Agri Articles
(e-Magazine for Agricultural Articles)
Volume: 02, Issue: 02 (MAR-APR, 2022)
Available online at http://www.agriarticles.com
©Agri Articles, ISSN: 2582-9882

Apple Functional Genomics

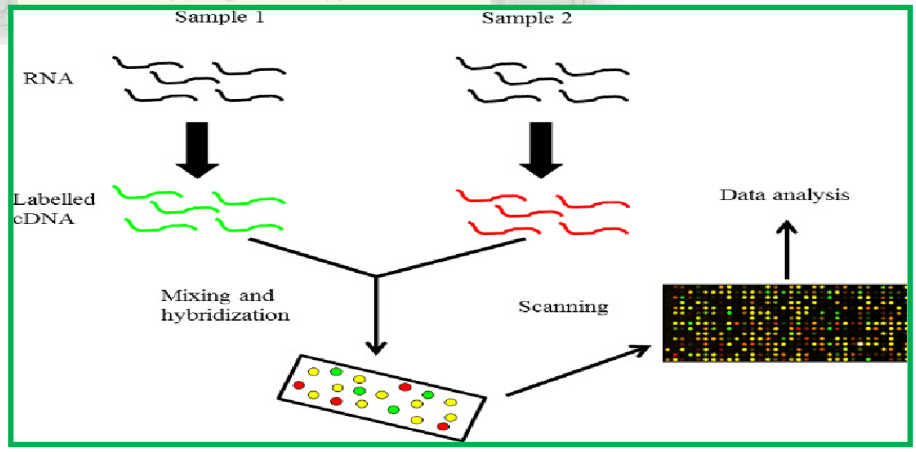
(*Shikha Jain)
Ph.D. Research Scholar, Division of Fruits and Horticulture, ICAR- Indian Agricultural Research Institute, New Delhi
* jain64235@gmail.com

General Apple Genomics

The *Malus domestica* Borkh. genome is currently recognized as a reference in the study of the molecular basis of regulation of many important features in woody plants. A wide sequential database may now be a valuable source of molecular markers complementary to the target genes, successfully used in genetic breeding applications. The ability to determine the genotype and its correlations with phenotype, as well as the description of important seedlings at an early developmental stage, shortening the breeding process, are all advantages of such markers. In the current effort of breeding and genetic selection of apple species, the complete genome sequence (7 Mb) of *M. domestica* is critical. The diploid Golden Delicious sequence, which is now available in a Rosaceae database, is being used as a reference for plant genome alignment and functional gene annotation. It is very useful for an accurate molecular definition of many important agronomical traits, development of high-density molecular markers, and allows accelerating the apple breeding process. Different DNA variants that characterize the Malus genome, including as single nucleotide polymorphisms (SNPs) and copy number variations (CNVs), can be easily detected based on the available sequence data.

Microarray – Fundamental Approach to Description of Apple Gene Function

The identification of functional genes affecting essential agronomical features is aided by reverse genetics, which was established in the recent decade. The cDNA microarray approach can be used without a sequence description in this project. Microarray technology was widely employed a few years ago to not only monitor the expression of hundreds of samples in a single experiment, but also to undertake a genome-wide analysis of variable transcript expression in normal and treated / infected plant samples. The technology is based on laborious fabrication of microchips (slides) by probe coverage and relies on the specific cDNA/DNA hybridization of the target samples. Furthermore, the microarray results must



DNA Microarray Technology

be confirmed using quantitative reverse transcriptase (qRT-PCR), a technology that allows for more precise quantification of gene expression levels based on a variety of criteria. Regardless of labour costs, the method provides useful information on gene expression profiling and genotype-to-genotype gene transcript comparisons.

Reading the Apple Gene Sequences – RNA-Seq

Massive throughput RNA sequencing-based transcriptome analysis is now the most effective method for identifying annotated functional genes as well as small RNA molecules introduced by infections. It was successfully used in the genome of Lord Lambourne cv. for detecting pathogenic RNA transcripts, regulating apple rubbery wood disease resistance, and providing valuable information about interactions between other viroid sequence coverage of plant genome, as well as allowing expression analysis of genes involved in lignin synthesis. Such knowledge has a significant impact on the breeding program's future directions. RNA-seq technology helps to create various sequence tag collections from various types of plant tissues, environmental circumstances, stress treatment, and other factors. The differentially expressed sequences are then compared to plant genome databases, identified, and used as functional molecular markers for desired features. The technology of RNA deep sequencing is based on qualitative and quantitative assessments of sequence copy numbers, allowing for the detection of changes in transcript variations. Profiling of poly-A RNA template capturing in cells or separation of the RNA molecule converted to cDNA can be used to accomplish this (cDNA libraries obtained after adapter attachment to one or both ends of the RNA molecule). Genes in *M. domestica* were functionally annotated using sequences from *A. thaliana*, papaya, rice, maize, grape, *Sorghum bicolor*, *Oryza sativa*, *Vitis vinifera*, and *Cucumis sativus*. This allowed researchers to classify the sequences of genes involved in metabolic pathways that produce volatiles, antioxidants, and pigments, as well as forecast their chromosome position and establish their origin.

Conclusion

Because the apple (*Malus domestica* Borkh.) exhibits self-incompatibility, outbreeding mode of reproduction, and a long generation cycle, the new generation technologies based on genome characterization can speed up time-consuming field evaluations. The current work detailed some of the current knowledge of modern technologies that have been used to apple genome investigations, resulting in the characterization of genome segments and the identification of a large number of accurately defined genes. The latest generation genotyping technologies appear to be excellent for random apple genome-wide association (GWA) research as well as pedigree-based analyses due to their great efficiency (few gaps between SNPs above 100 kpb were detected). Recent descriptions of the apple genome and transcriptome, as well as chromosome structure, are important deliverables that bridge the gap between scientific genetic research and its use in breeding, allowing for more efficient development of novel varieties (apple and other Rosaceae species). These new technologies have shown to be useful for transcriptome re-sequencing, the development of new molecular markers, the development of specialized sequencing assays such as microarrays/genotyping platforms, and gene expression profiling surveys of plant genetic variation. Finally, they are appropriate tools for studying gene alternative splicing as a phylogenetic, plant speciation, and adaptation process phenomenon