

GENETICAL ANALYSIS OF NUTRITIONAL DISEASE AND NUTRITION
TOXICITY CONTAIN IN TROPICAL MAIZE



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Abstract

The grain maize is one of the world's most important crops because it contains significant levels of components that produce energy, including lipids, proteins, carbs, and other such components. Maize kernels may be beneficial to human health due to the large number of secondary metabolites, trace elements, vitamins, and minerals they contain. However, maize does not have a very big pool of utilisable gene resources, which limits the food's potential to be improved in terms of its nutritional profile. In this study, we evaluated 246 orthologs in the genome of maize and found that they are identical to 145 genes from other plant species that are involved in nutritional content. These genes were shown to play a role in the composition of the plant's genome. In addition to locating and mapping all 246 potential maize gene resources, we also carried out an in-depth study of the expression patterns of those genes. Due to the expression profiles of these genes and their potential involvement in the enhancement of maize's nutritional value, genetic engineering of maize through editing or ectopic expression of these genes is anticipated to increase the amounts of resistant starch, oil, vital amino acids, vitamins, iron, zinc, and anthocyanin. This is because of the genes' potential to improve maize's nutritional value. As a direct outcome of our studies, there is now a greater availability of valuable gene resources that can be used to enhance the nutritional profile of maize.

Keywords: Maize Grain, Genetic, Species, Nutrients

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Introduction

There are many different and abundant physiologically active compounds present in plants grown for food [1]. While urban dwellers in rich nations have relatively simple access to nutrient-dense crops, those in rural poverty in developing nations frequently do not [2]. Implementing and maintaining dietary practises that guarantee everyone gets the vitamins and minerals they need in such societies may be difficult [3]. Too frequently, what is easily available and affordable is a monotonous diet that primarily consists of one crop, like rice [4]. Creation of nutrient-improved food crops is now possible thanks to recent developments in agricultural biotechnology, which have increased the quantity and bioavailability of vital components like iron and vitamin A [5]. These kinds of technological advancements have been used to treat cardiovascular disease and cancer [6]. Over two billion individuals are at risk of micronutrient deficiency due to the lack of micronutrients in daily meals [7]. The bulk of our food crops are unable to adequately produce essential nutrients because they are grown in mineral-deficient soils, which has resulted in nutrient stress. [8] Instead of tackling starvation, the majority of developing countries' agricultural production scenarios are concentrated on increasing grain yield and crop productivity. [9] Malnutrition, which puts the population's health and productivity in grave jeopardy, is one of the most important adverse health effects of climate change. Recent decades have seen an increase in global temperature that has been accompanied by either exceptionally little or a lot of precipitation [10]. The World Health Organization and the Intergovernmental Panel on Climate Change's Fifth Assessment Report list malnutrition as one of the five most detrimental effects of climate change on human health [11-13]. A number of causes, including as the quick depletion of natural resources, the scarcity of farm supplies, and the effects of climate change on agriculture in developing nations, have contributed to the rise in micronutrient malnutrition. [14] Fortunately, the output of nutrient-rich food crops has increased in this area as a result of creative breeding efforts by plant breeders [15]. This will address the issue of micronutrient deficit because staple food crops in many nations dominate daily diets and are poor in micronutrients. [16] Through a process known as biofortification, nutritional shortages can be permanently resolved. This is a long-term, sustainable solution to the issue of hidden hunger because once the biofortified crops are produced, there is no additional expense to purchase the fortificants and add

them to the food supply during processing [17]. In biofortification, crop nutrient density is increased through genetic and agronomic treatments [18]. By utilising biofortification, we may lessen our reliance on pricey, external additives while increasing the nutrient richness of our food [19]. A new prospective pathway for the development of nutrient-dense crops has now been made possible by techniques like traditional plant breeding, molecular breeding, transgenic methods, and agronomic practices [20]. The main focus of biofortification activities is on foods that are mainstays in the diets of the majority of people. These foods include starchy foods like potatoes and sweet potatoes as well as cereal crops including rice, wheat, maize, sorghum, millet, and legumes [21].

At ideal levels, the human body requires more than 40 essential nutrients. These substances come in different varieties, including minerals, macronutrients, and micronutrients. Micronutrients include iron, zinc, copper, manganese, iodine, selenium, molybdenum, cobalt, nickel, and vitamin A all play significant roles in a number of metabolic processes necessary for normal development and growth. Some minerals, including as sodium, magnesium, calcium, potassium, phosphorus, chlorine, and sulphur, are considered significant nutrients when they are present in trace amounts. These nutrients have a significant role in both our physical and mental development [22]. Instead of vitamins or minerals, food grains' high protein and fat content is what makes them most nutrient-dense. As a result, it is crucial to add supplements to the diets of resource-poor populations whose diets are based on grains like rice, wheat, cassava, and maize, which are deficient in many nutrients, including micronutrients, minerals, and proteins [23]. Particularly susceptible to the detrimental effects of climate change on nutrient food security are Africa and South Asia. Food crops' nutritional value will deteriorate if yields are decreased by climate change. Hundreds of millions of people may be at risk for protein, iron, or zinc shortages as CO₂ levels rise [24]. According to recent studies, rising atmospheric CO₂ causes rice, wheat, barley, and legumes to contain lower levels of iron, zinc, and protein. The contents of zinc and iron in cereal grains and legumes can be reduced by 3–11% as a result of today's higher than average CO₂ levels (550 ppm). If the CO₂ concentration is permitted to increase by another 690 parts per million, the majority of crops will lose between 5 and 10 percent of their iron, zinc, potassium, calcium, phosphorus, sulfur, magnesium, copper, and manganese content [25]. According

to estimates, 150-200 million people will be at risk of zinc deficiency due to the reduction in zinc content caused by the continuously rising CO₂ level. One strategy for reducing the effect of climate change on agricultural nutrition is the creation of biofortified food crops [26].

For the development of biofortified crops, finding germplasm with high vitamin and mineral content is crucial. The majority of the crops' wild relatives, landraces, and regional cultivars are rich in these nutrients, making it simple to utilise them in breeding programmes. The International [27]. Food Policy Research Institute and the International Center for Tropical Agriculture launched the Harvest Plus bio fortification program to raise the levels of vitamin A, iron, and zinc in staple crops in collaboration with the CGIAR centres [28]. The preferred crops were wheat, rice, and maize, which are rich in zinc, and beans and pearl millet, which are rich in iron, vitamin A, and cassava and sweet potatoes [29]. This project's only objective is to develop these micronutrient-rich crops and distribute those to underdeveloped regions of the world that are particularly hard struck by micronutrient deficiencies [30]. It is hard to enhance the quality qualities through conventional breeding because they are polygenic and quantitatively regulated [31-32]. Thanks to the quick advancement of improved genomic tools like molecular markers, it is now able to transfer these quantitatively inherited traits more successfully through plant breeding [33]. The use of molecular markers can substantially simplify breeding programmes by identifying the precise genomic region/QTL regulating the trait for nutrient content. Once QTLs have been identified, it is simple to transfer them to superior breeding materials with less nutritional value [34]. These markers' utility in QTL mapping was constrained because they were derived from biparental mapping populations [35]. Instead of the single or limited recombinations that are achievable in biparental mapping populations, genome-wide association studies (GWAS) offer a rare opportunity to use heterogeneous germplasm that has seen numerous meiotic events [36]. How successfully marker/trait correlations can be resolved depends on how much linkage disequilibrium there is in the panel. The markers that have been linked to QTL could be used for introgression and identification across all breeding stock [37]. In order to enhance the diets of entire communities and eradicate hunger, especially among food insecure children, our review's objective was to gather information on quantitative trait loci (QTLs) linked to nutrient content in important food

crops [38]. An overview of recent initiatives in agricultural biotechnology to improve global health is given in this article [39].

Nutrition and health equation

A well-known preventative approach is eating a healthy diet. Hippocrates said, paraphrasing, "Leave your drugs in the chemist's pot if you can heal your patient with food." Hippocrates delivered this advice to physicians in the year 800 B.C. additionally, it is generally known that everyone has different dietary demands [40]. Dietary factors may have an impact on the development or appearance of a disease. The interplay of genes and nutrition is often advantageous, but it can occasionally be fatal [41]. It is crucial to include both while providing care for a person because inherited and environmental factors interact to affect human health. The majority of past studies either concentrated on the influence of genes alone or the influence of the environment alone, but never both. Recent scientific research has focused on the relationship between genes and diet [42]. The study of nutrition is concerned with how food affects the cellular, tissue, and organ levels of the body's internal surroundings. Understanding nutrient-dependent interactions at the genetic, molecular, protein production, and metabolic profile levels is necessary for this field [43, 44]. As a result, molecular biology, genetics, and nutritional genomics have become part of the discipline of nutrition studies, which initially concentrated on epidemiology and physiology [45].

The interaction between diet and genetics (nutrition)

Genetic diversity and nutritional status

The information obtained during the Human Genome Project has been extremely useful for the study of nutritional genomics. It helps in the investigation of the intricate connections between heredity, food, and sickness [46]. The human genome's sequencing has revealed significant genetic diversity among various human populations. Numerous SNPs, or differences in a gene's DNA, have been connected to dietary patterns [47]. SNPs may have a significant impact on an individual's reaction to exposure, such as food, if they are found in genes involved in the metabolism of medications, environmental toxins, or dietary ingredients [48].

A continual balancing act between nutritional intake, metabolic rate, and gene expression is necessary for homeostasis. Nutrition-related or nutrition-dependent diseases have been

associated with multiple genes, not just one [49]. Genetic variations are the fundamental cause of why people react to the same food in such a variety of ways. Understanding how genetic variation impacts gene expression and identifying genetic variants as risk factors for human nutrition-dependent or -related disorders are the goals of the science of nutrigenetics [50]. Different plant species have different vitamin compositions and contents. Vitamin B1 is abundant in oats (*Avena sativa*) and green peas (*Pisum sativum*). As a result of our research, we can conclude that maize grain is a rich source of vitamins B1 and B6. A significant degree of thiamine variation was seen across maize lines, as shown by both the heat map and the violin plot, similarly to quinoa (*Chenopodium quinoa*, cassava and wheat. We may see that environmental conditions have a negligibly modest impact on PN and PMP concentrations by comparing violin plots across many sites. Additionally species-specific, vitamin B concentration and variation are found in legumes as opposed to cereal grains, with higher levels of thiamine and riboflavin. [51] Other studies have discovered variations in vitamin B1 and B2 in wheat and wheat-derived products, which may be influenced by genetics and variety [52]. According to study [53], maize kernels don't have enough vitamin B3. We discovered that maize grains from recognised lines are an acceptable supply of vitamins B1, B2, B3, and B6, and that dietary diversity will

make up for the lack of other vitamins B in maize-based foods. These findings are similar to those of Palacios. [54]

There are many levels of vitamin interactions in plant metabolism. Thiamine and pyridoxine interact with one another and have different effects on different metabolic pathways, according to studies [55]. In the current study, it was discovered that pantothenic acid (vitamin B5) and thiamine (vitamin B1) had beneficial relationships with total vitamin B6 levels. Therefore, it is crucial to consider the likelihood of vitamin-vitamin interactions when employing inbred lines as parental lines. The link between PN and PM as well as between PL and PM is explained by interconversions of these derivatives in the cytoplasm of plant cells [56]. Similar biochemical evidence was found in wheat by Shewry et al. [57] proving that riboflavin does not interact with other vitamin Bs. With greater investigation into the linkages involved, one vitamin in maize may be improved. Additionally, we found that the vitamin B1 and B6 content of the hybrids was much lower than that of the inbred lines in our study, indicating that the hybrids require improvement in order to achieve the highest nutritional quality. It could be required to genetically manipulate both parental lines simultaneously to optimise vitamin accumulation.

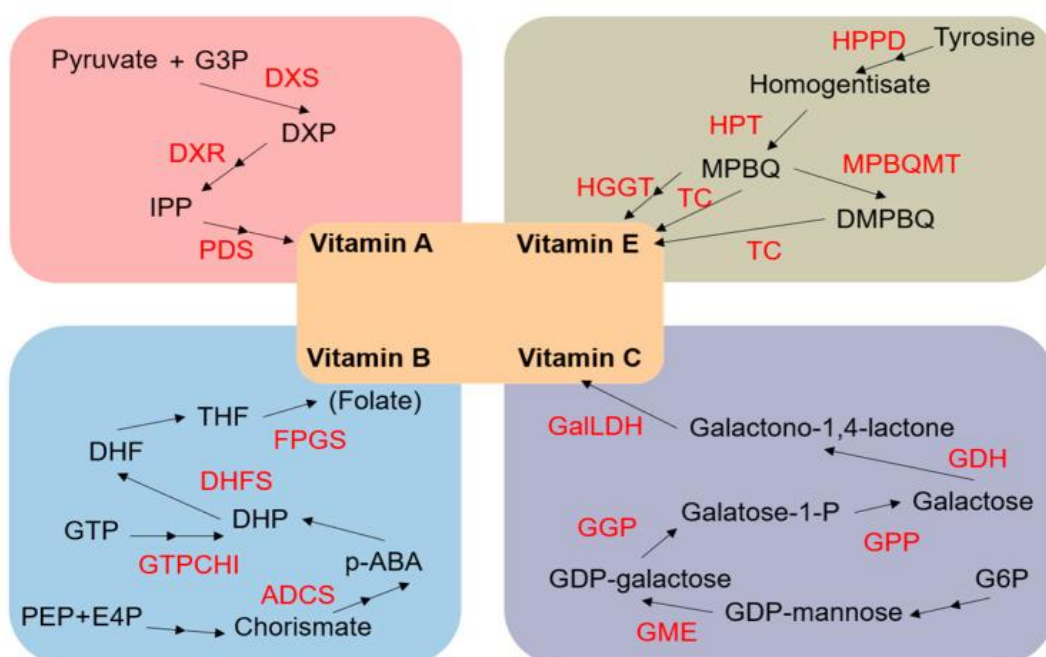


Figure 1: Simplified methods for vitamin production in plants are shown. Isopentenyl diphosphate (IPP), phytoene desaturase (PDS), -hydroxyphenylpyruvate dioxygenase (HPPD), homogentisate phytyltransfer, 1-deoxy-D-xylulose-5-phosphate (DXP), 1-deoxy-D-xylulose-5-phosphate reductoisomerase (DXR), (Nutrigenomics and Nutrigenetics) Nutritional genomics.

Relationships between food habits and human genetics exist. It is a signature that identifies and dates the gene expression and metabolic response. The individual's health and resistance to disease may be affected as a result [58]. First, a person's nutritional status, metabolic response, and susceptibility to diseases that are either directly or indirectly related to diet can be determined by their genetic composition [59]. Second, nutrients regulate the transcription factors that affect gene expression by raising or lowering it, which in turn affects metabolic reactions at the molecular level. Two new terminology have appeared to characterise the cause-and-effect link between food and the human genome: nutrigenetics and nutrigenomics [60].

It is proposed that the science is involved in handling the mechanism by which genetic variations define individual risk to diseases, nutrient daily requirements, cellular metabolic response, and behaviour towards the bioactive dietary components or nutritional therapy. The main objective of nutrigenetics is to clarify the impact of gene variability on the interaction between nutrients and diseases. The objective of the newly emerging scientific discipline known as "nutrigenomics" is to evaluate how food affects each and every cell in the body. The genome, transcriptome, proteome, and metabolome are all parts of the (-omes) subfield of biology, which is of particular interest [61]. Another essential component of nutrigenomics is characterising how dietary restrictions, nutritional supplement ingredients, and food-based nutrients affect gene expression. The emphasis will then move to how nutrients affect an organism's or cells entire genome as seen in variations in its transcriptome, proteome, and metabolome. Additionally, it will aid in defining and validating the genes that influence a person's propensity for diet-related illnesses. This information may also be useful in the early phases of diet-related and diet-dependent illnesses to understand how nutrients can change the metabolic pathways and how to obstruct these regulators [62].

To identify the pattern of gene expression, protein expression, and metabolite synthesis in response to dietary intake, Dolinoy and Jirtle [63] proposed a dietary signature. Therefore, the

aim of nutrigenomics is to understand how dietary patterns influence cellular activity and tissue balance within the body.

Principles of nutritional genomics

Four basic principles form the foundation of the area of nutritional genomics [64]. (1) In certain groups and environments, diet is regarded to be a significant risk factor for a number of diseases. Two) the human genome may be impacted by certain dietary elements that affect DNA structure and/or expression. (3) Individual variations in genotype can be used to explain how health and sickness coexist. (4) Dietary elements that control gene activity may affect how chronic diseases start, progress, and ultimately manifest. Four basic principles form the foundation of the area of nutritional genomics [65].

Examples of nutrigenomics

Dietary cholesterol inhibits the transcription of the hydroxymethylglutaryl-CoA reductase gene. By silencing mRNA for lipogenic enzymes, polyunsaturated fatty acids in the diet lower hepatocytes' capacity to generate fatty acid synthase mRNA. For this technique, the level of fatty acid unsaturation is crucial [66].

Phenylketonuria is a single-gene mutation example. Foods high in phenylalanine should be avoided by those with phenylketonuria. Many Asian cultures lack aldehyde dehydrogenase, the enzyme necessary for ethanol metabolism. Alcohol consumption by someone with the condition can make them feel uneasy. The disorder known as galactosemia is brought on by a genetic deficiency of one of three enzymes involved in galactose metabolism [67].

Effects on crop protection chemicals

Due to the selection criteria utilized, it was not possible to undertake an economic analysis or compare the use of insecticides and herbicides in GE maize to isolines and near isolines [68]. Other authors have predicted that the widespread application of GE HT and IR maize will result in reductions in herbicide and insecticide use of 10.1% and 45.2%, respectively, between 2011 and 2022. This study discovered that the usage of insecticides

was greatly reduced thanks to advancements in GE IR technology whereas the use of herbicides changed drastically with the introduction of GE HT crops. [69]

In earlier meta-analyses, [70] untreated non-Bt crops and insecticide-treated Bt crops were contrasted. According to the findings of these assessments, GE-enabled systems have also benefited from improved biological control of all pests that are resistant to the treatment. You may say that this is a byproduct of technology.

Effects that have quality

GE maize grain has significantly reduced amounts of mycotoxins (29%), fumonisin (31%), and thricotecens (37%), as compared to non-GE maize grain. In comparison to isolines and near isolines, insect damage was reduced by 59.6 percentage points in GE maize, indicating a relationship between the decreased mycotoxin concentration and the diminished frequency of insect attack. Insects promote colonisation by acting as carriers of fungal spores, and the wounds they cause in kernels during harvest and storage raise the possibility of mycotoxin buildup [71]. Markets frequently reject grain with a high mycotoxin concentration or reduce the price of grain due to the presence of mycotoxins because of the health concern they provide. In contrast, GE maize grain has lower mycotoxin levels, which may help lower the chance of consuming toxins that are bad for human health. In low-income nations, mycotoxin exposure is more likely to occur. Toxinogenic fungi are encouraged to proliferate by environmental factors such as drought stress during maize growing and a lack of infrastructure and technical tools for routine food monitoring. In a scenario of climate change where rainfall declines and temperatures rise, drought stress on maize enhances its sensitivity to fungal attack [72].

Genetically modified crops must be grown under authorization procedures that guarantee the finished product is chemically identical to non-GE crops. Our findings demonstrated that the protein, fat, ADF, NDF, and TDF contents of GE maize grain were comparable to those of the isolines, in contrast to mycotoxin levels. These results support the data on compositional equivalency between GE crops and non-GE comparators that have been gathered over the previous 20 years.

TO and NTO modifications

Section A-Research paper

The European corn borer (*Ostrinia nubilalis*) (Lepidoptera: Crambidae), Mediterranean corn stalk borer (*Sesamia nonagrioides* Lefebvre) (Lepidoptera: Noctuidae), and western corn rootworm (*Diabrotica virgifera virgifera* Le Conte) (Coleoptera: Chrysomelidae) are three pests that frequently attack maize. Only adequate data on the prevalence of *Diabrotica* spp. was available in our study to enable a trustworthy meta-analysis. Our study found that genetically modified (GM) maize considerably reduced *Diabrotica* spp. infestation by 89.7% compared to non-GE isolines. The data were all collected in untreated, natural environments. Our data show that this target has been met, making IR crops an effective tool against insect pests, which is the main goal of crop genetic engineering. Although the use of *Diabrotica* adult number might be viewed as an indicator that is not entirely reliable, since the damage is primarily caused by larvae, our data show that this target has been achieved. Furthermore, GE seed manufacturers claim that the most recent generation of maize hybrids only partially resists *Diabrotica*, and work is being done to improve this resistance trait using the ground-breaking technique of RNA interference (RNAi).[73][74]

Despite the great efficacy of IR crops, the development of pest resistance and the subsequent decline in the effectiveness of GE crops cannot be completely ruled out. Although refuges have been required in the US, EU, Australia, and other nations, resistance to Bt maize and cross-resistance have lately been found in the following places: *D. virgifera*, a Coleoptera species, was found in Puerto Rico, South Africa, [75] and Iowa [76]. The refuge method, which is based on the hunch that refuges, which are non-Bt host plants positioned close to or inside fields of Bt crops, generate vulnerable pests that breed with the few resistant individuals, uses several management techniques [77]. An illustration of a novel technique for delaying the emergence of pest resistance by the expression of multiple Cry toxins is multiple stacked/pyramided Bt crops [78-80].

Conclusion

Breeders' major focus right now is developing nutrient-dense, high-yield crop varieties to satisfy expanding dietary and demographic needs. The utilisation of biofortification, a terrific method to raise the nutrient density of plants, has a tonne of potential for maize. Transcriptomics and metabolomics advancements have provided valuable

information for understanding the biosynthesis processes of dietary substances. We list the genes associated with nutrient content in plants that have been previously published in this overview. On the assumption that plant homologous genes may have comparable roles across species, we mapped the chromosomal positions of 246 genes associated with nutritional quality in the maize genome and gave in-depth expression profiles in early seeds, kernels, and non-seed tissues. By raising the amount of starch, oil, protein, vitamins, minerals, and other secondary metabolites in maize kernels, these genes may be effective in improving the nutritional value of the grain. It is required to combine information from transcriptomic, proteomic, and metabolomic analyses to create transcriptional, proteomic, and metabolic roadmaps for maize kernels in order to confirm gene functions and support future breeding initiatives to improve nutritional quality.

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