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Review Article

# Nutrigenomics: A new approach to the diagnosis and prevention of diseases

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ABSTRACT

An expanding understanding of the ability to alter meals or dietary to enhance health and lower the probability of nutrition-related conditions is what has sparked interest in nutrigenomics. It is a newly developed field which incorporates the areas of bioinformatics, diet, molecular biology, the study of genomes epidemiology, and molecular medicine to reveal the effects of diet on gene activity. More research in this area requires immediate attention to assist people recognize the connection between nutrition and well-being and to make sure all individuals receive advantages from the genomic change. As people's eating behaviors and daily routines change, they turn more vulnerable to diet-related disorders. The implementation of high quantities genomics technologies in studies on nutrition is known as nutrigenomics. If executed correctly, it will advance knowledge of how nutrition affects the processes of metabolism and homeostatic management, how this restriction is hampered in the initial stages of diet-related disorders, and the point to which specific sensitizing genotypes are responsible for such diseases. Nutrigenomics will eventually enable successful dietary approaches to restore homeostasis and eliminate diet-related illnesses. It is possible to think of nutritional genomics, also known as nutrigenomics, as the intersection of molecular nourishment and genome. The expression of genes profiles (transcriptome), chromatin design (epigenome), expression of proteins patterns, including posttranslational modifications (proteome), and metabolite profiles (metabolome) are only a few of the many tissue- and organ-specific effects of bioactive nutrients.The term "Nutrigenomics" was coined to signify the scientific investigation of this gene-nutrient interplay. Therefore, nutrigenomics refers to the application of the field of biochemistry physiology, dietary intake, genomics, proteomics, metabolomics, transcriptomics, and epigenomics to identify and understand the molecular basis of the current reciprocal relationships among genes and nutrients.Nutritional genomics, also known as nutrigenomics, is a research field of gene-nutrient relationships and how they are utilized. By changing the way genes are expressed and/or arrangement of someone's genetic code, ordinary food nutrients might alter the ratio across well-being and illness. This genetic insight can be obtained by nutritional genomics. The study of nutrigenetics looks at the associations between a person's gene makeup and particular nutritional intake. This subfield examines how genetic variability affects dietary guidelines or the relationship between diet and disease. Though they have different short-term goals, dietary research's long-term mission is to enhance people's health and aid in illness prevention. Gene-specific dietary data has provided a wealth of information that has helped doctors develop therapeutic strategies for the medical management of complex chronic diseases. The aforementioned data can be used in the future to a vast community; however, practicality needs to be verified. An understanding of nutrigenomics should soon enable more specialized therapies.



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## 1. Introduction

The scientific investigation of the effects of nutrition on the entire genome is called nutrigenomics. According to nutrigenomics, nutrients are nutritional signals that are picked up by cellular biological sensors and alter the activity of genes as well as proteins, which in turn affects the creation of metabolites. Therefore, 'dietary signatures' can be thought of as sequences of gene expression, protein expression, and metabolite development when exposed to specific nourishment or dietary routines.By analysing these nutritional characteristics in particular cells, organs, and organisms, nutrigenomics aims to further clarify how nutrition affects homeostasis. Additionally, nutrigenomics seeks to understand the mechanisms underlying these genetic predispositions as well as discover the genes which impact the susceptibility to diet-related problems on the level of the genome.[1]

Nutrigenomics investigates the relationships among genes and nutrients or food biologically active substances and their impacts on human health.,[2,3] It tries to figure out the consequences of various nutrients, including micronutrients as well as macronutrients, on the genome.[4] The phrase "Nutrigenomics" also encompasses the scientific investigation of how nutrients affect gene expression, the activity of transcription, and the diverse response of gene modifications. The term "nutrigenomics" also refers to the analysis of biological processes applying functional genomic techniques in order to comprehend whether dietary components influence the processes of metabolism and homeostatic balance.Additional tools employed in nutrigenomics research include transcriptomics, proteomics, and metabolomics."Nutrigenomics" signifies the use of genomic approaches to the discovery of associations involving particular specific nutrients and genetic variables.[5]

The growth of serious illnesses like carcinoma, osteoporosis, diabetes, and heart diseases is largely influenced by genetics and nutrition. To examine how diet affects physical well-being, scientists use the technique called nutrigenomics, which combines nutritional research with genomics and applies additional high quantities 'omics' technologies like transcriptomics, proteomics, and metabolomics.[6]

## 2. Transcriptomics in Nutrition

The entire collection of active RNA transcripts is being investigated by means of transcriptomics.[8,9] Gene expression varies depending on the various situations and times of day because mRNAs that are created at a certain time and in a specific tissue of a determined organism.[10] When transcription variables are engaged, they are shipped to the nucleus, where they link to a particular DNA sequence in the promoter zone of genes and either promote or interfere with transcription.[11] The physiological signals that are stimulated by nutrients/bioactive food molecules or the metabolites generated from them, as well as hormones, pharmaceutical therapies, and illnesses, between somebody else, may induce these transcription variables.[12] They operate as sensors that are controlling or altering cellular transcription as necessary. Transcriptomics can help with nutritional investigations by supplying details on the processes or fundamental impacts of a specific nutrient or diet. Additionally, it can aid in finding and describing the pathways controlled by nutrients or bioactive molecules found in food, and it can also help to recognize genes, proteins, or metabolites which alter in the condition of prediseases.[13]

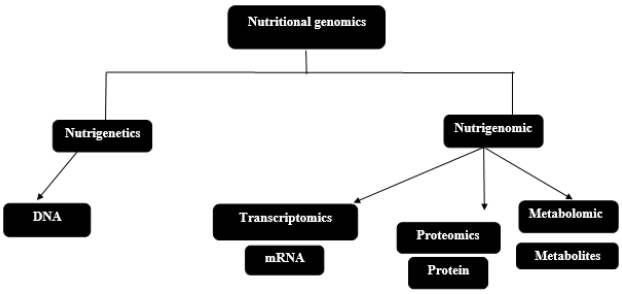


**Figure 1:** Research area of nutritional genomics[7]

### 2.1. Proteomics

The analysis of all the proteins that contribute to a particular type' biological functions is known as proteomics.[14] These proteins function in the cell, tissue, or organ in their usual states, but they may alter their expression stage or even how they operate under various physiological or pathological circumstances, similar to those in the transcriptomics.[8–10]

All living cells contain proteins, which are a crucial class of chemical compounds. In the cell, they perform a wide range of functions, including related to structure, mechanical, biochemical, signaling by cells, transportation, and storage.[15,16] Additionally, they are a crucial component of the human diet.An organism generates much more proteins than it does genes, which is a significant difference. The various posttranscriptional and translational alterations are responsible for this. Methods invented for investigating the structure and activity of proteins are used in proteomics.It accomplishes this by employing techniques like organellar proteome analysis, prefractionation of samples by extraction sequences of data, and chromatographic methods connected with electrophoresis, in addition.[11,17,18] Thus, proteomics serves as a foundational assets for nutrigenomics. Once it bridges the separation across genome sequences and cell behavior,

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it works as a biological means of figuring out how the genome is triggered in response to a given diet and how genetic function can be identified. As an illustration, consider how butyrate works to change the expression of various ubiquitin-proteasome system proteins. This modification shows that butyrate may influence critical proteins involved in the regulation of the cycle of cells, apoptosis, and division of cells through proteolysis.

### 2.2. Metabolomics

The bodily fluids and tiny primary/secondary metabolites of an organism or species compose its metabolome. The field related to functional genomics known as metabolomics analyses metabolite alterations with the aim of identifying and evaluating them.[17,19] The knowledge regarding how both the phenotype and genotype of someone are related might have been made easier by innovations in this field of studies. Metabolomics has several uses in nutrition, including the ability to understand the patterns and metabolic problems generated by an individual's dietary habits and how these modifications may impact the individual's well-being or illnesses.[10,20] As a result, metabolomics also examines how metabolism functions when subjected to genetic and environmental modifications,[9] with the aid of bioinformatics and statistical approaches.[21]

Microscopic organic compounds called metabolites, which are dispersed in the cell cytoplasm, communicate directly with protein molecules and other macromolecules. Primary and secondary metabolites are distinguished between them. Although secondary metabolites are more prevalent in both fungi and plants and serve as structural elements and safeguards, primary metabolites have a close relationship with the pathways of macromolecule production and breakdown. The metabolites found in living organisms have the potential to function as substrates, thereby including as enzyme inhibitors or activating agents, molecular precursors, waste products resulting from the production or breakdown of macromolecules, and so on.

Metabolomics in the field of nutrition enables an awareness of metabolic configurations and disturbances that result from or are influenced by diet. This advances our understanding of how an individual's well-being or disease may be impacted by an excess or deficiency of certain nutrients or chemicals (secondary metabolites) that exist in food. The metabolome routes are altered as an outcome of the associations across these substances (nutrients or not). For instance, under specific chemical-based stimulations, perilla alcohol (a monoterpene derived from strawberries) may operate as an anticancer component.[8,17,19]

### 2.3. Nutrigenomics's historical context

It has long been believed that nutrition affects health. Inborn errors of metabolism, referred to as nutrigenomic relationships among inheritable genes and food, are frequently corrected through modifying diet. Phenylketonuria (PKU), which is brought on by an alteration (mutation) in an individual gene, is one such instance. People who are affected need to stay away from food that contains phenylalanine.Another illustration is lactose intolerance; more than half of grown-ups globally are unable to consume dairy products due to the gene that codes for the digestive enzyme that breakdown lactose, lactase, is typically "turned off" after breastfeeding. Nevertheless, a variation in just one DNA nucleotide first showed up in northern Europeans approximately 10,000 and 12,000 years back. This one nucleotide polymorphism, or SNP, caused the lactase gene to keep trying developing itself into adolescence.Due to this SNP, individuals might gain benefit from nutrient-dense milk products in areas with limited growing seasons. With the advent of molecular genetics in the latter part of the 20th century, researchers went out to find more genes which communicate with dietary components. Organizations started promoting nutrigenomics in the 1980s. The scientific field of nutrigenomics was established by the Human Genome Project in the 1990s, that analyzed the complete human genome. By 2007, researchers have uncovered multiple connections between genes, diet, and illness.[22] A completely fresh approach to studies on nutrition is being brought through nutrigenomics. For example, high-throughput tools allow for the worldwide analysis of how genes are expressed in a cell or organism.Nutrigenomics would call for cooperation amongst professionals in genetics, health promotion, nutritional science, and culinary arts. Making food that tastes excellent is quite simple. It will taste better if you add a touch of butter or ghee to it. The difficulty lies in figuring out how to eliminate fat while still producing wholesome food that tastes pleasant. In light of the dire need for an improvement regarding public well-being and the rising prevalence of persistent conditions like type 2 diabetes and obesity, nutrigenomics may eventually demonstrate to be the answer.

## 3. Fundamentals of Nutrigenomics

Nutrigenomics is the scientific investigation of the manner in which genes influence nutrition (i.e., what a person consumes and how a person interacts to nutrients) as well as how nutrients affect genes (i.e., how they influence gene expression and function). The complete range of scientific methodologies, through fundamental cellular and molecular biology to clinical studies, the field of epidemiology and public health, can be included in nutrigenomics. The biological and operational component of heredity that is

transmitted from parent to child is the gene.Genes are sections of DNA which include the instructions needed to create a particular protein. Changes to the protein's design and function can occur from mutations in the DNA. Single nucleotide polymorphisms (SNPs), which are changes in a single nucleotide, are one type of genetic variance among many others. Alleles are different gene patterns found at certain chromosomal sites. The genotype, which is derived from the admixture of maternal and paternal alleles, represents the genetic make-up of an individual's genome for a particular genomic position. Genotypes are distinct from phenotypes because they do not always manifest as physical traits. A phenotype is an identifiable characteristic of someone's personality, such as a particular hair shade, elevated glucose levels, or a history of a particular medical condition. In light of their various circumstances, people with a similar genotype may exhibit diverse phenotypes.Sets of polymorphisms in genes are frequently accumulated simultaneously because a haplotype is an inherited collection of alleles. Nutrigenomics' goal is to sustain the physical well-being of a group of people who consume different kinds of food. The Human Genome Project developed as an outcome.

1. Will a person's wellbeing be affected by how their genes are expressed at the cellular level in response to metabolic processes?
2. Do relationships among genotype and environment/nutrients affect gene expression and metabolic reaction?
3. Recognizing how the association within a gene and nutrition works could help determine the best diet for each person.

Nutrigenomics was therefore developed with the objective to address such inquiries. The field of nutrition known as nutrigenomics makes use of molecular techniques to look up, availability, and comprehend the various reactions brought on by a particular dietary regimen administered to people or community categories. It looks into how a certain diet's elements (bioactive compounds) can influence the activity of genes that may have boosted or decreased a gene's potential. The reaction will be contingent on how the functioning or expression of the genes varies.[6,23]

## 4. Cardiovascular Diseases and Nutrigenomics

A report released by the World Health Organization, cardiovascular conditions accounted 17.5 million fatalities in 2012. Throughout circumstances of Cardio Vascular Diseases (CVD), intimal lesions emerge as a consequence of cellular death, lipid buildup, pus tissue cells, cells in the bloodstream, fibrosis, and inflammatory reactions in the arteries and veins.Cardiovascular disease can be cured and avoided with proper diet. A nutritious meal can influence many genes involved in metabolism and biosynthesis of lipids, including peroxisome proliferator (PPAR), fatty acid synthetase (FASN), lipoprotein lipase (LPL), arachidonate 5 lipoxygenase (ALOX5), apolipoprotein E (APOE), and many. The genes that produce distinct hormones, apolipoproteins and enzymes might vary, which can change an individual's vulnerability to heart disease.Investigations based on evidence have shown that the arachidonate 5 lipoxygenase (ALOX5) gene influences the production of leukotriene, chemokines, and cytokines because people with atherosclerotic lesions had higher levels of this gene, which would suggest a rise in the dispersion of immune cells. Leukotriene development is prevented by eating a diet composed of omega 3 polyunsaturated fatty acids, which alter eicosanoid biosynthesis.[5,24] Polyunsaturated fatty acids (PUFA) support the breakdown of carbs and lipids by affecting the activity of several genes. As a consequence of this, a patient who fed these essential fatty acids had decreased levels of LDL cholesterol in the body.[25] In certain racial or ethnic communities, such as African-Americans, a polymorphism (-504 cc) in the liver-derived lipase gene boosts protective HDL levels in relation to a high-fat dietary. By altering the flow of the membrane or by producing alternative ligands, PUFA regulates the expression of genes. The aforementioned justifications so suggest that dietary changes may be used to treat cardiac conditions depending on an individual's genotype.[5,26,27]

Inflammation has been demonstrated as the root of a number of long-term conditions, including CVD, which is the most prevalent diet-related chronic condition of the modern era. A collection of multipurpose diseases linked to being overweight, hypertension, atherosclerosis, and thrombosis is known as CVD. It is well known that all these kinds of pathogenic microbes have significant genetic and environmental links. Diet is regarded as a component of the environmental factors, and there is significant evidence between the structure of the diet and the risk of CVD.Polymorphic genes are associated with the regulation of energy control undoubtedly produce a "favorable" or "unfavorable" backdrop for the occurrence of heart disease (CVD), as obesity is a significant potential risk element. One in every five fatalities in America each year is attributable to coronary heart disease (CHD), one of the most common diseases in western culture.[28,29]

Low density lipoproteins (LDL) and high density lipoproteins (HDL) are two lipoproteins that are specifically mentioned as the primary objectives in the fight against CHD in epidemiological studies as well as long-term results of investigations. A exterior covering containing phospholipids, unesterified cholesterol, and certain proteins surrounds a lipid-rich center in a macromolecular compound known as a lipoprotein.Chylomicron (high lipid to protein ratio, highest in TG as% of weight), VLDL (very low density lipoprotein), IDL (intermediate density lipoprotein), LDL (highest in CE as% of weight), and HDL (high

protein to lipid ratio) are just a few of the associations that are present and are classified according to their chemical structure, which eventually impacts how dense they are. The initial stage of treatment, referred to as therapeutic modifications to lifestyle, consists of adjustments to the person's dietary and amount of exercise, together with any necessary changes in smoking and bodyweight. Pharmaceutical substances like statins, which have been shown to successfully suppress the function of hepatic 3-hydroxy-3-methylglutaryl CoA reductase (HMG-CoA reductase), are utilized as the next phase of therapy to lower the concentrations of circulating cholesterol in the body.[30]

These different levels of reactivity have been attributed to genetic variations in people across the globe, highlighting the significance of discovering the genes that are essential for the development of CHD or offer safeguards against it, as well as understanding how these genes communicate with prevalent food components. Current research has identified several potential genes and their common SNPs. Early research suggests that genetic variations in the genes for cholesterol ester transfer protein (CETP), lipoprotein lipase (LPL), hepatic triglyceride lipase (HL), LDL-receptor, apolipoprotein E (APOE), apolipoprotein A1 (APOA1), ATP binding cassette transporter A1 (ABCA1), and lecithin-cholesterol.[31] A nutrigenetic methodology has also started to show that some of the aforementioned genes and their polymorphisms, like APOA1 and LPL, are amenable to food modification and could alter the beginning of CHD.

## 5. Obesity and Nutrigenomics

Another major metabolic abnormality is obesity, a nutrition-related disorder that significantly raises tolerance to chronic conditions. Therefore, the management of energy levels in biologically predetermined manners defines an individual's susceptibility to obesity.[5,32] Owing to investigations, inherited factors account for approximately 80% of the variations in identical twins' Body Mass Index (BMI).[33] Multiple peripheral indicating peptides, which involves cholecystokinin, leptin, insulin, and ghrelin, along with a few connected test receptors in the body contribute to food consumption regulate because of polymorphisms in the genes and have an immediate connection with the management of weight. These genes have been published and play a role in encoding peripheral and central factors linked to energy consumption and dietary intake. The polymorphic traits of the genes that serve as regulators of energy consumption encoding have a significant role in the control of adipocyte growth and diversification in addition to protein separation. A polymorphic core oversight of consumption of energy is made up of elements of the melanocortin route, hypothalamic neuropeptide Y, and other important neuropeptides.[32]

Nutritional genomics may be able to reduce the persistent inflammation associated with obesity. Certain food items include bioactive substances that inhibit inflammation, such as quercetin (found in vegetables and fruits), caffeic acid (which are present in yerba mate), lycopene (which is primarily in guavas, melons, and tomatoes), and tyrosol (which can be found in fruits and veggies, as well as olive oil). Those bioactive substances prevent some genes from being expressed. Tocopherol, an antioxidant that is present in green tea, has been shown to lower inflammatory reactions and appears to be beneficial in safeguarding fat people. This substance may also be helpful for the medical management of obesity, according to some investigation.[34]

However it is obvious that these factors are not the by still primary causes of obesity, variations in genes definitely play a significant part in its growth. Behavioral and environmental variables are equally significant. It is mainly uncertain how socioeconomic and genetic factors interplay in human civilizations and what proportions they each bring about the emergence of obesity. Over six hundred DNA markers and chromosomal locations have been connected or related to individual obesity, according to the most current version of the human obesity genetic map.It reveals the vital function that these genes play and how they affect important functions, particularly appetite, which affect the onset of obesity. These medical conditions are incredibly uncommon, though, and consequently have no bearing on a great number of obese people.[35] In several latest investigations, techniques that can do parallel genotyping assessments for millions of SNPs from only one tiny tissue or blood specimen have been established. People worldwide, there are thought to be roughly 10 million SNPs. However, SNPs that are adjacent to one another in the DNA sequence on the exact same chromosome have a likelihood to be inherited jointly, even if this scale now beyond the capabilities of the newly developed advances.A "haplotype" is a collection of such related SNPs, and it appears out that there aren't many common haplotypes across many chromosome locations. Therefore, even though a chromosome location might include lots of SNPs, it's feasible that learning the majority of the data about the genetic variation profile in that location can come from studying just a small number of 'tag' SNPs. The International HapMap Project's objectives are to determine such haplotype blocks and the most trustworthy tag SNPs.[36]

## 6. Diabetes and Nutrigenomics

The number of people with diabetes is expected to increase from 387 million to 592 million until the year 2035. (The IDF, or International Diabetes Federation). Type I diabetes (T2DM), responsible for over ninety per cent of people with diabetes, is the most prevalent and complex illness. It is caused by the loss of the islets in the pancreas via T lymphocyte infiltration. Most people with diabetes mellitus are around the ages of 40 and 59.The development and pathophysiology of disease are significantly influenced by

a wide range of variables, including metabolic biography, genes, nutrition, modifications to the environment, and their relationship to one another. With the use of omics approaches, which facilitate the identification of substrates like proteins, genes, and how they communicate with nutrients, the effect of food elements on how genes operate was exainedm.[37]

Understanding nutrient-gene connections in the etiopathogenesis of various metabolic diseases is essential. These elements can control the expression of genes by altering signaling molecules in intricate mechanisms. A genomics investigation discovered a link between 65 (SNPs) and the likelihood of having type 2 diabetes.The latest advances regarding human genome decoding and genome sequencing have made it easier for people to conduct studies for the detection of (SNPs) connected to Type II diabetes, enabling patients to understand their genetic susceptibility to the disease's onset.[38]

A metabolic condition known as diabetes mellitus is distinguished by hyperglycemia brought on by impaired insulin secretion or metabolism.[39] Glycatedhemoglobin levels are used for the definitive identification of diabetes mellitus; in those who have the disease, successive levels of fasting plasma glucose will be 7 mmol/L or higher. In general, diabetes mellitus categories can be made based on signs and symptoms.

## 7. Cancer and Nutrigenomics

Cancer appears to be a complex process that begins when the expression of genes, function of proteins, and metabolite function start to behave abnormally. The cellular processes driving the start of carcinogenesis and its regulation by nutritional variables have provided crucial insights into this medical condition in the post-genomic period. One's possibility of acquiring cancer may rise as a result of inherited mutations in genes. In cases where there is a gene-diet relationship, your chance of getting cancer will significantly rise. Just under ten percent of twins with identical DNA will have identical instances of cancer, in accordance with the investigations on twins, proving that the surrounding environment has a significant impact on vulnerability to cancer.[40]In a lack of apparent involvement with genotoxins, confirmation that the genome and epigenome harm biological indicators are susceptible signs of inadequate levels of micro nutrients necessary as substrates or as elements of DNA-repairing enzymes, for service methylation of CpG sequences and avoidance of DNA oxidation and/or uracil incorporation into DNA.[41]Diet is seen as a supply of both safeguards (vitamins, antioxidants, substances that activate detoxification enzymes, etc.) or carcinogens (intrinsic or cooking-generated) included among particular meals. It is evident that polymorphisms that influence how a carcinogen undergoes metabolism may alter the likelihood that a carcinogen will come into touch with a target cell, operating at the cancer start phase. Without a doubt, eating habits can affect how hormones control themselves. Hormonal state is highly impacted by obesity. In addition, because phytoestrogens are believed to be metabolized through similar metabolic processes as testosterone and estrogen, their ability to prevent cancer can be affected by polymorphisms.

Cancer is a complex condition marked by aberrant protein, metabolite, and expression of genes. According to studies, many cancers can be prevented by managing food and nutrition well since they help control risk factors for the disease.[42] A poor nutritional environment is linked to over 70% of cancer cases and roughly 35% of individual malignancies.[43,44] Several genome and epigenome harm indicators that function as conscious biomarkers can be used to validate the lack of particular foodstuffs that are substrates of enzymes that repair DNA and also aid in the avoidance of uracil absorption in DNA.[45]

Polymorphisms in the chemical breakdown of carcinogens can influence the probability that a carcinogen will come into contact with a specific kind of cell and cause cancer to develop. Single nucleotide polymorphism has been associated with a decreased chance of developing cancer in the genes that produce particular hormones such androgen, progesterone, estrogen, and others.[5,46] Because the existence of a metabolic enzyme called N-Acetyl Transferase (NAT) with different polymorphs is linked to cancer problems, a high intake of red meat has been linked with an increased likelihood of colon cancer.

Wee-cooked meat from red meat may include N Acetyl Transferase, which is necessary for the acetylation of heterocyclic aromatic amines. When some amino acids combine with creatinine whilst the elevated temperatures processing of beef, heterocyclic aromatic amines (HAA) are created. Heterocyclic aromatic amines (HAA) can be acetylated to produce chemical compounds that link to DNA and promote cancer. Apparently NAT2 fast acetylators allow for this kind of operation. As a result, those with the N Acetyl Transferase (NAT) acetylator genotype are more likely to develop cancer, including endometrial, renal, and colon cancer.[47]The sodium chloride and additives, two food ingredients that have been identified as potential carcinogens, may contribute to the development of gastric cancer.[48] Electron acceptors that act as pharmacological biological sensitivity modifiers, anti-oxidants aid in controlling the progression of cancer. With continuously repeating redox reactions in order to eliminate reactive oxygen species or free radicals, many anti-carcinogenic medications function as antioxidants and are able to communicate with each other.[49]

The creation of dietary compounds that can alter the expression of specific genes engaged within the moderation of the reactive oxygen species serves as one

of the major achievements. Contrarily, phytoestrogens are substances obtained from plants that resemble human estrogen structurally. That might serve as an antagonist or agonist of estrogen receptors, vying with them for binding. Instances of these substances include lignans, isoflavones, coumestans, stilbenes, flavones, and flavanones. Isoflavones, a type of phytoestrogen, are abundant in soy-based goods such miso, tofu, soy milk, and textured soy protein. Lignans, the constituents of plant cell walls, are present in a wide variety of plants.Numerous meals, like veggies, whole-grain products, and tea, contain nutritional lignans. Earlier investigations have demonstrated the beneficial interaction between nutritional foodstuffs and anti-cancer medications.[50,51] According to earlier research on avoidance of cancer, particular nutritional intake has an impact on important biological processes that are altered in some malignancies. More than a thousand phytochemicals have the ability to safeguard against cancer.[52] Long-chain polyunsaturated fatty acids increase the impact of noncommunicable long-term degenerative conditions as well as expansion, neurological growth, and inherited and inborn immunity, which all contribute to the battle against cancer.[53–55]Owing to particular in vivo and in vitro studies, the ingestion of omega 3 fatty acids inhibits the growth of colonic tumors. Fruits and veggies both include several kinds of biologically active compounds that assist in speeding up the process of detoxification and thereby avoid cancer.[56,57]

## 8. Applications of Nutrigenomics

In order to enhance the nutritional profile of soybean seed oil as well as render it more palatable and sustainable for people to eat, the microsomal -6-desaturated gene from soybean was extracted. Bombyx mori L. proved that soyprotein extract supplemental intake plays a role in governing the fibroin gene expression at transcriptional level through raising fibroin mRNA transcription, which in turn produces a rise in the manufacturing of silk.There is no discernible distinction among fish supplemented with a diet consisting of fish meal (FM) and SBM diets, according to nutrigenomic investigation of intestinal reaction to 50% soybean meal (SBM) substitution in young Atlantic halibut (Hippoglossushippoglossus L.) fish.The hypoglycaemic ability of a processed the water-based extract of fenugreek seeds has been studied in vivo, and its consequences on the hormone insulin signaling networks in the main targets of insulin, adipocytes and liver cells, were examined in vitro, through mechanism-based cutting-edge modern techniques.[6,58] A significant oilseed crop, Brassica juncea, was subjected to genetic modification in an effort to effectively add natural tocopherol to human meals. Over-the-top consumption of tocopherol are linked to better immune system performance, a reduced likelihood of cardiovascular illness, and a reduced rate of development of a variety of destructive human diseases. For the avoidance and/or therapy of retinopathy caused by diabetes, curcumin and turmeric, its nutritional source, are essential. Real-time polymerase chain reaction (PCR) and immunoblotting analyses of the vascular-endothelial-growth-factor (VEGF) activity in diabetes-related rat retinal cells revealed that curcumin and turmeric, its nutritional source, can reduce VEGF development.[6,59]

### *8.1. Nutrigenomics applications in developing of food that has been genetically modified*

The production of dietary supplements can benefit from understanding the field of nutrigenomics. By changing specific genes, it is possible to create transgenic organisms or nutrigenomic consumables that are advantageous for both overall health and specialized pathological diseases.[60]

Synthesis of nutritional diets encouraging certain health advantages is tied to the advent of the post-genomic age. These claims regarding health are aided by cutting-edge technologies like DNA chip technology that is implemented in incorporated form on a genomics framework in an effort to give the community an appropriate diet that is full of nutrients and varied.[5,61]

Implementation of advanced methods such as genomics, proteomics, and metabolomics for expanding agricultural output and healthy sources of nourishment in the marketplace will additionally assist in reducing without flavor compounds such phytic acid, acrylamide amino acid, and thereby enhance nutrition.[62–65]

## 9. Conclusion

The field of nutrigenomics offers a fresh perspective on nutrition, providing more insight on the ways in which food alters an organism's genetic code, the manner in which that alteration affects its phenotypic, and the means by which the organism reacts to it.Personalized nutritional counseling founded on nutrigenomics has also emerged as a result of advancements in the nutrition sciences, promotional activities, and communication. Utilizing information gathered from both present and prospective sources, statistics show that India is experiencing significant issues as the country's insufficient and over-nutrition progresses as its populations grow more advanced. Considering metro percentages twice as high than countryside costs, India has a few of the greatest incidences of CHD in the entire globe. Furthermore, wealthy individuals people in the countryside and those living in metropolitan areas are experiencing significant rises in the incidence of both obesity and diabetes. We have looked at nutrigenomics studies conducted in India in light of the rising frequency of diet-related ailments (such as obesity, diabetes, cardiovascular diseases, neural tube abnormalities, cancer etc.) in India.Through the use of methods such as microarrays,


**Figure 2:** Representation of nutrigenomics applications, including polymorphism detection, diet selection based on genetic profile, cell signatures, building neuroprotective dietary mechanisms, and gene classification impacting diet-related illnesses.[66]

genome research, and single nucleotide polymorphisms (SNPs) to enhance the consumption of nutrients and ultimately advance general health and wellness. In order to better understand how genetic variation affects diet and disease, nutrition and genetics are combined. This allows for the development of long-term objectives for enhancing health and eliminating ailment. Having deliberate preparation and focused actions, this expertise must be used and used in the years to come for a broader population. The field of science as a whole must work together to assure success, as this will enable us to build a solid database that is validated and supported by substantial evidence, which will be beneficial to clinicians and dieticians alike.

## 10. Source of Funding

None.

## 11. Conflict of Interest

None.

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