IDLife

DNA

NUTRITION + FITNESS SIMPLIFIED

GENETIC TESTING SUMMARY

WEIGHT CATEGORY

GENE TESTED	GENETIC REPORT CATEGORY	SNP SYNOPSIS
FTO-1	Appetite Weight Regain Body Weight Dietary Fats Dietary Carbohydrates Fat Loss with Exercise	Substitutions on this SNP are associated with delayed satiety (less likely to feel full after eating), increased hunger, and an increased risk for T2DM and obesity. Several specific polymorphisms on this gene are associated with total food consumption, feeling of satiety with eating, increased body weight and BMI and the level of risk for obesity-related health problems such as Type II diabetes. It appears to play a role within the central nervous and cardiovascular systems influencing the level of satiety an individual would perceive.
MC4R	Appetite Weight Regain Body Weight	Substitutions on this SNP are associated with influencing appetite and satiation. Found in the hypothalamus close to an area associated with controlling appetite and satiety. Defects in this gene are the most commonly known and understood genetic defects causing a predisposition to obesity.
FTO-2	Appetite Weight Regain Body Weight Dietary Fats Dietary Carbohydrates Fat Loss with Exercise	Substitutions on this SNP are associated with less weight loss, making it more difficult to lose weight when dieting. This particular SNP, at this location, is associated with an individual's ability to lose weight. In one study, individuals with this substitution lost less weight after gastric band surgery than others without the substitution. This association was not Present following gastric bypass surgery.
ANKK1/DRD2	Addictive Tendencies & Impulsive Eating	The ANKK1-DRD2-TaqIA gene, located on chromosome 11 (11q23.2) is involved with the synthesis of dopamine in the brain that signals a "feel good" or rewarding sensations. Some SNPs here decrease the concentration of dopamine receptors resulting in the individual seeking more stimulation to feel an equivalent level of reward. For this panel's purpose, this gene functions by interacting with the reward feeling obtained by consuming pleasant tasting, palatable foods with a resulting increase in weight and a propensity for developing obesity.
APOA2	Dietary Fats	Substitutions on this SNP are involved with how the body metabolizes saturated fat. Being the second most abundant particles in the HDL-cholesterol, this is one of the "thrifty" energy genes. 'hunter-gatherers' in the past who might experience alternating periods of feast and famine, were benefited by this SNP. This gene interacts with a high fat diet to promote weight gain and obesity.
PPARG	Dietary Carbohydrates	Substitutions on this SNP are involved with how the body senses steroid and thyroid hormones. It regulates the distinction and the expression of other genes. It plays a role in energy stability, glucose balance, obesity, diabetes, Plaque accumulation on arterial walls, and colon & thyroid tumors.

DIET, METABOLISM & TASTE CATEGORY

GENE TESTED	GENETIC REPORT CATEGORY	SNP SYNOPSIS
CYP1A2	Caffeine	Substitutions on this SNP are involved with how the body metabolizes substances that would not otherwise be naturally present in an organism. While there is very little reliable information on the endogenous substrates, this enzyme figures prominently in the metabolism caffeine, acetaminophen and a number of other drugs. This enzyme is responsible for 95% of the body's metabolism of caffeine. Enzyme activity can be induced by the aromatic hydrocarbons found in cigarette smoke, as well.
MCM6	Lactose	This is a protein complex that plays a role in DNA replication by functioning as a helicase, temporarily unwinding, editing, replicating and transporting DNA. Its activity also modulates the expression of a nearby gene, LCT, responsible for lactase. It is the activity of this complex that is responsible for the increasing lactase intolerance in most of the world's population after the age of two years. Certain polymorphisms on this gene allow a persistence of lactase activity into and through adult life.
ALDH2	Alcohol	Substitutions on this SNP are associated with influencing enzymes responsible for metabolizing ethanol. This enzyme converts acetaldehyde to acetate, the second step in the metabolism of grain alcohol. Decreased activity in this step leads to higher levels of acetaldehyde which is toxic and results in aversive symptoms including anxiety, facial flushing, nausea, rapid heartbeat and a lower tolerance for alcohol. It is this step that is blocked by drugs used to treat alcoholics. While this gene does play a role, the question of whether any specific individual will become an alcoholic is influenced by environment and other factors and not solely on genetics.
TAS2R38	Bitter Taste	Polymorphisms on this gene dictate an individual's ability to taste. While there are only three genes that control how a person perceives "sweet" flavors, there are almost thirty genes that characterize how a person perceives what would be characterized as bitter flavors. While the ability to taste sweet implies the ability to identify fruits and carbohydrates, it is felt that the ability to identify and distinguish bitter flavors has enabled people to identify and avoid potentially noxious & toxic plants and substances. Because so many factors play a role in food preference such as a person's age, gender, taste status, available foods, etc., it is not clear how definite a role that these genetic factors play in one's overall diet over time. There is some correlation of these SNPs with BMI.
LEPR	Weight Regain	Substitutions on this SNP are involved the body's thermogenesis. Specifically, Leptin is a hormone that regulates energy balance by inhibiting hunger. Produced in the body by fat tissue, the more fat tissue present, the higher levels of leptin present. These SNP's bind to leptin receptors at various sites including the hypothalamus and play a role in signaling satiety and energy utilization (thermogenesis) by the body. Various mutations on the LEPR gene result in fewer leptin receptors or dysfunctional leptin receptors. This results in excessive hunger, weight gain, and in some instances decreased sex hormones, resulting in a condition where the male testes or the female ovaries produce little to no sex hormones.
NMB	Appetite Weight Regain	Substitutions on this SNP influence the central Nervous system's modulation of the Gastrointestinal tract. In one role, a peptide is released from the GI tract after eating and travels to the brain to inhibit further food intake. It appears to be the best candidate as the genetic link between eating behavior, disorder and obesity.
ANKK1/DRD2	Addictive Tendencies & Impulsive Eating	The ANKK1-DRD2-TaqIA gene, located on chromosome 11 (11q23.2) is involved with the synthesis of dopamine in the brain that signals a "feel good" or rewarding sensations. Some SNPs here decrease the concentration of dopamine receptors resulting in the individual seeking more stimulation to feel an equivalent level of reward. For this panel's purpose, this gene functions by interacting with the reward feeling obtained by consuming pleasant tasting, palatable foods with a resulting increase in weight and a propensity for developing obesity.

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ADIPOQ	Inflammation Dietary Carbohydrates	This substitution links to a collagen-like protein that is secreted exclusively by fat tissue which circulates within the system and plays a role in hormonal and metabolic processes. It protects against the formation of atheromas or Plaques in arteries, and It possesses significant-diabetic and anti-inflammatory properties. Higher levels of adiponectin, involved in regulating glucose levels as well as fatty acid breakdown, are associated with decreased insulin resistance and risk of diabetes.
FTO-1	Appetite Weight Regain Body Weight Dietary Fats Dietary Carbohydrates Fat Loss with Exercise	Substitutions on this SNP are associated with delayed satiety (less likely to feel full after eating), increased hunger, and an increased risk for T2DM and obesity. Several specific polymorphisms on this gene are associated with total food consumption, feeling of satiety with eating, increased body weight and BMI and the level of risk for obesity-related health problems such as Type II diabetes. It appears to play a role within the central nervous and cardiovascular systems influencing the level of satiety an individual would perceive.
LIPC	Cholesterol Response Dietary Fats	The LIPC gene is located on chromosome 15 (15q21.3) and codes for an enzyme, Hepatic triglycerol lipase. In plays a role in the regulation of triglycerides, LDL cholesterol and HDL cholesterol. In the general population, genetic factors account for 40-60% of the variability of HDL-cholesterol levels.
APOA2	Dietary Fats	Substitutions on this SNP are involved with how the body metabolizes saturated fat. Being the second most abundant particles in the HDL-cholesterol, this is one of the “thrifty” energy genes. ‘Hunter-gatherers’ in the past who might experience alternating periods of feast and famine, were benefited by this SNP. This gene interacts with a high fat diet to promote weight gain and obesity.
PPARG	Inflammation Cholesterol Response	Substitutions on this SNP are involved with how the body senses steroid and thyroid hormones. It regulates the distinction and the expression of other genes. It plays a role in energy stability, glucose balance, obesity, diabetes, Plaque accumulation on arterial walls, and colon & thyroid tumors.
FADS1	Inflammation Dietary Fats	Substitutions on this SNP are associated with the enzyme that desaturates fatty acids, forming polyunsaturated fatty acids (PUFAs). Thus linoleic (omega-6 fatty acid) and A-linolenic acids (omega-3) are desaturated to arachidonic acid and eicosapentinoic acid which are precursors for inflammatory molecules such as the eicosanoids. Of note is that minor alleles of a number of SNPs on this family of genes are associated with a decrease in frequency and severity of allergic rhinitis and atopic dermatitis.
KCTD10	Cholesterol Response Dietary Carbohydrates	This substitution links to a protein which plays a role in the regulation of HDL and LDL cholesterol in response to diet. Low levels of HDL and high levels of LDL are independently associated with an increased risk of heart disease. It has been shown that half of the individual variability in HDL levels is genetically determined.
MMAB	Cholesterol Response Dietary Carbohydrates	Substitutions on this SNP are associated with the production of adenosylcobalimin from Cyanocobalamin (vitamin B12) which in turn plays a role in the production of a co-Enzyme which helps break down certain proteins, fats and cholesterol.

VITAMINS CATEGORY

GENE TESTED	GENETIC REPORT CATEGORY	SNP SYNOPSIS
BCMO1	Vitamin A	Substitutions on this SNP are associated with an enzyme found in the liver, lungs, and kidneys, notably. Normally, 70-80% of active vitamin A in the body is derived from ingested carotenoids which are converted by this enzyme to active retinoids (vitamin A). From 27-45% of the general population in double blind trials are poor converters of carotenoids to active retinoids.
NBPF3	Vitamin B6	The NBPF3 gene, located on chromosome 1 (1q21.1) codes for neuroblastoma breakpoint family, member 3. A specific function for this protein has not been determined but it is felt to be a factor in cognitive development because of its large expansion in humans, and to a lesser extent in primates. It is a factor in a number of developmental and neurogenetic disorders such as microcephaly, macrocephaly, autism, schizophrenia, mental retardation, congenital heart disease, neuroblastoma, and congenital kidney and urinary tract anomalies. Altered expression of some gene family members is also associated with several types of cancer and it is suspected that it may serve as a tumor suppressor gene. This particular substitution is associated with pyridoxine (vitamin B6) levels.
MTHFR C677T	Folate Metabolism	The MTHFR C677T gene variant is a common mutation in the MTHFR gene, where the DNA base "C" (cytosine) is replaced by "T" (thymine) at the 677 position. This gene encodes the enzyme methylenetetrahydrofolate reductase (MTHFR), which is crucial for converting folate (Vitamin B9) into its active form, 5-methyltetrahydrofolate. The C677T variant results in a thermolabile enzyme with reduced activity, leading to higher levels of homocysteine in the blood. Homocysteine is potentially toxic to living cells and high levels have been associated with increased risk of cardiovascular disease. Consequently, this particular substitution results in decreased methylation activity and an increased homocysteine activity, particularly pronounced in individuals with low levels of folate in their diet. There is also an increased risk of a number of other disorders in individuals that carry this substitution, at least some of which can be ameliorated by dietary intervention. These disorders cover a range including spina bifida, various mental disorders, birth defects and other diseases.
MTHFR A1298C	Folate Metabolism	The MTHFR A1298C gene variant is a specific mutation in the MTHFR gene, where the DNA base "A" is replaced by "C" at the 1298 position. This gene provides instructions for making an enzyme called methylenetetrahydrofolate reductase (MTHFR), which plays a crucial role in processing amino acids, the building blocks of proteins. Unlike the more commonly discussed MTHFR C677T variant, the A1298C variant primarily affects the regulation of S-adenosyl methionine (SAMe), a key methyl group donor in the body. This regulation is essential for maintaining balanced levels of methyl groups, which are vital for numerous biochemical processes, including DNA methylation and neurotransmitter production. Mutations in the A1298C variant can lead to less effective regulation, potentially resulting in an overload of methyl groups and associated symptoms like mood swings, depression, and other health issues.
FUT2	Vitamin B12 Inflammation	Substitutions of this SNP are associated with an enzyme resulting in lower concentrations of the gut microbe, Bifidobacterium, as well as a greater predisposition towards elevated serum concentrations of Vitamin B-12. Non-secretors are more susceptible to inflammation and could benefit from probiotics. They also appear to have a greater resistance towards certain pathogenic infections such as H Pylori, as well as protection against certain viruses. Secretors are more susceptible to H. pylori and have lower B12 levels.
GC	Vitamin D	This substitution is associated with a vitamin D binding protein within the albumin Family. This binding facilitates their transportation to target tissues. It also serves as a macrophage activating factor (originating from white blood cells) and thus plays at least some role in the immune system and the protection from infections and various diseases. Inter-individual vitamin D levels can vary significantly. Only approximately 25% of this variability can be attributed season, and geographical location. Likely 50% or more of the variability between individuals is attributable to genetic factors and these genetic variant forms, as one of the mostly strongly correlated with vitamin D levels.
INTERGENIC	Vitamin E Dietary Fats	An intergenic area is a stretch of DNA between known genes and usually is composed of non-coding DNA. Intergenic areas are thought to comprise 80-90% of the human genome and likely to contain various promoters and enhancers. This particular SNP lies close to a gene associated with a protein which is involved in lipid metabolism and triglycerides and chylomicrons levels. Vitamin E is a fat-soluble vitamin and consists of eight related tocopherols of which a-tocopherol has the highest bioavailability. Genetics may be a strong factor in the level of *a*-tocopherol. The presence of an A gene variant at this position in this Intergenic region has a very strong association with *a*-tocopherol levels. It is important to note that this correlation is attenuated when corrected for the triglyceride level. This implies a possible correlation of relatively elevated triglyceride levels with the elevated *a*-tocopherol levels associated with this SNP.

EXERCISE CATEGORY

GENE TESTED	GENETIC REPORT CATEGORY	SNP SYNOPSIS
LIPC	Dietary Fats Cholesterol Response	The LIPC gene is located on chromosome 15 (15q21.3) and codes for an enzyme, Hepatic triglycerol lipase. In plays a role in the regulation of triglycerides, LDL cholesterol and HDL cholesterol. In the general population, genetic factors account for 40-60% of the variability of HDL-cholesterol levels.
PPARD	Aerobic Potential	There are a number of associations with this allele (gene and its variants) including a reduced height, altered cholesterol metabolism and a possible shift in fuel preference to lipids from glucose. This allele taken by itself is a poor predictor of training and performance, but when paired with the genotype of certain other genes, exhibits a significant correlation with athletic performance and endurance.
INSIG2	Fat Loss with Exercise	This gene's association with insulin, is involved with energy metabolism. Some studies have shown an increased BMI, particularly in females, when the allele is present, but this has been a weak association. It may be associated with a slight increase in cholesterol levels. At most, the presence of the altered allele here accounts for 1.1% of individual genotypic variability in subcutaneous fat content.
PPARGC1A	Aerobic Potential	co-activator that is present at higher levels in metabolically active tissues. The protein regulates genes involved in energy metabolism and appears to serve as a direct link between external physiologic stimuli and the regulation of mitochondrial biogenesis. The *PPARGC1A* protein governs muscle plasticity, mediates some of the beneficial effects of exercise and suppresses a broad inflammatory response.
ACTN3	Appetite Weight Regain Body Weight Dietary Fats Dietary Carbohydrates Fat Loss with Exercise	This gene is associated with a muscle protein which is found, almost exclusively in fast glycolytic Type II fibers which are important in strength based, "explosive" muscle movement. A mutation here indicates decreased protein and a preponderance of slow Type I fibers. There is some evidence that Type I muscle fibers are better suited to endurance type sports. There is little evidence distinguishing an individual with either of these genotypes from the general population. However, there is a clear distinction when comparing the genotypes of elite and Olympic level athletes in endurance sports from that of those athletes in strength-based sports. It is important to remember that fitness and training is multifactorial and response to training is influenced by several other conditions.
SLC30A8	Dietary Carbohydrates Recovery	This substitution is associated with an increased susceptibility to delayed onset muscle soreness (DOMS) which occurs 12-72 hours after a workout. Activities involving predominantly eccentric muscle contraction (e.g. weight lifting, jumping, jogging downhill, step aerobics) are associated with increased DOM compared to activities requiring predominantly concentric contractions (e.g. stair stepper, running level or up-hill, elliptical, swimming). There is no association with increased muscle mass following workouts compared with the alternative allele at this position. *Concentric* muscle contraction – The muscle shortens as it "contracts" or fires. *Eccentric* muscle contractions – The muscle lengthens as it "contracts" or fires. As seen when decelerating a body part, lowering a load or cushioning a blow or fall.
MMP3	Injury	This substitution is associated with an enzyme that is secreted as a pre-protein which must divide to become active. The enzyme, by its action of degrading cartilage and similar tissues, is involved in wound repair, tumor initiation, atherosclerosis and other actions. This allele also seems to have a mild protective effect on the diastolic blood pressure, but only in african american women.