



ELITE GENE LABS

GENETIC POTENTIAL FOR OPTIMAL PERFORMANCE

Gene Comprehensive Nutrigenomic Report

Accession Number: #####

Specimen Collected: ###/###/####

Specimen Received: ###/###/####

Report Generated: August 12, 2025

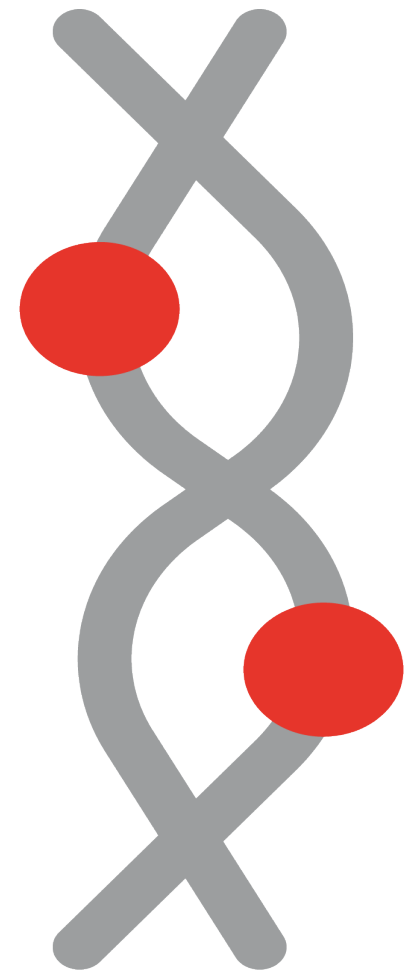
Specimen Type: Buccal Swab

Provider: #####

Patient Name: #####

Patient DOB: ###/###/####

Patient Gender: Female



Do not make any decisions about your health solely based on the information contained in this report.
Always consult with a licensed and experienced health practitioner when you receive this report.



– 21 – Female

(-/-) Normal Risk (-/+) Medium Risk (+/+) High Risk

rsID	Gene	Genetic Result	Therapeutics Associated With Positive Result	Highly Recommended Therapeutics	Provider Discretion: As Needed Formula Recommendations	Lifestyle Recommendations	Laboratory Recommendations
Immune Autoimmune Inflammatory							
Cellular Inflammation							
rs2250656	C3	T/T (+/+)	Anti-Inflammatory Therapy: Curcumin, Omega-3 Fatty Acids, Resveratrol, Quercetin, Low Dose Naltrexone (LDN), CBD Oil	PEA Calm Omega Calm	Cannab Calm+ Prescription Low Dose Naltrexone (LDN)	Consider Anti-inflammatory Diet and Lifestyle	General Inflammatory Markers: Serum High Sensitivity C-Reactive Protein, Serum Iron and Ferritin, Erythrocyte Sedimentation Rate, Serum Complement C3, Serum Interleukin 6 Lymphocyte Profile AND/OR Antibody Testing Additional Options: Adrenal Stress Profile, Sex Hormone Panel, Full Thyroid Panel, Food Allergy Panel, Comprehensive Micronutrient Testing, Microbial Titer (Candida, Epstein-Barr Virus, etc.), Toxic Metal Testing, Environmental Allergy Testing
rs2569190	CD14	A/G (+/-)					
rs2069812	IL5	G/G (+/+)					
rs2243250	IL4	C/C (-/-)					
rs1800925	IL13	C/C (-/-)					
rs11209026	IL23R	G/G (+/+)					
rs10181656	STAT4	C/C (-/-)					
rs1800795	IL6	G/G (+/+)					
rs1800629	TNF	G/G (-/-)					
rs3761847	TRAF1	G/G (+/+)					
rs9657182	IDO1	T/T (-/-)					
rs2069762	IL2	A/A (-/-)					
rs12722489	IL2RA	C/C (+/+)					
rs243324	SOCS1	A/A (+/+)					
rs231775	CTLA4	A/G (+/-)					



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Immune Autoimmune Inflammatory							
Essential Fatty Acid Metabolism							
rs174547	FADS1	T/T (-/-)	Long-chain essential fatty acids: EPA, DHA, AA				
Low Dose Naltrexone Response							
rs1076560	DRD2	C/C (-/-)	Increased Efficacy of Naltrexone				
Nitric Oxide Inducibility							
rs4795067	NOS2	A/A (-/-)	Inducible Nitric Oxide Synthase (iNOS) Activity, Anti-Infectives, Beta Glucans	Immune Defend	Reduced iNOS Activity May Increase Susceptibility to Infections Consider 3-Factor Immune Complex if Chronic Infections Are Common		
Vitamin D							
rs2228570	VDR	G/G (-/-)	Vitamin D, Vitamin K				



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rsID	Gene	Genetic Result	Therapeutics Associated With Positive Result	Highly Recommended Therapeutics	Provider Discretion: As Needed Formula Recommendations	Lifestyle Recommendations	Laboratory Recommendations
Immune Autoimmune Inflammatory							
Autophagy Efficiency							
rs510432	ATG5	C/C (+/+)	Curcumin, Lithium Orotate, D-Chiro-Inositol, Catechins, Resveratrol, 12+ Hour Fasting	Inositol Pro Intracellular Detox Complex		Intermittent Fasting (12-15 Hours) Exercise Regularly	Routine Blood Sugar, Insulin, and HbA1c
rs26538	ATG12	C/T (+/-)					
rs10210302	ATG16L1	C/T (+/-)					
rs2241880	ATG16L1	A/G (+/-)					
Detoxification							
rs234706	CBS	G/A (+/-)	Methyltetrahydrofolate, Methylcobalamin, Pyridoxal 5'-Phosphate (B6), Choline, Trimethylglycine, Serine, N-Acetyl Cysteine		Methylation Complete Pro if Homocysteine Levels Are High N-Acetyl Cysteine if Homocysteine Levels Are Low	Avoid Herbicides and Pesticides	Plasma Homocysteine
rs1021737	CTH	G/T (+/-)	N-Acetyl Cysteine, Glutathione, Pyridoxal 5'-Phosphate		N-Acetyl Cysteine, Especially if Exposed to Industrial Toxins, Anesthesia, Alcohol, Etc.		
rs6721961	NFE2L2	G/G (-/-)	Pterostilbene, Green Tea (Epigallocatechin Gallate), Tumeric, Sulforaphane, Endurance Exercise				
rs1695	GSTP1	A/A (-/-)	N-Acetyl Cysteine (NAC), Glutathione				



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rsID	Gene	Genetic Result	Therapeutics Associated With Positive Result	Highly Recommended Therapeutics	Provider Discretion: As Needed Formula Recommendations	Lifestyle Recommendations	Laboratory Recommendations
Immune Autoimmune Inflammatory							
Environmental Inflammation							
rs10156191	AOC1	C/T (+/-)	Poor Ability to Break Down External Histamine				
rs11558538	HNMT	C/C (-/-)					
rs12995000	HNMT	C/T (+/-)					
rs492602	FUT2	A/G (+/-)	Prebiotics and Probiotics Needed		Berry Good Immune	Consider Consumption of Prebiotic and Probiotic Foods	
rs2187668	HLA DQA1	C/C (-/-)	High Risk of Gluten and Casein Sensitivity, Broad Spectrum Enzyme				
rs7454108	HLA DQB1	T/T (-/-)					
rs2056131	ITGB3	A/G (+/-)	High Reactivity To Mold/Fungi			Highly Recommend Avoiding Mold/Fungal/Yeast Exposure	

Summary for Elite Autoimmune

Highly Recommended Therapeutics

Provider Discretion: As Needed Formula Recommendations

Lifestyle Recommendations

Laboratory Recommendations

Cellular Inflammation

- PEA Calm
- Omega Calm

- Cannab Calm+
- Prescription Low Dose Naltrexone (LDN)

- Consider Anti-inflammatory Diet and Lifestyle

- General Inflammatory Markers: Serum High Sensitivity C-Reactive Protein, Serum Iron and Ferritin, Erythrocyte Sedimentation Rate, Serum Complement C3, Serum Interleukin 6
- Lymphocyte Profile AND/OR Antibody Testing
- Additional Options: Adrenal Stress Profile, Sex Hormone Panel, Full Thyroid Panel, Food Allergy Panel, Comprehensive Micronutrient Testing, Microbial Titer (Candida, Epstein-Barr Virus, etc.), Toxic Metal Testing, Environmental Allergy Testing

- Immune Defend

- Reduced iNOS Activity May Increase Susceptibility to Infections
- Consider 3-Factor Immune Complex if Chronic Infections Are Common

Autophagy Efficiency

- Inositol Pro
- Intracellular Detox Complex

- Intermittent Fasting (12-15 Hours)
- Exercise Regularly

- Routine Blood Sugar, Insulin, and HbA1c

Detoxification

- Methylation Complete Pro if Homocysteine Levels Are High
- N-Acetyl Cysteine if Homocysteine Levels Are Low
- N-Acetyl Cysteine, Especially if Exposed to Industrial Toxins, Anesthesia, Alcohol, Etc.

- Avoid Herbicides and Pesticides

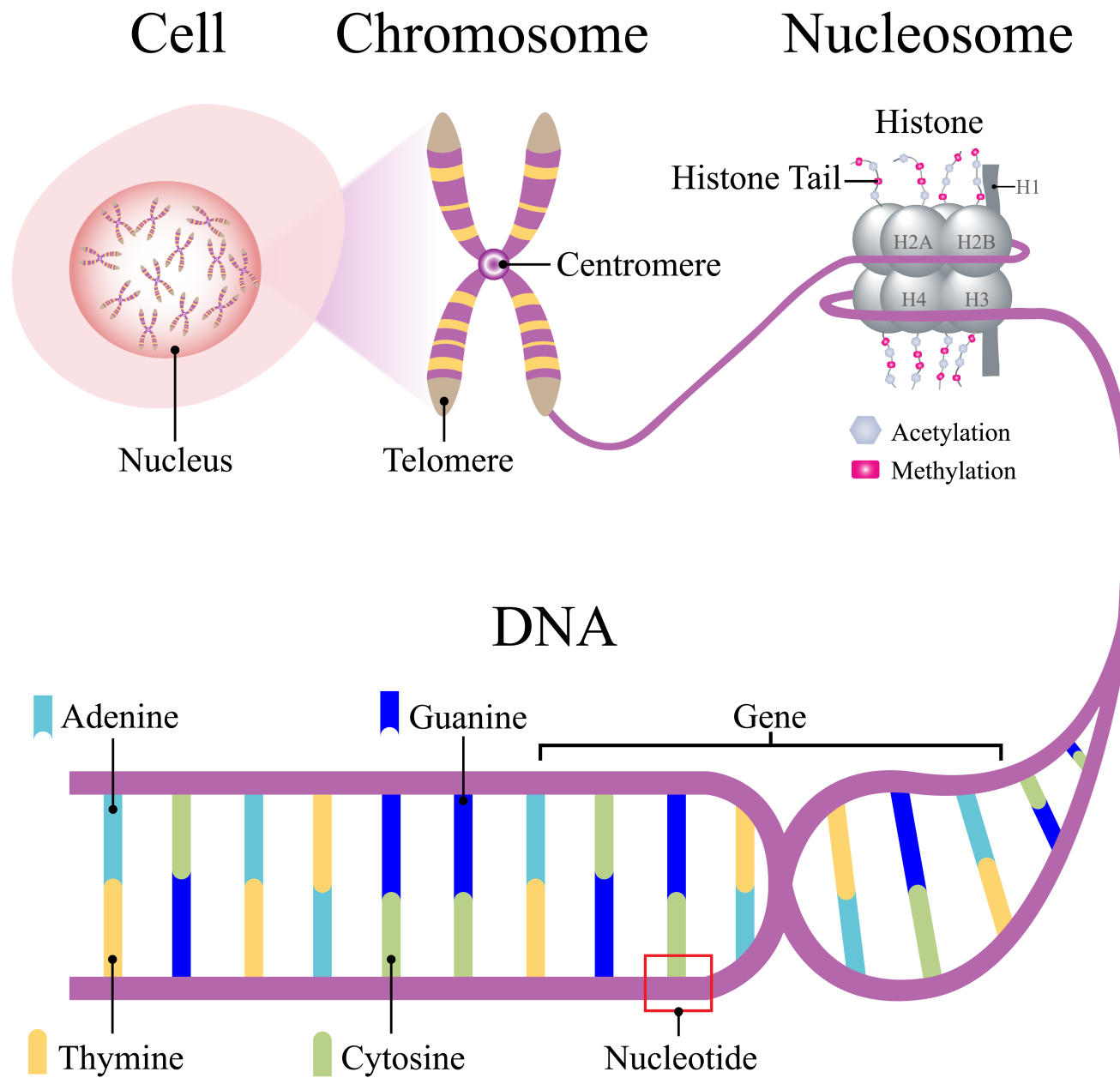
- Plasma Homocysteine

Environmental Inflammation

- Berry Good Immune

- Consider Consumption of Prebiotic and Probiotic Foods

- Highly Recommend Avoiding Mold/Fungal/Yeast Exposure



VITAMIN D

FOOD SOURCES



Tuna



Mushrooms



Eggs



Mackerel



Milk Products
(including fortified
alternatives such as
almond, coconut,
oat, etc.)



BENEFITS AS YOU AGE



Lower Risk
of Fractures



Improves
Heart Function



Supports
Immune System



Speeds
Wound Healing

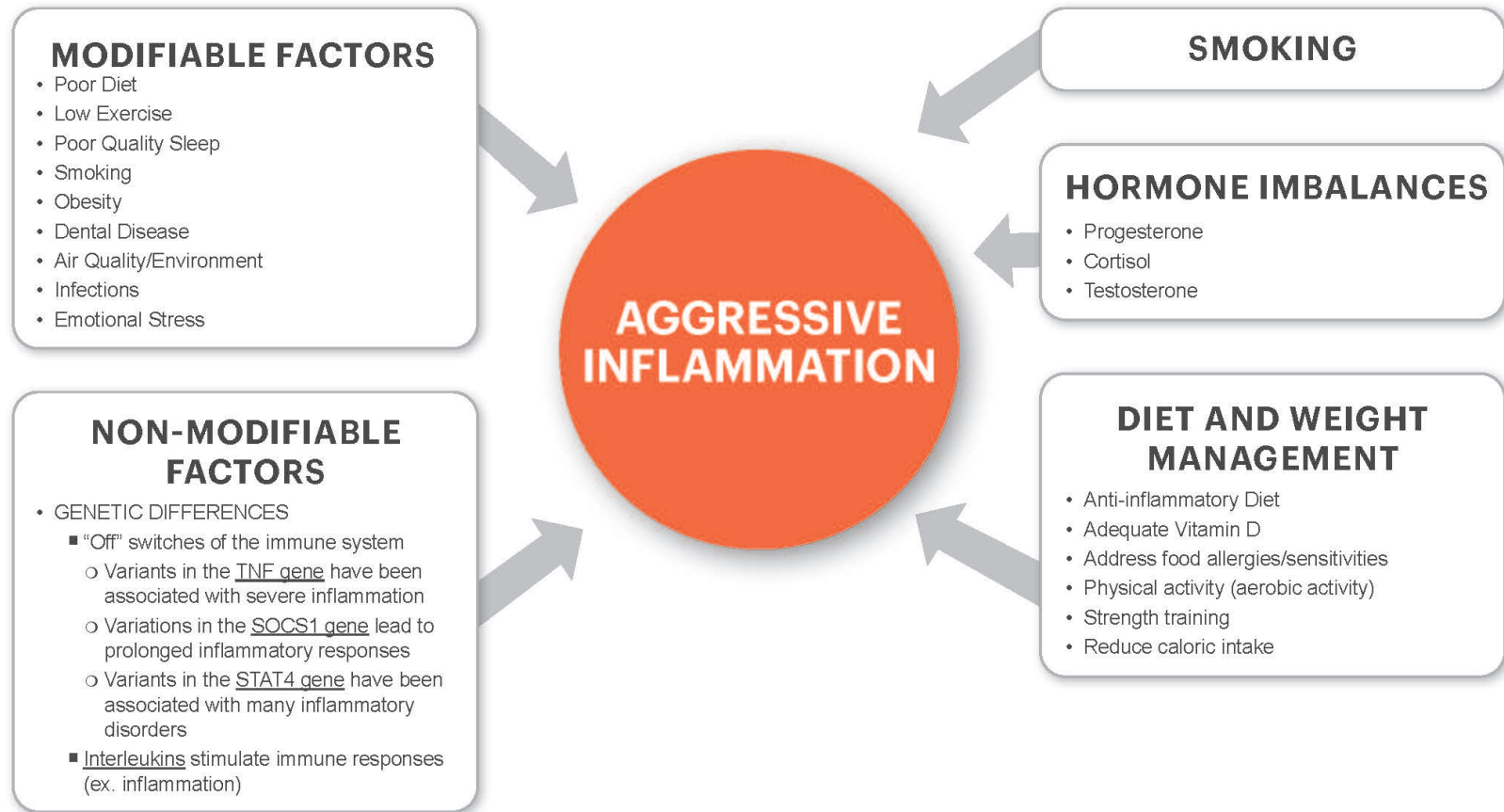
DEFICIENCY CAUSES

- Bone Pain
- Arthritis
- Obesity
- Backache
- Depression
- Diabetes
- Hypertension
- Osteoporosis
- Heart Disease
- Skin Conditions

ANTI-INFLAMMATORY

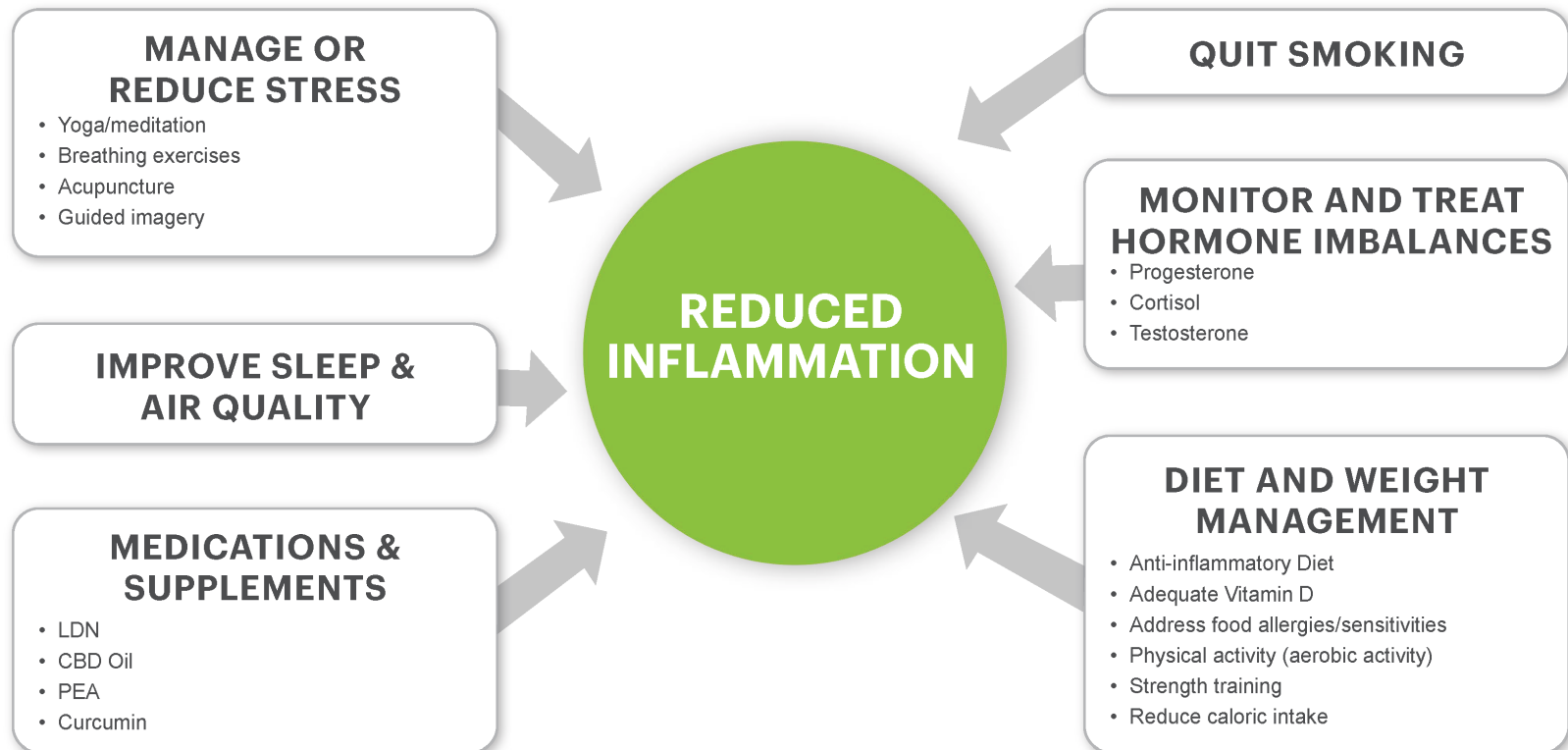
AN IMMUNE SYSTEM RESPONSE TRIGGERED BY HARMFUL STIMULI
(EX. PATHOGENS, DAMAGED CELLS, TOXIC COMPOUNDS, IRRADIATION)

DRIVERS OF INFLAMMATION



ANTI-INFLAMMATORY

WAYS TO REDUCE INFLAMMATION

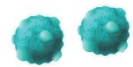


THE IMMUNE SYSTEM & AUTOIMMUNITY

WHAT DOES THE IMMUNE SYSTEM DO?

Prevent or limit infections by distinguishing between healthy and unhealthy cells

KEY PLAYERS & RELEVANT GENES

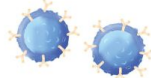


CYTOKINES

(ex. IL family, TNF-a)

- Helps with immune cell growth, activation, and function
- Interleukins (IL2, IL4, IL5, IL6, IL13, IL23R, IL2RA) stimulate the immune response
- SOCS1 & TNF are involved in cytokine signaling for the inflammatory response

activation



LYMPHOCYTES

(ex. B, T & Natural Killer cells)

- Identify & kill infected cells
- Produces antibodies to fight future infections
- IDO1, CTLA4 & CD14 are involved in the suppression of T-cells
- C3, STAT4 & TRAF1 activate, form and/or differentiate T-cells

IMMUNE AGGRESSION

The immune system begins to attack healthy tissue

COMMON SYMPTOMS



Fatigue



Hair loss



Achy muscles



Inflammation



Skin rashes



Pain



Low-grade fever



Numbness and tingling in hands and feet



Trouble concentrating

MALFUNCTIONS LEAD TO

- Chronic inflammation
- Allergic reactions
- Immune aggressive diseases (Inflammatory bowel disease, skin & neurological disorders)

LOW-INFLAMMATORY

FOODS TO EAT



Fruits: strawberries, blueberries, cherries, oranges



Fatty fish: salmon, mackerel, tuna, sardines



Spices - turmeric, ginger



Green leafy vegetables & tomatoes



Dark chocolate



Olive oil



LOW-INFLAMMATORY DIET

FOODS TO AVOID



Soda & other sugar-sweetened drinks



Dairy products



Fried foods



Red & Processed meats (hotdogs, sausage)



Refined carbohydrates: white bread, pastries



Margarine, shortening, lard

BENEFITS



Reduces inflammation



Reduces risk for cardiovascular disease & Type II diabetes

DETOXIFICATION

GLUTATHIONE IN DETOXIFICATION

Relevant genes for production are AHCY, CTH, GSTP1, GSTM1, GSTM3, GSR, MTRR & MTR

WHY IS IT IMPORTANT?



Maintains health by protecting the body from toxins



Regulates cell production and programmed cell death



Critical role in chemical detoxification



Vital for proper mitochondrial function

DEFICIENCY CAUSES

- Auto-immune diseases
- Cardiovascular diseases
- Neurodegenerative diseases
- Cell death
- Poor mitochondrial function



WAYS TO INCREASE GLUTATHIONE

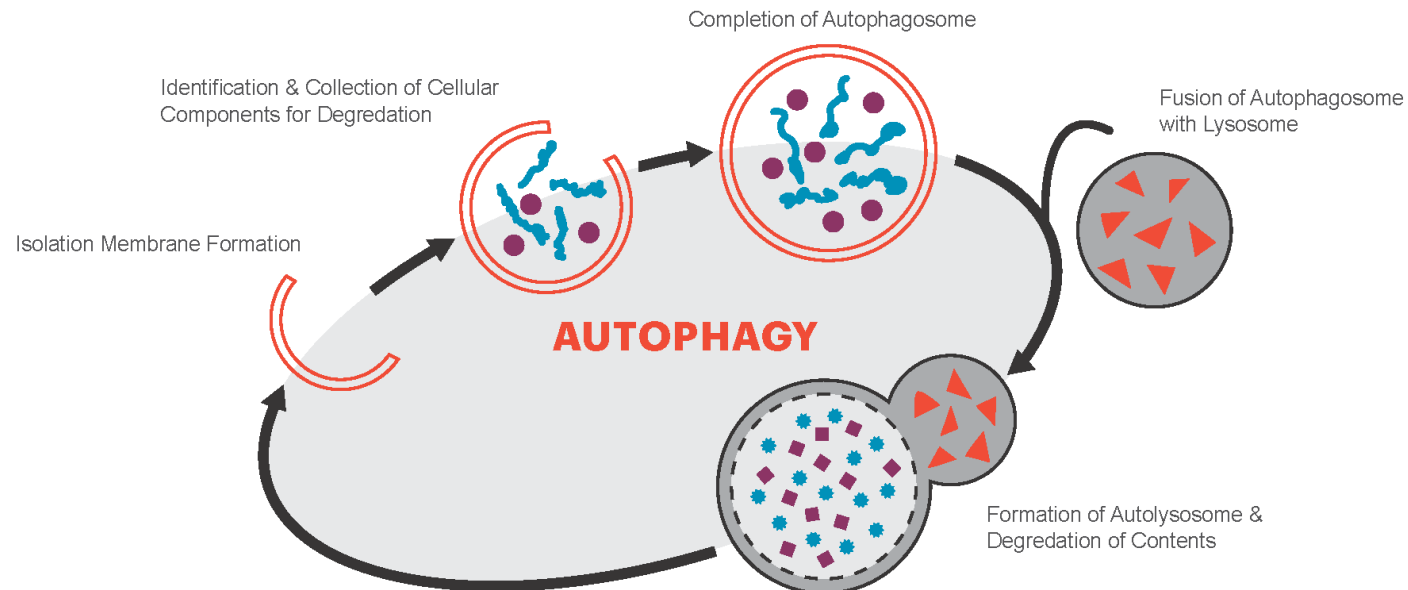
- Limit alcohol intake
- N-acetyl-cysteine (NAC)
- Glutathione therapies
- (ie. IV Glutathione, Glutathione suppository, Liposomal Glutathione)
- Include whey in diet, unless allergic or intolerant
- Methylation Support - if necessary

SUPEROXIDES & ANTIOXIDANTS

- SOD1, SOD2, SOD3 genes are important to transform superoxides to protect against mitochondrial damage
- Reactive Oxygen Species (ROS) can damage mitochondria and cause cell death.
- Antioxidants such as Vitamin A, Vitamin C and Vitamin E act as a defense against ROS

AUTOPHAGY: Cellular Housekeeping

VARIANTS IN THE ATG GENES HAVE BEEN ASSOCIATED WITH CELLULAR BLOCKAGE



DEFECTS LEAD TO:

- Neurodegenerative Diseases
- Aging
- Heart Disease
- Developmental Disorders
- Type II Diabetes
- Insulin Resistance
- Fatty Liver
- Cancers

WAYS TO INCREASE

-  Intermittent fasting or low-calorie diet
-  Routine Exercise
-  Ketogenic diets (high fat, low carbs)
-  Medications & Supplements
D-Chiro Inositol (B8)
Metformin

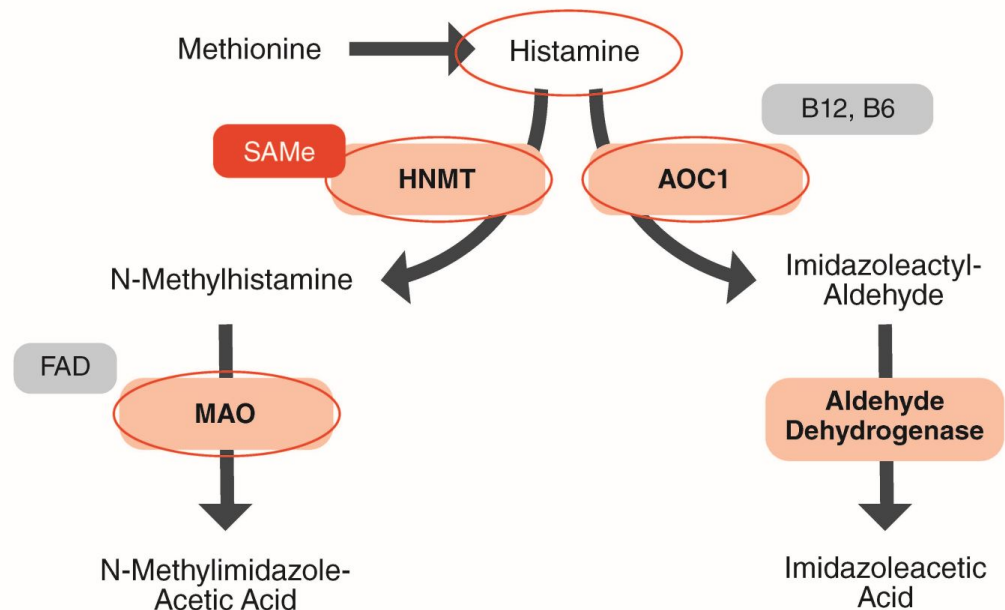
HISTAMINE

HISTAMINE

- Natural substance found in various foods

IMPLICATIONS

- Metabolic Enzymes: amine oxidases (ex. AOC1, MAO, DAO) & HNMT
- High histamine & low amine oxidase activity is associated with:
 - Diarrhea
 - Headaches
 - Nose congestion
 - Asthma
 - Hypotension
 - Arrhythmia
 - Flushing
 - Urticaria (hives)
 - Pruritus (itchy skin)
- Dietary histamine can be rapidly detoxified by amine oxidases, whereas persons with low amine oxidase activity are at risk of histamine toxicity



AOCI & HNMT POLYMORPHISM HISTAMINE

LOW HISTAMINE LEVEL FOODS



Meats & Fish
fresh meat (ex. chicken, turkey, pork and red meat), fresh fish (ex. hake, trout, plaice)



Milk substitutes
(Coconut milk, rice milk)



Cream cheese, butter



Egg yolk



Fresh fruits
(with the exception of strawberries)



Most cooking oils



Most leafy greens and herbs



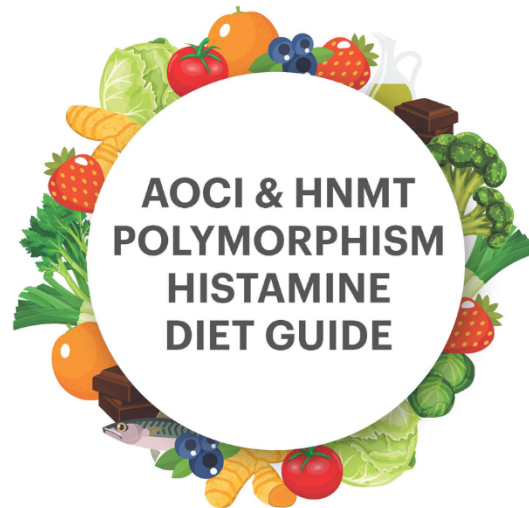
Fresh vegetables



Beverages
(non-citric fruit juices, herbal teas)



Grains



HIGH HISTAMINE LEVEL FOODS



Egg whites



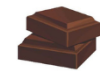
Processed, cured, smoked and fermented meats/fish (lunch meat, bacon, sausage, pepperoni, canned tuna)



Leftover meat
(After meat is cooked, the histamine levels increase due to microbial action as the meat sits)



Dairy products: All fermented milk products (ex. aged cheeses, yogurt, buttermilk, kefir)



Chocolate, cocoa



Bone broth



Fruits (oranges, grapefruit, lemons, lime, berries, dried fruit)



Vegetables (spinach, tomatoes, eggplant)



Artificial food colors and preservatives



Fermented & vinegar-containing foods (sauerkraut, kombucha, pickles, relishes, ketchup, prepared mustard)



Spices (cinnamon, chili powder, cloves, nutmeg, curry powder, cayenne)



Beverages (Black Tea, alcohol)

Gene Information Key

rsID	Gene	"-" variant	"+" variant
rs10156191	AOC1	C	T
rs26538	ATG12	T	C
rs10210302	ATG16L1	C	T
rs2241880	ATG16L1	A	G
rs510432	ATG5	T	C
rs2250656	C3	C	T
rs234706	CBS	A	G
rs2569190	CD14	G	A
rs1021737	CTH	G	T
rs231775	CTLA4	A	G
rs1076560	DRD2	C	A
rs174547	FADS1	T	C
rs492602	FUT2	A	G
rs1695	GSTP1	A	G
rs2187668	HLA-DQA1	C	T
rs7454108	HLA-DQB1	T	C
rs11558538	HNMT	C	T
rs12995000	HNMT	C	T

rsID	Gene	"-" variant	"+" variant
rs9657182	IDO1	T	C
rs1800925	IL13	C	T
rs2069762	IL2	A	C
rs11209026	IL23R	A	G
rs12722489	IL2RA	T	C
rs2243250	IL4	C	T
rs2069812	IL5	A	G
rs1800795	IL6	C	G
rs2056131	ITGB3	A	G
rs6721961	NFE2L2	G	T
rs4795067	NOS2	A	G
rs243324	SOCS1	G	A
rs10181656	STAT4	C	G
rs1800629	TNF	G	A
rs3761847	TRAF1	A	G
rs2228570	VDR	G	A

Definitions

C3 rs2250656	The C3 (complement C3) gene encodes an abundant protein in the complement cascade, a major component of the innate immune system. C3 is secreted into the bloodstream, and activation of C3 is essential for both classical and alternative complement activation. The polymorphism rs2250656 occurs in the fourth intron, and carriers of the T allele were shown to have increased plasma levels of C3 and C-reactive protein, two markers of inflammation. Additionally, increasing consumption of n-6 PUFAs, which are known to have a proinflammatory effect, further increased plasma levels of C3 in individuals with the TT genotype. Lastly, T allele carriers had a 2-fold higher risk for metabolic syndrome compared to individuals with the CC genotype, and the T allele was associated with severe COVID-19, suggesting that the T allele confers increased complement activity and inflammation.
CD14 rs2569190	The CD14 (CD14 molecule) gene encodes a crucial determinate of the innate immune response and protector from atopy. CD14 is an endotoxin receptor that is expressed on the surface of monocytes and macrophages. The polymorphism rs2569190 occurs in the promoter region of the gene, and mechanistic studies have shown that the variant encoded by the A allele is preferentially bound by RNA polymerase, suggesting that there is increased transcription of the A allele variant. Consistent with this mechanism, carriers of the A have been shown to have increased levels of CD14. Clinical studies have found that while A allele carriers have basal IgE levels that are lower than G allele carriers, IgE levels rise to a greater extent in A allele carriers when exposed to various forms of endotoxins. Moreover, A allele carriers are at increased risk for asthma or allergic disease when highly exposed to endotoxins, suggesting that A allele carriers are at increased risk for environmentally instigated inflammation. Lastly, A allele carriers may have increased risk for cardiovascular disease and inflammatory bowel disease, both of which are characterized by increased inflammation.
IL5	The IL5 (interleukin 5) gene encodes a cytokine that promotes the growth, differentiation, and activation of eosinophils. Therefore, it has an important role in Th2 immune responses and the development of allergic disease, which includes the promotion of IgE production and eosinophil response. The polymorphism rs2069812 is associated with a Th2-dominant autoimmune thyroid disease known as Graves' disease (GD). Carriers of the G allele have been shown to be at increased risk for GD as well as Graves' ophthalmopathy. Additionally, genome-wide association studies have linked the G allele with asthma, whereas the A allele has been associated with remission of GD and reduced risk of asthma.
IL4	The IL4 (interleukin 4) gene encodes a cytokine that signals to multiple cell targets in both the innate and adaptive immune systems. Its action is important for immunoglobulin production, fibrosis, allergic responses, and inflammation. IL4 has partially overlapping functions with IL13 as both cytokines share a receptor, and like IL13, IL4 activates Th2 immune responses, typically associated with IgE production and atopy, by promoting the differentiation of Th2 cells. Additionally, IL4 can antagonize the activity of Th1 cytokines, typically associated with proinflammatory responses related to microbial defense and autoimmunity. The polymorphism rs2243250 occurs in the promoter region of the gene, and mechanistic studies have shown that the T allele leads to increased expression of IL4, potentially increasing the potency of any immunological response stimulated by IL4. Numerous studies report that the T allele was associated with an increased risk for atopic inflammation. Carriers of the T allele have increased risk for asthma and allergies. Furthermore, the T allele has been associated with increased IgE production, a hallmark of atopic disease.
IL13	The IL13 (interleukin 13) gene encodes a cell signaling molecule that has a central role in the regulation of allergic inflammation. IL13 has a crucial role in the activation of Th2 immune responses, including the stimulation of B cells to synthesize IgE, a type of immunoglobulin that mediates allergic reactions. The polymorphism rs1800925 is located in the promoter region of the gene, and functional studies have shown that the variant encoded by the T allele increases transcription of IL13 by increasing the binding of STAT transcription factors to the promoter region. Consistent with these studies, the TT genotype was found to be more prevalent in individuals with asthma and atopic dermatitis, and it has been associated with increased risk of sensitization to food and outdoor allergens. Additionally, the TT genotype was associated with increased risk for appendicitis, and the T allele was associated with increased risk for chronic obstructive pulmonary disease (COPD).
IL23R	The IL23R (interleukin 23 receptor) gene encodes the receptor for IL23, a pro-inflammatory cytokine mainly secreted by activated macrophages and dendritic cells. The activation of IL23R by IL23 results in signaling through the JAK-STAT and NF- κ B pathways and differentiation of T cells. More specifically, the activation of IL23R leads to the production of Th17 cells, which produce another pro-inflammatory cytokine, IL17, and overproduction of IL17 is associated with autoimmune disease. The polymorphism rs11209026 results in a glutamine substitution for an arginine residue at position 381 in the IL23 receptor. The A allele, which encodes a glutamine residue, has been associated with reduced protein levels of IL23R, and it confers reduced risk of autoimmune disease. More specifically, the A allele has been shown to be protective against inflammatory bowel disease, such as Crohn's disease and ulcerative colitis. Furthermore, the A allele was shown to be protective against ankylosing spondylitis, a condition in which IL23R expression is significantly elevated.
STAT4	The STAT4 (signal transducer and activator of transcription 4) gene encodes a transcription factor that responds to extracellular growth factors and cytokines. It is present in the cytosol, and following cytokine signaling at the cell surface, STAT4 is phosphorylated and translocates to the nucleus, initiating the expression of cytokines, receptors, and signaling factors. The polymorphism rs10181656 occurs in the third intron, and cell-based experiments indicate that the G allele results in overexpression of STAT4, suggesting that the variant regulates gene expression. The G allele has also been associated with increased risk for numerous autoimmune diseases, such as rheumatoid arthritis, type 1 diabetes, lupus, and autoimmune thyroid disease. Furthermore, multiple studies support that there is additional disease risk for individuals carrying two copies of the G allele (GG genotype) compared to single allele carriers (GC genotype).
IL6	The IL6 (interleukin 6) gene encodes a cytokine with pro- and anti-inflammatory functions depending on the context; however, continuous and dysregulated synthesis of IL6 plays a key role in both acute and chronic inflammation. Additionally, IL6 is a crucial link between the innate and adaptive immune systems, and the gene is known to be mainly regulated at the transcriptional level. The polymorphism rs1800795 occurs in the promoter region of the gene, and mechanistic studies showed that the C allele yielded lower levels of IL6 than the G allele. As a result, the G allele has the potential to increase the potency of any immunological response stimulated by IL6, and the G allele has been associated with conditions of high inflammation. For example, the G allele may increase the risk for rheumatoid arthritis, IBS, and various types of liver disease. Additionally, the GG genotype may increase the risk for psoriasis, poly cystic ovarian syndrome, and pre-term birth, all conditions associated with high levels of circulating IL6.

TNF-?	The TNF-? (tumor necrosis factor alpha) gene encodes an important pro-inflammatory cytokine that is mainly secreted by activated macrophages and monocytes. TNF-? functions in a plethora of biological functions from pathogen defense to tissue remodeling as it plays a role in cell survival, growth, and differentiation. Given its pro-inflammatory nature, dysregulation of TNF-? is also associated with numerous pathological conditions. The polymorphism rs1800629 occurs in the promoter region of the gene, and mechanistic studies have shown that the variant encoded by the A allele results in increased transcription and secretion of TNF-?. Therefore, the A allele has the potential to increase the potency of any immunological response stimulated by TNF-?. Consistent with this mechanism, the A allele has been associated with increased susceptibility to autoimmune disease, such as asthma, Graves' disease, psoriatic arthritis, and lupus. Additionally, individuals with the AA genotype were less responsive to TNF-? blockers for the treatment of autoimmune disease, and A allele carriers experienced fewer anti-inflammatory benefits of physical activity compared to individuals with the GG genotype. Similarly, obese individuals with the AA genotype were less responsive to a hypocaloric diet high in polyunsaturated fats as an intervention to improve metabolic markers. In summary, these results suggest that the inflammation generated by increased transcription of TNF-? caused by the A allele variant is markedly resistant to repression.
TRAF1	The TRAF1 (TNF receptor-associated factor 1) gene encodes an intracellular protein that mediates cell signaling through tumor necrosis factor receptors. Moreover, TRAF1 plays a role in negatively regulating cytokine signaling by minimizing pro-inflammatory signals from the Toll-like and NOD-like receptors. Studies in animal models have shown that loss of TRAF1 leads to exaggerated T cell proliferation and activation in response to stimulation with tumor necrosis factors (TNF). The polymorphism rs3761847 occurs in an intronic region of TRAF1; however, preliminary studies indicate that rs3761847 interacts with long non-coding RNAs, which are known to impact gene expression. Numerous clinical studies have shown that the G allele is associated with rheumatoid arthritis, an autoimmune disease that can present with increased populations of pro-inflammatory T cells. In summary, these results suggest that the G allele might reduce expression of TRAF1, leading to increased inflammation.
IDO1	The IDO1 (indolamine 2,3 dioxygenase 1) gene encodes a heme enzyme responsible for the first and rate-limiting step of tryptophan degradation to kynurenine. IDO1 is activated by proinflammatory cytokines, such as interferon gamma (IFN-?) and tumor necrosis factor alpha (TNF-?), and its activity produces kynurenine metabolites and reduces tryptophan availability for the production of serotonin. As a result, increased IDO1 activity can have neurotoxic and depressogenic effects. The polymorphism rs9657182 occurs in the promoter region of the gene. In clinical studies, individuals with the CC genotype have been shown to have an increased risk for the development of depression when receiving treatment with interferon alpha (IFN-?), which can be used to treat infectious diseases and cancer. These results suggest that rs9657182 has a role in inflammation-induced behavioral changes. Additionally, the C allele is associated with increased risk for schizophrenia.
IL2	The IL2 (interleukin 2) gene encodes a cytokine that has numerous immune-stimulatory and immune-regulatory functions. For example, IL2 stimulates proliferation and enhances function of T cells, natural killer (NK) cells, and B cells. However, it also has a crucial role in maintaining regulatory T cells, which are essential for suppression of the immune response and self-tolerance. The polymorphism rs2069762 is located in the promoter region of the gene. Mechanistic studies have shown that the T allele may preferentially bind transcriptional repressors, presumably reducing transcription, whereas the G allele has been shown to increase expression of IL2 in cell-based assays. Clinical studies have shown that the C allele is associated with conditions of high inflammation. Moreover, the C allele has been associated with psoriasis and endometriosis, and the CC genotype was associated with increased risk for ulcerative colitis.
IL2RA	The IL2RA (interleukin 2 receptor subunit alpha) gene encodes the alpha chain of a high-affinity interleukin-2 (IL2) receptor. The IL2 receptor is expressed on the cell surface where it is available to bind to circulating IL2 to promote the expansion and survival of activated T cells. It also has an essential role in the production of regulatory T cells, which are important for quenching inflammation and sustaining self-tolerance. The polymorphism rs12722489 is located in the first intron of IL2RA, and allelic variation in expression is likely determined by epigenetic changes. Numerous clinical studies have shown that carriers of the C allele are more susceptible to multiple sclerosis and Crohn's disease.
SOCS1	The SOCS1 (suppressor of cytokine signaling 1) gene encodes an intracellular protein that is the primary negative regulator of cytokine signaling. SOCS1 expression is induced by cytokines, and its activity prevents immune dysregulation and prolonged pro-inflammatory signaling. Because it is well known that the immune system must be tightly regulated to block an autoimmune response, it is congruent that the absence of SOCS1 leads to systemic inflammation. Furthermore, clinical studies have defined the A allele of rs243324 as a risk factor for multiple sclerosis (MS), specifically relapsing remitting/secondary progressive MS. These results suggest that the A allele might lead to increased inflammation, possibly due to less SOCS1 activity.
CTLA4	The CTLA4 (cytotoxic T-lymphocyte associated protein 4) gene encodes a cell-surface receptor that acts as an important inhibitor of T cell activity and T cell-mediated immune responses. Therefore, CTLA4 has a crucial role in T cell homeostasis and self-tolerance, the loss of which can lead to the development of autoimmunity. The polymorphism rs231775 results in an alanine substitution for a threonine residue in the receptor at position 17, and the G allele, which encodes the alanine variant, results in decreased expression and cell surface localization of CTLA4 and increased proliferative response of T cells. Furthermore, clinical studies found that the G allele was associated with a variety of autoimmune diseases, such as autoimmune thyroid disease, type 1 diabetes, and rheumatoid arthritis. Additionally, the GG genotype was associated with positivity for insulinoma associated-2 autoantibodies (IA-2A) in patients with type 1 diabetes.
FADS1 rs174547	The FADS1 (fatty acid desaturase 1) gene encodes an enzyme that desaturates omega-3 and omega-6 polyunsaturated fatty acids (PUFA) to produce long-chain PUFAs, such as eicosatetraenoic acid (EPA), arachidonic acid (AA), and docosahexaenoic acid (DHA). These long-chain PUFAs are essential for the integrity of cellular membranes. The polymorphism, rs174547, occurs in the ninth intron, and studies have found that T allele carriers had higher levels of DHA whereas C allele carriers had lower levels of EPA. This suggests that the enzyme encoded by the C allele has reduced capacity to synthesize long-chain PUFAs.
DRD2	The DRD2 (dopamine receptor D2) gene encodes the D2 subtype of the dopamine receptor, which plays a role in locomotion, attention, sleep, memory, learning, and reward behavior. The D2 receptor is a G-protein coupled receptor that decreases dopamine signaling by inhibiting adenylyl cyclase activity. There are two splice variants of DRD2: long, which is primarily expressed postsynaptically, and short, which is primarily expressed presynaptically. The polymorphism rs1076560, located in intron 6, results in less expression of the short variant, leading to increased excitability. Carriers of the risk allele, A, were shown to have increased brain activity while performing various tasks with decreased performance of the task. Lastly, the A allele has been associated with alcoholism, opiate addiction, and increased risk for schizophrenia.

NOS2	The NOS2 (nitric oxide synthase 2) gene encodes an isoform of an enzyme that can be induced by pro-inflammatory agents like lipopolysaccharide and cytokines to produce nitric oxide (NO), a potent signaling molecule that can influence immune activation, inflammation, and cell survival. NOS2 can be conditionally activated in many cell types, but it is especially important for the function of immune cells, like macrophages. While NO is needed to defend against invading pathogens and unregulated cellular proliferation, excessive NO can damage healthy tissue. Carriers of the G allele for rs4795067 have an increased ratio of nitrite to nitrate in plasma. Because NO is quickly metabolized to nitrite in the body, nitrite is considered to be a measure of NO reserve, suggesting that carriers of the G allele have increased production of NO. Additionally, the G allele is associated with psoriasis, and NOS2 expression has been shown to be increased in psoriatic lesions. In summary, studies suggest that G allele carriers for rs4795067 produce increased amounts of NO, which can lead to inflammation.
VDR rs2228570	The VDR (vitamin D receptor) gene encodes a receptor for vitamin D3 that is highly expressed in the intestines. VDR is a member of the nuclear hormone receptor superfamily, so when activated by vitamin D, it can impact transcription of many genes involved in mineral metabolism, cell proliferation, and immune activation. The polymorphism rs2228570, sometimes termed FokI for the restriction enzyme that can detect it, results in a threonine substitution for a methionine residue in the first codon of the protein, altering the translation start site. As a result, translation of the receptor produced by the A allele, which does not contain the FokI restriction site (f) and encodes a methionine residue, is 427 amino acids in length, whereas the receptor produced by the G allele, which does contain the FokI restriction site (F) and encodes a threonine residue, is three amino acids shorter. Mechanistic studies indicate that the shorter variant encoded by the G allele has greater capacity to bind vitamin D and more transcriptional activity in response to vitamin D. Consistent with these findings, A allele carriers were less responsive to vitamin D supplementation, and A allele carriers were shown to have reduced calcium absorption and bone mineral density. Furthermore, vitamin D supplementation was less effective at reducing inflammatory markers in carriers of the A allele, and the A allele is associated with risk for celiac disease and type 2 diabetes.
ATG5	The ATG5 (autophagy-related 5) gene is an important intracellular mediator of the autophagy response, which is essential for maintaining homeostasis. The polymorphism rs510432 occurs in the promoter region of ATG5, and individuals homozygous for the C allele have been shown to have increased mRNA expression of ATG5. Additionally, individuals homozygous for the C allele are at an increased risk for developing childhood asthma, but they have a reduced risk for developing sepsis. Individuals who are heterozygous or homozygous for the T allele have been shown to have reduced levels of C-reactive protein.
ATG12	Autophagy-related 12 protein is part of the core autophagy machinery inside the cell. Autophagy, a form of cellular "recycling" is necessary for many cell functions. ATG12 is specifically involved in turning off the innate immune response. Mutations in the ATG12 gene are predicted to lead to increased activity of the innate immune response, and overall inflammation.
ATG16L1 rs10210302	The ATG16L1 (autophagy related 16 like 1) gene encodes a protein that is part of a major protein complex essential for autophagy, a process of digesting cellular components for nutrient sensing and cellular regulation. The polymorphism rs10210302 occurs in the promoter region of the gene, and a comprehensive study has linked the T allele with Crohn's disease, an inflammatory bowel disease.
CBS rs234706	The CBS (cystathionine beta-synthase) gene encodes an enzyme that catalyzes the first step in the transsulfuration pathway. More specifically, CBS, a pyridoxal 5'-phosphate-dependent enzyme, consumes serine to convert homocysteine to cystathionine, which is further catabolized to generate substrate for glutathione synthesis. Therefore, homocysteine clearance and glutathione synthesis converge on the function of CBS. The polymorphism rs234706 results in a nucleotide substitution in exon 8. Carriers of the G allele have been found to have higher levels of homocysteine and lower levels of cystathionine and betaine, consistent with reduced CBS activity. Furthermore, individuals with the GG genotype had higher plasma homocysteine following the ingestion of a methionine load, and individuals with the GG genotype were less responsive to folate supplementation to lower homocysteine levels. Lastly, the GG genotype is associated with increased risk for coronary artery disease.
CTH	The CTH (cystathionine gamma-lyase) gene encodes an enzyme that catalyzes the last step in the transsulfuration of L-methionine to L-cysteine. More specifically, it converts cystathionine, derived from methionine, into cysteine, which is utilized in the liver to synthesis glutathione, a ubiquitous antioxidant. As a results, CTH has an important role in glutathione production. The polymorphism rs1021737 results in an isoleucine substitution for a serine residue in the enzyme at position 403. The T allele, which encodes the isoleucine variant, has been associated with an accumulation of homocysteine.
NFE2L2 rs6721961	The NFE2L2 (NFE2 like bZIP transcription factor 2) gene encodes a transcription factor, known as NRF2, that has a crucial role in the regulation of a network of antioxidant genes. NRF2 activates expression of genes with a conserved promoter sequence called the antioxidant response elements (ARE). Genes with an ARE include superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPX), etc. Therefore, NRF2 is a master regulator of oxidant and antioxidant balance. The polymorphism rs6721961 occurs in the promoter region of NFE2L2, and mechanistic studies have found that the variant encoded by the T allele has reduced promoter activity and mRNA levels. Consistent with these findings, carriers of the T allele have been shown to have lower total antioxidant capacity. T allele carriers had less SOD, CAT, GPX, and glutathione activity. Furthermore, T allele carriers are at increased risk for insulin resistance and vascular stiffness.
GSTP1	The GSTP1 (glutathione S-transferase pi 1) gene encodes a cytosolic enzyme that has a keystone role in cellular detoxification. It conjugates cytotoxic and carcinogenic substances to glutathione for elimination, thereby aiding in antioxidant defense and preserving DNA integrity. The polymorphism rs1695 results in a valine substitution for an isoleucine residue in the enzyme at position 105, which is a region of the protein that is known to undergo several post-translational modifications. Mechanistic studies have shown that the protein produced by the G allele, which encodes a valine residue, has reduced substrate binding capacity and enzymatic activity. Numerous clinical studies have shown that the GG genotype is a risk factor for asthma, especially when individuals are exposed to environmental toxins, such as cigarette smoke or traffic-related air pollution. Additionally, the G allele is associated with increased risk for heart failure, and the frequency of the G allele is decreased in populations of older, living adults, suggesting it does not confer increased longevity.
AOC1	The AOC1 (amine oxidase copper-containing 1) gene encodes for the diamine oxidase (DAO) enzyme, which is one of two enzymes that breaks down pro-inflammatory amines such as histamine and putrescine. DAO is active in intestinal mucosal cells, and a deficiency of its activity results in the accumulation of high levels of histamine, which can cause a wide range of neurological, gastrointestinal, and epidermal disorders. The polymorphism rs10156191 results in a methionine substitution for a threonine residue in the enzyme at position 16. The T allele, which encodes the methionine variant, results in an enzyme with lower metabolic capacity than the enzyme encoded by the C allele, possibly resulting in reduced ability to break down histamine.

HNMT Thr105Ile	The HNMT (histamine N-methyltransferase) gene encodes an enzyme that catalyzes the first step of histamine breakdown, and it requires S-adenosyl-L-methionine as a methyl donor. HNMT is a cytosolic protein that metabolizes intercellular histamines, and it is of particular importance for the central nervous system because it is the only pathway that can degrade histamines in the brain. The polymorphism rs11558538 results in an isoleucine substitution for a threonine residue in the protein at position 105. Mechanistic studies have shown that the isoleucine variant, which is encoded by the T allele, has reduced thermostability. As a result, the T allele variant results in a reduction in the enzyme and its activity. Additionally, the T allele has been associated with asthma.
FUT2	The FUT2 (fucosyltransferase 2) gene encodes an enzyme involved in the synthesis of histoblood group antigens (HBGA), which are found on the intestinal mucosa and various bodily fluids. HBGA are oligosaccharide molecules, and in the intestinal mucosa, they act as an attachment site and nutrient source for intestinal bacteria. The polymorphism rs492602 is in near perfect linkage disequilibrium with rs601338, meaning that the alleles are nonrandomly associated and inherited together. Therefore, the G allele for rs492602 indicates the inheritance of the minor allele for rs601338, which results in a stop gain mutation that produces a truncated version of FUT2 that is unable to secrete the oligosaccharide molecules. As a result, individuals of the GG genotype for rs492602 are considered "non-secretors". Carriers of the G allele were found to have compositional and functional changes to the gut microbiota and reduced microbial diversity. Furthermore, G allele carriers had increased susceptibility for inflammatory bowel disease.
HLA-DQA1	The HLA-DQA1 (major histocompatibility complex, class II, DQ alpha 1) gene encodes a cell surface protein that plays a central role in the function of the immune system and the development of autoimmune disease. HLA-DQA1 is a class II, human leukocyte antigens (HLA), which are expressed on the surface of antigen presenting cells where HLA can bind antigens or substances that induce an immune response for recognition by T cells. HLA-DQA1 encodes a component of HLA-DQ2, a serotype or distinct variation among the HLA structure that determines its antigenic complements. More specifically, the T allele for the polymorphism, rs2187668, can be used to identify HLA-DQ2.5, a high-risk factor for gluten sensitivity and celiac disease. Consistently, genome-wide association studies have found the T allele is associated with celiac disease.
HLA-DQB1 rs7454108	The HLA-DQB1 (major histocompatibility complex, class II, DQ beta 1) gene encodes a cell surface protein that plays a central role in the function of the immune system and the development of autoimmune disease. HLA-DQB1 is a class II, human leukocyte antigens (HLA), which are expressed on the surface of antigen presenting cells where HLA can bind antigens or substances that induce an immune response for recognition by T cells. More specifically, the C allele for the polymorphism, rs7454108, can be used to identify HLA-DQ8, a serotype or distinct variation among the HLA structure that determines its antigenic complements. HLA-DQ8, for example, is a high-risk factor for gluten sensitivity and celiac disease.
ITGB3 rs2056131	The ITGB3 (integrin subunit beta 3) gene encodes an integrin subunit, and integrins are transmembrane adhesion receptors that mediate cellular interactions to regulate cell proliferation, activation, and migration. The polymorphism rs2056131 occurs in the first intron, and in adults with asthma, the G allele was associated with increased risk of mold sensitization or mold allergy.

Disclaimers

TESTING:

Testing Performed By: AC

METHODOLOGY AND LIMITATIONS DISCLAIMER:

Testing for genetic variation/mutation on listed genes was performed using ProFlex PCR and Real-Time PCR with TaqMan® allele-specific probes on the QuantStudio 12K Flex. All genetic testing is performed by GX Sciences, LLC d/b/a Fagron Genomics US ("Fagron Genomics US") (807 Las Cimas Pkwy, Suite 145, Austin, TX. 78746). This test will not detect all the known alleles that result in altered or inactive tested genes. This test does not account for all individual variations in the individual tested. Test results do not rule out the possibility that this individual could be a carrier of other mutations/variations not detected by this gene mutation/variation panel. Rare mutations surrounding these alleles may also affect our detection of genetic variations. Thus, the interpretation is given as a probability. Therefore, this genetic information shall be interpreted in conjunction with other clinical findings and familial history for the administration of specific nutrients. Patients should receive appropriate genetic counseling to explain the implications of these test results. Details of assay performance and algorithms leading to clinical recommendations are available upon request. The analytical and performance characteristics of this laboratory developed test (LDT) were determined by Fagron Genomics US's laboratory (Laboratory Director: James Jacobson, PhD) pursuant to Clinical Laboratory Improvement Amendments (CLIA) requirements (CLIA #: 45D2144988).

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