**Recent Progress in the Detection of Key Genes Linked to Multiple Fruit Development Biosynthesis by Transcriptomic Analysis: A Review**

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**Abstract**

**Fruits constitute a vital part of the human diet and an excellent source of nutrients as well.** **Most of the indigenous fruits are the key source of foreign exchange earnings and also provide a sufficient amount of income to the fruit growers worldwide in the form of fresh and processed products.** **However, besides production, multiple yield-declining factors are involved and responsible for affecting its production, which ultimately disintegrates the fruit crop improvement programs. Therefore, it is important to understand the mechanism of gene expression involved in different fruits like anthocyanin accumulation and biosynthesis, ripening and brisk fruit senescence, fruit color development, fruit drop, fruit pericarp pigmentation and fruit development. For this, transcriptomics or transcriptome sequencing (RNA-Seq) is the high-throughput approach used for the detection of genes, studying the genomes of fruits and providing novel pathways to counter biotic and abiotic stresses. Furthermore, the study of fruits through transcriptomics has enabled the researchers to analyze the functional genes and provide ample knowledge to understand the regulatory mechanisms involved in various fruits. Furthermore, advances in biotechnological tools like next-generation sequencing (NGS) technology and transcriptomic research** **have the potential to solve or minimize the problems and hurdles faced by fruit plants. In this article, we review the recent achievements in the field of transcriptomics of important fruit plants, including their significance in the discovery of trait-specific genes and their roles in particular biological processes.**

**KEYWORDS**: Anthocyanin biosynthesis, Biotic and abiotic stresses, Fruit quality, RNA sequencing, Next-Generation Sequencing, Transcriptome