

Differential Gene Expression Studies: A Possible Way to Understand Bearing Habit in Fruit Crops

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Abstract

India is still by far the major producer of various fruit crops, but its relative share in the world production has been gradually declining. Alternate bearer fruit cultivars present a serious economic problem to fruit growers. An alternate bearing plant is the one that does not bear a regular crop year-after-year; rather heavy yields are followed by extremely light yield. This complex phenomenon could be solved by transcriptome analysis resulted in numerous differentially expressed genes (DEGs), allowing the partial identification of mechanisms that convert 'on' into 'off' buds. Several candidate genes would be identified in future studies whose differential expression can be correlated with growth habit and architectural variation in another perennial fruit crops. The information generated will be utilized for identification of potential parents, desired hybrids in early nursery stage, thus would assist breeders by bringing precision breeding and also make available fruits during off years.

Keywords: Alternate bearing; Fruits; Differential gene expression; Transcriptomic

Short Communication

India is the major producer of various fruit crops like mangoes, banana, citrus, etc. In the world, although its relative share in the world production has been gradually declining. The decline in production is attributed not only due to incidence of pests and diseases, but also influenced by other factors like poor germination percentage, lack of efficient rootstocks, irregular bearing etc. During a good year, a tree can be loaded with bumper yield; however, crop quality fluctuates from year to year, so that in the year following a good crop, there are relatively few fruits. Alternate bearer fruit cultivars present a serious economic problem to fruit growers. The major problem associated with this alternate bearing habit is the loss of the fruits and yield, which affects the overall crop production. Various research workers throughout the world have studied the phenomenon of alternate bearing in different fruit crops and associated several horticultural traits with this complex phenomenon. Furthermore, transcriptome analysis resulted in numerous differentially expressed genes (DEGs), allowing the partial identification of mechanisms that convert 'on' into 'off' buds (Table 1). RNA-seq can be used to look for allele specific expression in heterozygous organisms. This is best done with hybrids between very divergence genotypes. This data can be utilized to infer the presence of cis-regulatory variation that influences gene expression levels, to find out regulatory regions and their function in fruit crops. Several candidate genes would be identified in future studies whose differential expression can be correlated with growth habit and architectural variation in another perennial fruit crops. A detailed study is required to coordinate the regulation among chromatin structure, transcription, regulatory genes 'on' and 'off' mechanism and alternative splicing during vegetative to flowering and fruiting transition. Transcriptome profiling is needed for both types of mRNAs and small regulatory RNAs to study the regular and alternate bearing behavior of perennial fruit crops. Fundamental to the task of analyzing gene expression data is the need to select those genes whose patterns of expression are related to a specific phenotype of interest. The present article is aimed to study genes that control the flowering behavior in regular and irregular bearing fruit genotypes. RNA profiling is needed for both types of mRNAs and small regulatory RNAs to study the regular and alternate bearing behavior in fruit crops. Differential expression analysis is based on gene regulation, that is, under different physiological situations, or when experiencing different stimulation, the regulation of gene expression is

increased or decreased. Construction of cDNA libraries is one of the strategies used to obtain differentially expressed sequences and is useful for the identification of genes involved in contrasting situations. These sequences are then used in a microarray or subjected to RT-PCR to confirm the differential expression of genes. To achieve the objectives, transcriptomic data of regular and irregular varieties of different fruit crops, available on public domain like NCBI could be utilized. The genes involved in cellular signaling and metabolism related regular bearing habit have not been fully identified, while the function(s) of many of those which have are as yet incompletely characterized in fruit crops [1-3]. Flowering involves the sequential action of two groups of genes, i.e. those that switch the fate of the meristem from vegetative to floral (floral meristem identity genes), and those that direct the formation of the various flower parts (organ identity genes). A thorough understanding of the floral transition with complex genetic network, regulated by multiple environmental and endogenous clues is a primary requirement. Research on tree crops is expensive, slow, and has often been focused on limits on production in horticultural species. Recently, the development of genomic and transcriptomic tools has contributed to a better understanding of the metabolic and molecular processes involved in floral biology. The availability of the draft genome sequence of some fruit crops is expected to greatly assist future molecular genetic studies, like identification of the complete gene set of regulatory genes, focusing the selection of candidate genes for the final analysis of biological function. Gene expression analyses for flowering in fruit crops allow the identification of genes and the study of their relationship with reproductive processes. Understanding the cellular and molecular mechanisms involved in regular and irregular bearing fruit varieties assists in the development of flowering, identification of regulatory regions and factors implicated for regularity

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Fruit tree	Study	Core findings	Reference
Olive tree (<i>Olea europaea</i> L.)	Differential expression of transcripts under different Temporal phases and organs.	Studies revealed that nutritional control had a remarkable impact on the alternate bearing of olive, Moreover, hormonal control and flowering processes also played important roles in this phenomenon. Transcript related to flower development (GO243632_1) was altered among the "on" and "off" year leaves. The expression of GO243632_1 was two-fold higher in the "off" year leaves as compared to the "on" year ones in the olive tree.	[13]
Olive tree (<i>Olea europaea</i> L.)	miRNA- oeu_miR156 oeu_miR159 oeu_miR393 etc.	Regulation of miRNA under different developmental phases and tissues indicated that control of nutrition and hormone, together with flowering processes had a noteworthy impact on the olive tree alternate bearing.	[14]
Mandarin	Citrus flowering locus T and suppressor of over expression of constants	The "off" year leaves showed significantly increased expression levels of the genes <i>cift</i> and <i>soc1</i> , which are responsible for flowering, as compared with those from the "on" year leaves in Mandarin	[15]
Citrus	Global gene expression	Fruit removal resulted in relatively rapid changes in global gene expression, including induction of photosynthetic genes and proteins. Altered regulatory mechanisms included abscisic acid (ABA) metabolism and auxin polar transport. Genes associated with Ca ²⁺ -dependent auxin polar transport were remarkably induced in buds of OFF-Crop and de-fruited trees. Hormone analyses showed that auxin levels were reduced in these buds as compared with ON-crop buds.	[16]
Citrus	Squamosa promoter binding like (SPL)	Among genes induced in OFF-crop trees was one homologous to SPL, which controls juvenile-to-adult and annual phase transitions, regulated by miR156.	[12]
Mango	FT like and gibberellin Metabolism genes in biennial-bearing mango trees	The expression of FT, AP1 and LFY in mango was induced in leaves during the flowering induction period, with OFF trees showing higher levels of expression of FT and AP1.	[2]

in bearing Hence, there is immense scope of thorough research in this area. In recent years, sequencing of expressed genes (transcriptomes) using Next Generation Sequencing (NGS) technologies such as SOLiD, Illumina and 454, has been used for gene discovery and allele mining [4,5]. This method, also known as RNAseq, has been used in many plant and animal species. Transcriptomic data could be utilized for the synthesis of SSR and SNPs markers. From among many types of molecular markers that have been developed during the past three decades, SSR and SNP are highly informative for the breeders [6,7]. Recently, development of RNA sequencing (RNA-seq) methodology has facilitated the analysis of transcriptomes of a number of crop and medicinal plants [8,9]. High quality genetic analysis of perennial crops such as mango, apple, citrus, etc. requires large numbers of informative polymorphic markers for genetic or comparative mapping and quantitative trait loci identification. Recently, the transcriptome of mango cvs. Langra and Zill have been reported [10,11]. Recent studies have indicated that epigenetic modification, alternative splicing, antisense RNA and chromatin silencing regulatory mechanisms play an important role in this process by regulating related flowering gene expression. Dynamic changes between chromatin states facilitating or inhibiting DNA transcription regulate the expression of floral induction pathways in response to environmental and developmental signals. Genomic analysis resulted in numerous differentially expressed genes (DEGs), allowing the partial identification of mechanisms that convert 'on' into 'off' buds [12].

Conclusion

Genome resources developed by the way of segmental and whole transcriptome data will be utilized for better understanding of genetics of regular bearing habit in fruit crops. The information generated will be utilized for identification of potential parents, desired hybrids in early nursery stage, thus would assist breeders by bringing precision breeding and also make available fruits during off years. The improved production and productivity in various fruit crops, though development of regular bearing hybrids would boost the economic conditions of the

growers.

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References

- Zhang X, Garretton V, Chua NH (2005) The AIP2 E3 ligase acts as a novel negative regulator of ABA signaling by promoting ABI3 degradation. *Genes Dev* 19: 1532-1543.
- Nakagawa M, Honsho C, Kanzaki S, Shimizu K, Utsunomiya N (2012) Isolation and expression analysis of *FLOWERING LOCUS T*-like and gibberellins metabolism genes in biennial-bearing mango trees. *Scientia Horticulturae* 139:108-117.
- De los Santos-Villalobos S, Parra-Cota FI, de-Folter S, Peña-Cabrales JJ (2012) Primers to amplify *flowering locus T (FT)* transcript in mango (*Mangifera indica*) and their potential use in other angiosperms. *Plant Omics Journal* 5: 453-457.
- Barabaschi D, Guerra D, Lacrima K, Laino P, Michelotti V, et al. (2012) Emerging knowledge from genome sequencing of crop species. *Molecular Biotechnology* 50: 250-266.
- Egan AN, Schlueter J, Spooner DM (2012) Applications of next-generation sequencing in plant biology. *American Journal of Botany* 99: 175-185.
- Buschiazzo E, Gemmill NJ (2006) The rise, fall and renaissance of microsatellites in eukaryotic genomes. *BioEssays* 28: 1040-1050.
- Kelkar YD, Tyekucheva S, Chiaromonte F, Makova KD (2008) The genome-wide determinants of human and chimpanzee microsatellite evolution. *Genome Research* 18: 30-38.
- Duangjit J, Bohanec B, Chan AP, Town CD, Havey MJ (2013) Transcriptome sequencing to produce SNP-based genetic maps of onion. *Theory of Applied Genetics* 126: 2093-2101.
- Xu J, Li Y, Ma X, Ding J, Wang K, et al. (2013) Whole transcriptome analysis using next-generation sequencing of model species *Setaria viridis* to support C4 photosynthesis research. *Plant Molecular Biology* 83: 77-87.
- Azim KM, Khan IA, Zhang Y (2014) Characterization of mango (*Mangifera indica* Linn) transcriptome and chloroplast genome. *Plant Mol Biol* 85:193-208.
- xia Wua H, Jiaa H, Mab X, Wangb S, Yao Q, et al. (2014) Transcriptome and proteomic analysis of mango (*Mangifera indica* Linn) fruits. *Journal of proteomics* 105: 19-30.

12. Shalom L, Samuels S, Zur N, Shlizerman L, Zemach H, et al. (2012) Alternate bearing in citrus: changes in the expression of flowering control genes and in Global Gene Expression in 'ON'- versus 'OFF'-Crop Trees. *PLoS ONE* 7: 46930.
13. Turktas M, Inal B, Okay S, Erkilic EG, Dundar E Hernandez P, et al. (2013) Nutrition Metabolism Plays an Important Role in the alternate bearing of the olive tree (*Olea europaea* L.). *PLoS One* 8: e59876.
14. Yanik H, Turktas M, Dundar E, Hernandez P, Dorado G, et al. (2013) Genome-wide identification of alternate bearing-associated microRNAs (miRNAs) in olive (*Olea europaea* L.). *BMC Plant Biology* 13: 10.
15. Munˆoz-Fambuena N, Mesejo S, Gonz'ales-Mas MC, Primo-Millo E, Agusti M, et al. (2011) Fruit regulates seasonal expression of flowering genes in alternate bearing 'Moncada' mandarin. *Ann Bot-London* 108: 511-519.
16. Shalom L, Samuels S, Zur N, Shlizerman L, Doron-Faigenboim A, et al. (2014) Fruit load induces changes in global gene expression and in abscisic acid (ABA) and indole acetic acid (IAA) homeostasis in citrus buds. *Journal of Experimental Botany* 65: 3029-3044.

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