

Delivering More Than a Test Result

ASHI No. 10-4-OR-03-1 CLIA No. 38D1058476

CARDIAC HEALTH GENOTYPING REPORT

Patient Name: Johnny Health **Date Sample Collected:** 00/00/14 DOB: 01/01/1980 Date Sample Received/Tested: 00/00/14 Lab ID Number: 000000000 Date Reported: 00/00/14 **Ordering Physician:** Dr. KCL **Ordering Facility:** Acme Center

Genes Tested: 9P21 Factor II Prothrombin

AGT Factor V Leiden

eNOS/NOS3 APOE MTHFR SLCO1B1*5

KEY: GREEN: NON-RISK ALLELE RED: RISK ALLELE

9p21 Mutation

BACKGROUND

Results: [C/C]

INDICATIONS

C/C allele carriers may have an increased coronary artery disease risk of up to 50%.

Coronary artery disease (CAD) risk is approximately 40-60% genetically determined.¹ One of the first and most researched risk factors associated with coronary artery disease is 9p21.² The 9p21 variant is located in a non-protein coding region near the tumor suppressor genes, cyclin-dependent kinase inhibitors 2A and 2B (CDKN2A, CDKN2B), both of which exhibit anti-proliferative activity in the vascular endothelium.³ Expression studies show the 9p21 variant to be associated with decreased expression of CDKN2a/b, which may be a source for the development of atherosclerosis.⁴

Presence of the 9p21 C allele is associated with CAD, atherosclerotic changes, and multi-vessel disease.^{2,4-7} Multiple studies have shown that the degree of CAD risk is determined by the number of risk alleles present. Heterozygous carriers have an increased CAD risk however homozygous C/C allele carriers may double their risk of CAD, atherosclerotic severity, and a greater number of vessels involved in CAD.⁴⁻⁷ The presence of the risk allele increases CAD risk independent of other risk factors such as cholesterol.⁴

 ${\it G/G}$ allele carriers do not possess the 9p21 risk alleles associated with increased risk of coronary artery disease or atherosclerosis.

G/C heterozygous allele carriers may have up to a 25% increased risk of coronary artery disease, an increased risk of atherosclerosis, and increased risk in number of vessels involved in CAD. **C/C** allele carriers may be associated with up to a 50% increased risk of CAD, higher severity of atherosclerosis, and a two-fold higher risk of three-vessel coronary artery disease.

- 1. Roberts R. Genetics of Coronary Artery Disease. Circ Res. 2014; 114:1890-1903.
- 2. The Wellcome Trust Case Consortium, Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature. 2007; 447(7145): 661-678.
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- 4. Roberts R and Stewart A. 9p21 and the Genetic Revolution for Coronary Artery Disease. Clinical Chemistry. 2012; 58(1):104-112.
- 5. Ye S et al. Association of Genetic Variation on Chromosome 9p21 with Susceptibility and Progression of Atherosclerosis. JACC 2008; 52(5): 378-384.
- 6. Munir M et al. The association of 9p21-3 locus with coronary atherosclerosis: a systematic review and meta-analysis. BMC Medical Genetics. 2014; 15:66.
- 7. Dandonna S et al. Gene Dosage of the Common Variant 9p21 Predicts Severity of Coronary Artery Disease. J Am Coll Cardiol. 2010; 56(6):479-488.

AGT Mutation

Results: [C/C]

INDICATIONS

C/C allele carriers do not possess the risk alleles, and may not be at increased risk for coronary artery disease.

BACKGROUND

Angiotensinogen is the protein produced by the AGT gene. This is the precursor to the active peptide angiotensin II (Ang II), a hormone that causes blood pressure to increase through vasoconstriction and sodium retention. The more precursor available in the blood, the more Ang II is produced, and increased levels of the hormone are significantly correlated with blood pressure in patients with hypertension. Hundreds of epidemiological studies in various populations have focused on a few common polymorphisms in the AGT gene associated with increased AGT activity and high blood pressure. High blood pressure is known to be a risk factor for cardiovascular disease and early mortality. While evidence indicates there are many genes involved with this disease condition, there is ample evidence that this variant allele in AGT is associated with poor cardiovascular health and in particular may be a marker indicating risk for developing coronary artery disease.

C/C allele carriers do not possess the AGT risk alleles, and may not be at increased risk for coronary artery disease.

C/T allele carriers possess one risk allele and may be at increased risk of coronary artery disease. **T/T** allele carriers possess two copies of the risk allele and are often found to be at increased risk of coronary artery disease.

- 1. Touyz RM and EL Schiffrin. Signal Transduction Mechanisms Mediating the Physiological and Pathophysiological Actions of Angiotensin II in Vascular Smooth Muscle Cells. Pharmacol Rev. 2000; 52(4):639-672.
- 2. Catt KJ et al. Angiotensin II blood-levels in human hypertension. The Lancet. 1971; 297:459-464.
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- 4. Wang WZ. Association between T174M polymorphism in the angiotensinogen gene and risk of coronary artery disease: a meta-analysis. J Geriatr Cardiol. 2013; 10:59-65.
- 5. Li X et al. AGT gene polymorphisms (M235T, T174M) are associated with coronary heart disease in a Chinese population. J Renin Angiotensin Aldosterone Syst. 2013; 14(4):354-9.
- 6. Gardemann A et al. Angiotensinogen T174M and M235T gene polymorphisms are associated with the extent of coronary atherosclerosis. Atherosclerosis. 1999; 145(2):309-14.

eNOS/NOS3

BACKGROUND

Results: G/T

INDICATIONS

G/T allele carriers have one risk allele and may have a reduced ability to synthesize nitric oxide.

Endothelial nitric oxide synthase (eNOS/NOS3) is the key enzyme responsible for maintaining baseline vascular nitric oxide (NO) levels.¹ Nitric oxide is responsible for vasodilation, or the relaxation of vascular smooth muscle cells allowing greater blood flow and reduced blood pressure.² eNOS is also involved in preventing platelet and leukocyte adhesion to vascular walls, modulating thrombosis, inhibiting vascular smooth cell migration and proliferation, limiting oxidation of LDL, and participating in insulin sensitivity.³-5 The eNOS variant results in an amino acid change that causes the protein to undergo proteolytic cleavage thought to result in a functional consequence to the enzyme.⁶ Individuals with this variant allele may have an increased risk of ischemic heart disease, ischemic stroke, and myocardial infarction in young patients, while the risk for hypertension seems to be dependent upon ethnicity.⁷⁻¹⁰

G/G allele carriers do not possess the risk allele and are expected to have normal nitric oxide synthase activity.

G/T allele carriers have one risk allele and may have a reduced ability to synthesize nitric oxide.

T/T allele carriers have two risk alleles and may have reduced enzyme function and increased susceptibility to ischemic heart disease, ischemic stroke, hypertension, and myocardial infarction.

References

- 1. Marsden PA et al. Structure and chromosomal localization of the human constitutive endothelial nitric oxide synthase gene. J Biol Chem. 1992; 68:17478-17488.
- 2. Cosentino F and Luscher TF. Maintenance of vascular integrity: role of nitric oxide and other bradykinin mediators. Eur Heart J. 1995; 16 Suppl K:4-12.
- 3. Huang PL. eNOS, metabolic syndrome and cardiovascular disease. Trends Endocrinol Metab. 2009; 20(6):295-302.
- 4. Hogg N et al. Inhibition of low-density lipoprotein oxidation by nitric oxide. Potential role in atherogenesis. FEBS Lett. 1993; 334(2):170-174.
- 5. Radomski MW et al. Endogenous nitric oxide inhibits human platelet adhesion to vascular endothelium. Lancet. 1987; 2:1057-1058.
- 6. Tesauro M et al. Intracellular processing of endothelial nitric oxide synthase isoforms associated with differences in severity of cardiopulmonary diseases: cleavage of proteins with aspartate vs. glutamate at position 298. *Proc Natl Acad Sci U S A*. 2000; 6:2832-2835.
- 7. Casas JP et al. Endothelial Nitric Oxide Synthase Genotype and Ischemic Heart Disease: Meta-Analysis of 26 Studies Involving 23,028 Subjects. Circulation. 2004; 109:1359-1365.
- 8. Niu W and Y Qi. An Updated Meta-Analysis of Endothelial Nitric Oxide Synthase Gene: Three Well-Characterized Polymorphisms with Hypertension. Plos One. 2011; 6(9):e24266.
- 9. Wang M et al. Association of G894T polymorphism in endothelial nitric oxide synthase gene with the risk of ischemic stroke: A meta-analysis. Biomed Rep. 2013; 1(1):144-150.
- 10. Zigra AM et al. eNOS gene variants and the risk of premature myocardial infarction. Dis Markers. 2013; 34(6):431-436.

Folate (Vitamin B9) MTHFR Mutations

MTHFR-1: C677T Results: C/T

MTHFR-2: A1298C Results: A/C

INDICATIONS

MTHFR-1: C677T

C/T allele carriers have one risk allele but are not at risk for elevated levels of homocysteine.

MTHFR-2: A1298C

A/C allele carriers may have reduced levels of enzyme activity, but typically do not have increased homocysteine levels.

BACKGROUND

The MTHFR (methylenetetrahydrofolate reductase) gene produces an enzyme that helps in processing folate and regulating homocysteine levels in the body. Folate is a critical nutrient involved in methylation, DNA synthesis and amino acid metabolism. Impaired folate metabolism due to MTHFR enzyme inactivity, or a low folate level, results in elevated plasma homocysteine. Homocysteine is an amino acid synthesized by the body through demethylation of methionine. In the presence of adequate B-vitamins, homocysteine is either irreversibly degraded to cysteine or it is re-methylated back to methionine, an essential amino acid. An elevated homocysteine level has been identified as an independent risk factor for ischemic stroke, thrombotic and cardiovascular diseases. However, it is important to remember that this is a multifactorial condition, involving a combination of genetic, physiologic, and environmental factors, and clinical relevance of MTHFR testing should be interpreted in light of clinical information.

Two single nucleotide variants known to affect MTHFR function are C677T (a change from cytosine to thymine at position 677 within the gene) and the A1298C mutation (a change from adenine to cytosine at position 1298 within the gene). It is not uncommon for some individuals to have both MTHFR variants. Clinical relevance for hyperhomocysteinemia is associated with homozygosity for the C677T variant allele.

MTHFR-1: C677T

C/C allele carriers do not carry the risk allele and are not at risk for elevated levels of homocysteine.
C/T allele carriers have one risk allele but are not at risk for elevated levels of homocysteine.
T/T allele carriers of two risk alleles are associated with increased homocysteine levels.

In general, these genotypes produce an MTHFR enzyme with reduced function and activity.

MTHFR-2: A1298C

A/A allele carriers have full enzymatic activity and most often do not exhibit high levels of homocysteine. **A/C** allele carriers may have reduced levels of enzyme activity, but typically do not have increased homocysteine levels.

C/C allele carriers have two risk alleles and are often found to have decreased enzyme activity but not elevated homocysteine levels.

References

- 1. Wagner C. Biochemical role of folate in cellular metabolism. In: Bailey LB, editor. Folate in health and disease. New York, NY: Marcel Dekker Inc.; 1995. p. 23–42.
- 2. Bailey LB and JF Gregory III. Polymorphisms of Methylenetetrahydrofolate Reductase and Other Enzymes: Metabolic Significance, Risks and Impact on Folate Requirement. J Nutr. 1999; 129(5):919-22.
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- 6. Cotlarciuc I et al. Effect of genetic variants associated with plasma homocysteine levels on stroke risk. Stroke. 2014; 45(7):1920-4.
- 7. Van der Put NM et al. A second common mutation in the methylenetetrahydrofolate reductase gene: an additional risk factor for neural-tube defects? Am J Hum Genet. 1998; 62(5):1044–51.
- 8. Weisberg I et al. A second genetic polymorphism in methylenetetrahydrofolate reductase (MTHFR) associated with decreased enzyme activity. Mol Genet Metab. 1998; 64:169–72.

Factor II Prothrombin

BACKGROUND

Results: G/G

INDICATIONS

G/G allele carriers do not possess the risk alleles and are typically not at increased risk for thrombosis. Coronary heart disease and stroke remain the leading causes of death and disability for individuals of most ethnicities within the United States. ^{1,2} The prothrombin gene, also known as coagulation Factor II (F2) has been considered as a candidate gene for venous thrombosis and stroke. ³ Prothrombin is the precursor protein of thrombin, a component of the coagulation cascade. ⁴ Thrombin is the key enzyme involved in the processes of hemostasis and thrombosis that exhibits procoagulant, anticoagulant, and antifibrinolytic activities. Individuals with this particular mutation in F2 have a 2-3-fold increased risk for developing thrombosis and venous thromboembolism (VTE). ^{3,5,7} Additionally, for individuals carrying both the F2 and the Factor V Leiden mutations, the risk of VTE is even further increased. This mutation is also associated with significantly increased stroke risk in adults ≤55 years. ^{6,8}

G/G allele carriers do not possess the risk alleles and are typically not at increased risk for thrombosis.
G/A heterozygotes may be associated with increased risk for thrombosis and embolism.

A/A allele carriers possess two copies of risk alleles and are often associated with increased risk of thrombosis, embolism and stroke.

- 1. Murphy SL et al. Deaths: Final data for 2010. Natl Vital Stat Rep. 2013; 61(4).
- 2. Go AS et al. Heart disease and stroke statistics—2014 update: a report from the American Heart Association. Circulation. 2014; 129: e28-e292.
- 3. Poort SR et al. A common genetic variation in the 3'-untranslated region of the prothrombin gene is associated with elevated plasma prothrombin levels and an increase in venous thrombosis. Blood. Nov 15 1996;88(10):3698-703.
- 4. Bertina RM et al. Thrombin, a link between coagulation activation and fibrinolysis. Ann NY Acad Sci. 1992; 667:239.
- 5. Simone B et al. Risk of venous thromboembolism associated with single and combined effects of Factor V Leiden, Prothrombin 20210A and Methylenetethraydrofolate reductase C677T: a meta-analysis involving over 11,000 cases and 21,000 controls. Eur J Epidemiol. 2013; 28(8):621-47.
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- 7. Gohil, R et al. The Genetics of Venous Thromboembolism: A meta-analysis involving ~120,000 cases and ~180,000 controls. Journal of Thrombosis and Haemostasis. 2009; 102: 360-370.
- 8. Casas JP et al. Meta-analysis of genetic studies in ischemic stroke: thirty-two genes involving approximately 18,000 cases and 58,000 controls. Arch Neurol. 2004 Nov; 61(11):1652-61.

Factor V Leiden

Results: A/A

INDICATIONS

A/A allele carriers possess two copies of risk alleles and are at increased risk for thrombophilia, VTE and stroke.

BACKGROUND

Factor V Leiden thrombophilia is an inherited blood clotting disorder. Factor V Leiden is a rare variant of the human factor V protein that causes an increase in blood clotting (hypercoagulability).¹ The mutation prevents efficient inactivation of factor V; prolonged activation of factor V allows for the overproduction of thrombin. Thrombin catalyzes the formation of fibrin, a key protein involved in clot formation. In people with the factor V mutation, excess fibrin is formed causing excess clotting.² In a comprehensive meta-analysis it was determined that individuals that are heterozygous for the factor V mutation have a fivefold increased relative risk for idiopathic venous thromboembolism (VTE), while those who are homozygous for the mutation have a nine to tenfold increase in risk.³ Additionally, there have been statistically significant associations with deep vein thrombosis, ischemic stroke, as well as pre-eclampsia also identified for factor V Leiden.⁴-6

G/G allele carriers do not possess the risk alleles.

G/A heterozygous allele carriers possess one risk allele and may be at increased risk for thrombophilia and VTE.

A/A individuals carry two copies of risk alleles and are at increased risk for thrombophilia, VTE and stroke.

- 1. Kujovich J et al. GeneReviews; 1999 "Factor V Leiden Thrombophilia".
- 2. Bertina RM et al. Mutation in blood coagulation factor V associated with resistance to activated protein C. Nature. 1994; 369(6475):64-7.
- 3. Gohil R et al. The Genetics of Venous Thromboembolism: A meta-analysis involving ~120,000 cases and ~180,000 controls. Journal of Thrombosis and Haemostasis. 2009; 102:360-370.
- 4. Dudding TE et al. Factor V Leiden is associated with pre-eclampsia but not with fetal growth restriction: a genetic association study and meta-analysis. J Thromb Haemost. 2008 Nov; 6(11):1869-75.
- 5. Dentali F et al. Role of factor V Leiden or G20210A prothrombin mutation in patients with symptomatic pulmonary embolism and deep vein thrombosis: a meta-analysis of the literature. J Thromb Haemost 2012;10:732–7.
- 6. Casas JP et al. Meta-analysis of genetic studies in ischemic stroke: thirty-two genes involving approximately 18,000 cases and 58,000 controls. Arch Neurol. 2004; 61(11):1652-61.

APOE

APOE -1 Results: [C/T]

APOE-2 Results: [C/C]

Genotype: [E3/E4]

INDICATIONS

APOE-1/APOE-2 allelic variants are associated with cardiovascular health.

APOE-1: C/T; APOE-2; C/C =<u>E3/E4</u> allele carriers are at increased risk for heart disease and may have higher triglycerides, and LDL cholesterol, with lower HDL levels.

BACKGROUND

Apolipoprotein E (APOE) is a serum glycoprotein synthesized by most tissues in the body, and is involved in the transport of lipids throughout the body.¹ It accumulates on the surface of very low density lipoprotein (VLDL) particles and chylomicrons as they travel through the bloodstream and helps to direct the metabolism of cholesterol and triglycerides.¹ ApoE genetic polymorphisms are thought to contribute up to 10% of the variation in cholesterol levels, and 20–40% of variability in triglyceride levels seen in the general population.¹ The three variants of apoE are commonly reported as a phenotype that represents the isoform present on each chromosome, such as E3/E3 or E2/E3. This is determined by cysteine and arginine amino acid substitutions at two residues in the protein. Depending on the amino acid present at these locations, the apoE protein changes conformation, which in the case of ApoE2, affects its ability to interact with the LDL receptor.¹ ApoE2/E2 is also associated with type III hyperlipidemia (HLP III) (dysbetalipoproteinemia), however most individuals with this condition will present as normolipidemic and it may be decades before deleterious cardiovascular changes due to secondary factors, become evident. Ultimately out of all the phenotypes, ApoE4/E4 carriers are associated with the highest risk of heart disease.

The Three Isoforms and their Phenotypes

ApoE2 allele carriers **(E2/E2 and E3/E2)** have a significantly lower ability to bind LDL receptors, and are associated with risk of type III HLP, higher ApoE levels, higher triglyceride levels, but lower cholesterol levels.¹

ApoE3 homozygous allele carriers (E3/E3) are the most common in the general population and considered the non-risk group for cardiovascular disease. 1-3

ApoE4 allele carriers (E4/E4 and E4/E3) are at increased risk for heart disease associated with decreased apoE and HDL levels, increased triglycerides⁴ and cholesterol levels (both total and LDL).¹

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- 2. Eichner JE et al. Apolipoprotein E Polymorphism and Cardiovascular Disease: A HuGE Review. Am J Epidemiol. 2002; 155(6):487-495.
- 3. Villeneuve S et al. The potential applications of Apolipoprotein E in personalized medicine. Front Aging Neurosci. 2014; 6:154.
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SLCO1B1*5

Results: [C/C]

INDICATIONS

C/C - poor metabolizer

These patients have a significantly decreased ability to metabolize statins. They are less responsive to statin therapy and achieve less LDL-c lowering from the statin that they receive. High dose statin therapy may not be advisable.

BACKGROUND

The SLCO1B1 gene encodes the organic anion transporting polypeptide B1 (OATPB1). This protein mediates the liver's uptake of many compounds, including the class of medications called statins.¹ Variants in this gene affect the function of the transport protein, causing changes in the amount of statin medication that can be taken up into the liver.¹ Presence of the variant allele markedly reduces the uptake of certain statins which in turn reduces the efficacy of the stain medication and allows statin accumulation in the bloodstream. Due to the adverse effects of statin-induced myopathies and myalgias being dosedependent, it may be advisable to avoid high dose statin therapy in these variant allele carriers.¹

T/T – normal metabolizer

These patients are able to metabolize statins appropriately. Standard doses are recommended for LDL-C reduction and CVD risk reduction.²

T/C – intermediate metabolizer

These patients have a decreased ability to metabolize statins. They are less responsive to statin therapy and achieve less LDLD-c lowering from the statin that they receive. Consider routine creatine kinase (CK) monitoring.

C/C – poor metabolizer

These patients have a significantly decreased ability to metabolize statins. They are less responsive to statin therapy and achieve less LDL-c lowering from the statin that they receive. Consider routine creatine kinase (CK) monitoring. High dose statin therapy may not be advisable.

References:

- 1. Niemi M et al. Organic Anionic Transporting Protein 1B1: a Genetically Polymorphic Transporter of Major Importance for Hepatic Drug Uptake. Pharm Review. 2011; 63(1): 157-181.
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^{*}Additional information will be supplied to your provider to help inform treatment options.