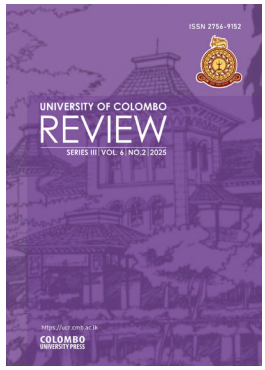

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Nutrigenomics: Linking diet, genes, and health for a personalized future

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ABSTRACT

'Nutrigenomics', which is defined as the study of how nutrients and bioactive food components influence gene expression and function, is an emerging discipline with profound implications for personalized nutrition and preventive healthcare. By integrating genomics, transcriptomics, metabolomics, and epigenomics; nutrigenomics offers insights into the molecular mechanisms by which diet modulates metabolic pathways, disease risk, and overall health outcomes. This review summarizes the current evidence on the role of nutrigenomics in the prevention and management of chronic diseases such as cardiovascular disease, type 2 diabetes, obesity, and certain cancers. Special emphasis is placed on bioactive dietary compounds—including polyphenols, omega-3 fatty acids, vitamins, and dietary fiber—that regulate gene activity and confer measurable health benefits. Challenges related to scientific reproducibility, ethical considerations, and the accessibility of genetic testing in low- and middle-income settings are discussed. Finally, the potential for integrating nutrigenomics into Sri Lanka's public health strategies is explored, especially focusing the high burden of diet-related non-communicable diseases. The review underscores the need for local research to align traditional dietary practices with genomic insights for improved health outcomes.

KEYWORDS:
Chronic disease prevention, Gene–diet interaction, Nutrigenomics, Nutrigenetics, Personalized nutrition, Sri Lanka

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Introduction

Nutrition and genetics are intrinsically interconnected, with dietary factors influencing gene expression, metabolic regulation, and disease susceptibility (Fenech et al., 2019). The field of 'nutrigenomics', distinct from 'nutrigenetics' focuses on how nutrients and bioactive compounds in food alter gene expression and cellular function. While nutrigenetics investigates how genetic variation influences dietary responses, nutrigenomics examines the reverse relationship: how diet shapes genomic expression and downstream biological effects (Corella & Ordovás, 2018).

The rise of high-throughput sequencing, microarrays, and multi-omics platforms has accelerated the growth of nutrigenomic research (Ferguson et al., 2016). By mapping the interplay between diet and gene expression, scientists have begun to identify dietary strategies tailored to individual genetic profiles; an approach that holds promise for 'precision nutrition' and the reduction of non-communicable diseases (NCDs).

Globally, NCDs such as cardiovascular disease, type 2 diabetes, obesity, and certain cancers are the leading causes of mortality, accounting for 74% of all deaths in 2019 (World Health Organization [WHO], 2022). In Sri Lanka, NCDs represent a significant and growing public health challenge, contributing to approximately 83% of all annual deaths (Ministry of Health, 2021). Dietary risk factors including excessive consumption of refined carbohydrates, low fruit and vegetable intake, and high sodium levels play a pivotal role in this trend (Katulanda et al., 2019).

Nutrigenomics offers a framework for mitigating these risks by aligning dietary recommendations with genetic profiles. For example, individuals with salt-sensitive hypertension may benefit from targeted sodium reduction strategies, while those carrying certain fat mass and obesity-associated (FTO) gene variants may respond more favorably to higher-protein diets for weight control (Qi et al., 2014). Moreover, bioactive compounds in traditional Sri Lankan foods such as turmeric, cinnamon, and coconut-based products present untapped potential for expressional modulation of genes and health promotion (Aggarwal & Harikumar, 2009; Ranasinghe et al., 2013; Lima et al., 2015).

The core objective of this review is to outline the scientific principles of this field, specifically gene–diet interactions and the mechanisms of epigenetic regulation by nutritional components. Furthermore, the review summarizes current evidence demonstrating nutrigenomics' efficacy in the prevention and management of chronic diseases. A key focus involves highlighting specific bioactive compounds that exhibit gene-modulatory potential. Finally, the discussion addresses the significant challenges and limitations to the practical application of nutrigenomics, particularly within low- and middle-income contexts, and explores its future integration into the healthcare and research landscape of Sri Lanka. Furthermore, by bridging molecular nutrition science and population health, nutrigenomics has the potential to transform

dietary guidelines from generalized recommendations into precision strategies that optimize individual health outcomes.

Scientific Foundations of Nutrigenomics

Nutrigenomics is an emerging interdisciplinary field that investigates how nutrients, dietary patterns, and other bioactive food components influence gene expression, thereby affecting metabolic pathways, physiological processes, and disease susceptibility or progression (Ferguson et al., 2016; Mutch et al., 2005). It bridges the gap between molecular nutrition and genomics, offering insights into how diet can modulate biological systems at the genetic level. By uncovering the mechanisms of diet–gene interactions, nutrigenomics aims to fuel the design of personalized nutrition plans that optimize health outcomes and reduce the risk of diet-related diseases.

At its core, nutrigenomics investigates how environmental exposures, in this case, dietary components, interact with the genome to influence transcriptomic, proteomic, and metabolomic profiles. These interactions may explain why individuals respond differently to identical dietary patterns and why certain populations are more vulnerable to specific nutrient-related diseases. This section explores four key scientific foundations: gene–diet interactions, the distinction between nutrigenomics and nutrigenetics, epigenetic regulation by diet, and integration with other omics sciences.

Gene–Diet Interactions

Gene–diet interactions describe the bidirectional relationship between dietary components and gene function. Specific nutrients and bioactive molecules can directly or indirectly regulate gene expression by different means. Certain lipophilic nutrients, such as fatty acids and fat-soluble vitamins, act as ligands for nuclear receptors such as transcription factors that control gene transcription. Moreover, nutrients can influence the phosphorylation, acetylation, or stability of transcription factors, thereby altering gene transcription rates. In addition, some nutrients such as glucose and amino acids can influence nutrient-sensing intracellular signaling pathways like mTOR committed to regulate cell growth and metabolism.

Polyunsaturated fatty acids (PUFAs), especially omega-3 fatty acids from fish oil, regulate lipid metabolism by activating peroxisome proliferator-activated receptors (PPARs). This affects genes involved in fatty acid oxidation, lipogenesis, and triglyceride storage, with implications for cardiovascular health (Jump et al., 2013). Similarly, Sodium intake influences the renin–angiotensin–aldosterone system (RAAS). Individuals with certain angiotensin-converting enzyme (ACE) gene polymorphisms exhibit pronounced blood pressure responses to sodium, a phenomenon known as salt sensitivity (Poch et al., 2001).

In Sri Lanka, salt intake exceeds the WHO-recommended limit of 5 g/day (Jayatissa et al., 2021). Thus, understanding gene–diet interactions could enable targeted interventions for hypertension. For instance, genetic screening for salt-sensitive alleles could help to identify individuals at high risk of hypertension, guiding personalized sodium-reduction strategies. Similarly, populations with high prevalence of dyslipidemia could benefit from dietary omega-3 interventions tailored to PPAR gene expression profiles. In addition to the above examples, numerous gene–diet interactions have been well documented in the literature. For instance, Vitamin D status influences immune function in our body. However, its effect varies depending on polymorphisms in the vitamin D receptor (VDR) gene (Uitterlinden et al., 2004). The dietary dairy recommendations can be tailored based on the lactase activity of patients with lactose intolerance, based on the variants of the genes that regulate the lactase enzyme activity (Enattah et al., 2002).

Nutrigenomics vs. Nutrigenetics

Although the terms Nutrigenomics and Nutrigenetics are often used interchangeably in popular literature, they represent distinct but complementary fields. Nutrigenetics examines how genetic variation affects an individual's response to nutrients. For instance, individuals with the MTHFR C677T polymorphism have reduced enzyme activity in folate metabolism, resulting in elevated homocysteine levels and increased cardiovascular risk. Such individuals may require higher folate intake to achieve normal biochemical function (Li et al., 2016).

Nutrigenomics focuses on the reverse: how dietary factors influence gene expression and function. An example is the effect of sulforaphane from cruciferous vegetables on upregulating detoxification genes in the *Glutathione S transferase* (GST) family (Clarke et al., 2008a). Sulforaphane, a phytochemical in cruciferous vegetables such as broccoli, induces phase II detoxification enzymes by activating nuclear factor erythroid 2–related factor 2 (Nrf2) pathways. This enhances the expression of glutathione S-transferase (GST) genes, improving cellular defense against oxidative stress.

Understanding both perspectives is essential for implementing personalized nutrition strategies that are genetically informed yet adaptable to changing dietary exposures. This dual approach allows for dietary strategies that account for fixed genetic traits while also leveraging dietary modulation to influence gene expression in real time.

Epigenetic Regulation by Diet

Epigenetics refers to heritable changes in gene expression that do not involve alterations in the DNA sequence. Dietary factors can profoundly influence epigenetic modifications, including DNA methylation, Histone modification and

microRNA (miRNA) modulation. In DNA methylation, methyl groups are added to cytosine residues, leading to silencing the gene expression. nutrients such as folate, vitamin B12, and choline donate methyl groups for the methylation of cytosine residues, influencing gene silencing or activation (Anderson et al., 2012). In histone modification, chemical alterations such as acetylation or methylation of histone proteins influence chromatin structure and gene accessibility. For example, Butyrate, a short-chain fatty acid produced by gut microbial fermentation of dietary fiber, inhibits histone deacetylases (HDACs), leading to relaxed chromatin structure and increased transcription (Davie, 2003). Plant polyphenols like curcumin and epigallocatechin gallate (EGCG) can alter miRNA profiles, affecting pathways related to inflammation, apoptosis, and carcinogenesis (Milenkovic et al., 2021).

In Sri Lanka, maternal undernutrition and micronutrient deficiencies are prevalent in some regions, raising concerns about epigenetic programming of chronic disease risk in offspring. For instance, inadequate maternal folate intake during pregnancy could lead to persistent DNA methylation changes in genes regulating metabolism and neurodevelopment (Atukorala et al., 2020a). Interventions ensuring adequate micronutrient intake before and during pregnancy could have long-lasting transgenerational benefits.

Integration with Other Omics

Nutrigenomics rarely functions in isolation. Integrating other omics disciplines including transcriptomics, proteomics, metabolomics, and microbiomics, enhances its predictive and explanatory power (Afman & Müller, 2012). In combination with transcriptomics, nutrigenomics approaches can measure global mRNA expression changes in response to dietary interventions (van Ommen et al., 2008). On the other hand, coupling with proteomics, it can evaluate alterations in protein abundance and function caused by nutrient–gene interactions (Hernandez et al., 2012). Nutrigenomic approaches can profile metabolites, while providing a snapshot of metabolic health and revealing biomarkers of dietary intake, hand in hand with metabolomics approaches (Guiraud et al., 2017). With the integration of microbiomics, nutrigenomics approaches are used to characterize gut microbial composition and functional capacity, which can modulate nutrient metabolism and influence host gene expression (Zhernakova et al., 2016).

Traditional Sri Lankan diets are rich in rice, lentils, coconut-based curries, and diverse spices such as turmeric and cinnamon, all of which contain bioactive compounds with potential gene-modulating effects (Aggarwal & Harikumar, 2009; Nevin & Rajamohan, 2010; Ranasinghe et al., 2013; Lima et al., 2015). Integrating nutrigenomics with metabolomics could help identify unique biomarkers of such dietary patterns and link them to chronic disease risk reduction (Guiraud et al., 2017). Furthermore, microbiome analyses could uncover how local plant-based

diets influence gut microbial diversity and, in turn, modulate host epigenetics and metabolism.

The complex interplay between diet, genes, and environment is summarized schematically in Figure 1, which illustrates the key molecular mechanisms by which nutritional compounds modulate gene expression.

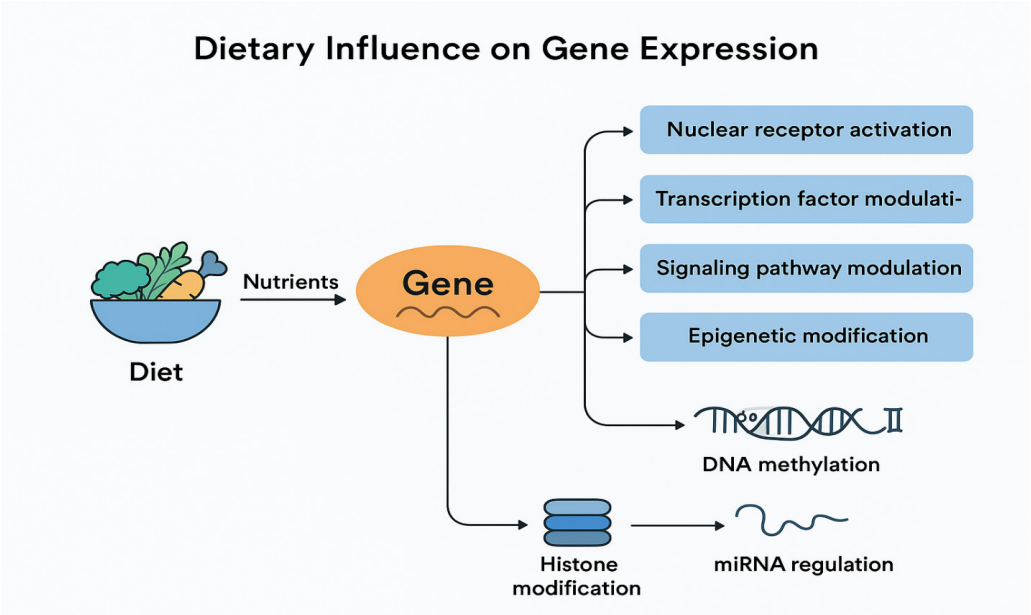

Figure 1: Key Mechanisms of Nutrigenomic Modulation of Gene Expression

Gut Microbiome and Nutrigenomics

The gut microbiome plays a pivotal role as a mediator between dietary components, host genetics, and health outcomes (Zmora, Suez, & Elinav, 2019). It consists of trillions of microorganisms, including bacteria, archaea, fungi, and viruses, residing primarily in the colon. These microbes contribute to numerous physiological processes such as digestion, nutrient absorption, immune modulation, and the maintenance of intestinal barrier integrity (Thursby & Juge, 2017). Recent advances in nutrigenomics reveal that the microbiome is not merely a passive bystander but an active regulator of gene expression, metabolic pathways, and epigenetic modifications in the host (Valdes et al., 2018).

Microbial Metabolites as Epigenetic Modulators

The gut microbiota metabolizes dietary components into bioactive metabolites that can influence host gene expression. Among these, short-chain fatty acids (SCFAs), notably butyrate, propionate, and acetate, are key players. SCFAs

act as histone deacetylase (HDAC) inhibitors, promoting histone acetylation and enhancing chromatin accessibility, thereby upregulating the transcription of genes involved in anti-inflammatory and metabolic homeostasis (Ríos-Covián et al., 2016; Davie, 2003). Butyrate also functions as an energy source for colonocytes, supporting gut barrier integrity and reducing systemic inflammation.

Beyond SCFAs, the microbiome produces metabolites such as secondary bile acids, indole derivatives, and trimethylamine-N-oxide (TMAO), which interact with nuclear receptors like FXR and PXR, influencing lipid and glucose metabolism. These interactions exemplify how the microbiome can act as an epigenetic and transcriptional modulator, linking diet to gene expression patterns.

Diet–Microbiome Interactions in Nutrigenomics

Diet is the primary determinant of gut microbiome composition and functionality. High-fiber, plant-based diets favor the growth of saccharolytic bacteria such as *Bifidobacterium* and *Lactobacillus*, enhancing SCFA production. In contrast, westernized dietary patterns characterized by high fat, refined carbohydrates, and low fiber lead to dysbiosis, reduced SCFA levels, and increased endotoxin-producing bacteria. This imbalance promotes metabolic inflammation, a recognized precursor of obesity, type 2 diabetes, and cardiovascular diseases (Deehan & Walter, 2016).

Nutrigenomic evidence suggests that these microbial shifts influence host gene expression related to lipid metabolism, glucose regulation, and immune responses. For example, SCFAs regulate G-protein-coupled receptor (GPCR) signaling pathways, which impact energy homeostasis and inflammatory gene networks (Kasubuchi et al., 2015).

Gene–Diet–Microbiome Interactions

The microbiome's role extends beyond metabolic signaling to host–microbe genetic interactions. Specific host genetic polymorphisms can shape microbial diversity and functionality, which in turn determines how nutrients are metabolized. For instance, variations in genes involved in bile acid metabolism affect microbial bile salt hydrolase activity, altering lipid digestion and cholesterol homeostasis (Sonnenburg & Bäckhed, 2016). This bidirectional interaction highlights the complexity of nutrigenomic responses and supports the need for personalized nutrition strategies based on microbiome profiling.

Sri Lankan Context

Sri Lanka presents a unique dietary landscape, where traditional eating patterns coexist with rapid nutritional transitions. Historically, Sri Lankan diets rich in rice, lentils, leafy greens, and fermented foods (e.g., curd, pittu) have supported a diverse gut microbiome beneficial for metabolic health. These foods

provide prebiotics (non-digestible fibers) that stimulate SCFA production. However, increasing urbanization and Western dietary habits, high in processed foods, fats, and added sugar pose a risk of microbiome dysbiosis, which may exacerbate the already rising prevalence of obesity, diabetes, and cardiovascular diseases in the country (Jayawardena et al., 2021).

Furthermore, cultural practices such as the use of probiotics through fermented dairy (e.g., curd) and plant-based diets offer opportunities for microbiome-targeted interventions. Future nutrigenomic studies in Sri Lanka should incorporate microbiome sequencing, dietary assessments, and host-genome analyses to establish population-specific recommendations. Evidence shows that gut microbiota composition influences dietary responses, microbial metabolism affects energy balance and metabolic risk, and diet-induced microbiome shifts can modulate gene expression via epigenetic mechanisms (Zmora, Suez, & Elinav, 2019; Thursby & Juge, 2017). Integrating these layers allows for precision nutrition strategies tailored to Sri Lankan populations, which are currently underrepresented in multi-omics research.

Therapeutic and Research Implications

Understanding gut microbiome–nutrigenomic interactions opens new avenues for precision nutrition and disease prevention, encompassing different strategies such as prebiotic and probiotic supplementation to restore microbial balance, promotion of taking functional foods enriched with bioactive compounds (e.g., polyphenols, resistant starch) to modulate gene expression via microbial metabolites, and introducing microbiome-driven personalized diets tailored to individual genetic and microbial profiles. Emerging technologies such as metagenomics, metabolomics, and transcriptomics will be essential to map these interactions comprehensively. Such approaches can inform targeted interventions for NCD prevention in Sri Lanka and globally.

In summary, the intricate relationship between the gut microbiome, dietary components, and host genetics, including the influence of SCFAs and bile acids, is detailed in Table 1, with a specific focus on dietary examples relevant to the Sri Lankan context.

Table 1: Summary of Gut Microbiome–Diet–Gene Interaction Mechanisms and Examples

Mechanism	Microbial Metabolite / Factor	Effect on Host Gene Expression	Dietary Influence	Sri Lankan Context
SCFA production (e.g., butyrate)	Butyrate, acetate, propionate	Inhibits HDAC → ↑ histone acetylation → ↑ anti-inflammatory genes	High-fiber foods (whole grains, legumes, vegetables)	Traditional rice, lentils, leafy greens, jackfruit
Bile acid metabolism	Secondary bile acids	Modulates nuclear receptors (FXR, PXR) → lipid/glucose metabolism	High-fat diets increase bile acid production	Increased Western-style diets in urban Sri Lanka
Tryptophan metabolism	Indole derivatives	Activates AhR receptor → immune gene regulation	Protein intake from meat, legumes	Fish curry and pulses as protein sources
Trimethylamine-N-oxide (TMAO)	TMAO from choline metabolism	Associated with ↑ inflammation, ↑ cardiovascular risk	High-choline diets (red meat, eggs)	Urban diets with increased processed meat consumption
Microbial regulation of miRNAs	Modulation via microbial metabolites	Influences post-transcriptional gene silencing	Polyphenol-rich foods (turmeric, green tea)	Turmeric (curcumin) and Ceylon tea widely consumed
Dysbiosis effects	LPS (lipopoly-saccharides)	↑ NF-κB signaling → ↑ pro-inflammatory gene expression	High-fat, low-fiber diets	Shift toward processed fast foods in urban areas

Nutrigenomics in Disease Prevention and Management

Nutrigenomics represents a frontier in precision nutrition, offering the ability to understand how dietary components interact with individual genetic profiles to influence health outcomes. Unlike conventional dietary recommendations, which adopt a one-size-fits-all approach, nutrigenomics integrates genomic information to identify how specific nutrients can modulate gene expression, metabolic pathways, and signaling networks. This approach has significant potential for preventing and

managing chronic non-communicable diseases (NCDs), which represent the leading causes of morbidity and mortality worldwide and pose a growing public health challenge in Sri Lanka. NCDs such as obesity, type 2 diabetes mellitus (T2DM), cardiovascular disease (CVD), and certain cancers are multifactorial in nature, influenced by complex interactions between genetic susceptibility and lifestyle factors, particularly diet. By elucidating these gene–diet interactions, nutrigenomics provides opportunities for personalized nutritional interventions that could improve disease prevention and therapeutic outcomes.

This section explores key chronic diseases in the context of nutrigenomics, highlighting evidence-based gene–diet interactions, mechanisms by which dietary components influence gene expression, and implications for population health in Sri Lanka. Special emphasis is placed on culturally relevant dietary patterns, local food bioactives, and the challenges of urbanization and dietary transition.

Obesity

Obesity is a complex metabolic disorder arising from the interplay of genetic, epigenetic, and environmental factors. It is characterized by excessive accumulation of adipose tissue, which increases the risk of T2DM, CVD, and certain cancers. Among genetic contributors, the FTO (fat mass and obesity-associated) gene is one of the most extensively studied loci associated with obesity susceptibility (Loos & Yeo, 2022). Variants in FTO, particularly the rs9939609 polymorphism, are linked to increased caloric intake, reduced satiety, and higher body mass index (BMI) (Qi & Cho, 2008). Similarly, polymorphisms in MC4R (melanocortin 4 receptor) and LEPR (leptin receptor) genes influence appetite regulation and energy homeostasis, further modulating obesity risk.

Nutrigenomic studies demonstrate that dietary interventions tailored to genetic profiles can improve weight management outcomes. For example, individuals carrying FTO risk alleles show enhanced weight loss when adhering to high-protein diets or reduced-fat regimens compared to standard dietary advice (Qi & Cho, 2008). These findings suggest that personalized nutrition strategies based on genotype can optimize obesity prevention and therapeutic approaches.

In Sri Lanka, the prevalence of overweight and obesity has risen sharply over the past two decades, with an estimated 25% of adults affected (Katulanda et al., 2019). This increase coincides with a nutrition transition characterized by higher consumption of energy-dense, nutrient-poor foods, increased intake of sugar-sweetened beverages, and a decline in traditional plant-based diets. Urbanization and sedentary lifestyles exacerbate this trend, particularly among middle- and upper-income groups. Nutrigenomic approaches could be particularly valuable in Sri Lanka, where culturally tailored dietary interventions incorporating local foods and spices may enhance adherence and effectiveness. For example, incorporating

protein-rich legumes and traditional cereals in personalized meal plans could mitigate the obesogenic effects of urban diets. Moreover, early identification of genetically susceptible individuals could facilitate targeted lifestyle counseling, reducing the long-term burden of obesity-related complications.

Type 2 Diabetes Mellitus (T2DM)

T2DM is a chronic metabolic disorder characterized by impaired insulin secretion, insulin resistance, and hyperglycemia. It represents a major public health concern in Sri Lanka, where prevalence has increased in parallel with rising obesity rates, urbanization, and lifestyle changes. Genetic polymorphisms significantly influence T2DM risk, disease progression, and response to dietary interventions. One of the most prominent susceptibility genes is TCF7L2 (transcription factor 7-like 2), which regulates insulin secretion and glucose metabolism. Individuals carrying risk alleles exhibit altered beta-cell function and higher sensitivity to dietary carbohydrates, making them more prone to hyperglycemia when consuming high-glycemic diets (Grant et al., 2006; Cornelis & Hu, 2012).

Nutrigenomic evidence suggests that dietary modification tailored to genotype can enhance glycemic control. For instance, carriers of TCF7L2 risk alleles benefit from diets emphasizing low-glycemic index (GI) carbohydrates, high fiber intake, and moderate protein, which improve postprandial glucose levels and insulin sensitivity. Moreover, bioactive compounds present in traditional Sri Lankan foods, such as cinnamon (Cinnamomum verum), have been shown to exert glucose-lowering effects through modulation of insulin signaling pathways, potentially influencing the expression of genes like GLUT4, IRS1, and PPARγ (Ranasinghe et al., 2013). Similarly, polyphenols from local fruits and spices may enhance beta-cell function and reduce systemic inflammation, further supporting T2DM management.

From a public health perspective, nutrigenomic-informed dietary interventions offer a culturally relevant approach to diabetes prevention. In Sri Lanka, where rice is a staple food, optimizing portion sizes, combining with protein-rich lentils, and incorporating low-GI vegetables can reduce postprandial glucose excursions, particularly in genetically susceptible individuals. Additionally, identifying at-risk populations through genotyping could guide early lifestyle interventions, thereby preventing or delaying disease onset.

Cardiovascular diseases (CVDs)

CVDs encompass a range of disorders affecting the heart and blood vessels, including coronary artery disease, hypertension, stroke, and heart failure. It remains the leading cause of mortality globally and in Sri Lanka. The pathogenesis of CVD is influenced by both genetic and environmental factors, particularly dietary intake. Genetic variants affecting lipid metabolism, such as APOE, PCSK9, and LPL,

modulate serum lipid profiles and cardiovascular risk. For example, individuals carrying the APOE ε4 allele exhibit elevated LDL cholesterol levels and higher susceptibility to atherosclerosis, especially in the context of high saturated fat intake (Ordovás & Corella, 2004). Similarly, polymorphisms in genes regulating blood pressure, including ACE and AGT, interact with dietary sodium to influence hypertension risk.

Nutrigenomic research demonstrates that dietary fatty acids and bioactive nutrients can modulate gene expression related to inflammation, lipid metabolism, and vascular function. Omega-3 polyunsaturated fatty acids (PUFAs), primarily EPA and DHA, activate peroxisome proliferator-activated receptors (PPARs) and other transcription factors to reduce systemic inflammation, improve endothelial function, and lower triglyceride levels (Kwak et al., 2018). Dietary fiber from whole grains, fruits, and vegetables similarly exerts cardioprotective effects through modulation of cholesterol metabolism and gut microbiome-mediated production of short-chain fatty acids, which influence gene expression in vascular and hepatic tissues.

Sri Lankan diets traditionally include fish rich in omega-3 PUFAs, particularly in coastal regions. However, urbanization and Western dietary influences have led to increased consumption of processed foods, refined carbohydrates, and saturated fats, contributing to rising CVD prevalence (Jayawardena et al., 2017). Nutrigenomic-informed interventions could promote the retention of protective dietary patterns while personalizing advice based on genetic susceptibility. For instance, individuals with APOE ε4 genotype may particularly benefit from diets low in saturated fats and enriched with omega-3 fatty acids, while those with salt-sensitive hypertension could adopt sodium-restricted meal plans tailored to local culinary practices.

Cancer

Cancer development involves a multistep process of genetic mutations, epigenetic alterations, and dysregulated cellular signaling. Diet plays a critical role in modulating these processes, both by influencing DNA damage and repair mechanisms and through epigenetic regulation of oncogenes and tumor suppressor genes. Specific dietary bioactive compounds, such as sulforaphane from cruciferous vegetables and curcumin from turmeric, have demonstrated chemo-preventive properties by activating detoxification enzymes (e.g., GST family genes), reducing oxidative DNA damage, and modulating inflammatory pathways like NF-κB (Clarke et al., 2008b; Prasad et al., 2014).

In Sri Lanka, oral, esophageal, and gastrointestinal cancers are prevalent, with strong associations with tobacco and betel quid use (Amarasinghe et al., 2010; Jayarajah, U et al., 2023; Talagala, I. A., 2018). Nevertheless, dietary factors also contribute significantly to cancer risk. High intake of fruits, vegetables, and spices rich in bioactive compounds is associated with reduced oxidative stress, improved DNA

repair, and modulation of apoptosis-related genes, providing a rationale for cancer-preventive nutritional strategies. Integrating nutrigenomics into cancer prevention may involve identifying individuals with genetic predispositions to certain cancers (e.g., BRCA1/2, TP53 variants) and advising diets rich in bioactive compounds that target relevant signaling pathways.

Promoting the use of locally available bioactive-rich foods such as turmeric, curry leaves, green leafy vegetables, and tropical fruits can harness nutrigenomic potential in cancer prevention. Additionally, understanding gene–diet interactions can guide public health recommendations, emphasizing personalized approaches alongside conventional cancer prevention strategies, such as tobacco cessation and vaccination programs.

Bioactive Nutrients with Gene-Modulatory Potential

Bioactive food components play a central role in mediating the health-promoting effects of diet through gene regulation. These compounds act on multiple molecular targets, influencing transcription factors, epigenetic modifications, and intracellular signaling pathways, ultimately affecting metabolism, inflammation, and cell proliferation.

Polyphenols

Polyphenols are a diverse group of phytochemicals abundantly found in fruits, vegetables, teas, and spices. They exert antioxidant, anti-inflammatory, and epigenetic effects, influencing gene expression and cellular function. For example, curcumin, widely used in Sri Lankan cuisine, modulates signaling pathways including NF-κB, STAT3, and AP-1, reducing inflammation, inhibiting cancer cell proliferation, and enhancing apoptosis (Prasad et al., 2014). Similarly, EGCG from green tea regulates DNA methylation and histone acetylation, affecting genes involved in oxidative stress, apoptosis, and cell cycle control (Khan & Mukhtar, 2018).

Polyphenols also influence metabolic health by regulating genes involved in lipid metabolism, insulin sensitivity, and adipogenesis. For instance, flavonoids can upregulate PPARγ and adiponectin, promoting improved glucose homeostasis and reduced adiposity (Yang et al., 2017). These effects are particularly relevant in Sri Lanka, where traditional diets and spice usage offer a rich source of polyphenols that can be leveraged in nutrigenomic-informed dietary strategies (Ranasinghe et al., 2013).

Omega-3 Fatty Acids

Long-chain omega-3 fatty acids, notably EPA and DHA, exert profound effects on gene transcription by activating nuclear receptors such as PPARs and retinoid

X receptor (RXR). These receptors regulate genes controlling lipid metabolism, inflammation, and glucose homeostasis, providing protective effects against CVD and metabolic disorders (Calder, 2020). Additionally, omega-3 PUFAs influence epigenetic modifications, including histone acetylation and DNA methylation, further modulating gene expression.

In Sri Lanka, coastal populations traditionally consume diets rich in omega-3 fatty acids through fish intake (Wijesundera et al., 2016). However, shifts toward urban dietary patterns have reduced omega-3 consumption, increasing susceptibility to CVD and metabolic syndrome (Wijeratne et al., 2019). Nutrigenomic-guided interventions could reinforce fish consumption, promote omega-3 supplementation, and provide personalized recommendations for individuals with genetic risk factors affecting lipid metabolism and cardiovascular health (Rasmussen et al., 2018).

Vitamins and Minerals

Micronutrients, including vitamins and trace minerals, serve as cofactors in enzymatic processes that regulate gene expression and epigenetic modifications. Vitamin D, through the vitamin D receptor (VDR), regulates genes involved in immune function, inflammation, and cell proliferation (Hossein-nezhad & Holick, 2013). Deficiencies in vitamin D and other micronutrients, such as zinc and selenium, are linked to impaired DNA repair, oxidative stress, and increased disease risk (Atukorala et al., 2020b).

In Sri Lanka, micronutrient deficiencies remain a concern, particularly among populations with limited dietary diversity, malabsorption issues, or reliance on polished rice and refined foods. Nutrigenomic approaches can identify individuals at risk and guide dietary or supplemental interventions to restore optimal micronutrient status, thereby supporting gene regulation and reducing disease susceptibility.

Dietary Fiber

Dietary fiber contributes to health primarily through interactions with the gut microbiota, producing short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate. SCFAs function as histone deacetylase (HDAC) inhibitors and ligands for G-protein coupled receptors (GPCRs), modulating gene expression related to inflammation, energy metabolism, and immune regulation (Dalile et al., 2019).

Traditional Sri Lankan diets, rich in plant-based foods, legumes, and whole grains, support gut -microbial diversity and SCFA production, promoting cardiometabolic and gastrointestinal health (Deehan & Walter, 2016; Lou et al, 2014). Nutrigenomic insights highlight how dietary fiber can epigenetically influence gene expression, enhancing disease prevention and health maintenance at both individual and population levels. Personalized fiber interventions, tailored to

genetic and microbial profiles, may optimize SCFA production and confer maximum health benefits.

Collectively, nutrigenomics provides a framework for understanding the intricate interplay between diet, genetics, and chronic disease. By integrating genomic information with dietary patterns, bioactive nutrient profiles, and culturally relevant food practices, it is possible to develop personalized nutrition strategies that optimize disease prevention and management. In Sri Lanka, where nutrition transition, rising NCD prevalence, and traditional dietary practices coexist, nutrigenomics holds promise for shaping population health policies, designing individualized interventions, and ultimately improving long-term health outcomes. Future research should focus on expanding genetic studies in Sri Lankan populations, characterizing gene–diet interactions specific to local foods, and translating these findings into actionable public health and clinical strategies.

Each class of bioactive nutrient from polyphenols to dietary fiber collectively exerts its benefits by targeting specific molecular pathways. The full spectrum of these compounds, their genetic targets, and resulting health implications are consolidated in Table 2.

Table 2: Summary of Bioactive nutrients, their molecular targets, gene-modulatory effects and health implications

Bioactive Nutrient	Sources	Molecular/Genetic Targets	Gene-Modulatory Effects	Health Implications
Polyphenols	Fruits, vegetables, teas, spices (e.g., curcumin in turmeric, EGCG in green tea)	NF-κB, STAT3, AP-1; DNA methylation; histone acetylation; PPARγ; adiponectin	Anti-inflammatory, antioxidant, epigenetic modulation; regulate lipid metabolism, insulin sensitivity, adipogenesis	Reduces inflammation, cancer cell proliferation, oxidative stress; improves metabolic health
Omega-3 Fatty Acids (EPA, DHA)	Fatty fish, seafood	PPARs, RXR; histone acetylation; DNA methylation	Modulate genes controlling lipid metabolism, inflammation, glucose homeostasis	Protective against cardiovascular disease (CVD) and metabolic syndrome

Vitamins and Minerals	Vitamin D (sunlight, fortified foods), zinc (nuts, seeds), selenium (seafood, grains)	Vitamin D receptor (VDR); cofactor for epigenetic enzymes	Regulate immune function, inflammation, cell proliferation; DNA repair	Deficiency linked to oxidative stress, impaired DNA repair, increased disease risk
Dietary Fiber	Whole grains, legumes, fruits, vegetables	Gut microbiota → SCFAs (acetate, propionate, butyrate); HDAC inhibition; GPCR signaling	Epigenetic modulation of genes regulating inflammation, energy metabolism, immune response	Supports gut health, cardiometabolic and gastrointestinal function

Challenges and Future Perspectives

Nutrigenomics offers unprecedented opportunities for personalized nutrition and chronic disease prevention by elucidating the complex interactions between genes and dietary components. However, several challenges must be overcome before its full potential can be realized, particularly in the Sri Lankan context where genomic research is still in its nascent stages and local dietary patterns are diverse and culturally specific.

Challenges

One of the foremost challenges in nutrigenomics is the inherent complexity of gene–diet interactions. The human genome contains thousands of genes, many of which interact with one another in ways that are influenced by epigenetic modifications, environmental exposures, and lifestyle factors. This complexity makes it difficult to disentangle specific gene–nutrient relationships that can be translated into actionable dietary recommendations (Corella & Ordovás, 2014). For example, polymorphisms in genes involved in lipid metabolism may influence individual responses to dietary fats, but these effects are often modified by other genetic variants, age, gender, and overall dietary context, which complicates the formulation of precise nutritional advice.

A second critical challenge is the limited availability of genetic and nutritional data specific to Sri Lankan populations. Most nutrigenomic research to date has been conducted in Western populations, which differ significantly in genetic background, dietary habits, and environmental exposures compared to South Asian populations. Consequently, applying findings from these studies to Sri Lanka may be misleading or ineffective. Local research is urgently needed to map the unique

genetic variants prevalent in Sri Lankan ethnic groups and understand how these interact with traditional diets, which are rich in spices, legumes, coconut-based foods, and bioactive compounds (Rajapakse et al., 2019). Without this population-specific evidence, nutrigenomics-guided dietary interventions risk being poorly tailored and less effective.

Ethical and privacy concerns also pose significant barriers to the implementation of nutrigenomics. The collection, storage, and use of genetic information raise issues regarding informed consent, confidentiality, and the potential for genetic discrimination in employment, insurance, and social contexts. Addressing these concerns requires the establishment of robust legal frameworks, transparent data governance policies, and active public engagement to build trust and ensure ethical use of genetic data (Kaye et al., 2015). Without such safeguards, public skepticism may hinder participation in nutrigenomic research and adoption of personalized nutrition recommendations.

Economic and infrastructural barriers further limit the integration of nutrigenomics into public health and clinical practice in Sri Lanka. Nutrigenomics research and application necessitate sophisticated laboratory infrastructure, advanced genomic sequencing platforms, bioinformatics tools, and skilled personnel. Currently, such resources are limited, particularly outside major urban centers, constraining the ability to conduct large-scale studies and implement personalized nutrition programs nationwide (Perera et al., 2020). The high cost of genetic testing and dietary counseling also poses a challenge, particularly for low- and middle-income populations, raising concerns about equitable access to the benefits of nutrigenomics.

Finally, public awareness and acceptance of nutrigenomics are currently low. Healthcare professionals, nutritionists, and the general public may have limited understanding of the scientific principles and practical implications of gene–diet interactions. This knowledge gap can reduce adherence to nutrigenomics-informed dietary advice and limit the perceived relevance of personalized nutrition interventions (Horne et al., 2018). Educational campaigns and training programs are therefore essential to ensure that both providers and recipients of nutrigenomic services are informed and engaged.

Future Perspectives

Despite these challenges, the future of nutrigenomics in Sri Lanka is promising, particularly if research, infrastructure, and policy initiatives are strategically aligned. Integrative “omics” approaches, which combine genomics with epigenomics, transcriptomics, metabolomics, and microbiomics, can provide a holistic understanding of how dietary components interact with genetic and metabolic pathways to influence health outcomes. Such approaches have the potential to identify novel biomarkers for disease risk and to tailor dietary interventions with

greater precision than traditional methods (Pinu et al., 2019).

Expanding population-specific research is another critical priority. Conducting large-scale nutrigenomic studies within Sri Lanka will generate data that reflect local genetic diversity, dietary patterns, and environmental exposures. This will enable the development of evidence-based dietary guidelines that are culturally relevant and genetically informed, improving the effectiveness of personalized nutrition strategies (Jayasinghe et al., 2022). By focusing on Sri Lankan ethnic groups and their unique dietary practices, researchers can identify gene–nutrient interactions that may be overlooked in studies conducted in Western populations.

Capacity building is essential to support these research initiatives and facilitate the translation of findings into practice. Investments in laboratory infrastructure, bioinformatics capabilities, and training of multidisciplinary teams, including nutritionists, geneticists, and public health professionals are critical to advancing nutrigenomics research and its clinical application. Additionally, fostering interdisciplinary collaboration will ensure that research findings are effectively translated into practical dietary interventions and public health policies.

Policy development will also play a central role in the responsible application of nutrigenomics. Establishing ethical guidelines for the collection, storage, and use of genetic information is crucial to protecting privacy and preventing discrimination. Integrating nutrigenomics into public health strategies requires clear frameworks that ensure equitable access, informed consent, and regulatory oversight, thereby promoting trust and social acceptance.

Finally, technology and digital health solutions offer significant opportunities to scale nutrigenomics interventions. Mobile health applications, wearable devices, and artificial intelligence-driven dietary assessment tools can facilitate the delivery of personalized nutrition advice based on individual genetic and lifestyle data. These innovations have the potential to overcome geographical and economic barriers, making nutrigenomics-guided interventions more accessible to a broader population (Khurana et al., 2020). By leveraging technology, Sri Lanka can bridge gaps in healthcare delivery while promoting preventive health through precision nutrition.

Conclusion and Recommendations

Nutrigenomics represents a transformative frontier in nutrition science, providing insights into how individual genetic variation interacts with dietary components to influence health outcomes. Personalized nutrition approaches have considerable potential for preventing and managing chronic diseases prevalent in Sri Lanka, including obesity, type 2 diabetes, cardiovascular diseases, and cancer. By integrating traditional Sri Lankan dietary patterns, which are naturally rich in bioactive compounds, with modern genomic insights, health interventions can be tailored to individual genetic profiles, maximizing health benefits and disease

prevention.

However, realizing the full potential of nutrigenomics requires overcoming significant challenges, including limited local genomic data, ethical and privacy concerns, infrastructural constraints, and low public awareness. Addressing these challenges necessitates a multi-pronged approach encompassing research, policy, capacity building, and technology adoption. Large-scale, population-specific studies, interdisciplinary collaboration, and investments in infrastructure and training are essential to generate actionable insights and facilitate the translation of research into practice.

Recommendations for advancing nutrigenomics in Sri Lanka include expanding local research to investigate gene–diet interactions across diverse ethnic groups, fostering collaboration between nutritionists, geneticists, bioinformaticians, and public health experts, and developing robust infrastructure and trained personnel. Establishing ethical guidelines and policy frameworks will safeguard privacy and promote equitable access, while public education initiatives will increase awareness and acceptance of personalized nutrition strategies. Leveraging digital health technologies and artificial intelligence can further support the scalable implementation of nutrigenomics interventions.

By prioritizing these actions, Sri Lanka can harness the potential of nutrigenomics to improve health outcomes, reduce the burden of chronic diseases, and move towards precision nutrition tailored to its unique genetic and cultural landscape. This integrative approach represents a critical step toward a future in which dietary recommendations are not only evidence-based but also individualized, culturally relevant, and sustainable.

Declaration of conflict of interest

The author has no conflict of interest to declare.

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