



Draft Genome of Some Important Fruits: Source of Finding New Antioxidant Molecules

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Antioxidants are molecules which work to protect our cells from the damage of free radicals and other oxidative molecules. Free radicals/oxidants are the molecular by-products during conversion of food into energy in cells. The cells in our body continuously fighting against the threat of these free radicals which have the potential to damage our cells and genetic material. Two of the best-known antioxidants are vitamin C and vitamin E, which helps to slow down or stop the processes that damages the cells in our body. Many fruits which are rich in vitamin C and phenolic compounds, including stress-linked phytochemicals are recommended for consumption to fight against oxidants/free radicals. Plant polyphenols, which are the products of plant secondary metabolism, thus as dietary antioxidants in human health and disease might protect against oxidative damage. It is well-known that normally consumed fresh and processed fruits along with some vegetables, for instance, apples, grapes, berries, pears, tomatoes and jams, are the main sources of phenolic compounds. Some of the major phenolic compounds isolated and identified from these fruits peels, flesh, skin and seeds are anthocyanins, chlorogenic acids, quercetin glycosides, flavan-3-ols, gallaocatechin, (-)-epicatechin, (+)-catechin, rosmarinic acid, ellagic acid, resveratrol, coumaric acid, L-DOPA etc. These natural polyphenols with health benefits fight against many heart diseases, obesity, diabetes, cancers and aging-related diseases.

With respect to polyphenol biosynthesis, identification of new antioxidants, characterization of novel genes which encode different enzymes involved in the polyphenol biosynthesis are essential. For this, genomes of few fruits were sequenced, and draft genomes were made. Grapes are important fruits, known for the production of natural polyphenol, resveratrol, which has many health benefits. To understand the biosynthesis of this polyphenol and other secondary metabolites in grapes, grapevine genome was sequenced. Using an inbred variety Pinot Noir (PN40024), the grapevine genome got sequenced, and access to the grapevine genome enabled the annotation of stilbene synthase

that led to the synthesis of resveratrol. In another grapevine clone UY11 (Uruguayan Tannat clone), which accumulates high levels of polyphenols in the berry skin and seed, revealed 1,873 genes in its sequence data that were not present in PN40024 genome [1]. In relation to polyphenol biosynthesis, 141 novel UY11 genes that encode 19 different enzymes involved in polyphenol biosynthesis and expression of cultivar-specific genes associated with altered polyphenol accumulation in UY11 were identified. The fruit of apple is also a rich source of phytochemicals including phenolic compounds, and is main sources of phenolic compounds in the human diet. The fruit contains some important phenolic compounds including quercetin glycosides, anthocyanins, procyanidins, flavan-3-ols etc. To understand the involvement of structural genes in phenolic compounds/phenylpropanoid biosynthetic pathway, and to understand the role of epigenetic marks on fruit development, apple genome sequence, draft genome and genetic analysis of metabolites were used. Through genetic analysis of metabolites in apple fruits and detection of Metabolic Quantitative Trait Loci (mQTLs) hotspot, a number of quercetin conjugates were shown to have mQTLs on linkage group LG1 or LG13 [2]. However, the most important mQTL hotspot with the largest number of phenolic compound related metabolites (33 apple peel-related and 17 flesh-related) was detected on LG16. Structural genes involved in the phenylpropanoid biosynthetic pathway were also located, the gene, leucoanthocyanidin reductase and the genes for seven transcription factors were in the mQTL hotspot on LG16. To understand the potential role of epigenetic marks on apple fruit development, genome-wide DNA methylation maps were constructed that compared different tissues and two isogenic apple lines (GDDH13 and GDDH18) that produce large or small fruits [3]. The fruit size difference between two apple lines was investigated. As two of the key determinants, that are known to alter plant organ size are cell number and cell size, the number of cell layers in the parenchyma of GDDH13 fruits increased more rapidly than those in the parenchyma of the smaller GDDH18 with

significant differences being observed as early as 21 DAP (Day After Pollination). Three genes that potentially contributed to the cell number difference and difference in fruit size between two apple lines and these contained DMRs (differentially methylated regions) in their promoter regions. Content of phenolic compounds in different sizes and varieties of apples and their relationship with various kinds of free radical associated diseases was extensively studied. Another important fruit, jujube fruit important for its medicinal value obtained from Chinese jujube, oldest cultivated fruit trees, native to China. The plant contains various therapeutically important phenolics and flavonoids and its fruits are highly rich in antioxidant Vitamin C. Recent data of genome sequencing and draft genome of jujube provided insights into the ascorbic acid metabolism and detected key genes involved in the biosynthetic process [4]. Combined genomics and transcriptomics data established that L-galactose pathway is the major synthesis pathway for antioxidant Vitamin C.

Further characterization of many novel genes and unknown

enzymes/metabolic pathways of these important and unexplored medicinal fruits will definitely help in the future identification of many new antioxidant molecules/drugs.

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