

Genetic Testing

Genetic testing is the laboratory analysis of DNA to identify variations that may influence health, disease risk, or response to nutrients. In the context of personalized nutrition, understanding the terminology associated with genetic testing is essential for interpreting results, designing individualized dietary recommendations, and communicating findings to clients. The following glossary presents the most frequently encountered terms, organized by thematic categories, and includes practical examples, applications, and common challenges.

DNA (deoxyribonucleic acid) is the hereditary material that carries the genetic instructions for the development and function of all living organisms. It is composed of two complementary strands that form a double helix. Each strand consists of a sequence of four nucleotides—adenine (A), thymine (T), cytosine (C), and guanine (G). The order of these nucleotides encodes the information required to build proteins, the workhorses of the cell. In nutrition, variations in the DNA sequence can affect enzymes involved in metabolism, transporters that move nutrients across cell membranes, and receptors that sense dietary signals.

Gene refers to a specific segment of DNA that contains the instructions for producing a particular protein or functional RNA molecule. Humans have roughly 20,000 protein-coding genes. For example, the LCT gene encodes lactase, the enzyme responsible for breaking down lactose in the small intestine. Individuals with certain variants of the LCT gene retain lactase activity into adulthood (lactase persistence), while others experience a decline that leads to lactose intolerance. Knowledge of a client's LCT genotype can guide recommendations regarding dairy consumption, lactose-free alternatives, or enzyme supplementation.

Allele is one of several possible forms of a gene that occupy the same position (locus) on a chromosome. Because humans are diploid, each individual carries two alleles for most genes—one inherited from each parent. Alleles can be identical (homozygous) or different (heterozygous). In the context of the FTO gene, which is linked to body mass index (BMI), the risk allele "A" at the rs9939609 single nucleotide polymorphism (SNP) is associated with a modest increase in obesity risk. A person who is homozygous "AA" may benefit from more aggressive lifestyle interventions compared with a "TT" individual.

Genotype describes the specific genetic makeup of an individual at a particular locus or across the entire genome. When a test reports the genotype "GG" for the rs1801133 SNP in the MTHFR gene, it indicates that the person carries two copies of the G allele. The genotype provides the raw data that clinicians interpret to predict phenotypic outcomes, such as folate metabolism efficiency. Accurate genotype determination requires high-quality DNA extraction, reliable assay design, and appropriate quality control measures.

Phenotype is the observable characteristic or trait that results from the interaction of genotype with

environmental factors, including diet, lifestyle, and exposure to chemicals. For example, the phenotype of “high plasma homocysteine” can result from the MTHFR “TT” genotype combined with low dietary intake of folate, vitamin B12, and B6. Understanding the genotype-phenotype relationship enables nutrition professionals to tailor interventions that address both genetic predisposition and modifiable environmental influences.

Single nucleotide polymorphism (SNP) is the most common type of genetic variation, representing a single base-pair change at a specific location in the genome. SNPs are catalogued in public databases such as dbSNP and are often used as markers in association studies. An SNP can be synonymous (no change in the amino acid sequence), missense (substitutes one amino acid for another), or nonsense (creates a premature stop codon). In nutrigenetics, the rs662 SNP in the PON1 gene influences the enzyme’s ability to protect lipids from oxidative damage; carriers of the “C” allele may experience greater benefits from antioxidant-rich foods.

Copy number variation (CNV) refers to structural alterations in the genome that result in the duplication or deletion of large DNA segments, ranging from a few kilobases to several megabases. CNVs can affect gene dosage and therefore influence metabolic capacity. For instance, a duplication of the AMY1 gene, which encodes salivary amylase, is associated with higher amylase activity and improved starch digestion. Individuals with multiple AMY1 copies may tolerate high-carbohydrate diets more readily than those with fewer copies.

Insertion–deletion (indel) describes a type of mutation where short segments of DNA are inserted into or deleted from the genome. Indels can cause frameshifts if they occur within coding regions, potentially leading to loss-of-function proteins. An example relevant to nutrition is the 2-base pair deletion in the promoter region of the TCF7L2 gene, which has been linked to altered glucose regulation and type 2 diabetes risk. Detecting indels requires sequencing or specialized genotyping platforms that can accurately resolve length differences.

Whole genome sequencing (WGS) is a comprehensive method that determines the complete DNA sequence of an individual’s genome, including coding and non-coding regions, regulatory elements, and mitochondrial DNA. WGS provides the most detailed view of genetic variation, capturing SNPs, CNVs, indels, and structural rearrangements. In personalized nutrition, WGS can uncover rare variants that influence nutrient metabolism, such as loss-of-function mutations in the PCSK9 gene that affect cholesterol homeostasis. However, the sheer volume of data generated by WGS poses challenges for interpretation, data storage, and privacy protection.

Whole exome sequencing (WES) focuses on sequencing only the exons—the protein-coding portions—of the genome, which represent roughly 1–2% of the total DNA but contain the majority of known disease-causing mutations. WES is a cost-effective alternative to WGS when the primary interest lies in identifying variants that directly alter protein structure. For nutrition professionals, WES may reveal pathogenic variants in genes like G6PD, which affect red blood cell stability and can influence

recommendations regarding certain foods (e.G., Fava beans) and supplements.

Targeted gene panel testing examines a pre-selected set of genes that are known to be relevant for a particular clinical or nutritional question. Panels for nutrigenomics typically include genes involved in lipid metabolism (APOE, LPL), carbohydrate handling (TCF7L2, GCK), and micronutrient processing (MTHFR, SLC23A1). Targeted panels are advantageous because they reduce sequencing costs, simplify data analysis, and limit incidental findings. Nonetheless, they may miss novel or rare variants outside the selected regions, which could be important for a comprehensive assessment.

Genome-wide association study (GWAS) is a research approach that scans the genomes of large populations to identify statistical associations between genetic markers (usually SNPs) and specific traits or diseases. GWAS have identified numerous loci linked to dietary patterns, nutrient biomarkers, and metabolic outcomes. For example, a GWAS discovered an association between the rs174547 SNP in the FADS1 gene and plasma levels of long-chain polyunsaturated fatty acids. Individuals carrying the "C" allele may have reduced conversion of alpha-linolenic acid to eicosapentaenoic acid, suggesting a potential benefit from direct EPA supplementation.

Polygenic risk score (PRS) aggregates the effects of many genetic variants across the genome into a single numeric value that estimates an individual's genetic predisposition to a trait. PRS are calculated by weighting each variant according to its effect size derived from GWAS data. In nutrition, a PRS for obesity could combine risk alleles from FTO, MC4R, TMEM18, and others to stratify clients into low, moderate, or high genetic risk categories. While PRS can enhance risk stratification, their predictive power varies across ethnic groups, and they should be interpreted alongside lifestyle and environmental factors.

Epigenetics describes heritable changes in gene expression that do not involve alterations to the underlying DNA sequence. The most studied epigenetic mechanism is DNA methylation, which typically occurs at cytosine-phosphate-guanine (CpG) sites and can silence gene transcription. Nutrients such as folate, choline, and betaine serve as methyl donors, influencing the epigenetic landscape. For instance, maternal intake of folic acid during pregnancy can modify DNA methylation patterns in offspring, potentially affecting long-term metabolic health. Epigenetic testing can therefore provide insight into how diet interacts with the genome to shape phenotypic outcomes.

DNA methylation is the addition of a methyl group to the 5-carbon of cytosine residues, often within CpG islands located near gene promoters. Methylation status can be measured using techniques like bisulfite conversion followed by sequencing. In the context of nutrition, hypermethylation of the PPARGC1A promoter has been linked to reduced mitochondrial biogenesis and impaired fatty-acid oxidation, suggesting that dietary strategies aimed at modifying methylation (e.G., Increased intake of methyl-rich foods) could support metabolic flexibility.

Nutrigenomics is the study of how an individual's entire genome influences their response to nutrients, dietary patterns, and bioactive food components. This field integrates high-throughput omics technologies

(genomics, transcriptomics, proteomics, metabolomics) to elucidate complex gene-diet interactions. A nutrigenomic investigation might examine how a high-fat diet alters the expression of genes involved in lipid transport in individuals with different APOE genotypes. The goal is to move beyond single-gene approaches and capture the systemic impact of nutrition on the genome.

Nutrigenetics focuses specifically on how genetic variation affects an individual's nutritional needs, metabolism, and susceptibility to diet-related diseases. It is the primary lens through which most personalized nutrition services operate. For example, nutrigenetic testing may reveal that a client carries the "GG" genotype for the rs1801282 SNP in the PPARG gene, which is associated with improved insulin sensitivity when the diet is rich in monounsaturated fats. The practitioner can then recommend a Mediterranean-style eating plan to optimize the client's metabolic response.

Gene-diet interaction refers to the phenomenon where the effect of a dietary factor on health outcomes depends on the individual's genotype. This concept is illustrated by the interaction between the APOE ϵ 4 allele and saturated fat intake: Carriers of ϵ 4 experience a greater increase in LDL-cholesterol when consuming high-saturated-fat diets compared with non-carriers. Recognizing gene-diet interactions enables nutrition professionals to customize macronutrient distribution, micronutrient supplementation, and lifestyle advice based on genetic risk.

Pharmacogenomics (also called pharmacogenetics) examines how genetic variation influences drug metabolism, efficacy, and toxicity. Although primarily associated with medication, pharmacogenomics is relevant to nutrition because many nutrients act as pharmaceuticals or modulate drug pathways. For instance, the CYP2C19 enzyme metabolizes both the antiplatelet drug clopidogrel and certain flavonoids. A client with a loss-of-function CYP2C19 allele may experience reduced activation of clopidogrel and altered metabolism of dietary flavonoids, affecting both cardiovascular risk and antioxidant status.

Metabolomics is the comprehensive analysis of small-molecule metabolites in biological samples such as blood, urine, or saliva. Metabolomic profiling can identify biochemical signatures that reflect both genetic background and dietary intake. A practical application is the measurement of plasma carotenoid levels to assess fruit and vegetable consumption, which may be influenced by genetic variants in transport proteins like SCARB1. Metabolomics therefore serves as a bridge between genotype, phenotype, and environmental exposure.

Transcriptomics studies the complete set of RNA transcripts produced by the genome under specific conditions. Dietary interventions can cause rapid changes in gene expression, detectable through RNA-sequencing. For example, a high-protein meal may up-regulate genes involved in amino-acid catabolism, an effect that can be modulated by polymorphisms in the BCAT2 gene. Understanding transcriptomic responses helps nutritionists predict how different foods will influence metabolic pathways in genetically diverse populations.

Proteomics analyzes the entire complement of proteins expressed in a cell, tissue, or organism. Protein

abundance and post-translational modifications can be affected by both genetic variants and nutrient status. A case in point is the influence of the GSTT1 null genotype on the activity of glutathione-S-transferase enzymes, which detoxify reactive metabolites derived from processed meats. Proteomic data can therefore inform recommendations on antioxidant intake for individuals with reduced detoxification capacity.

Microbiome refers to the collection of microorganisms (bacteria, archaea, fungi, and viruses) residing in the human body, particularly the gastrointestinal tract. The gut microbiome interacts with host genetics to shape nutrient absorption, immune function, and metabolic health. Certain host genetic variants, such as those in the FUT2 gene that determine secretor status, influence the composition of the intestinal microbiota and the production of short-chain fatty acids. Incorporating microbiome profiling alongside genetic testing can enhance the precision of dietary recommendations.

Secretor status is determined by functional variants in the FUT2 gene, which encodes an enzyme that adds fucose to mucosal glycans. Secretors (functional FUT2) express these glycans on the intestinal surface, providing substrates for specific bacterial taxa. Non-secretors lack this capability, leading to distinct microbial communities. Secretor status has been linked to susceptibility to infections, vitamin B12 absorption, and response to prebiotic fibers. Testing for FUT2 variants can guide the selection of probiotic or prebiotic interventions.

Genetic risk factor denotes a specific allele or combination of alleles that increases the probability of developing a disease or condition. In nutrition, a well-known genetic risk factor is the APOE ε4 allele, which raises the risk of coronary heart disease and Alzheimer's disease, partly through its effect on lipid transport. Identifying such risk factors enables proactive dietary modifications—such as limiting saturated fat and emphasizing omega-3 fatty acids—to mitigate the heightened risk.

Protective genetic factor is a genetic variant associated with reduced disease risk or enhanced physiological function. The ACTN3 R577X polymorphism illustrates this concept: Individuals homozygous for the "X" allele lack functional α-actinin-3 protein in fast-twitch muscle fibers, which may confer endurance advantages and lower susceptibility to certain muscle injuries. Recognizing protective factors can inform exercise and nutrition prescriptions that capitalize on inherent strengths.

Variant of uncertain significance (VUS) describes a genetic alteration whose impact on protein function or health outcomes is not yet established. VUS are common in comprehensive sequencing reports because many rare variants have not been studied extensively. When a VUS is identified in a gene relevant to nutrient metabolism, such as a novel missense mutation in SLC5A2 (a glucose transporter), the practitioner should convey uncertainty, recommend monitoring of relevant biomarkers, and avoid making definitive dietary changes until further evidence emerges.

Pathogenic variant is a genetic alteration that has been demonstrated to cause disease or significantly impair biological function. Pathogenic variants in the PAH gene, for example, lead to phenylketonuria (PKU),

a condition requiring strict dietary restriction of phenylalanine. In personalized nutrition, the detection of a pathogenic variant obligates the practitioner to provide evidence-based medical nutrition therapy, often in collaboration with a clinical geneticist or physician.

Carrier status indicates that an individual possesses one copy of a recessive pathogenic variant but does not express the associated disease phenotype. Carrier testing is common for conditions like hereditary hemochromatosis (mutations in HFE) or thalassemia (mutations in HBB). Carriers may still experience mild phenotypic effects, such as increased iron absorption in heterozygous HFE C282Y carriers, which can influence recommendations for iron intake and monitoring.

Genetic counseling is a professional service that provides information, support, and guidance to individuals undergoing genetic testing. In the nutrition context, counselors help clients understand the implications of test results, assess psychosocial impacts, and make informed decisions about dietary changes. Effective counseling incorporates risk communication, cultural sensitivity, and clear explanation of technical concepts, ensuring that clients do not misinterpret probabilistic information as deterministic.

Informed consent is a foundational ethical requirement that ensures individuals understand the purpose, benefits, risks, and potential outcomes of genetic testing before agreeing to proceed. Consent forms for nutrigenomic testing typically address issues such as data storage, sharing with third parties, and the possibility of incidental findings unrelated to nutrition. Obtaining genuine informed consent protects client autonomy and aligns with professional standards.

Incidental finding (also called secondary finding) is an unexpected result that emerges from a genetic test but falls outside the primary scope of inquiry. For example, a whole-genome test ordered to assess nutrient metabolism may reveal a pathogenic BRCA1 mutation that confers high breast-cancer risk. Handling incidental findings requires established protocols, including pre-test counseling about the possibility of such results, clear pathways for referral to appropriate medical specialists, and respect for the client's preferences regarding disclosure.

Data privacy concerns the protection of personal genetic information from unauthorized access, misuse, or commercial exploitation. Regulations such as the General Data Protection Regulation (GDPR) in Europe and the Health Insurance Portability and Accountability Act (HIPAA) in the United States set standards for secure storage, de-identification, and permissible sharing of genetic data. Nutrition professionals must implement robust security measures, obtain explicit consent for data use, and be transparent about data handling practices.

Population stratification describes the presence of systematic genetic differences between subpopulations that can confound association studies. If a study cohort includes individuals of diverse ancestry without accounting for genetic background, false associations may arise. In practice, this means that a SNP identified as a risk factor for high cholesterol in a European cohort may not have the same effect in an Asian or African population. Nutrition professionals should therefore interpret genetic risk scores within the

context of the client's ethnic background and use ancestry-adjusted reference data whenever possible.

Reference genome is a standardized DNA sequence that serves as a template for aligning individual genetic data. The most widely used reference is GRCh38/hg38 for the human genome. Aligning a client's reads to the reference enables identification of variants relative to the "normal" sequence. However, the reference genome does not capture all human diversity; therefore, using population-specific reference panels can improve variant calling accuracy, especially for under-represented groups.

Allele frequency denotes the proportion of a specific allele in a given population. Minor allele frequency (MAF) is often used to describe how common the less frequent allele is. For instance, the rs174537 SNP in FADS1 has a MAF of approximately 0.30 in European populations but varies widely across continents. Knowledge of allele frequencies helps interpret the clinical relevance of a variant; rare alleles may have larger effect sizes but affect fewer individuals, whereas common alleles often contribute modestly to risk.

Effect size quantifies the magnitude of the association between a genetic variant and a trait, typically expressed as an odds ratio, beta coefficient, or percentage change. In nutrition, the effect size of the FTO rs9939609 "A" allele on BMI is roughly 0.3 Kg/m² per copy, indicating a modest influence that can be amplified by lifestyle factors. Understanding effect sizes prevents over-interpretation of single-gene results and supports a balanced view of genetic contributions.

Heritability measures the proportion of phenotypic variance in a trait that can be attributed to genetic variation within a specific population. Heritability is expressed as a value between 0 and 1 (or as a percentage). For example, the heritability of serum vitamin D levels is estimated at 0.5, indicating that genetics accounts for about half of the variability, with the remainder driven by sun exposure, diet, and other environmental factors. Recognizing heritability informs expectations about how much genetic testing can explain and guides the emphasis on modifiable lifestyle components.

Gene expression refers to the process by which information encoded in a gene is transcribed into messenger RNA and then translated into a functional protein. Gene expression can be up-regulated or down-regulated in response to dietary cues. A classic illustration is the induction of the CYP1A2 enzyme by caffeine consumption; individuals with the "AA" genotype at rs762551 may exhibit faster caffeine metabolism, influencing recommendations regarding coffee intake and timing.

Gene silencing involves mechanisms that reduce or eliminate the expression of a particular gene. RNA interference (RNAi) and CRISPR-based approaches can achieve targeted silencing. Although not yet routine in clinical nutrition, experimental studies have used gene silencing to down-regulate SREBF1, a transcription factor that promotes lipogenesis, thereby exploring potential therapeutic avenues for fatty-liver disease.

Gene editing denotes technologies that directly modify the DNA sequence, with CRISPR-Cas9 being the most prominent tool. Gene editing holds promise for correcting pathogenic variants that affect nutrient metabolism, such as mutations in the GLUT2 transporter that impair glucose sensing. However, ethical, regulatory, and safety considerations currently limit its application in nutrition practice, confining its use to

research settings.

Clinical utility assesses whether a genetic test provides information that can meaningfully influence health outcomes, such as improving disease prevention, guiding therapy, or informing lifestyle changes. In personalized nutrition, a test that identifies a variant affecting folate metabolism (e.g., MTHFR “TT”) may have clinical utility if it leads to targeted folate supplementation that corrects elevated homocysteine levels and reduces cardiovascular risk. Demonstrating clinical utility requires robust evidence from intervention trials.

Analytical validity evaluates the accuracy, reliability, and reproducibility of a genetic test in detecting the intended genetic variant. Parameters include sensitivity (ability to detect true positives), specificity (ability to exclude false positives), and concordance with reference methods. A test with high analytical validity is essential before any clinical or nutritional recommendations are made, as erroneous results can misguide interventions.

Clinical validity measures how well a genetic test predicts a specific health outcome. For example, the clinical validity of the APOE ε4 test for predicting Alzheimer’s disease risk is moderate, with a relative risk increase of 2–3-fold. In nutrition, the clinical validity of a SNP associated with caffeine metabolism determines whether caffeine-related advice (e.g., Timing of consumption before exercise) is justified.

Clinical significance reflects the practical importance of a genetic finding for patient care. A variant may be analytically and clinically valid but still have limited clinical significance if the effect size is negligible or if effective interventions are unavailable. For instance, a SNP that modestly influences the taste perception of bitterness may have low clinical significance for dietary counseling compared with a variant that dramatically affects lipid metabolism.

Pharmacogenomic panel is a collection of genes that influence drug response, often including enzymes such as CYP2D6, CYP2C19, and transporters like SLCO1B1. While primarily used for medication management, these panels intersect with nutrition because many nutrients share metabolic pathways with drugs. A nutritionist working with a client on a low-dose aspirin regimen might consider the client’s SLCO1B1 genotype to anticipate potential interactions with statin therapy and dietary sources of cholesterol.

Biomarker is a measurable indicator of a biological state, such as a nutrient level, metabolic product, or gene expression pattern. Genetic biomarkers include specific SNPs, while phenotypic biomarkers encompass plasma triglycerides, fasting glucose, or urinary nitrogen excretion. Combining genetic and biochemical biomarkers enables a more comprehensive assessment of nutritional status and risk.

Risk assessment integrates genetic, phenotypic, and lifestyle data to estimate an individual’s probability of developing a condition. In personalized nutrition, risk assessment may involve calculating a PRS for type-2 diabetes, measuring fasting insulin, and evaluating dietary patterns. The resulting risk profile guides the intensity and focus of nutritional interventions, such as recommending a low-glycemic-index diet for

high-risk individuals.

Evidence-based practice emphasizes the use of scientifically validated information to inform clinical decisions. For genetics-guided nutrition, evidence-based practice requires systematic review of the literature on gene-diet interactions, assessment of study quality, and application of findings that demonstrate reproducible benefits. Practitioners must remain vigilant about emerging data, as the field evolves rapidly and early studies may be later contradicted.

Gene-environment interaction ($G \times E$) captures the dynamic interplay between genetic predisposition and external factors such as diet, physical activity, and exposure to toxins. A classic $G \times E$ example is the interaction between the TCF7L2 risk allele and high-carbohydrate intake, which together amplify the risk of impaired glucose tolerance more than either factor alone. Understanding $G \times E$ relationships helps nutritionists prioritize interventions that can offset genetic risk.

Gene-gene interaction (epistasis) occurs when the effect of one gene is modified by one or more other genes. For instance, the impact of the APOE $\epsilon 4$ allele on LDL-cholesterol may be attenuated in individuals who also carry a protective variant in the LIPG gene. Recognizing epistatic effects prevents oversimplified interpretations of single-gene tests and encourages a more holistic view of the genome.

Genotype-phenotype correlation describes the relationship between a specific genetic variant and the observable trait it influences. Strong genotype-phenotype correlations, such as the link between PAH mutations and phenylalanine levels, provide clear guidance for dietary management. Weak correlations, as often seen with complex traits like obesity, require integration of multiple data sources and caution in translating findings into practice.

Allelic dosage refers to the number of copies of a particular allele an individual possesses. For a dosage-dependent effect, each additional copy may incrementally increase risk or benefit. The APOE $\epsilon 4$ allele exhibits allelic dosage: Heterozygous carriers have a moderate increase in LDL-cholesterol, while homozygous carriers experience a larger elevation, necessitating more aggressive dietary fat restriction.

Haplotype is a set of alleles at neighboring loci that are inherited together on the same chromosome. Haplotypes can capture the combined effect of multiple SNPs better than single-marker analysis. For example, a haplotype spanning the FADS1 and FADS2 genes may more accurately predict plasma omega-3 levels than any individual SNP alone, allowing refined recommendations for fish oil supplementation.

Linkage disequilibrium (LD) describes the non-random association of alleles at different loci. High LD means that neighboring SNPs are often inherited together, which is exploited in GWAS to tag regions of interest without sequencing every base. Understanding LD patterns is essential when selecting proxy SNPs for a gene of interest; a tag SNP in strong LD with a functional variant can serve as a reliable surrogate in a nutrigenetic panel.

Phasing is the process of determining which alleles reside on the same chromosome (haplotype) versus

opposite chromosomes. Accurate phasing can clarify whether two risk alleles are in cis (same chromosome) or trans (different chromosomes), influencing the interpretation of combined effects. In clinical nutrition, phasing may be relevant for compound heterozygous variants in the GCK gene, where the arrangement of mutations can affect enzyme activity.

Imputation is a statistical technique that predicts untyped genetic variants based on known LD patterns and reference panels. Imputation expands the coverage of genetic data without additional laboratory testing, facilitating more comprehensive risk assessment. For nutrition professionals using pre-designed SNP arrays, imputed data can provide insight into additional loci that influence nutrient metabolism, though the confidence of imputed calls must be evaluated.

Quality control (QC) procedures ensure the reliability of genetic data by filtering out low-quality samples, checking for contamination, verifying sex concordance, and assessing call rates. QC metrics such as Hardy-Weinberg equilibrium, heterozygosity rates, and duplicate concordance are standard in research laboratories. Implementing QC in commercial testing pipelines safeguards against erroneous genotype assignments that could mislead dietary recommendations.

Hardy-Weinberg equilibrium (HWE) is a principle that predicts genotype frequencies in a stable population under random mating. Deviations from HWE in a test dataset may signal genotyping errors, population stratification, or selection pressures. Nutrition analysts routinely assess HWE for each SNP in a cohort to confirm data integrity before proceeding with association analyses.

Minor allele is the less common allele at a given SNP within a specific population. The term is synonymous with "rare allele" when the minor allele frequency is below 0.01. Identifying the minor allele is important for interpreting risk direction; a study may report that the minor "G" allele of a certain SNP is associated with increased vitamin D levels, guiding supplementation strategies for carriers.

Minor allele frequency (MAF) quantifies how prevalent the minor allele is in a reference population. MAF values inform decisions about which variants to include in a nutrigenetic test: Common variants (MAF > 0.05) are typically prioritized because they affect larger numbers of people, while rare variants may be reserved for specialized panels or research contexts.

Genomic imprinting is an epigenetic phenomenon where gene expression depends on the parent of origin. Imprinted genes, such as IGF2, can have dosage effects that influence growth and metabolism. While imprinting is not a primary focus of most nutrigenetic services, awareness of imprinting can be relevant for conditions like Prader-Willi syndrome, where dietary management must consider altered appetite regulation.

Loss-of-function (LoF) variant is a mutation that reduces or eliminates the activity of the encoded protein. LoF variants in the PCSK9 gene lower LDL-cholesterol by decreasing receptor degradation, providing a natural model for cholesterol-lowering therapies. Detecting LoF variants can inform personalized recommendations, such as the potential for reduced reliance on statins or the need for monitoring lipid

levels more closely.

Gain-of-function (GoF) variant enhances the activity of a protein relative to the wild-type. A GoF mutation in the SCN5A gene, for example, can increase sodium channel activity, affecting cardiac electrophysiology and potentially interacting with caffeine intake. Recognizing GoF variants helps anticipate adverse reactions to certain foods or supplements that may exacerbate the underlying physiological change.

Pharmacokinetics describes how the body absorbs, distributes, metabolizes, and eliminates a substance. Genetic variants in metabolic enzymes, such as CYP1A2, influence the pharmacokinetics of both drugs and dietary compounds like caffeine. Understanding these relationships enables nutritionists to advise clients on optimal timing of nutrient intake relative to medication schedules.

Pharmacodynamics concerns the biological effects of a substance on the body, including receptor binding and downstream signaling. Genetic differences in receptor genes, such as DRD2 (dopamine receptor), can modify the reward response to sugar and influence dietary preferences. Tailoring dietary advice to account for such genetic influences may improve adherence to healthier eating patterns.

Metabolic pathway is a series of enzymatic reactions that convert substrates into products, ultimately generating energy or biosynthetic precursors. Genetic variants can disrupt specific steps within a pathway. For example, polymorphisms in the SLC22A5 carnitine transporter affect fatty-acid oxidation, suggesting that carriers might benefit from increased dietary carnitine or medium-chain triglycerides to support mitochondrial function.

Enzyme activity refers to the rate at which an enzyme catalyzes a biochemical reaction. Enzyme activity can be quantified in vitro or inferred from genotype. The LCT lactase enzyme exhibits reduced activity in individuals with the "CC" genotype at rs4988235, leading to lactose malabsorption. Providing lactase enzyme supplements or recommending lactose-free dairy alternatives directly addresses the enzymatic deficiency.

Transporter protein facilitates the movement of molecules across cellular membranes. Variants in transporters such as SLC23A1 (vitamin C transporter) or SLC30A8 (zinc transporter) can alter nutrient absorption efficiency. For a client with a reduced-function SLC23A1 allele, higher dietary vitamin C intake or targeted supplementation may be necessary to achieve adequate plasma concentrations.

Receptor is a protein that binds specific ligands (e.g., Hormones, neurotransmitters, nutrients) and initiates a cellular response. Genetic differences in receptors can modify sensitivity to dietary components. The bitter taste receptor gene TAS2R38 determines perception of phenylthiocarbamide (PTC) and influences preference for certain vegetables; individuals with the "PAV" haplotype perceive bitterness strongly and may require culinary strategies to increase vegetable intake.

Metabolic syndrome is a cluster of risk factors—including abdominal obesity, dyslipidemia, elevated blood pressure, and insulin resistance—that increase cardiovascular disease risk. Genetic testing can identify

variants that predispose individuals to components of metabolic syndrome, such as the ADIPOQ SNP rs1501299, which is associated with lower adiponectin levels and higher insulin resistance. Tailored dietary plans focusing on fiber, low-glycemic carbohydrates, and healthy fats can mitigate genetically driven risk.

Obesity-related gene is any gene whose variants have been statistically linked to body weight regulation. Besides FTO, other obesity-related genes include MC4R, TMEM18, and BDNF.