Mango Nutrigenomics for Nutritional Security

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Abstract

Nutrition is all about the study of food and the intake of food to stay healthy. As the community is developing, the world is also facing substantial challenges, such as malnutrition or hyperalimentation. Due to the imbalance of nutrition, chronic disease rates are also drastically increasing in the world. Furthermore, it is leading to high rates of obesity and diabetes in cities and villages. High rise in diet-related disorders such as obesity, cardiovascular diseases, diabetes etc., have resulted in seriousness regarding "Genomics of Nutrition" research worldwide. Therefore, the present global growth of the epidemic needs to be addressed through the promises of nutrigenomics. How genes and diet jointly may affect a person's health and risk of developing the illness could be well studied by nutrigenomics. The goal of nutrigenomics is to study the interaction of nutrients with the genome, proteome, and metabolome,

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C. Kole (ed.), *Compendium of Crop Genome Designing for Nutraceuticals*,
https://doi.org/10.1007/978-981-19-4169-6_46

and it describes the affinity between these specific nutrients and nutrient regimes for quality health. A result of consolidated analyses that comprised fruit and vegetable utilization was connected to preventing coronary artery disease, cancer, and fatality, with similar results seen when fruits were scrutinized independently from vegetables. Mango (*Mangifera indica* L.) is one of the excellent tropical fruits in the world. Most of the mango tree parts are a rich reserve of bioactive compounds, which reside in leaves, bark, and fruit (pulp, peel, and stone). Contemporary studies have proven the presence of significant bioactive components of remedies in fruit waste parts like mango peel and kernel. Mangiferin, flavonoids, catechin, phenolic acids, and gallic acid are a few of the biologically active components contained in this fruit. Hence, the study of nutrigenomics in mango is very important to mitigate malnutrition and coronary diseases.

Keywords

Mango · Diet-gene interaction · Nutrigenomics · Nutrition · Food supplement

Abbreviations

BaCs	Bioactive compounds
BCO1	*Beta-carotene oxygenase 1*
BMI	Body mass index
DM	Dry matter
EA	Ellagic acids
FAO	Food and Agriculture Organization
FW	Fresh weight
GT	Gallotannins
IU	International units
MAB	Marker-assisted breeding
MTHFD1	Methylenetetrahydrofolate dehydrogenase
MTHFR	Methylenetetrahydrofolate reductase
NCDs	Noncommunicable diseases
NHANES	National Health and Nutrition Examination Survey
OECD	Organization for Economic Cooperation and Development
PKU	Phenylketonuria
PP	Polyphenols
QTL	Quantitative trait locus
RAE	Retinol activity equivalents
RDA	Recommended dietary allowances
SNP	Single nucleotide polymorphism
UFGT	Udp glucose: flavonoid-3-O-glucosyltransferase
US	United States
USDA	United States Department of Agriculture

1 Introduction

Nutrigenomics is defined as the relationship between nutrients, diet, and gene expression. It is a fascinating, upcoming field that explains the role of nutrition on gene expression. It brings together the science of bioinformatics, nutrition, molecular biology, genomics, epidemiology, and molecular medicine. The present chapter highlights the nutrigenomics research in mango. It includes the common outlook of nutrigenomics, relevant diseases, the role of single nucleotide polymorphism (SNP) in gene alteration, diet supplementation, and public consciousness in general and specifically in the fruit crop mango. It is very clear that with the accelerated changes in food habits and lifestyles, individuals are becoming more susceptible to diet-related disorders. Therefore, there is an imperative need to accelerate more research in this area so that the relationship between diet and health could be better understood and everyone could be benefitted from the genomic revolution (Neeha and Kinth 2013).

The new science of nutrigenomics teaches us what specific foods tell your genes and how food affects a person's genes and how a person's genes affect the way the body responds to food. What you eat directly determines the genetic messages your body receives. These messages, in turn, control all the molecules that constitute metabolism: the molecules that tell your body to burn calories or store them. "If you can learn the language of genes and control the messages and instructions, they give your body and metabolism, you can radically alter how food interacts with your body, lose weight, and optimize your health" (Hyman 2006; Aswini and Varun 2010). The nutritional phenotype of individuals could be more precisely accessed *via* the science of omics (Collins et al. 2003; German et al. 2011). It is cardinal to understand human health both by the role of diet in the fluctuating declaration of a genome and the role of genetics in the uncertain responses to diet (Gopalan 1992; Ghoshal et al. 2003; Ghosh 2010; Ghosh and Gorakshakar 2010). It is quite obvious and understandable that individuals respond distinctively to the same dietary consumption. The most manifest goal of actively preventing disease and improving the health of all individuals, of all ages, becomes nutrition's greatest golden chance and its strenuous provocation will be in establishing these basic relationships and implementing them (Gobard and Hurlimann 2009; Godbole et al. 2009). The comprehensive retort of metabolism to the quislings of the lifestyle and food choices, environmental oscillations, the status of nutrients, hereditary background, and epigenetic changes, within an individual at a discrete point in time (e.g., metabolic recessive) is possibly a susceptible and actionable reflection of nutritional and metabolic status (Zivkovic and German 2009). In India, some the diseases like epilepsy, type 2 diabetes, and neural tube defect disease are found to be associated with low nutrient uptake (Menon et al. 2010; Mohan et al. 2007a, b; Naushad et al. 2010). Further, nutritional status was observed in the Indian population (Rao 2001; Raj et al. 2007).

2 Need of Nutrigenomics Study for Fruit Crops Like Mango

It is a treasure house of nutrition and supports the economic stamina of the territory (FAO 2020) in newly industrialized countries, where tropical fruits are mostly grown. The acceleration in worldwide production of tropical fruits elevated rapidly from 5% to as high as 23% in 2019, based on the approximate anticipation that it will be one of the flourishing agricultural sectors (OECD/FAO 2020). Tropical fruits contain multitudinous health-promoting bioactive compounds such as phenolic acids, carotenoids, flavonoids, anthocyanins, vitamins, minerals, fatty acids, and fiber. These fruits comprise tremendously bountiful antioxidants, and phytochemicals rank them a predominant nutritional source with good medicinal properties (Rymbai et al. 2013; Acham et al. 2018; Laldinchhana Lalrengpuii et al. 2020) and assist in accomplishing nutritional security for an ever-increasing world population. As a result, to circumvent nutritional forfeiture and superior merchantability, fruits need to be harvested at the perfect phases. Postharvest deprivation is around 20–40% (Bantayehu and Alemaye 2019; Rajapaksha et al. 2021) because of their highly decaying character. Accommodating an integrated "multi-omics" perspective supports escalating the genomic knowledge and its implementation in developing improved cultivars. A study on 15,000 adults in several US communities emphasized that both high and low percentages of carbohydrates as part of routine uptake were associated with high mortality, although a 50% reduction in carbohydrate uptake lowers the risk (Seidelmann et al. 2018). Higher salt and low-quality fat due to the intake of more animal protein and decreased consumption of fruits and vegetables lead to higher mortality risk (Mazidi et al. 2019). Therefore, the nutritionist suggests to take more veggies in a routine manner as it maintains sound health. Increased intake of certain fruits like mango corresponds with a medley of beneficial health outcomes. It not only lowered the risk of obesity but also decreased chronic illness (Slavin and Lloyd 2012; Dreher et al. 2018).

Cardiovascular diseases and all-cause mortality (Aune et al. 2017) may be auxiliary with low risk with the excessive intake of fruits (apples, pears, and citrus fruits) and vegetables (green leafy and cruciferous vegetables). Studies on the intake of mango and its correlation with nutrient quality and health outcomes emphasize restricted information. Former research using NHANES 2001–2008 illustrated that the intake of mango in kids and adults corresponded with increased nutrients in comparison to those who did not consume mangoes. One cup (165 g) of raw mango give 100 kcal, 3 g dietary fiber, 277 mg potassium, 70 μg folate, DFE, 60 mg vitamin C, 90 μg vitamin A, RAE, 1060 μg beta-carotene, and 12 mg choline (USDA Database 2015). Therefore, it is considered as the supreme source of a healthy diet, although it is still less consumed in the United States. Papanikolaou and Fulgoni (2022) studied nutrient intakes, diet quality, and health results using data from NHANES 2001–2018 in children and adult mango consumers ($n = 291$; adults $n = 449$) compared with mango nonconsumers (children $n = 28{,}257$; adults $n = 44{,}574$). Children who consumed mangoes had a significantly lower daily intake of added sugar, sodium, and total fat, and a higher intake of dietary fiber, magnesium, potassium, total choline, vitamin C, and vitamin D, compared with nonconsumers. In adults, mango consumers had significantly higher daily intakes of dietary fiber, magnesium, potassium, folate, vitamin A, vitamin C, and vitamin E and significantly lower intakes of added sugar and cholesterol, compared with nonconsumers. Mango consumption was also associated with better diet quality versus mango nonconsumers ($p < 0.0001$). Mango consumption in youngsters was associated with lower BMI z-scores, compared with nonconsumption. In adults, BMI scores, waist circumference, and body weight were significantly lower only in male mango consumers compared to mango nonconsumers. The key findings comprise a healthy nutrient pattern (more consumption of vegetables and fruits, whole grains, and less animal protein foods). The present data are affiliated with previously published data documenting numerous benefits associated with the inclusion of fruit within healthy dietary patterns.

3 Mango and Dietary Benefits

Mango (*Mangifera indica* L.) is a member of the Anacardiaceae family (more than 70 genera and 1000 varieties) and is known as the "king of fruits." It is widely consumed due to its exotic flavor, succulence, and sweet taste. Mango leaves, bark, and fruit (pulp, peel, and stone) are rich sources of bioactive compounds (BaCs). It contain proteins [0.36–0.40 g 100 g^{-1} fresh weight (FW) of pulp; 1.76–2.05% (w/w) of peel; 66.1 g kg^{-1} of kernel flour; and 3.0% (w/w) of leaves], vitamin A [0.135–1.872 mg 100 g^{-1} FW of pulp; 15.27 International Units (IU) in kernels; 1490 IU in leaves], vitamin C [7.8–172.0 mg 100 g^{-1} FW of pulp; 188–349 μg g^{-1} FW of peel; 0.17 g kg^{-1} DW of kernel flour; 53 mg 100 g^{-1} dry matter (DM) in leaves], carotenoids (0.78–29.34 μg g^{-1} FW of pulp; 493–3945 μg g^{-1} FW of peel), mangiferin (1690.4 mg kg^{-1} DM in peel; 4.2 mg kg–1 DW of kernel extract), phenolic compounds, dietary fiber (DF), carbohydrates, minerals, and other antioxidants known to have medicinal, nutritional, and industrial benefits. Certain diseases related to oxidative stress need several bioactive compounds due to their antioxidant properties. In mango fruit, only the pulp is used, while all other parts are relinquished that could be better utilized due to its therapeutic properties. Thus, there is an exigency to conduct research on all the bioactive constituents present in mango. These compounds not only provide substantial medical and nutritional properties but also have industrial applications, as well as role in defending the plant. The present-day, ascendant worldwide population leads to the dual challenges of nutritional insecurity and dietary disorders, engendering to health problems such as obesity, cancer, and cardiovascular disease (Clugston and Smith 2002). Mango encloses a complex mixture of antioxidants including xanthones and polyphenols whereby can help protect us from many diseases (Berardini et al. 2005). Mangoes are ingested as fresh fruit or are processed into enriched products such as nectar, puree, squash, or juice. In all instances, only the pulp is used, while the stones and peel are discarded, which results in a considerable waste of organic material. Details of nutrient composition of mango are given in Table 1.

Table 1 Nutrient composition of ripe mango pulp (Masibo and He 2008)

Component	Value (100 g–1 FW)	Component	Value (100 g–1 FW)
Water (g)	78.90–82.80	Calcium (mg)	6.10–12.80
Carbohydrate (g)	16.20–17.18	Phosphorus (mg)	5.50–17.90
Fiber (g)	0.85–1.06 Ash (g)	Iron (mg)	0.20–0.63
Protein (g)	0.36–0.40	Vitamin A (mg)	0.135–1.872
Fat (g)	0.30–0.53	Thiamin (mg)	0.020–0.073
Riboflavin (mg)	0.025–0.068	Ascorbic acid (mg)	7.80–172.00
Niacin (mg)	0.025–0.707	Tocopherol (mg)	1.12
Tryptophan (mg)	3.00–6.00	Lysine (mg)	32.00–37.00
Methionine (mg)	4.00	Lycopene (mg)	0.35

Polyphenolics: polyphenolics (PP) are the most widely distributed secondary metabolites and serve as the dominant antioxidant compounds. Gallic acid and six hydrolyzable tannins constituted 98% of the total polyphenolics. Other polyphenolics reported in mango pulp include flavonoids, xanthones, phenolic acids, and gallotannins (Berardini et al. 2005); m-hydroxybenzoic acid, vanillic acids, and apigenin (Masibo and He 2008); and hydroxybenzoic acid, m-coumaric acid, coumaric acid, ferulic acid, myricetin, mangiferin, catechins, epicatechin, quercetin, ellagic acids (EA), benzoic acid, and protocatechuic acid (Kim et al. 2007; Jasna et al. 2009; Gorinstein et al. 2011) (Table 2).

4 Therapeutic Potentials of Bioactive Compounds from Mango Fruit Wastes

Mango contains a congregation of several bioactive compounds and has been used as a significant herb in the traditional and Ayurvedic medicinal system for centuries (Shah et al. 2010). Bioactive components (mangiferin, flavonoids, catechin, phenolic acids, gallic acid, and gallic acid derivatives) of therapeutic nature were identified in the kernel and peel of mango. The medicinal value of these compounds has been assessed *in vitro* and minimal pre-clinically (Asif et al. 2016). The seed of mango is an important source of therapeutic health benefits (Momeny et al. 2012). Mango contains 20–60% seed of the whole and the kernel is 45–75% of the whole seed fruit (Maisuthisakul and Gordon 2009). Peel is a waste product of the mango processing industry. It consists of 15–20% of mango weight (Masibo and He 2008). Various important compounds are distributed in various concentrations in different parts of mango fruit like seed, peel, and pulp (Ignat et al. 2011;Ghuniyal 2015; Parvez 2016; Torres-León et al. 2016). Several polyphenols like alkylresorcinol, flavonols, gallotannins, xanthones, and benzophenone derivatives have been reported in mango fruit waste; peel and seed kernel antimicrobial (Gadallah and Fattah 2011; Shabani and Sayadi 2014), anti-inflammatory (Robles-Sánchez et al. 2009), antidiabetic (Ediriweera et al. 2017), analgesic, immune modulator (Sahu et al. 2007), and antioxidative (Khandare 2016), Wauthoz et al. 2007).

Table 2 Medicinal properties of polyphenols and vitamins present in mango

Polyphenols	Vitamins/carotenoids	Lupeol
1. Gallic acid acts as a substrate for polyphenol oxidase (PPO) in the pulp 2. Ellagitannins inhibit cancer cell proliferation *in vitro* 3. Gallic acid, mangiferin, myricetin, and flavan-3-ols (e.g., catechin and epicatechin) can prevent membrane lipid peroxidation and protect cells from Parkinson's disease 4. These antioxidants prevent coronary atherosclerosis lowering the levels of low-density lipoprotein cholesterol and triglycerides	1. Ascorbic acid is known to be a potent antioxidant that can eliminate reactive oxygen species (ROS) and maintain the membrane-bound antioxidant 2. Tocopherol, in its reduced state, act as a cofactor for the activity of a number of key enzymes and act as a substrate for oxalate and tartrate biosynthesis 3. Play roles in stress resistance and the synthesis of collagen, hormones, and neurotransmitters 4. Lower risk of degenerative diseases such as cancer, heart disease, inflammation, arthritis, immune system decline, brain dysfunction, and cataracts 5. b-carotene was the dominant carotenoid in mango plays a vital role against degenerative diseases such as cancer, cataracts, and muscular diseases, as well as neurological, inflammatory, and immune disorders	1. It is a pentacyclic triterpene. It possesses pharmacological properties, acting as a strong antioxidant, antimutagenic, anti-inflammatory, and antiarthritic agent 2. Lupeol also prevented 7, 12 dimethylbenz(a)anthracene-induced strand breaks in DNA, thereby reducing the incidence of tumors, lowering the tumor body burden, and causing a significant delay in the latency period of tumor appearance

Mango seed consists of about 29% shells, 68% kernel, and 3% testa (Diarra 2014). The composition of mango seed kernel varies according to different varieties (Barreto et al. 2008). Based on dry weight, 11% fat, 6.0% protein, 77% carbohydrate, 2.0% ash, and 2.0% crude fiber are the average composition of mango seed kernel. Mango seed kernel is high in minerals such as sodium, potassium, phosphorus, calcium, and magnesium (Sandhu et al. 2007). The mango seed kernel encompasses 52–56% unsaturated fatty acids and 44–48% saturated fatty acids (primary stearic acid). The mango seed kernel also comprehends a substantial amount of essential amino acids (lysine, leucine, and valine). Bioactive components that are embodied in mango kernel incorporate phytosterols (stigmasterol, campesterol, and also consists of vitamin K), sitosterol (β-sitosterols), tocopherols, and polyphenols (Soong and Barlow 2006).

The mango peel contains a prominent proportion of total dietary fiber (45–78%), distributed into soluble (16–28%) and insoluble (29–50%) fractions (Ajila et al. 2007). Furthermore, the mango peel also contains cellulose, hemicelluloses, pectin, lipids, proteins, carotenoids, and polyphenols. Apart from this, mango peel also has an appreciable amount of reducing sugars, and due to reducing sugars, mango peel is also harnessed for the fermentation process, bioenergy, and various value-added products (Barreto et al. 2008). Sandhu et al. (2007) chronicled that mango peel comprises an elevated quantity of pectin (10–15%), and the soaking process before the extraction of pectin increases its yield to about 21%. The bioactive compounds or the polyphenolic connotations in 100 g of mango seed kernel comprise 20.7 mg tannin, 6.0 mg gallic acid, 12.6 mg coumarin, 7.7 mg caffeic acid, 20.2 mg vanillin, 4.2 mg mangiferin, 10.4 mg ferulic acid, 11.2 mg cinnamic acid, and 7.1 mg unknown compounds (Masibo and He 2008). Polyphenols include mangiferin pentoside, quercetin, syringic acid, and ellagic acid (Ajila et al. 2007).

5 Gene and Genomics to Study Nutrigenomics

Genomic data of both eukaryotes and prokaryotes are essential to understand the complete science of food. These genome sequences pave the way to get thorough knowledge about the composition of nutrients and their availability. Further, processing strategies and safety standards could be determined in a systematic way. It allows unlocking of a novel method to the post-genomic era that allows nutritionists to screen the genetic background and observe the omics as a whole (transcriptome, proteome, and metabolome). Genome science has resulted in development of new dietary strategies, targeted to supply the optimum nutrition for every person. These tools are the pivot of the ascending domain of nutrigenomics (Fig. 1a, b). The tools of genomics research come in to use to design markers from the candidate genes. It not only improves the health of humans but other living entities as well. Further, it accelerates the breeding efficiency of crops for quality traits and imparts better resistance against diseases (EFSA 2008; Kogel et al. 2010; Polesani et al. 2010). It allows breeders to design a genotype *in silico* based on the desired phenotype by the knowledge procured from recognizing the alleles at all places in a population. As far as the domains of food science, proteomics offers opportunities for discovering functional foods with metabolic effects. It is exceptionally pertinent in the research of proteins of fauna and flora for designer crop breeding (Agrawal et al. 2010), identifying new biomarkers (Pavlou and Diamandis 2010), and discovering therapeutic targets (Katz-Jaffe et al. 2009). By applying measurements of single biomarkers using traditional biochemical methods (Bakker et al. 2010), metabolomics is more helpful in identifying the complexities of metabolic regulation. Due to polyploidy in plants, genomes tend to be stupendous. Hence, because of the scale of the projects, the progression of entire plant genomes lags somewhat beyond other life forms. However, sequencing in a variety of agriculturally important genomes is complete or nearing completion and is forming the basis of a vital knowledge resource for food research. These genomes appraise from the frame of reference of production with agricultural nutritionists who are still struggling with the fundamental strategies for moving beyond the discovery of genes associated with essential nutrients to maximize their agricultural suitability and nutrient bioavailability under the Darwinian selection pressures that guided the organism's development (Lagaert et al. 2009). A genome of organisms represents the culmination of its evolutionary

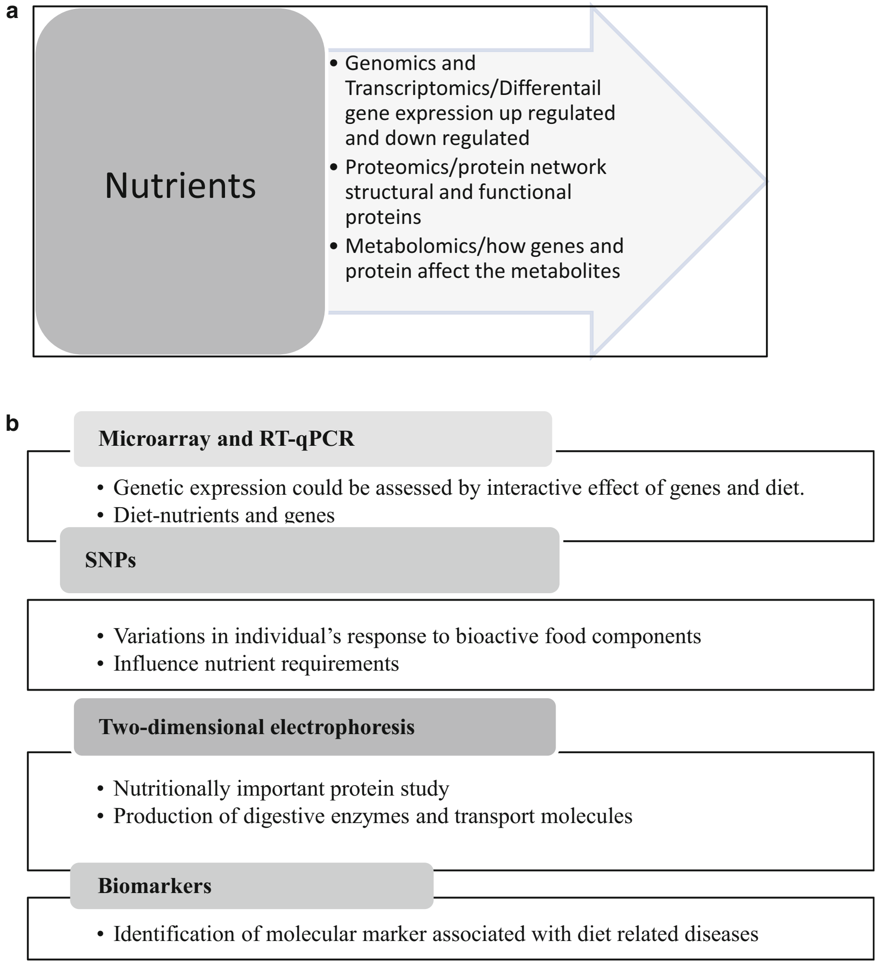

Fig. 1 (**a**, **b**) Conceptual nutrigenomics approach in mango for sound health. The model summarizes the proposed roles for various molecular tools to study the interaction among diet-nutrient and genes

history and the ensemble of genes emerging. Genetics could also influence nutrient and vitamin levels in individuals and changed gene expression. Hence, nutrigenetics emerges as a new science for unlocking the individual pedigree and their composition of nutrients. In mango, molecular markers like simple sequence repeats (SSRs) associated with fruit weight, width, volume, total soluble solid (TSS), titrable acidity, ascorbic acid, and total sugars, additionally reducing sugars, and succors will facilitate screening for varieties/seedlings with preferable fruit traits. Spongy tissue is a consequential physiological disorder influencing the palatable standard of mango drupes, producing a metabolic profile consisting of stress-related and flavor-suppressing metabolites that differ among different stages of the fruit (Ajila et al. 2007; Masibo and He 2008). Genes also affect the absorption, transportation, and activation of nutrients and vitamins. There are studies on markers like single nucleotide polymorphisms (SNPs) which affect vitamin availability and cause deficiency (Rubab et al. 2022). Recently transcriptome-based grouping study showed the impact of mango fruit as dietary intake on cardiometabolic health that appears to have interindividual variability (Keathley et al. 2022). A study on the expression of genes involved in carotenoids and anthocyanins during ripening in fruit peel of green-, yellow-, and red-colored mango cultivars was carried out (Karanjalker et al. 2018). Various genes involved in bioactive and metabolites' production in mango like *UDP-glucose: flavonoid-Oglycosyl-transferase* (UFGT), *dihydroflavonol* (UFGT), *dihydroflavonol 4reductase*, and *anthocyanin synthase* are responsible for flavonoid synthesis (Karanjalker et al. 2018). Similarly, *lycopene-β-cyclase* is responsible for carotenoid synthesis. The gene *MiUFGT2* synthesizes cyanidine-3-O-monoglucosides and peonidin-3-O-glucosides bioactive compounds (Bajpai et al. 2018). Transcriptomes (a set of RNA) are transcribed at a cellular level. Functional products derived through RNA not only affect physiological functioning but also impart knowledge about disease progression (Passos 2015). Although, gene response may be variable, environmental interaction also change the expression of the cell. Some nutrition composition improves the health of humans *via* transcriptomic modulation. Further, "Omics" science could identify new therapeutic targets relevant to variable conditions (Chambers et al. 2019). The transcriptomic analyses provide insights to identify new metabolic pathways affected by mango consumption in individuals who responded to the intervention (Ducheix et al. 2018; Stefania et al. 2021). A network of pathways such as hydrogen peroxide, cofactor catabolic and metabolic processes, gases (oxygen, carbon dioxide) transport, and transcriptional regulation (by *RUNX1* and *TP53*) play a key role in this process. Metabolic pathways also modulated by mango consumption such as *RUNX1* have been demonstrated to be one of the most frequently mutated genes in several hematological malignancies (Sood et al. 2017). Further, *TP53* was found as expressed protein variant in human carcinoma (Khurana et al. 2016). Insulin resistance, diabetes, cardiovascular disease, and chronic diseases like cancer and kidney illness are regulated by hydrogen peroxide metabolism (Lismont et al. 2019). Previous studies with mango extracts have demonstrated beneficial health effects related to these conditions (Awodele et al. 2015; Fomenko and Chi 2016; Imran et al. 2017). Differential gene expression includes *TNFAIP3, API5*, and *TAL1*, etc., as up- and downregulated genes, that regulate the physiological processes. Based on these mechanistic findings, it appears that mango consumption could have a beneficial cardiometabolic effect. Moreover, a reduction in blood pressure following mango consumption is observed (Fang et al. 2018). Research on mangiferin component shows key inflammatory pathways involved in cancer progression (Gold-Smith et al. 2016; Imran et al. 2017; Piccolo et al. 2022). These mechanistic findings provide partial evidence supporting the anticancer potential of mangos.

6 Research Gaps and Future Prospects

The propagation of tropical fruit trees for ameliorating fruit traits is intricate due to several constraints like long gestation period, heterozygous nature, variable embryonic nature, and lack of high-quality genome sequences (Mathiazhagan et al. 2021). New advanced molecular tools supplement conventional breeding efforts. Numerous genomics strategies have recently progressed to accommodate and compliment to traditional breeding methods. DNA-based markers associated with fruit burgeoning and fruit quality characteristics were identified in perennial fruit crops. Furthermore, it could be utilized in association mapping.

7 Conclusion

With the availability of genome sequences of fruit crops, identification of SNP variants/Indels, QTLs, functional genes, etc., could be utilized in quality fruit production. Hence, the fruit superiority was accredited through multi-omics perspectives. Moreover, the recognition and measurements of transcripts involved in sugar-starch metabolism, fruit development and ripening, genomic selection (GS), and genetic modifications *via* transgenics have paved the way for studying gene function and developing varieties with improved quality traits of fruit crops by overcoming long breeding cycles.

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