

Sports Nutrigenomic

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Introduction

Every human has a unique genetic the template for nutrition. The study of gene-nutrient relationships, or nutrigenomics, can result in the creation of individualized dietary guidelines for preserving good health and warding off disease. The bioavailability of nutrients and their metabolism may be impacted by the genetic diversity among different ethnic groups. As a result, testing for particular genetic polymorphisms may prove to be beneficial in managing weight loss and fully understanding the relationships between genes and nutrients. Genes control the intake and metabolism of various nutrients, and nutrients can influence the expression of multiple genes in a positive or negative way (Kiani et al., 2022). By customizing nutritional advice to a person's genetic profile, personalized nutrition for athletes and fitness fans seeks to optimize nutrition status, body composition, and exercise performance. The genetic makeup has been shown to impact food biological agents and nutrient uptake, absorbtion, excretion, which can change the activity of metabolism. Utilizing genomic data and DNA testing methods, nutrigenomics and nutrigenetics are experimental methodologies that investigate how individual genetic variations affect an athlete's reaction to nutrients or other chemicals found in food and nutritional supplements. Nonetheless, an increasing quantity of study is establishing a connection between gene-diet relationships and nutrient intake and health biomarkers (Guest et al., 2019).

Aim of The Study

The aim of this study is to examine the relationship between food-gene-sports and to summarize the current literature on the subject.

Material and Methods

To obtain the data for this study, Google Scholar, Pubmed and Sportdiscus databases were searched for the last 10 years with the keyword "Sports Nutrigenomic". The data obtained were evaluated and summarized.

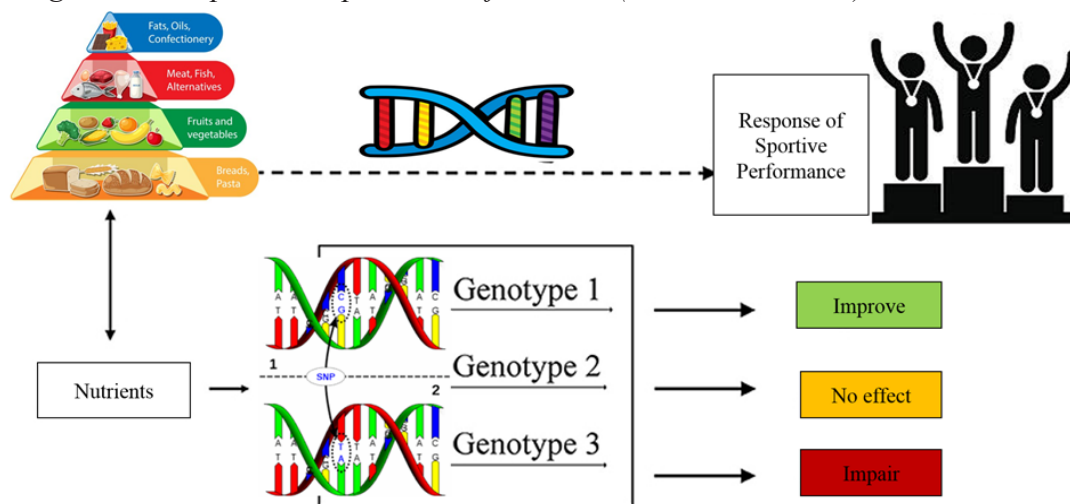
Nutrigenomic

In the developing field of nutrigenomics, the impacts of dietary nutrients on the DNA and gene activity, as well as the impact of genetic variants on the consumption of nutrients, are investigated using cutting-edge genomics techniques. The relationship between nutrients and genes is referred to as nutrigenomics. Thus, biochemistry, transcriptomics nutrition, metabolomics, bioinformatics, genetics and proteomics are all linked by nutrigenomics (Sales et al., 2014). Enhancing sports performance may represent one of the greatest beneficial uses of nutritional genomics. To be able to optimize the development of muscles and sports outcomes, athletes participating in sports like bodybuilding, running,

soccer, etc., these days need to combine exercise with a customized nutritional regimen. Genetic variation amongst people can impact a variety of human specific phenotype including strength of muscles, skeletal organization heart and lung stature, tendon flexibility, etc., which may eventually affect an athlete's performance. According to DNA testing, the likelihood of an individual possessing an ideal sporting genetic makeup is less than one in twenty million cases, and the score reduces in proportion to the number of polymorphisms. Athlete performance may additionally be impacted by nutritional factors, psychological factors, muscle fiber structure, hormonal activity, and variations in genetic makeup. In addition, in order to decide what kinds of nutrients ought to be coupled for every person and which are unnecessary or potentially harmful, additional study is required to explain the complex structure of gene-nutrient connections (Puthuchear et al., 2011).

Figure 1.

Nutrigenomic Response in Sportive Performance (Guest et al., 2019).



Briefly, individuals' responses to the product they consume depend on their own version of the gene or genotype. In words one of syllable, fast metabolizers with the AA genotype in the Cytochrome P450 1A2 (CYP1A2) gene show a positive or improved (sportive performance) to caffeine. Those who have the CYP1A2 AC or CC genotype report none from caffeine use, or performance impairment (Guest et al., 2018).

Genes Associated with Sports Nutrition

Both genetic and environmental factors have an impact on humans; therefore, both must be taken into account equal in order to sustain an individual's normal state of health. Studies on the connection between genes and nutrition has just been developed (Elsamanoudy et al., 2016). This section examines how genetic variation affects how different macro or micronutrients, as well as biologically active substances like caffeine, respond to outcomes related sportive performance (Table 1).

Table 1.

Genes that Association between Dietary Factors and Outcomes Related Sportive Performance (Guest et al., 2019).

Genes	Dietary factor and sources	Outcomes related sportive performance
CYP1A2	Caffeine (chocolate, tea, energy drinks and coffee)	Endurance and CV health
ADORA2A		Fatigue
GSTT 1	Vitamin-C (strawberry, pineapple, red pepper, orange)	Exercise-induced ROS production
PEMT	Choline (fish, egg, salmon, poultry)	Muscle damage
LAT 1-2	Protein (tofu, chicken, cheese, lentil, red meat, egg, fish, yoghurt)	Optimizing body composition

Abbreviations: CV: Cardiovascular; ROS: Reactive oxygen species

Caffeine

Caffeine (1,3,7-trimethylxanthine) is one of the more commonly utilized ergogenic substances. Caffeine's ability to improve sportive performance has been understood for more than a century (Guest et al., 2019). The differences in reactions after consuming caffeine are multifaceted phenomena, driven by several interacting genes. Single nucleotide polymorphisms linked to this actions have been found in some genome-wide association investigations (Guest et al., 2019). One single nucleotide polymorphism in the CYP1A2 gene influences how quickly caffeine is metabolized. Those who are fast metabolizers, or AA homozygotes, usually generate more of this enzyme and as a result, break down caffeine faster. On the other hand, people with the C allele who are slow metabolizers typically clear caffeine more slowly (Pickering & Kiely, 2018). While slow metabolizers are more likely to experience the long-term adverse consequences of adenosine blockage and/or restricted blood flow, fast metabolizers can rapidly metabolize caffeine and reap the advantages of caffeine metabolites as physical activity progresses or exceed the brief duration of harmful consequences. The overwhelming body of research points to CYP1A2's function in regulating the impact of caffeine consumption on physical activity that involves muscular endurance or aerobics (Higgins & Babu, 2013). An additional possible genetic alteration of the impact of caffeine on athletic performance is the Adenosine A2A receptor (ADORA2A) gene. It has been demonstrated that the adenosine Adenosine 2A receptor, which is created by the ADORA2A gene, controls the demand for oxygen in the heart and increases coronary flow through vasodilation (Pickering & Kiely, 2018). Additionally expressed in the brain, the Adenosine 2A receptor controls the flow of glutamate and dopamine, which has implications for pain and sleeplessness. Caffeine's antagonistic effects on adenosine receptors may vary depending on the ADORA2A genotype, which could impact dopamine signals. Dopamine may play a role in the manifestation of varying responses to caffeine because it can be linked to enthusiasm and exertion in exercisers (Salamone et al., 2018). Moreover, the cerebral cortex expresses the Adenosine 2A receptor, which controls the release of glutamate and dopamine and has implications

for pain and sleeplessness. The way that caffeine binds to adenosine receptors can vary depending on the ADORA2A genotype, which can change how dopamine is signaled. Dopamine has been linked to drive and dedication in exercisers, and this could be the process underlying the manifestation of different reactions to caffeine (Bodenmann et al., 2012). Literature suggests that people with the ADORA2A gene's TT genotype may perform more effectively, respond more quickly, and experience less sleep disturbance after consuming caffeine (Guest et al., 2018).

Choline

In carbon metabolic processes, which provides the majority of the methyl donors for cellular methylation reactions, choline plays a crucial role. These reactions consist of DNA methylation, cell division, crucial DNA synthesis and fix steps, and amino acid synthesis (Morton & Close, 2015). Specifically, acetylcholine synthesizing, cell-membrane signals (phospholipids), methyl-group metabolic processes, and the production of neurotransmitters are just a few of the biological processes in which choline is essential. A number of these processes may be strained during prolonged physical activity, which would raise the need for choline as a metabolic material (Penry et al., 2008). Although people may synthesize choline endogenously via the hepatic phosphatidylethanolamine N-methyltransferase (PEMT) pathway, a single nucleotide polymorphism in the PEMT gene, was demonstrated to increase the risk of choline a shortage and the distribution of more dietary choline toward PC biosynthesis instead of betaine synthesis. In contrast to people with the GG genotype, those who carry the C allele of the PEMT gene have been demonstrated to exhibit symptoms of choline deficiency and organ dysfunction, specifically in the liver and skeletal muscles (da Costa et al., 2014). Damage to the muscles is a natural result of extensive, high intensity training for athletes. There are reports of decreases in plasma choline linked to intense exercise, including marathon running and triathlons. Because acetylcholine, a neurotransmitter that regulates attention, recall, and learning, requires enough choline, a decrease in its release may be a factor in the emergence of fatigue and damage in sporting efficiency. Supplementing with choline may also enhance lipid metabolism because it has been linked to a more desirable body type and the capacity to facilitate quick muscle loss in weight class sports (Elsawy et al., 2014). Briefly, choline deficiency or inadequate status can put further strain on an athlete's capacity to heal, rebuild, and adjust to a given training stimuli.

Vitamin-C (Ascorbic Acid)

Oxidative stress-related variants in genes are currently linked to numerous possibly significant discoveries. Reduced defense against oxidative stress may arise from variations in the amounts or activities of antioxidant enzymes caused by a number of single nucleotide polymorphisms (SNPs). A family of phase 2 detoxify enzymes known as glutathione S-transferases (GSTs) is present in all eukaryotic cells. They are essential for the detoxification of xenobiotics (substances that are not found naturally) as well as tumor-causing agents, contaminants from the natural world, and reactive oxygen species. glutathione S-transferase Theta-1 (GSTT1) and glutathione S-transferase Mu-1 (GSTM1) are the two main isoforms (Block et al., 2011). The cytoplasmic enzymes GST-μ (mu) and GST-θ (theta) are encoded by the glutathione S-transferases M1 (GSTM1) and T1 (GSTT1) genes, as well. The conjugation responses among decreased glutathione (GSH) and various electrically conductive substances are catalyzed by these enzymes. Thus, variations in that family of genes may have an impact on the oxidative stress brought on by exercise as well as athletic performance (Cho et al., 2005). A class

of water-soluble, non-enzymatic antioxidants, vitamin C (ascorbic acid), can react with singlet oxygen and eliminate radicals from various sources. It performs several vital cofactor roles in various reactions, including hydroxylation (Peterkofsky et al., 1991). Vitamin C has the potential to keep the mitochondria and lessen the production of excess ROS. Moreover, it can lessen inflammation in muscle mass as well as other tissues. As a result, it might enhance both sports performance and recovery duration (Beck et al., 2021). For instance, inside human muscle cells, consuming 1000 mg/day of vitamin C inhibits the development of Peroxisome proliferator-activated receptor- α coactivator (PGC1- α) and mitochondrial biogenesis, along with important endogenous antioxidant enzymes. Thus, elevated mitochondrial biogenesis is a significant response to skeletal muscle exercise training, with PGC1- α regarded as the primary controller of mitochondrial biogenesis (Fernandez-Marcos & Auwerx, 2011). People have a number of widespread GST polymorphisms that have been linked to either a higher or less prone to disease, especially if paired with other biological and environmental variables like smoking, exposure, or eating habits. Deletion polymorphisms in the GSTM1 and GSTT1 genes, which are significant members of the GST family, cause a whole lack of GSTM1 and GSTT1 molecules (Polinikov et al., 2010). It appears that the GST enzymes guard against serum Vitamin-C deficiency when dietary vitamin C is inadequate because those with GST null genotypes were more likely to develop a lack of it if they did not reach the Recommended Dietary Allowance for vitamin C (Cahill et al., 2009). According to the literature, it is recommended that athletes, regardless of genotype, should receive adequate levels of vitamin-C (Peterkofsky et al., 1991).

Protein

Building muscle is dependent on protein consumption as well as the digestion and utilization of amino acids. Variations in genetic makeup can impact the quantities of biologically active peptides obtained from proteins and, in turn, their utilization for muscle development and action. The quantity of restricting amino acids present in proteins varies amongst foods. For instance, leucine is essential for the synthesis of proteins and increases the activity of important kinases that control the initiation of the transformation procedures, like the regulatory Mammalian target of rapamycin (mTOR) path. Genetic variations in the L-type amino acid transporters, (LAT1 and LAT2 genes) which code for the Branched-chain amino acid (BCAA) carriers (Kühne et al., 2007). Neutral amino acid sodium independent transporters, such as L-type amino acid transporters (LAT) 1 and LAT2, are responsible for carrying out branched-chain amino acid transportation. BCAAs can be transported in cells by LAT1, LAT2, and other mechanisms. The brain, spleen, liver, skeletal muscle, stomach, and placenta all exhibit LAT1 and LAT2 (Fraga et al., 2005). Branched-chain amino acids regulate the metabolic process of muscle proteins by preventing the catabolism process and promoting anabolism through the action of mTOR. Leucine plays a major role in maintaining the equilibrium of glucose via the glucose-alanine cycle by promoting a rise in serum levels of insulin, which in turn has a flexible effect on the production of proteins in the absence of amino acids and affects the sustainability of muscle protein synthesis (Kawaguchi et al., 2008). Genetic variations that cause the mTOR paths to work abnormally have an effect on the creation of proteins and nutrient absorption, which in turn affects muscle development and sports performance. Nutritional techniques pertaining to the amount of protein and carbohydrates consumed through diet and supplements need to be appropriately implemented in light of this genetic proof (Chou et al., 2012).

Conclusion

Future research should concentrate on this as there aren't many gene-diet interaction investigations that have been done in professional athletes and have established outcomes related to performance. Nonetheless, it is known that dietary consumption and/or serum concentrations of a number of nutrients and food biologically active substances can affect the physique and general health, which can then have minor to significant effects on the performance of athletes. With many studies showing the altering impact of genetic modifications with athletic results, caffeine seems to have the most powerful proof to date on endurance performance. In order to optimize sports performance, sport medical professionals, dietitians, and mentors may find that DNA analysis for specific food preferences is a further instrument that they can use to guide the preparation of food and dietary advice (Guest et al., 2019). In conclusion, by creating individualized nutrition plans based on a person's genetic composition, the emerging field of nutrigenomics presents an intriguing strategy toward improving sports performance.

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