Stroke GENOME screen Report

Stroke Genome Screen				
	Institution		Sample ID	
	Name		Medical record No.	
	Age / Sex		Accepted	
	Sample type		Reported	

The test result of

Test Description

This is a brief description of stroke genome screening.

This analysis, being the latest gene analysis technique, analyses genes that can cause stroke and reviews the results of existing research papers to provide personalized information to help people manage their health. Even if any pathogenic variant(PV) associated with hereditary stroke is found, individuals may have no symptoms(reduced penetrance). However, such individual may have higher risk of stroke compared to the general population, measures to reduce the stroke risk and regular thorough examinations for early detection are recommended.

Summary of Test Results

A Likely Pathogenic Variant (LPV) in the APOE gene related to Familial Hypercholesterolemia was detected

Gene	DNA Change	Predicted AA change	Zygosity	Class
APOE	c.388T>C	p.(Cys130Arg)	Het	LPV

Medical Technologist : M-K Lee M.T(20058) MKlee

Lab Director(medical doctor) : Chang-Seok Ki M.D(547) CSKi

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Interpretation

The APOE c.388T>C (p.Cys130Arg) variant has been classified as a LPV or PV in Clinvar (Variation ID: 17864) and as a Disease-associated polymorphisms with supporting functional evidence in HGMD. The minor allele frequency of this variant is estimated to be 0.1 in the Asian population (gnomAD).

The APOE gene encodes an apolipoprotein E which combines with fats (lipids) in the body to form molecules called lipoproteins. Lipoproteins are responsible for packaging cholesterol and other fats and carrying them through the bloodstream.

A combination of this variant (rs429358) with a wild type allele of rs7412 is called an APOE e4 allele, which is known to cause hyperlipoproteinemia, coronary artery disease, Alzheimer disease, lipoprotein glomerulopathy, etc.

Clinical correlation and, if necesary, family testing are recommended.

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Stroke screen Report

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The test result of

Relevant Disease Information

Disease	Test guidebook
Familial Hypercholesterolemia	**03.Prevention and Treatment page41~43**

Familial hypercholesterolemia (FH) is an autosomal dominant hereditary disease and is characterized by blood low-density lipoprotein cholesterol (LDL-C) increase, normal triglyceride, tendinous xanthoma, premature coronary sclerosis, etc. The homozygous type has abnormality in both sides of genes with the LDL-C value of 500-900 mg/dL and the total cholesterol (TC) value of 600 mg/dL or higher, and the heterozygous type has abnormality in one side of genes with the LDL-C value of 150-420 mg/dL and the TC value of 230-500 mg/dL. This disease causes severe coronary sclerosis. Therefore, it is important to find and treat this disease in the early stage.

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The test result of

The result details and related diseases

* Large artery and small artery occlusion (lacunar) ischemic stroke

An ischemic stroke caused by blockage of large or small arteries that are branching in the brain due to genetic cause.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Beta thalassemia	HBB	☐	☑
Hyperhomocysteinemia	CBS	☐	☑
Fabry disease	GLA	☐	☑
Pseudoxanthoma elasticum	ABCC6	☐	☑

* Small artery occlusion (lacunar) ischemic stroke

An ischemic stroke caused by clogging of small arteries that spread deep into the brain due to genetic abnormality.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
CADASIL	NOTCH3	☐	☑
CARASIL	HTRA1	☐	☑
Retinal vasculopathy with cerebral leukodystrophy (RVCL)	TREX1	☐	☑

* Cardioembolic Stroke

A stroke cause by a variety of cardiac disorders such as arrhythmia. In such conditions the heart pumps unwanted materials into the brain circulation.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Long QT Syndrome	KCNQ1	☐	☑
	KCNJ2	☐	☑
	SCN5A	☐	☑

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	Age / Sex		Accepted	
	Sample type		Reported	

The test result of

The result details and related diseases

* Ischemic stroke of other etiologies

An ischemic stroke occurs by a connective tissue abnormality or inflammation affecting cerebral blood vessels.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Vascular Ehlers-Danlos syndrome	COL3A1	☐	☑
Marfan syndrome	FBN1	☐	☑
Polyarteritis nodosa	ADA2	☐	☑
Arterial tortuosity syndrome	SLC2A10	☐	☑

* CADASIL D/Dx (migrane)

A category of migraine with aura requiring differential diagnosis with CADASIL, of which first symptom can be migraine.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Familial hemiplegic migraine	CACNA1A	☐	☑
	ATP1A2	☐	☑
	SCN1A	☐	☑

* Moyamoya

Chronic progressive cerebrovascular disease is a genetic cause associated with stenosis or closure at the beginning of the entire cerebral artery and middle cerebral artery.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Moyamoya disease	RNF213	☐	☑
	ACTA2	☐	☑
	GUCY1A1	☐	☑

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	Sample type		Reported	

The test result of

The result details and related diseases

* Intracerebral hemorrhage

Cerebrovascular disorder caused by hemorrhage of blood vessels in the brain due to genetic abnormality.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Cerebral amyloid angiopathy	APP	☐	☑
	CST3	☐	☑
	ITM2B	☐	☑
Brain small vessel disease	COL4A1	☐	☑
Porencephaly	COL4A2	☐	☑

* Hyperlipidemia

A genetic cause of hypercholesterolemia which is main risk factor of ischemic stroke.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Familial Hypercholesterolemia	LDLR	☐	☑
	APOB	☐	☑
	PCSK9	☐	☑
	APOE	☑	☐

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	Sample type		Reported	

The test result of

The result details and related diseases

* Thrombophilia

A congenital abnormality of blood coagulation that increases the risk of thrombosis.

Disease	Gene	Pathogenic Variant	
		Detected	Not detected
Factor V Leiden Thrombophilia	F5	☐	☑
Prothrombin-Related Thrombophilia	F2	☐	☑
Thrombophilia due to antithrombin III deficiency	SERPINC1	☐	☑
Thrombophilia due to protein C deficiency	PROC	☐	☑
Thrombophilia due to protein S deficiency	PROS1	☐	☑

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Stroke GENOME screen Report

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What is Stroke Genome Screen?

Stroke is a neurological deficit that occurs when cerebral blood vessels are blocked (cerebral infarction) or cerebrovascular burst accident (cerebral hemorrhage). The major risk factors for stroke are hypertension, diabetes, hyperlipidemia, smoking, drinking, hemostatic disorders, coronary artery disease, and periodontal disease, and also there are a variety of genetic factors associated with it. Some of the strokes can be caused by genetic abnormality, and the most common genetic diseases causing stroke are moyamoya disease and CADASIL (Cerebral Autosomal Dominant arteriopathy with Subcortical Infarcts and Leukoencephalopathy). Younger patient without stroke risk factors such as hypertension, diabetes, hyperlipidemia, smoking, and alcohol may need to suspect a hereditary stroke disease if they have cerebral infarction or cerebral hemorrhage. Stroke Genome Screen is a test that can be expected to prevent, diagnose early, and improve the treatment effects regarding hereditary stroke by examining 34 genes known to increase the risk of developing hereditary stroke with NGS test.

Hereditary stroke have these characteristics.

- Even if pathogenic variant(PV) is found in genes related to hereditary stroke, disease does not occur 100% (Reduced Penetrance). The time of onset and clinical patterns of diseases vary widely from person to person.
- Hereditary stroke is part of total hyperlipidemia or dyslipidemia, and the mechanism and clinical manifestations of hereditary stroke may vary depending on the gene involved.
- Hereditary stroke included in this test may be associated with stroke as well as various other clinical manifestations and diseases.
- Even if genetic testing related to hereditary stroke does not identify any disease-related PV, there is still a possibility of stroke occurrence due to non-hereditary causes such as environmental effects and lifestyle.

Medical Technologist : M-K Lee M.T(20058) MKlee

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Disease Associated Genes

Stroke genome screen tests following diseases and genes according to the recommendation of the American College of Medical Genetics and Genomics (ACMG).

	Diseases	Gene
Large artery and small artery occlusion (Lacunar) ischemic stroke	Beta thalassemia	HBB
	Hyperhomocysteinemia	CBS
	Fabry disease	GLA
	Pseudoxanthoma elasticum	ABCC6
Small artery occlusion (lacunar) ischemic stroke	CADASIL	NOTCH3
	CARASIL	HTRA1
	Retinal vasculopathy with cerebral leukodystrophy (RVCL)	TREX1
Cardioembolic Stroke	Long QT Syndrome	KCNQ1
		KCNJ2
		SCN5A
Ischemic stroke of other etiologies	Vascular Ehlers-Danlos syndrome	COL3A1
	Marfan syndrome	FBN1
	Polyarteritis nodosa	ADA2
	Arterial tortuosity syndrome	SLC2A10
CADASIL D/Dx (migrane)	Familial hemiplegic migraine	CACNA1A
		ATP1A2
		SCN1A
Moyamoya	Moyamoya disease	RNF213
		ACTA2
		GUCY1A1
Intracerebral hemorrhage	Cerebral amyloid angiopathy	APP
		CST3
		ITM2B
	Brain small vessel disease	COL4A1
	Porencephaly	COL4A2
Hyperlipidemia	Familial Hypercholesterolemia	LDLR
		APOB
		PCSK9
		APOE
Thrombophilia	Factor V Leiden Thrombophilia	F5
	Prothrombin-Related Thrombophilia	F2
	Thrombophilia due to antithrombin III deficiency	SERPINC1
	Thrombophilia due to protein C deficiency	PROC
	Thrombophilia due to protein S deficiency	PROS1

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The reports and limitation of test

- Genetic variation is divided into five categories, pathogenic variant (PV), likely pathogenic variant (LPV), variant of unknown significance (VUS), likely benign variant (LBV), and benign variant (BV), according to 2015 ACMG/AMP.

- The disease relevance of sequence variation according to 2015 ACMG/AMP guidelines is analyzed by a specialist in the department of laboratory medicine, combining various evidences such as allele frequency in population databases, frequency, function analysis and computer prediction, and papers and mutation databases. However, the interpretation of the variation could be changed as additional evidence builds up after the results are reported.

- In this test, it is a rule to report mainly pathogenic variant and likely pathogenic variant, which have high or very high disease relevance, and not to report variant of unknown significance, likely benign variant, and benign variant.

- The genes included in the test include the entire exon, but in some areas sequencing may not be sufficiently covered. In addition, if a highly homologous sequence exists, the sequencing of the base may not be accurate, and variations in large deletions or duplications or non-protein-coding sequence areas may be difficult to detect.

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Test Information

Specimen	Peripheral Blood Leukocytes
Method	Next-Generation Sequencing; NGS

Next-Generation Sequencing Test

This technique breaks down the genome into many pieces, reads each piece at the same time, and combines the data obtained with bioinformatics techniques to quickly decode vast amounts of genome information.

Reference Transcript					
ABCC6	NM_001171.5	CST3	NM_000099.3	LDLR	NM_000527.4
ACTA2	NM_001613.2	F2	NM_000506.3	NOTCH3	NM_000435.2
APOB	NM_000384.2	F5	NM_000130.4	PCSK9	NM_174936.3
APOE	NM_000041.3	FBN1	NM_000138.4	PROC	NM_000312.3
APP	NM_000484.3	GLA	NM_000169.2	PROS1	NM_000313.3
ATP1A2	NM_000702.3	GUCY1A1	NM_000856.5	RNF213	NM_001256071.2
CACNA1A	NM_001127221.1	HBB	NM_000518.4	SCN1A	NM_001165963.1
CBS	NM_000071.2	HTRA1	NM_002775.4	SCN5A	NM_198056.2
ADA2	NM_001282225.1	ITM2B	NM_021999.4	SERPINC1	NM_000488.3
COL3A1	NM_000090.3	KCNJ2	NM_000891.2	SLC2A10	NM_030777.3
COL4A1	NM_001845.5	KCNQ1	NM_000218.2	TREX1	NM_033629.4
COL4A2	NM_001846.2				

Reference

1. The Human Gene Mutation Database (http://www.hgmd.cf.ac.uk)
2. Gene Reviews (http://geneclinics.org)

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Clinical significance of each tested gene

Even in people with positive result in the test, the onset and symptoms of the disease vary and it doesn't mean that necessarily the disease necessarily occur. In addition, even in people with negative result, the disease can be caused by other genes that have not been tested or other factors.

Genes with high clinical significance

CACNA1A	COL3A1	FBN1	GLA	HBB	HTRA1	KNCQ1	LDLR	NOTCH3
PROC	PROS1	RNF213	SCN5A					

Genes with clinical significance partially proven

ABCC6	*MedlinePlus*
	More than 200 ABCC6 pathogenic variants that cause pseudoxanthoma elasticum (PXE) have been identified. PXE is a condition characterized by abnormal accumulation of calcium and other minerals in elastic fibers, a component of connective tissues that provide strength and flexibility to structures throughout the body. The ABCC6 pathogenic variants involved in this condition lead to an absence of MRP6 protein or an altered protein that does not function properly.
ACTA2	*MedlinePlus*
	More than 30 ACTA2 pathogenic variants have been identified in people with familial thoracic aortic aneurysm and dissection (familial TAAD). This disorder involves problems with the aorta, which is the large blood vessel that distributes blood from the heart to the rest of the body. The aorta can weaken and stretch, causing a bulge in the blood vessel wall (an aneurysm). Stretching of the aorta may also lead to a sudden tearing of the layers in the aorta wall (aortic dissection). Aortic aneurysm and dissection can cause life-threatening internal bleeding.
ADA2	*MedlinePlus*
	More than 60 pathogenic variants in the ADA2 gene have been found to cause adenosine deaminase 2 deficiency, a disorder characterized by abnormal inflammation of various organs and tissues, particularly the blood vessels (vasculitis). These pathogenic variants severely reduce or eliminate the function of adenosine deaminase 2. Researchers do not fully understand how a shortage (deficiency) of this enzyme's activity leads to vasculitis and immune system abnormalities. They speculate that the enzyme deficiency may disrupt the balance between pro-inflammatory and anti-inflammatory macrophages in various tissues, leading to a buildup of pro-inflammatory macrophages and abnormal inflammation.
APP	*MedlinePlus*
	At least six pathogenic variants in the APP gene have been found to cause hereditary cerebral amyloid angiopathy, a condition characterized by stroke and a decline in intellectual function (dementia), which begins in mid-adulthood.
ATP1A2	*MedlinePlus*
	More than 30 pathogenic variants in the ATP1A2 gene have been identified in people with familial hemiplegic migraine type 2 (FHM2). This condition is characterized by migraine headaches with a pattern of neurological symptoms known as aura.
CBS	*MedlinePlus*
	More than 150 pathogenic variants that cause homocystinuria have been identified in the CBS gene.Clinically, affected patients present with eye, skeleton, central nervous system, and most importantly, vascular system abnormalities. Thromboembolic events affect arteries and veins of all parts of the body, representing a major cause of morbidity and mortality.
COL4A1	*GeneReviews*
	Pathogenic variants in the COL4A1 gene have been found to cause COL4A1-related brain small-vessel disease. This condition is part of a group of conditions called COL4A1-related disorders that have overlapping signs and symptoms involving fragile blood vessels. COL4A1-related brain small-vessel disease is characterized by stroke and eye abnormalities.

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COL4A2	*GeneReviews*
	Seven heterozygous COL4A2 pathogenic variants have been characterized in individuals with either porencephaly (porencephaly type 2; OMIM 614483) or intracerebral hemorrhage (OMIM 614519). Neurologic presentation of individuals with porencephaly type 2 was similar to that observed in COL4A1-related porencephaly.
CST3	*MedlinePlus*
	At least one pathogenic variant in the CST3 gene has been found to cause hereditary cerebral amyloid angiopathy, a condition characterized by stroke and a decline in intellectual function (dementia), which begins in mid-adulthood. The CST3 pathogenic variant that has been identified causes a form of hereditary cerebral amyloid angiopathy known as the Icelandic type. This pathogenic variant replaces the protein building block (amino acid) leucine with the amino acid glutamine at position 68 in the cystatin C protein (written as Leu68Gln or L68Q).
GUCY1A1	*Clinical Genetics 2016;90(4):351-360*
	Moyamoya disease (MMD) is a progressive vasculopathy characterized by occlusion of the terminal portion of the internal carotid arteries and its branches, and the formation of compensatory moyamoya collateral vessels. Homozygous pathogenic variants in GUCY1A3 have been reported as a cause of MMD and achalasia.
ITM2B	*J Biol Chem 2020;296:100054*
	Pathogenic variants in the ITM2B gene, which codes for a protein called BRI2, cause familial British and Danish dementia (FBD and FDD). A prominent neuropathological finding in FBD and FDD patients is the accumulation of amyloid proteins in the walls of small arteries with a widespread distribution.
PCSK9	*MedlinePlus*
	More than 50 pathogenic variants in the PCSK9 gene have been identified that cause familial hypercholesterolemia. The enhanced activity of the altered PCSK9 protein causes low-density lipoprotein receptors to be broken down more quickly than usual, reducing the number of receptors on the surface of liver cells. With fewer receptors to remove LDLs from the blood, people with gain-of-function variants in the PCSK9 gene have very high blood cholesterol levels. As the excess cholesterol circulates through the bloodstream, it is deposited abnormally in tissues such as the skin, tendons, and arteries that supply blood to the heart (coronary arteries).
SCN1A	*MedlinePlus*
	At least seven pathogenic variants in the SCN1A gene have been identified in people with familial hemiplegic migraine type 3 (FHM3), a form of migraine headache that runs in families. Each of these pathogenic variants changes a single protein building block (amino acid) in the NaV1.1 channel, which alters the channel's structure. The abnormal channels stay open longer than usual, which increases the flow of sodium ions into neurons. This increase triggers the cell to release more neurotransmitters. The resulting changes in signaling between neurons make people with FHM3 more susceptible to developing these severe headaches.
SLC2A10	*MedlinePlus*
	At least 23 SLC2A10 pathogenic variants have been identified in people with arterial tortuosity syndrome, a connective tissue disorder characterized by abnormal curving and twisting (tortuosity) of the blood vessels that carry blood from the heart to the rest of the body (arteries) and other health problems. The pathogenic variants that cause arterial tortuosity syndrome reduce or eliminate GLUT10 function. A lack (deficiency) of functional GLUT10 protein leads to overactivity (upregulation) of TGF-β signaling. Excessive growth signaling results in elongation and tortuisity of the arteries.
TREX1	*MedlinePlus*
	At least 82 pathogenic variants in the TREX1 gene have been identified in people with Aicardi-Goutières syndrome, a disorder that involves severe brain dysfunction (encephalopathy), skin lesions, and other health problems. Most of these pathogenic variants are believed to prevent the production of the 3-prime repair exonuclease 1 enzyme. The absence of this enzyme results in an accumulation of unneeded DNA and RNA in cells. These DNA and RNA molecules may be mistaken by cells for the genetic material of viral invaders, triggering immune system reactions that damage the brain, skin, and other organs and systems and result in the signs and symptoms of Aicardi-Goutières syndrome.

Medical Technologist : M-K Lee M.T(20058) MKlee

Lab Director(medical doctor) : Chang-Seok Ki M.D(547) CSKi

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▶ **Genes with low clinical significance**
*** The following genes are lacking objective validity for action related to health.**

APOB	APOE	F2	F5	KCNJ2	SERPINC1

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Lab Director(medical doctor) : Chang-ahn Seol M.D(1037) ChangAhnSeol

GC Genome

CAP ACCREDITED COLLEGE of AMERICAN PATHOLOGISTS

www.gcgenome.com 107 Ihyeon-ro, 30 beon-gil, Giheung-gu, Yongin-si, Gyeonggi-do 16924 South Korea Tel 031-280-9900 Q&A https://gccs.channel.io/

Stroke GENOME screen Report

Stroke Risk Screen

Institution		Sample ID	
Name		Medical record No.	
Age / Sex		Accepted	
Sample type		Reported	

The test result of

Test Description

A brief description of the stroke risk screen.

This test uses the genetic analysis techniques to check for genetic factors that may increase the risk of stroke. Previous research findings are analyzed to provide individually tailored information that may help with health management. However, the test is not relevant to the diagnosis of illnesses, and therefore a physician must be consulted in order to obtain a diagnosis and make treatment decisions.

Summary of Test Results

Disease information	Ischemic stroke		Moyamoya disease	CADASIL
Overall result	Standard		Standard	Standard
Level of risk	Standard	Standard	Standard	Standard
Gene tested	APOE	MTHFR	RNF213	NOTCH3

* The genotypes associated with increased risk of ischemic stroke was not detected.
* The genotypes associated with increased risk of Moyamoya disease was not detected.
* The genotypes associated with increased risk of CADASIL was not detected.

Medical Technologist : M-K Lee M.T(20058) MKlee

Lab Director(medical doctor) : Chang-Seok Ki M.D(547) CSKi

Lab Director(medical doctor) : Chang-ahn Seol M.D(1037) ChangAhnSeol

Stroke GENOME screen Report

Stroke Risk Screen

Institution		Sample ID	
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Sample type		Reported	

The test result of

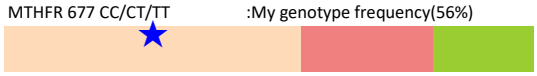
Test Results

Ischemic Stroke A description of the genetic risk factors of ischemic stroke. **Standard**

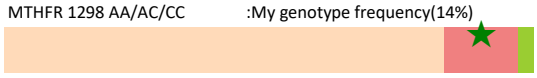
Genetic risk factors for Ischemic Stroke		
0 out of 3 risk		
Gene	My genotype	
	Standard	High-risk
APOE ★	e3e3	
MTHFR ★	CC	
MTHFR ★	AC	

APOE e2e2/e2e3/e2e4/e3e3/e3e4/e4e4 :My genotype frequency(71%)

MTHFR 677 CC/CT/TT :My genotype frequency(56%)



MTHFR 1298 AA/AC/CC :My genotype frequency(14%)



※ Genotype frequency of subject for the tested gene (based on East Asian population)

What is an ischemic stroke?

Strokes can be divided into ischemic strokes (cerebral infarctions), where a part of the brain is damaged due to blocked arteries, and hemorrhagic strokes (cerebral hemorrhages), which are caused by ruptured blood vessels in the brain. Cerebral infarctions are generally more common than cerebral hemorrhages, and about 82% of strokes in Korea are ischemic.

APOE gene information

The APOE gene synthesizes apolipoprotein E. It is involved in the regulation of serum lipid concentration and cholesterol delivery in the nervous system. Meta-analyses have reported an association between high-risk APOE genotypes and ischemic strokes.

MTHFR gene information

The MTHFR gene synthesizes MTHFR enzymes, which convert homocysteine to methionine. High-risk MTHFR genotypes reduce enzyme activity and therefore increase serum homocysteine concentration, consequently increasing the risk of stroke by damaging vascular walls and promoting thrombus formation.

Interpretation of results

- The genotype of APOE is e3e3. The genotype associated with increased risk of ischemic stroke was not detected.
- The genotype of MTHFR 677 position is CC. The genotype associated with increased risk of ischemic stroke was not detected.
- The genotype of MTHFR 1298 position is AC. The genotype associated with increased risk of ischemic stroke was not detected.

Recommendations

- Although the genetic risk factor of ischemic stroke was not detected, prevention for ischemic stroke by lifestyle is recommended.

Medical Technologist : M-K Lee M.T(20058) MKlee

Lab Director(medical doctor) : Chang-Seok Ki M.D(547) CSKi

Lab Director(medical doctor) : Chang-ahn Seol M.D(1037) ChangAhnSeol

Stroke GENOME screen Report

Stroke Risk Screen

Institution		Sample ID	
Name		Medical record No.	
Age / Sex		Accepted	
Sample type		Reported	

The test result of

Test Results

Moyamoya disease A description of the genetic risk factors of Moyamoya disease. **Standard**

Genetic risk factor for Moyamoya disease		
0 out of 1 risk		
Gene	My genotype	
	Standard	High-risk
RNF213 ★	GG	

RNF213 c.14429 GG/GA/AA :My genotype frequency(99.0%)

※ Genotype frequency of subject for the tested gene (based on East Asian population)

What is Moyamoya disease?

Moyamoya disease is a cerebrovascular disorder with the highest incidence occurring in Korea and Japan. It causes certain parts of the blood vessels in both sides of the brain to develop thicker inner walls, and produces abnormal blood vessels in the surrounding area. Pediatric patients usually present with ischemic symptoms as high brain activity requires large amounts of blood but only a small amount of blood is supplied. Adults mainly present with cerebral hemorrhage symptoms with the rupturing of small blood vessels

RNF213 gene information

The exact function of the RNF213 gene is unknown, but research findings suggest that the proteins synthesized by the gene are involved in vascular development. The high-risk RNF213 genotype is commonly found in patients with Moyamoya disease.

Interpretation of results

- The genotype of RNF213 is GG. The genotype associated with increased risk of Moyamoya disease was not detected.

Recommendations

- This test is not for the diagnosis of Moyamoya disease, but for the screening of Moyamoya disease based on genotype.
- Although most of Moyamoya disease patients have the increased risk genotype of RNF213, the disease can occur in individuals with standard risk genotype. Therefore, medical consultation is recommended for accurate diagnosis, if Moyamoya disease is suspected.

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Stroke GENOME screen Report

Stroke Risk Screen

Institution		Sample ID	
Name		Medical record No.	
Age / Sex		Accepted	
Sample type		Reported	

The test result of

Test Results

CADASIL A description of the genetic risk factors of CADASIL. **Standard**

Genetic risk factor for CADASIL		
0 out of 1 risk		
Gene	My genotype	
	Standard	High-risk
NOTCH3 ★	CC	

NOTCH3 c.1630 CC/CT/TT :My genotype frequency(99.8%)

※ Genotype frequency of subject for the tested gene (based on East Asian population)

What is CADASIL?

Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) is a cerebrovascular disease that causes blood flow disorders by damaging the walls of fine blood vessels. It usually affects relatively young persons aged 40 to 50 years and causes strokes, dementia, and migraines accompanied by an aura. CADASIL should be suspected when a young patient with no stroke risk factors such as hypertension, diabetes, or smoking presents with cerebral infarction symptoms.

NOTCH3 gene information

The NOTCH3 gene is associated with the NOTCH signal pathway, which plays a key role in vascular development. A high-risk NOTCH3 genotype may cause degeneration of vascular smooth muscle cells associated with CADASIL due to abnormal NOTCH signals.

Interpretation of results

- The genotype of NOTCH3 is CC. The genotype associated with increased risk of CADASIL was not detected.

Recommendations

- This test is not for the diagnosis of CADASIL, but for screening of CADASIL based on genotype.
- Although the analyzed position of NOTCH3 in this test is one of the position on which the pathogenic variant was recurrently detected in the CADASIL patients, the disease can occur if pathogenic mutations exist in areas other than those analyzed. Therefore, medical consultation is recommended for accurate diagnosis, if CADASIL is suspected. In addition, Stroke Genome Screen test is recommended for comprehensive analysis of NOTCH3 gene.

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Stroke GENOME screen Report

Stroke Risk Screen

Institution		Sample ID	
Name		Medical record No.	
Age / Sex		Accepted	
Sample type		Reported	

The test result of

Other Risk Factors Associated with Stroke

Risk factors other than genetic factors that increase the risk of stroke, and the degree of increased risk.

Check the applicable boxes (☑) to determine the level of risk due to lifestyle habits.

Lifestyle factors \ Disease	Stroke
Stroke risk screen results for 양성(여)122	Standard
☐ Hypertension	About 2.8 times
☐ Smoking	About 1.9 times
☐ Obesity	About 1.4 times
☐ Diabetes	About 1.3 times
☐ Alcohol	About 2.8 times
☐ Stress	About 2.8 times
☐ Cardiovascular disease	About 2.8 times

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Stroke screen Report

Stroke Risk Screen				
	Institution		Sample ID	
	Name		Medical record No.	
	Age / Sex		Accepted	
	Sample type		Reported	

Stroke Prevention

A description of simple ways to prevent strokes.

The following stroke-related risk factors should be addressed.

Hypertension | Smoking | Obesity | Diabetes | Alcohol | Stress | Cardiovascular disease

Diet guideline

Serum lipids are influenced by such factors as excessive intake of saturated fatty acids and cholesterol, imbalance between caloric intake and expenditure, excessive intake of sugars, inadequate intake of dietary fiber, and excessive intake of alcohol. Serum cholesterol and saturated fatty acid concentration should be reduced, and sugars should be limited to not more than 60% of total calories.

Good

Bad

Exercise guideline

Type of exercise	Walking	Running	Stretching	Cycling	Swimming
Intensity	Similar to aerobic exercise				
Frequency	5 days a week, 30 to 60 minutes per session				

References

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