: 27 August 2024 / Accepted: 28 October 2024
Published online: 26 November 2024

References

1. Horvath DP, Anderson JV, Chao WS, Foley ME. Knowing when to grow: signals regulating bud dormancy. Trends Plant Sci. 2003;8(11):534–40.
2. Guo L, Dai J, Ranjitkar S, Yu H, Xu J, Luedeling E. Chilling and heat requirements for flowering in temperate fruit trees. Int J Biometeorol. 2014;58(6):1195–206.
3. Fan S, Bielenberg DG, Zhebentyayeva TN, Reighard GL, Okie WR, Holland D, Abbott AG. Mapping quantitative trait loci associated with chilling requirement, heat requirement and bloom date in peach (Prunus persica). New Phytol. 2010;185(4):917–30.
4. Jiménez S, Reighard GL, Bielenberg DG. Gene expression of DAM5 and DAM6 is suppressed by chilling temperatures and inversely correlated with bud break rate. Plant Mol Biol. 2010;73(1):157–67.
5. Celton J-M, Martinez S, Jammes M-J, Bechti A, Salvi S, Legave J-M, Costes E. Deciphering the genetic determinism of bud phenology in apple progenies: a new insight into chilling and heat requirement effects on flowering dates and positional candidate genes. New Phytol. 2011;192(2):378–92.
6. Romeu JF, Monforte AJ, Sánchez G, Granell A, García-Brunton J, Badenes ML, Ríos G. Quantitative trait loci affecting reproductive phenology in peach. BMC Plant Biol. 2014;14(1):52.
7. Ruiz D, Campoy JA, Egea J. Chilling and heat requirements of apricot cultivars for flowering. Environ Exp Bot. 2007;61(3):254–63.
8. Olukolu BA, Trainin T, Fan S, Kole C, Bielenberg DG, Reighard GL, Abbott AG, Holland D. Genetic linkage mapping for molecular dissection of chilling requirement and budbreak in apricot (Prunus armeniaca L). Genome. 2009;52(10):819–28.
9. Erez A. Overcoming dormancy in Prunus Species under conditions of Insufficient Winter Chilling in Israel. Plants. 2024;13(6):764.
10. Yang Q, Wu X, Gao Y, Ni J, Li J, Pei Z, Bai S, Teng Y. PpyABF3 recruits the COMPASS-like complex to regulate bud dormancy maintenance via integrating ABA signaling and GA catabolism. New Phytol. 2023;237(1):192–203.
11. Moser M, Asquini E, Miolli GV, Weigl K, Hanke M-V, Flachowsky H, Si-Ammour A. The MADS-Box Gene MdDAM1 Controls Growth Cessation and Bud Dormancy in Apple. Front Plant Sci 2020, 11.
12. Cantin CM, Wang X-W, Almira M, Arús P, Eduardo I. Inheritance and QTL analysis of chilling and heat requirements for flowering in an interspecific almond x peach (Texas x Earlygold) F2 population. Euphytica. 2020;216(3):51.
13. Kitamura Y, Habu T, Yamane H, Nishiyama S, Kajita K, Sobue T, Kawai T, Numaguchi K, Nakazaki T, Kitajima A, et al. Identification of QTLs controlling chilling and heat requirements for dormancy release and bud break in Japanese apricot (Prunus mume). Tree Genet Genomes. 2018;14(2):33.
14. Campoy JA, Ruiz D, Egea J. Dormancy in temperate fruit trees in a global warming context: a review. Sci Hort. 2011;130(2):357–72.
15. Chen S, Zhou Y, Chen Y, Gu J. Fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics. 2018;34(17):i884–90.
16. International Peach Genome I, Verde I, Abbott AG, Scalabrin S, Jung S, Shu S, Marroni F, Zhebentyayeva T, Dettori MT, Grimwood J, et al. The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nat Genet. 2013;45(5):487–94.
17. Verde I, Jenkins J, Dondini L, Micali S, Pagliarani G, Vendramin E, Paris R, Aramini V, Gazza L, Rossini L, et al. The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. BMC Genomics. 2017;18(1):225.
18. Kim D, Langmead B, Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. Nat Methods. 2015;12(4):357–60.
19. Pertea M, Pertea GM, Antonescu CM, Chang T-C, Mendell JT, Salzberg SL. StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. Nat Biotechnol. 2015;33(3):290–5.
20. Love MI, Huber W, Anders S. Moderated estimation of Fold change and dispersion for RNA-seq data with DESeq2. Genome Biol. 2014;15(12):550.
21. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol. 1990;215(3):403–10.
22. Zhang W. RNA-seq of peach with different CR. Figshare. 2024. https://doi.org/10.6084/m9.figshare.26838976.v1.
23. Zhang W. Peach RNA-seq in different stages. BioProject 2024, https://identifiers.org/bioproject:PRJNA1152946

Publisher's note