Review

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Nutrigenomics: SNPs correlated to physical activity, response to chiropractic treatment, mood and sleep

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Abstract

Nutrigenomics, a rapidly evolving field that bridges genetics and nutrition, explores the intricate interactions between an individual's genetic makeup and how they respond to nutrients. At its core, this discipline focuses on investigating Single Nucleotide Polymorphisms (SNPs), the most common genetic variations, which significantly influence a person's physiological status, mood regulation, and sleep patterns, thus playing a pivotal role in a wide range of health outcomes. Through decoding their functional implications, researchers are able to uncover genetic factors that impact physical fitness, pain perception, and susceptibility to mood disorders and sleep disruptions. The integration of nutrigenomics into healthcare holds the promise of transformative interventions that cater to individual well-being. Notable studies shed light on the connection between SNPs and personalized responses to exercise, as well as vulnerability to mood disorders and sleep disturbances. Understanding the intricate interplay between genetics and nutrition informs targeted dietary approaches, molding individual health trajectories. As research advances, the convergence of genetics and nourishment is on the brink of reshaping healthcare, ushering in an era of personalized health management that enhances overall life quality. Nutrigenomics charts a path toward tailored nutritional strategies, fundamentally reshaping our approach to health preservation and preventive measures. ***Clin Ter 2023; 174 Suppl. 2 (6):183-192 doi: 10.7417/CT.2023.2486***

Key words: *Nutrigenomics, physical activity, chiropractic treatment, mood, sleep, SNPs, polymorphism*

Introduction

The discipline of nutrigenomics, at the intersection of genetics and nutrition, stands as a promising frontier, poised to uncover the intricate connection between an individual's genetic makeup and their response to various nutrients (1). This multidisciplinary field holds the potential to reshape how we approach health maintenance through personalized nutrition plans and strategies (2). Central to this realm is the intriguing exploration of Single Nucleotide Polymorphisms (SNPs), genetic variations that wield significant influence over a person's physiological state, encompassing a broad spectrum of facets such as physical performance, emotional demeanor, and sleep patterns (3-5).

The distinct genetic composition intrinsic to each person plays a pivotal role in shaping their unique interaction with nutrients and the environment (6). This interplay between genetics and nutrition forms the basis for tailoring dietary interventions that align with individual requirements and enhance overall health outcomes (7). Researchers and medical practitioners delve into this nexus to unravel how genetic predispositions influence responses to different dietary components (8).

As already mentioned, the bedrock of nutrigenomics lies in the scrutiny of SNPs, the most common form of genetic variation within the human genome (9). These variations involve minute changes in a single nucleotide at specific points in the DNA sequence (10). While some SNPs may have inconspicuous effects, others exert profound impacts on health and susceptibility to diseases (11). This genetic diversity underpins the intriguing variations observed in how individuals react to various dietary elements, serving as the cornerstone for personalized nutrition strategies (12).

Nutrigenomics delves into genetic influences on physical activity and its impact on health. Research has unveiled links between genetic variants and activity levels, sleep, and cardio-metabolic health. Specific genes like ACTN3, ACE, and PPARGC1A play roles in muscle strength, power, endurance, and metabolic adaptation to exercise (13-15). Insights from genetic studies offer potential for personalized fitness strategies and improved performance outcomes (16). Various genetic variants have been associated with

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power, endurance, and muscle function, offering a deeper understanding of the genetic basis of exercise-related traits (17). The impact of genetics on mental well-being and sleep patterns is another facet of nutrigenomics worth exploring. Genetic factors play a crucial role in mood disorders, sleep patterns, and sleep disorders, revealing complex interactions and potential therapeutic avenues (18, 19). The interplay between genetics and sleep has led to the identification of genes impacting sleep timing, structure, and homeostasis, while research on mood disorders has transitioned from single genes to polygenic risk factors and gene-environment interactions (20). Furthermore, genetic insights into sleep disturbances among children with autism and the role of clock genes in sleep homeostasis highlight the intricate relationship between genetics and sleep (21). Genome-wide association studies have contributed to the understanding of genetic links to sleep disorders and mood conditions, offering potential avenues for tailored interventions and improved health outcomes (22).

In this review article, the realm of nutrigenomics reveals an unfolding comprehension of the dynamic interplay between an individual's genetic blueprint and their response to nutrients, as genetics and nutrition converge. Through the lens of Single Nucleotide Polymorphisms (SNPs), this multidisciplinary field presents the prospect of personalized health management, fundamentally reshaping our approach to well-being. Genetic revelations encompassing physical activity, sleep patterns, and mood disorders provide alluring insights into the intricate matrix of interactions that mold human health.

SNPs and Physiological Status

SNPs are variations in a single nucleotide at specific positions in the DNA sequence (23) that can lead to divergent physiological responses to nutrients and environmental stimuli (24). Notably, some SNPs have the potential to exert substantial effects on an individual's physiological status (25). For instance, research has elucidated the influence of certain SNPs on the metabolism of nutrients, such as vitamin absorption, lipid metabolism, and glucose regulation (26). In this context, SCARB1 gene is vital in the reverse cholesterol transport process and lipid metabolism. Research indicates its potential influence on plasma lipid levels and response to interventions. In the GOLDN study, the SCARB1_G2S variant was linked to greater responsiveness to fenofibrate in reducing triglycerides, suggesting its value in predicting lipid level variations and treatment outcomes (27). Another study showed that TLR diversity is positively linked to physiological condition, particularly affecting hemoglobin, albumin, and triglyceride levels, suggesting associations between TLR variation and health indicators in wild avian populations (3). In addition, Yvert et al. assessed a polygenic profile linked to endurance performance using 21 genetic polymorphisms in Japanese endurance runners and controls. The results suggest that while the analyzed genotype score did not significantly influence endurance athlete status, there were some marginal trends indicating potentially higher frequencies of specific genotypes in international athletes (28).

Genetic traits like resistance to stress and physical capacity are crucial for athletes. Examining the COMT gene's rs4680 polymorphism, this study found that athletes with the Met allele had better psychological stability and specific gender-related differences in psychophysiological traits (29). In this context, calpain-calpastatin system is vital for skeletal muscle growth. Research aimed to identify calpastatin gene polymorphisms in sheep and their connection to growth traits; although no significant genotype-trait relationships were found, certain alleles/genotypes showed potential for growth rate preferences (30).

Nutrigenomics: Decoding the Relationship Between Genetics and Physical Activity

At the core of nutrigenomics lies the captivating exploration of polymorphisms and their possible effects on physical activity (31, 32). These genetic variations can exert a profound influence on how the human body metabolizes nutrients and responds to exercise stimuli (33). By unraveling the genetic code underlying nutritional interactions, nutrigenomics opens up new avenues for developing personalized fitness regimens, optimizing training outcomes, and enhancing physical performance (34).

Physical activity, a crucial determinant of health, displays considerable variability among individuals, in part due to genetic factors (35). Qi et al. conducted groundbreaking research using wrist accelerometry data from 88,411 UK Biobank participants, identifying 5 new genetic loci linked to physical activity, sleep duration, and chronotype. Associations extended to activity patterns, sleep, and blood and immune system involvement, with secondary effects on the digestive and endocrine systems (36). Foraita et al. explored the genetic influence on aerobic fitness (AF) measured by maximal oxygen uptake (VO2max), observing a significant familial aggregation of AF and estimating its heritability at 40%. Above-average AF was associated with reduced overweight/obesity risk (37). Angelen et al. investigated the impact of physical activity (PA) and sitting time on cardiometabolic diseases, discovering that low PA and high sitting time significantly increased the risk of cardiovascular disease and metabolic syndrome (38).

Numerous studies highlight the diverse health benefits of regular exercise, which include decreased risk of chronic diseases and enhanced mental health and cognitive function (39). Bailey et al. demonstrated that combining high calcium intake with childhood exercise boosts bone mass accrual and density, especially during the pre-pubertal period (40). Tou et al. examined the complex interplay between activity and body weight regulation, revealing the multifactorial nature of the determinants of physical activity and their implications for weight control (41). Liprinzi et al. revealed an association between physical activity and hearing sensitivity in diabetic U.S. adults, showing that those with hearing loss engaged in less moderate-to-vigorous physical activity (42). Maffulli et al. delved into single-nucleotide polymorphisms (SNPs) in the NDUFV2 gene's connection to lumbar disc degeneration (LDD), finding SNP rs145497186 significantly associated with LDD and chronic low back pain (43).

The Impact of Genetics on Physical Activity: Insights from SNPs

Research has uncovered specific SNPs associated with physical activity and training outcomes. Notably, the ACTN3 gene, with its rs1815739 SNP, has been linked to variations in muscle strength and power performance (44). Individuals with specific genotypes of this SNP may possess a genetic advantage in activities that require explosive power, such as sprinting and powerlifting (45). Similarly, the ACE gene, with its rs4343 SNP, has been associated with an individual's response to endurance training. This SNP influences the enzyme angiotensin-converting enzyme (ACE), which plays a role in cardiovascular function (15). Different ACE genotypes can impact an individual's aerobic capacity and adaptability to sustained physical activity, highlighting the role of genetics in shaping endurance performance. Moreover, the PPARGC1A gene, with its rs8192678 SNP, has implications in metabolic adaptation to exercise. PPARGC1A is a key regulator of mitochondrial biogenesis and oxidative metabolism, influencing an individual's ability to burn energy efficiently during physical activity (14). Genetic variations in this gene can impact an individual's endurance and overall exercise performance.

Table 1 shows some of SNPs involved in physical activity and response to chiropractic treatment.

Exploring the interplay between the ciliary neurotrophic factor (CNTF) 1357 G --> A polymorphism and muscle strength response to upper arm resistance training, Walsh et al. discovered that women with the CNTF GG genotype displayed superior gains in following isometric and dynamic strength trainings (47). Analyzing genetic polymorphisms linked to favorable muscle traits in Italian athletes, Persi et al. identified significant imbalances in ACTN3 R577X and CNTF IVS1-6G>A polymorphisms among athletes compared to controls. The ACTN3 577X/X polymorphism was associated with athlete anaerobic thresholds, hinting at implications for sport performance, training, and neuromuscular disease (13). Genetic variants contributing to elite athlete status were reviewed by Naureen et al., emphasizing that genetic interactions alone do not ensure championship success, due to epigenetic factors and the environment. Genetic testing for sport performance-related polymorphisms was noted to aid in talent identification and training potential assessment (48). Investigating the connection between polymorphisms in the nuclear respiratory factor (NRF2) gene and endurance capacity, He et al. found that certain NRF2 SNPs were associated with variations in endurance capacity and response to training in young Chinese men (80).

Eynon et al. delved into the NRF2 gene variants (rs12594956 and rs8031031) among endurance athletes and sprinters, discovering that specific NRF2 genotypes and alleles were overrepresented in endurance athletes, hinting at their potential role in enhanced endurance performance (50). PPARα G/C polymorphism (rs4253778) was studied among endurance-oriented athletes, power/endurance-oriented athletes, and non-athletes, revealing no significant genotype or allele frequency differences, indicating that the PPARα gene polymorphism might not be a distinct marker for endurance and mixed sport disciplines (51,81). Examining the impact of the PPARA intron 7 G/C polymorphism (rs4253778) on anaerobic power output in elite Czech ice hockey players, Petr et al. found that C allele carriers exhibited higher anaerobic power during the Wingate Test, suggesting a metabolic advantage toward anaerobic metabolism (82). A meta-analysis by Ahmetov et al. demonstrated that the PPARGC1A Gly482Ser polymorphism was significantly associated with sports performance, particularly in power sports and among Caucasian individuals (54). Investigating the influence of PPARGC1A rs8192678 (Gly482Ser) polymorphism on muscle fitness in Chinese schoolchildren, another study unveiled potential associations between this genetic variant and muscle fiber types in girls (55). A study examining the EPAS1 gene's influence on athletic performance found certain genotypes of rs1867785 and rs11689011 underrepresented in sprint/power athletes, suggesting predictive value for sprint/power athletic success (58). Similarly, in elite endurance athletes, EPAS1 gene variations were linked to differences in aerobic and anaerobic metabolism, influencing maximum sustainable metabolic power (57). Investigating the role of genetic variations in AMPD1, CPT2, and PYGM genes in Chronic Fatigue Syndrome (CFS), a study found no major genetic variations associated with CFS in these genes (59). Analyzing the C34T mutation in the AMPD1 gene among top-level Caucasian male endurance athletes and non-athletes, the frequency of the mutant T allele was lower in elite endurance athletes (60). A study on muscle AMPD deficiency in mice revealed no significant impact on muscle performance during different exercise protocols (61). Understanding the cardioprotective effect of the AMPD1 gene variant associated with improved survival in heart failure patients, the study highlighted the metabolic-chronotropic response during exercise as a critical factor (62). Investigating the influence of adenosine in endotoxemia-induced injury, the study found that the AMPD1 variant did not significantly affect inflammation-induced injury during human experimental endotoxemia (63). Exploring the AMPD1 C34T genetic polymorphism in Lithuanian athletes, the study found that the CC genotype was prevalent in sprint/power-oriented athletes and linked to higher short-term explosive muscle power (64).

The influence of genetic variants on exercise reinforcement, tolerance, and moderate-to-vigorous physical activity was studied, revealing associations between certain genotypes and exercise behaviors (65). In a similar way, the association of a DRD2 gene variant with physical activity levels was found to be specific to gender and ethnicity (66). Genetic influences on physical activity were explored further, uncovering associations with genes related to sensation-seeking behaviors (67). Investigating the impact of the AGT gene M235T polymorphism on athletic status and performance level, a study indicated that the CC genotype was overrepresented in power athletes (68); additionally, the very same polymorphism was associated with power-related improvements following aerobic dance training (69). A meta-analysis revealed significant associations between power athlete status and genetic polymorphisms in various genes (70). The AGTR2 rs11091046 polymorphism was found to be associated with sprint/power athlete status in men from Japanese and East European backgrounds (71). The use of ACTN3 R577X genetic polymorphism for personalized training guidelines was explored, linking the gene

Table 1. SNPs Associated with Physical Activity and Response to Chiropractic Treatment.

RsID	Gene	Function	Alleles	wt/mt	References
rs1800169	CNTF	Better response to chiropractic treatment	G/G	mt/mt	(46)
		Typical	G/A	wt/mt	(47)
		Typical	A/A	wt/wt	(13)
rs7181866	GABPB1 (NRF2)	Likely worse in endurance sports	G/G	mt/mt	(48, 49)
		Intermediate phenotype	G/A	wt/mt	(49)
		Likely better in endurance sports and better aerobic capacity	A/A	wt/wt	(50)
rs4253778	PPARA	Likely better in endurance sports and better aerobic capacity	GG	mt/mt	(48)
		Intermediate phenotype	GC	wt/mt	(51)
		Likely better in power sports and lower aerobic capacity	C/C	wt/wt	(52)
rs8192678	PPARGC1A	Likely worse in endurance sports; lower mitochondrial biogenesis and lower increase in insulin sensitivity on aerobic training; likely lower VO2max and higher levels of lactate in blood	A/A	mt/mt	(48, 53)
		Intermediate phenotype	A/G	wt/mt	(54)
		Likely better in endurance sports; higher mitochondrial biogenesis and higher increase in insulin sensitivity on aerobic training; likely normal VO2max and lower levels of lactate in blood	G/G	wt/wt	(55)
rs1867785	EPAS1	Variant rare in the sprint/power athletes	A/A	mt/mt	(48, 56)
		Intermediate phenotype	A/G	wt/mt	(57)
		Typical	G/G	wt/wt	(58)
rs17602729	AMPD1	Loss of enzyme function. May experience muscle soreness in exercise. Possible benefit on cardiovascular function	A/A	mt/mt	(59-62)
		Reduced enzyme function. May experience muscle soreness in exercise. Possible benefit on cardiovascular function	A/G	wt/mt	(63)
		Typical	G/G	wt/wt	(64)
rs6454672	CNR1	Likely to tolerate more high-intensity training	T/T	mt/mt	(65)
		Typical	C/T	wt/mt	(66)
		Typical	C/C	wt/wt	(67)
rs699	AGT	Risk of high blood pressure. Likely to be better in power sports	G/G	mt/mt	(68, 69)
		Slightly higher risk of high blood pressure. Likely to be better in power sports	A/G	wt/mt	(70)
		Typical	A/A	wt/wt	(71)
rs1815739	ACTN3	Functioning protein. More fast, type II muscle fiber. Optimal for elite power athletes	C/C	mt/mt	(48, 72)
		Functioning protein. Optimal for elite power athletes	C/T	wt/mt	(44)
		Non-functioning protein. More likely to be an endurance athlete than power athlete	T/T	wt/wt	(73)
rs1799722	BDKRB2	Typical	C/C	mt/mt	(48)
		Probably better endurance performance, than power performance	C/T	wt/mt	(74)
		Probably better endurance performance, than power performance	T/T	wt/wt	(75)
rs1805086	MSTN	Greater muscle mass	C/C	mt/mt	(46, 76, 77)
		Greater muscle mass	C/T	wt/mt	(76)
		Typical muscle mass, better jumping ability	T/T	wt/wt	(77)
rs2010963	VEGFA	Higher protein levels. Higher improvements in VO2max seen with aerobic training	C/C	mt/mt	(78)
		Higher protein levels. Higher improvements in VO2max seen with aerobic training	C/G	wt/mt	(79)
		Lower protein levels. Lower improvements in VO2max seen with aerobic training	G/G	wt/wt	(79)

variant to muscle phenotypes (72). Investigating the ACTN3 gene's impact on athletic performance and muscle function, the study found that overexpression of α-actinin-3 altered muscle metabolism and fatiguability, challenging previous assumptions (73). The influence of genetic polymorphisms on endurance performance was examined, revealing specific gene variants (BDKRB2 and ADRB2) with potential implications for endurance performance among habitual runners (74). The associations between gene variants in muscle afferents and exercise pressor responses were explored, with specific variants in TRPV1 and BDKRB2 receptors showing significance (75). Genetic polymorphisms (MSTN 2379 A > G and FST -5003 A > T) were examined in relation to muscle size and strength responses to resistance training across various ethnic groups (76). In the context of the MSTN K153R polymorphism, a study indicated that the KR genotype was linked to lower performance in vertical jumps, suggesting its potential influence on muscle power during contractions (77).

Nutrigenomics: Decoding the Relationship Between Genetics and Pain Perception

Chiropractic is an alternative therapy based on the body's self-healing ability and the relationship between body structure and health (46). It is widely used for chronic pain treatment, but the exact molecular mechanisms are not fully understood. Animal studies suggest that chiropractic impacts neuroplasticity through neurotrophin modulation. No published research has explored the interaction between neurotrophin gene polymorphisms and chiropractic treatment. The study identified potential genes and polymorphisms correlated with a better response to chiropractic therapy. However, more association studies are needed to confirm these findings.

The study explored associations between NTRK1 gene SNPs and pain perception in a Han Chinese population (4). Nine tag-SNPs of NTRK1 showed significant associations with pressure pain thresholds, leading to hyper- or hyposensitivity. Specifically, four tag-SNPs (rs1800880, rs6334, rs2644604, and rs943552) were highly associated with lower mechanical pain sensitivity to sharp pressure pain, and individuals with the haplotype CTCC exhibited hyposensitivity to sharp pressure pain compared to other haplotypes.

A research investigation centered on the molecular mechanisms of chiropractic therapy employed "chiropractic," "neuroplasticity," and "neurotrophin gene polymorphism" as focal points. The analysis revealed specific genes and functional polymorphisms that might be linked to a more favorable response to chiropractic therapy (46). Another study delved into the connections between NTRK1 gene SNPs and pain perception in Han Chinese females. Nine tag-SNPs of NTRK1 displayed significant associations with pressure pain thresholds, manifesting as either hyper- or hyposensitivity. Notably, certain tag-SNPs (rs1800880, rs6334, rs2644604, and rs943552) were markedly related to reduced mechanical pain sensitivity, with the CTCC haplotype particularly linked to hyposensitivity (4).

Genetics, Mood, and Sleep

The impact of genetic factors on mood and sleep patterns is an area of increasing interest (5). Specific genetic variants have been associated with an increased risk of mood disorders, such as depression and anxiety, while others may influence an individual's sleep quality and circadian rhythms (18). In this context, a meta-analysis of large-scale studies involving over 807,000 individuals revealed significant associations between 102 variants, 269 genes, and 15 gene-sets with depression, shedding light on its genetic complexity and potential treatment avenues (19). Children on the autism spectrum often experience sleep problems, which can worsen emotional and behavioral challenges. This study aimed to identify genetic variants associated with sleep disturbance and melatonin levels in autistic children, revealing potential distinct biological mechanisms underlying these issues (20). Circadian and sleep-homeostatic processes both influence sleep timing and structure. Recent evidence suggests that clock genes, traditionally associated with circadian rhythms, also play a role in sleep homeostasis, impacting sleep duration, structure, and EEG delta power across species (21). Researchers observed increased expression of circadian clock-genes in the cerebral cortex during sleep deprivation (SD), with the magnitude of increase corresponding to the extent of sleep rebound after SD in different mouse strains. Specifically, elevated per2 expression persisted in mice with limited sleep rebound, suggesting its potential role in negatively influencing recovery sleep (87). Rare variants in specific genes have been linked to Mendelian sleep conditions, but their effects in the general population are unclear. This study examined these variants in large cohorts and found that they are not highly penetrant for extreme sleep

Table 2. SNPs Associated with Pain Perception

RsID	Gene	Function	Alleles	wt/mt	References
rs6746030	SCN9A	Increased perception of pain	A /A	mt/mt	(46)
		Somewhat increased perception of pain	A /G	wt/mt	(83)
		Typical	G /G	wt/wt	(84)
rs6334	NTRK1	Increased pain perception during acupuncture	A/A	mt/mt	(4, 46)
		Somewhat increased pain perception during acupuncture	A/G	wt/mt	(85)
		Typical	G/G	wt/wt	(86)

or circadian phenotypes, suggesting that their impact may differ in a broader population context (88).

Mood disorders have a strong genetic component, and research in this field has evolved from focusing on single genes to polygenic risk factors and gene-environment interactions. This scientometric analysis highlights shifts in research trends, from monogenic studies to genome-wide association studies and the exploration of genetic overlaps with other psychiatric conditions, as well as the increasing importance of gene-environment interactions in understanding mood disorder risk (22). As the number of previous depressive episodes increases, the link between stressful life events and the onset of major depression weakens. This study investigated the impact of genetic risk factors on this phenomenon and found that individuals at high genetic risk for depression tend to experience depressive episodes without major environmental stressors, suggesting a "pre-kindling" effect rather than an accelerated kindling process (89). Genetic variants associated with cardiovascular and metabolic diseases, as well as mood disorders, have been identified through meta-analyses and candidate gene studies. This article reviews and analyzes shared genes, linked to both cardiometabolic diseases and mood disorders, identifying 24 potential pleiotropic genes and revealing significant shared pathways (90). Sleep is vital, yet its functions remain largely unknown, and disruptions can lead to health issues. Genetic factors influence sleep variation and disorders. Genome-wide association studies have identified genetic variants associated with sleep disorders, like insomnia and sleep apnea, offering valuable insights for prevention and treatment (91).These findings underscore the importance of considering genetic factors in tailoring therapeutic interventions for mood-related conditions (92). Investigating the connection between the neurotrophin Nerve Growth Factor (NGF) and pain perception, another study disclosed that mutations in NGF-related genes led to hereditary pain insensitivity disorders (HSAN IV and HSAN V), along with diverse cognitive neurological effects. Specifically, the R100W mutation in mature NGF reduced pain-inducing activity in mice, offering insights into HSAN V clinical manifestations and the role of NGF receptors and signaling cascades in pain sensitization (93).

Table 3 shows some of SNPs involved in mood and sleep activities.

Discussion

The study of SNPs correlated to physical activity, pain perception, mood, and sleep patterns has significant implications for personalized nutrition and healthcare interventions (5, 36, 93). Understanding an individual's genetic predisposition to these various aspects of health can inform targeted interventions and improve overall well-being (100).

The investigation of SNPs correlated to physical activity holds immense significance, offering valuable insights into optimizing exercise regimens and promoting overall well-being (101). By understanding an individual's genetic predisposition to various aspects of physical performance, nutrigenomics empowers healthcare practitioners to design exercise programs that capitalize on genetic strengths and address weaknesses, thereby optimizing training outcomes and enhancing physical performance. Certain genes have emerged as key players in the context of physical activity and chiropractic response, warranting further investigation. Genes such as ACTN3, ACE, PPARGC1A, OPRM1, COMT, and SCN9A play critical roles in shaping an individual's physical performance and pain perception (102, 103). Delving deeper into the interactions between these genes and their associated SNPs will unlock new possibilities for targeted interventions, personalized healthcare, and improved treatment outcomes.

Likewise, insights into the genetic influences on mood and sleep patterns offer opportunities for personalized mental health management (18). Indeed, understanding the genetic influences on mood and sleep patterns presents exciting prospects for personalized mental health management (104), in order to help millions of people worldwide managing conditions like depression, anxiety, and sleep disorders (105). However, the susceptibility to these conditions and response to treatment can vary widely among individuals (106). Nutrigenomics offers a novel perspective, by investigating how genetic factors contribute to mood regulation and sleep patterns, potentially revolutionizing mental health care (107).

Table 3. SNPs Involved in Mood and Sleep and Response to Chiropractic Treatment

RsID		Gene	Function	Alleles	wt/mt	References
rs334558		GSK3B	Increased risk for severe insomnia	G/G	mt/mt	(94)
		GSK3B	Increased risk for severe insomnia	A/G	wt/mt	(95)
		GSK3B	Typical	A/A	wt/wt	(96)
rs73598374		ADA	Typical	C/C	wt/wt	(97)
		ADA	Reduced clearance of adenosine. May lead to more deep sleep, but sleepiness when waking up	C/T	wt/mt	(98)
		ADA	Reduced clearance of adenosine. May lead to more deep sleep, but sleepiness when waking up	T/T	mt/mt	(99)
rs6330	NGF		More anxiety in females, less anxiety males	C/C	mt/mt	(92)
			Typical	T/C	wt/mt	(92)
			More anxiety in males, less anxiety females	T/T	wt/wt	(93)

The identification of specific SNPs associated with mood disorders has been a focus of extensive research. In this context, Fraizer et al. found associations between specific genetic variants (ANK3, BDNF, CACNA1C, DGKH) and mood disorders, cognition, and brain regions involved in affect regulation. Among these variants, CACNA1C carriers showed larger fronto-limbic brain volumes, increased IQ, and potential associations with mood disorder-related systems, suggesting a potential marker for neuropsychiatric risk (108). Similarly, research into anxiety-related SNPs, such as those in the COMT gene, sheds light on the genetic basis of anxiety susceptibility (109). By understanding the genetic variants associated with anxiety risk, mental health practitioners can better tailor treatment plans, including psychotherapy and pharmacotherapy, to suit individual needs.

Moreover, sleep is a vital component of overall well-being, and genetic factors can significantly impact an individual's sleep patterns (109). The study by Riestra et al. (2017) on SNPs in the CLOCK gene revealed how genetic variations could influence sleep duration and quality (110). This finding opens up opportunities for personalized sleep management strategies, such as chronotherapy or personalized sleep hygiene recommendations, to address sleep disturbances effectively.

Integrating nutrigenomics into mental health management can lead to more precise and targeted interventions (111). For instance, identifying an individual's genetic susceptibility to depression may inform treatment decisions, guiding the selection of medications that are more likely to be effective for that specific genetic profile (112). Additionally, personalized lifestyle modifications, including dietary and exercise recommendations tailored to the individual's genetic makeup, can complement conventional therapies and improve treatment outcomes (113, 114).

However, while nutrigenomics offers great promise, several challenges must be addressed for its successful integration into mental health care (115). Ethical considerations related to genetic testing and privacy must be carefully navigated, to ensure that individuals' rights and autonomy are respected (116). Genetic counseling should be made readily available, to help individuals understand the implications of their genetic information and make informed decisions about their mental health management (117).

Furthermore, the complexities of gene-environment interactions should be thoroughly investigated to comprehensively understand the interplay between genetics, lifestyle, and environmental factors in mental health (118). This knowledge will enable a holistic approach to personalized mental health care that considers the dynamic interactions between genes and the environment.

Conclusions

Nutrigenomics, with its focus on understanding the interplay between genetics and nutrition, represents a pioneering approach to personalized medicine and healthcare. The investigation of Single Nucleotide Polymorphisms (SNPs) and their correlations to physical activity, pain perception, mood, and sleep patterns provides invaluable insights into individual health and well-being. By leveraging genetic information, personalized nutrition plans and exercise regimens can be tailored to maximize health benefits and optimize fitness outcomes. Understanding an individual's genetic predisposition to various health aspects can guide targeted interventions, promoting physical activity, pain perception, and sleep and mood patterns. In the realm of mental health, nutrigenomics presents exciting opportunities for personalized mental health management. Identifying specific genetic markers associated with physical activity, pain perception, mood disorders, and sleep patterns can facilitate early detection and intervention, leading to more effective treatment approaches. As nutrigenomics continues to evolve, further research and advancements are needed to fully unlock its potential in transforming healthcare. Embracing the possibilities of nutrigenomics could move us towards a future of precision medicine, where healthcare is tailored to each individual's unique genetic composition, ultimately enhancing overall health and quality of life.

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Conflicts of interest statement

Authors declare no conflict of interest.

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