

Genetic and Proteomic Contributions to the Pathophysiology of Moyamoya Angiopathy and Related Vascular Diseases

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Kirsten B Dorschel^{1,*}
John E Wanebo^{2,3,*}

¹Heidelberg University Medical School, Ruprecht-Karls-Universität Heidelberg, Heidelberg, Germany; ²Department of Neurosurgery, Barrow Neurological Institute, Phoenix, Arizona, USA; ³Department of Neuroscience, HonorHealth Research Institute, Scottsdale, AZ, USA

*These authors contributed equally to this work

Rationale: This literature review describes the pathophysiological mechanisms of the current classes of proteins, cells, genes, and signaling pathways relevant to moyamoya angiopathy (MA), along with future research directions and implementation of current knowledge in clinical practice.

Objective: This article is intended for physicians diagnosing, treating, and researching MA.

Methods and Results: References were identified using a PubMed/Medline systematic computerized search of the medical literature from January 1, 1957, through August 4, 2020, conducted by the authors, using the key words and various combinations of the key words “moyamoya disease,” “moyamoya syndrome,” “biomarker,” “proteome,” “genetics,” “stroke,” “angiogenesis,” “cerebral arteriopathy,” “pathophysiology,” and “etiology.” Relevant articles and supplemental basic science articles published in English were included. Intimal hyperplasia, medial thinning, irregular elastic lamina, and creation of moyamoya vessels are the end pathologies of many distinct molecular and genetic processes. Currently, 8 primary classes of proteins are implicated in the pathophysiology of MA: gene-mutation products, enzymes, growth factors, transcription factors, adhesion molecules, inflammatory/coagulation peptides, immune-related factors, and novel biomarker candidate proteins. We anticipate that this article will need to be updated in 5 years.

Conclusion: It is increasingly apparent that MA encompasses a variety of distinct pathophysiologic conditions. Continued research into biomarkers, genetics, and signaling pathways associated with MA will improve and refine our understanding of moyamoya’s complex pathophysiology. Future efforts will benefit from multicenter studies, family-based analyses, comparative trials, and close collaboration between the clinical setting and laboratory research.

Keywords: genetics, moyamoya, pathophysiology, proteomics, stroke

Introduction

Moyamoya angiopathy (MA) is a chronic, progressive, occlusive arteriopathy of the intracranial circulation that predominantly affects the major branches of the internal carotid artery (ICA); it is associated with dilated distal basal collateral arteries, reflecting aberrant angiogenesis, arteriogenesis, and vasculogenesis.^{1–5} Adults with MA typically present with ischemic (50–75%) or hemorrhagic (10–40%) stroke, whereas children may also present with transient ischemic attacks (including drop attacks).^{1,3,6–8} In 2013, Hishikawa et al reported that 9% of MA patients experience a type of stroke involving both ischemia and hemorrhage.^{9,10} In hemorrhagic MA,

Correspondence: John E Wanebo
c/o Neuroscience Publications; Barrow
Neurological Institute, St. Joseph’s
Hospital and Medical Center, 350 W.
Thomas Road, Phoenix, AZ, 85013, USA
Tel +1 602 406 3593
Fax +1 602 406 4104
Email Neuropub@barrowneuro.org

recurrent hemorrhages were found to appear with an average annual incidence of 4.5% and are associated with increased mortality; smoking and hypertension are modifiable risk factors.¹¹ About 20% of MA patients, including pediatric and younger MA patients, may exhibit headaches of vascular origin with migrainous features; a decrease in cerebral blood flow or cerebrovascular reserve and spreading cortical depression are possible pathophysiological mechanisms for these features.^{9,12} Chorea, choreoathetosis, dyskinesia, dystonia, limb-shaking, epilepsy-partialis continua, and optic disk enlargement with concomitant retinovascular anomalies are observed in MA patients, with chorea being the characteristic movement pattern.^{1,9} Ischemia of the basal ganglia-thalamocortical circuits, increased sex hormones, and hyperthyroidism are possible pathophysiological mechanisms for these characteristics.⁹

MA was first reported in 1957¹³ and initially defined according to radiographic criteria in 1969.¹⁴ It has since become increasingly evident that the angiographic findings of moyamoya represent a variety of distinct pathophysiological processes, manifesting a shared radiographic appearance.² Accordingly, by definition, MA refers to an isolated bilateral arteriopathy. Moyamoya syndrome (MMS) is either a unilateral arteriopathy or an arteriopathy with an associated medical disorder.² MMS encompasses a heterogeneous group of arteriopathies with variable penetrance of the cerebrovascular phenotype and various modes of inheritance.⁴ When the term moyamoya is used alone, independently of the cause, it refers exclusively to distinctive angiographic findings.¹ By convention, the arteriopathies are collectively referred to as moyamoya disease or moyamoya angiopathy (the term used in this paper).²

Ideally, biomarkers should unequivocally identify the presence or absence of a disease with a high degree of sensitivity and specificity. A genetic mutation reproducibly linked to a distinct disease phenotype is an essential discovery in biomedical research. The association of specific genes with MA is complex and likely due to the heterogeneity of disorders that share a common phenotype.^{1,2} The initial efforts to elucidate the genetic markers of MA reflected this complexity, with a wide range of genes, chromosomes, and hereditary diseases reported to be potential markers (Table 1).^{1–6,9,15–119} The current literature on familial MA suggests a low penetrance, autosomal dominant inheritance at loci on chromosomes 3p24.2–p26, 6q25, 8q23, 10q23.31, 12p12, and 17q25 (Table 1).^{6,7,16,40,51,52,68,73,93} Polymorphisms of *PDGFRB*, *MMP3*, *TIMP2*, *RNF213*,

TGFBI, *RPTOR*, and *NOS3* genes may be associated with MA (Table 1).⁴⁸ (See the [Supplemental Data](#) for definitions of gene symbols, proteins, and additional terminology.) Meyer et al¹²⁰ reported a 2-year-old girl with MMS, pseudoxanthoma elasticum, and an *ABCC6* (16p13.11) mutation.

Whether a putative biomarker is uniquely causative of MA or is a secondary by-product of the arteriopathy can be difficult to ascertain.^{2,16} Two major approaches to biomarker discovery have been used. In hypothesis-driven discovery, specific molecules are selected a priori because of suspected roles in pathophysiological processes. In proteomic screening, the entire proteome of specimens from MA patients is compared to matched controls for differences in expression.² In searching for candidate biomarkers for MA, both approaches have been applied. Proteome analysis of the cerebrospinal fluid (CSF) has been used by many research groups worldwide.² Categorizing subgroups of molecules by their function is an additional method of organizing biomarker discovery. The broad classes of proteins linked to MA as a result of hypothesis-driven biomarker discovery include enzymes, growth factors, transcription factors, adhesion molecules, inflammation and coagulation peptides, immune-related factors, biomarker candidates, and gene mutation products (Table 2).^{2,5,6,9,15–24,38,39,45–47,49,50,52,54–56,59–71,76–79,87–92,106,108–115,117,118,121–149} Houkin et al¹⁵⁰ proposed a double-hit hypothesis in which, in addition to the *RNF213* mutation, environmental factors such as inflammation and/or infection, autoimmune disease, ischemia, and hemodynamic stress are essential in inducing the first step of MA pathophysiology (Figure 1).

Heterogeneity in clinical presentation, progression, and response to therapy has encouraged research to define MA more precisely and focus on developing techniques to improve diagnosis and prognosis.² Identifying genes, proteins, cells, and signaling pathways involved in MA may provide insights into pathophysiological models and allow the discovery of potential candidates for targeted treatment strategies (Figure 1–4 and Table 1).^{2,4}

Methods

References were identified using a systematic computerized search of the medical literature from January 1, 1957, through August 4, 2020, conducted by the authors, using the PubMed, EMBASE, BIOSIS Previews, and Medline databases and various combinations of the key words “moyamoya disease,” “moyamoya syndrome,” “genetics,” “proteomics,” “biomarker,” “stroke,” “angiogenesis,” “cerebral arteriopathy,” “pathophysiology,” and “etiology.”

Table I Chromosomes and Genetic Defects Related to Moyamoya Angiopathy

Chromosome	Genetic Defects—Factors Affecting:		
	Vascular Stenosis*	Aberrant Angiogenesis†	Vascular Stenosis and Aberrant Angiogenesis
Chromosome 1 ^{4–6,16–37}	1p36.22 <i>MTHFR</i> (677C>T, C677T/A1298C, rs9651118); 1p31.3 <i>ROR1</i> ; 1p13.3 <i>PSRC1</i> (rs599839 [A/G]); 1q42.13 <i>OBSCN</i>	1p34.2 <i>TIE1</i> ; 1p21.2 <i>VCAM1</i> ; 1q24.2 <i>SELE</i>	1p13.2 <i>NRAS</i> : Noonan syndrome; 1p12-p11 <i>NOTCH2</i> : Alagille syndrome; 1q21.3 <i>SI00A4</i>
Chromosome 2 ^{4,5,20,35,38,39}	2q14.1 <i>IL1B</i>	2q24.2 <i>GCG</i> , Oxyntomodulin (P01275)	2p22.1 <i>SOS1</i> : Noonan syndrome
Chromosome 3 ^{4,21,35,36,38,40–43}	3q21.3 <i>ZXDC</i> (p.P562L)	3p26-p24.2 <i>MYMY1</i> (D3S3050): von Hippel-Lindau disease, Marfan syndrome; 3p22.1 <i>CTNNB1</i> ; 3p21.31 <i>CAMP</i> , antibacterial protein LL-37 (P49913); 3p21.31 <i>UCN2</i> , urocortin-2 (Q96RP3); 3q22.2 <i>CEP63</i> : Seckel syndrome; 3q23 <i>ATR</i> : Seckel syndrome	3p25.2 <i>RAF1</i> : Noonan syndrome
Chromosome 4 ^{4,5,20,44–47}		4q32.1 <i>GUCY1A3</i> or <i>GUCY1A1</i> , sGC α 1 β 1 loss, sGC α 2 β 1 residual	4q28.1 <i>FGF2</i>
Chromosome 5 ^{21,38,48–50}		5q31.1 <i>LEAP2</i> , liver-expressed antimicrobial peptide 2 (Q969E1)	5q14.3 <i>EDIL3</i> ; 5q32 <i>PDGFRB</i> (rs3828610 [A/C])
Chromosome 6 ^{1,5,6,16,20,38,51–58}		6p21.1 <i>VEGFA</i> (VEGF-634C); 6p12.3 <i>DEFB133</i> , beta-defensin 133 (Q30KQ1)	6p22.1 <i>HLA-A</i> ; 6p21.33 <i>HLA-B</i> ; 6p21.32 <i>HLA-DRA</i> ; 6p21.32 <i>HLA-DRB1</i> (DRB1*1510, DRB1*03, DRB1*13, DRB1*1302); 6p21.32 <i>HLA-DQA1</i> (DQA1*01021); 6p21.32 <i>HLA-DQA2</i> ; 6p21.32 <i>HLA-DQB1</i> (DQB1*0502, DQB1*0620, DQB1*0609); 6q25 (D6S441); 6q25.1 <i>ULBP3</i>
Chromosome 7 ^{4–6,17,35,37,59–67}	7p21.1 <i>HDAC9</i> (rs2107595); 7q11.23 <i>ELN</i> (rs34208922 [–/A], rs8326 [C/G])	7p15.3 <i>IL6</i>	7q21.11 <i>HGF</i> ; 7q31.2 <i>CAVI</i> ; 7q34 <i>BRAF</i> : Noonan syndrome; 7q36.1 <i>NOS3</i> (a-4b-G haplotype)
Chromosome 8 ^{24,38,52,53,68,69}		8p23.1 <i>ANGPT2</i> ; 8q12.1 <i>PENK</i> , proenkephalin-A (143–183) (P01210); 8q23.1 <i>ANGPT1</i>	8q22.3 <i>KLF10</i> ; 8q22.3 <i>UBR5</i> ; 8q23 (D8S546); 8q23.2 <i>EBAG9</i>
Chromosome 9 ^{24,59,70–72}	9q34.11 <i>ENG</i>	9p21.2 <i>TEK</i> or <i>TIE2</i>	
Chromosome 10 ^{2,4,6,16,19,73–77}	10q23.31 <i>ACTA2</i> (R179, p.R258C/H)	10q11.21 <i>CXCL12</i> (rs501120 [A/G])	
Chromosome 11 ^{3–5,20,78–85}	11p15.4 <i>HBB</i> : sickle cell disease; 11q22.2 <i>MMP3</i> (–1171 5A/6A (rs3025058)); 11q22.2 <i>MMP12</i>		11p15.5 <i>HRAS</i> : Costello syndrome

(Continued)

Table 1 (Continued).

Chromosome	Genetic Defects—Factors Affecting:		
	Vascular Stenosis*	Aberrant Angiogenesis†	Vascular Stenosis and Aberrant Angiogenesis
Chromosome 12 ^{4,35,52,68,85,86}			12p12.1 <i>KRAS</i> : Noonan syndrome, Costello syndrome; 12p12 (D12S1690); 12q24.13 <i>PTPN11</i> , hyperactive SHP-2: Noonan syndrome
Chromosome 13 ^{4,42,43,87,88}		13q12.12-q12.13 <i>CENPJ</i> : Seckel syndrome; 13q14.11 <i>FOXO1</i> , nuclear forkhead box protein O1	
Chromosome 14 ^{4,18,42,43,59,70,71,89}	14q23.2 <i>HIF1A</i> ; 14q32.13 <i>SERPINA1</i>	14q22.1 <i>NIN</i> : Seckel syndrome	14q32.33 <i>IGHG1</i> , immunoglobulin heavy constant gamma 1
Chromosome 15 ^{4,16,35,42,43,90–92}		15q21.1 <i>CEP152</i> : Seckel syndrome	15q21.3 <i>ALDH1A2</i> ; 15q22.31 <i>MAP2K1</i> : Noonan syndrome; 15q25.1 <i>CRABP1</i>
Chromosome 16 ⁶		16q12.2 <i>MMP2</i> (MMP-2-1575GA/-1306CC)	
Chromosome 17 ^{2,4,6,9,19–21,37,48,53,74,93–105}	17q11.2 <i>NFI</i> : Neurofibromatosis type I; 17q25.3 <i>CENPX</i> ; 17q25.3 <i>GPS1</i> ; 17q25.3 <i>TIMP2</i> (heterozygous <i>TIMP2-418</i> (rs8179090 [G/C]))	17q12 <i>CCL2</i> ; 17q12 <i>CCL5</i> ; 17q25.3 <i>BAIAP2</i> ; 17q25.3 <i>RNF213</i> (c.14576G>A, rs9916351, rs112735431, rs148731719, p.R4859K, p.R4810K); 17q25.3 <i>RPTOR</i> (ss161110142 [G/A])	17q25 (D17S939; 9-cM region between D17S785 and D17S836); 17q25.3 (D17S704; candidate interval 3.5Mb between D17S1806 and the telomere of 17q)
Chromosome 18 ^{4,42,43}		18q11.2 <i>RBBP8</i> : Seckel syndrome	
Chromosome 19 ^{5,9,16,17,20,74,106–114}	19p13.3 <i>PRTN3</i>	19p13.2 <i>ICAM1</i>	19q13.2 <i>TGFB1</i> (rs1800471 [C/G])
Chromosome 20 ^{4,6,25–34,74}		20q11.3 <i>SAMHD1</i>	20p12.2 <i>JAG1</i> : Alagille syndrome; 20q13.12 <i>MMP9</i> (dominant type (GG vs GA+AA) of MMP-9 Q279R (rs17576))
Chromosome 21 ^{4,21,42,43,115,116}	21q21.3 <i>APP</i>	21q22.13 <i>DSCR3</i> : Down syndrome (trisomy 21); 21q22.3 <i>PCNT</i> : MOPDII, Seckel syndrome	
Chromosome 22 ^{20,37,108,117,118}	22q12.2 <i>TCN2</i> (rs117353193)		22q13.1 <i>PDGFB</i>
Chromosome X ^{4,6,20,119}	Xp11.3 <i>TIMP1</i>	Xq28 <i>BRCC3/MTCP1</i>	

Notes: *Vascular stenosis includes intimal thickening, media attenuation, and internal elastic lamina damage. †Aberrant angiogenesis includes capillary sprouting.

Abbreviations: See [Supplemental Data](#).

Relevant articles on MA and supplemental basic science articles published in English were included. Reference lists of relevant articles and supplemental articles were reviewed for additional sources, and 206 articles were included in the final manuscript. The review reports by

Smith² and by Guey et al⁴ served as substantial references to this manuscript. Biomarkers involved in the pathophysiology of MA may be classified as genetic biomarkers of MA and molecular biomarkers of MA.² In this literature review, each biomarker has been described and specified

Table 2 Molecular Biomarkers of Moyamoya Angiopathy by Protein Class

Biomarker	Level in Moyamoya Angiopathy:		
	Increased	Increase Suspected	Decreased
Enzymes			
Alpha-I antitrypsin ^{89*}	✓		
MMP-2 ^{6,†}	✓		
MMP-3 ^{5,20,78,79*}			✓
MMP-9 ^{5,6,15,20,39,52,54,121–123,‡}	✓		
MMP-12 ^{20*}	✓		
TIMP-1, -2 ^{6,20*}			✓
MTHFR ^{6*}	✓		
RALDH2 ^{16,90,‡}			✓
eNOS ^{6,‡}	✓		
Growth factors			
VEGF ^{5,6,16,20,54–56,†}	✓		
Endoglin ^{59,70,71*}	✓		
PDGF-BB ^{20,108,117,118,‡}	✓		
HGF ^{5,63,65–67,‡}	✓		
bFGF ^{5,20,45–47,‡}	✓		
TGF-β ^{5,9,17,108–114,‡}	✓		
ANG(PT)/Tie ^{24,56,68,69,87,88,124–129,†}		✓	
Caveolin-1 ^{16,76,130–133,‡}			✓
EPCs ^{2,5,16,77,134–140,‡}	✓(adult MA)		✓(pediatric MA)
Smooth muscle progenitor cells ^{2,16,135,141,†}		✓	
Transcription factors			
HIF-1α ^{59,70,71*}	✓		
Adhesion molecules			
VCAM-1 ^{5,16,20,†}	✓		
ICAM-1 ^{5,16,20,†}	✓		
E-selectin ^{5,16,20,†}	✓		
CRABPI ^{16,91,92,‡}	✓		
Inflammation/coagulation			
MCP-1 ^{20,†}	✓		
IL-1β ^{5,20,39*}	✓		
IL-6 ^{60–64,†}	✓		
p-ANCA ^{106*}	✓		
D-dimer ^{142*}	✓		
SDF-1α ^{76,77,†}	✓		
CCL5 ^{143,144,†}	✓		
Immune-related factors/ autoantibodies			
S100A4 protein and immunoglobulinG ^{18,19,‡}		✓	
Anti-alpha-fodrin autoantibodies ^{145*}		✓	
APP ^{21,115*}	✓		
Catenin beta-1 ^{21,†}	✓		
EDIL3 ^{21,49,50,‡}	✓		

(Continued)

Table 2 (Continued).

Biomarker	Level in Moyamoya Angiopathy:		
	Increased	Increase Suspected	Decreased
ROR1 ^{21–23*}	✓		
GPS1 ^{21*}	✓		
STRA13 ^{21*}	✓		
Biomarker candidates			
Gla-42 transthyretin ^{146*}	✓		
Complement C1 inhibitor protein ^{147*}	✓		
Apolipoprotein C-III ^{147*}			✓
Apolipoprotein-E ^{148*}			✓
Apolipoprotein E precursor ^{148*}			✓
Apolipoprotein-J ^{148*}			✓
Alpha-I-B-glycoprotein ^{148*}	✓		
Oxyntomodulin (P01275) ^{38,†}		✓	
Urocortin-2 (Q96RP3) ^{38,†}		✓	
Beta-defensin 133 (Q30KQ1) ^{38,†}		✓	
Antibacterial protein LL-37 (P49913) ^{38,†}		✓	
Liver-expressed antimicrobial peptide 2 (Q969EI) ^{38,†}		✓	
Proenkephalin-A (143–183) (P01210) ^{38,†}		✓	
4473Da ^{2,149,†}	✓		
Haptoglobin ^{148,†}	✓		

Notes: *Indicates that the factor affects vascular stenosis (intimal thickening, media attenuation, and internal elastic lamina damage). †Indicates that the factor affects aberrant angiogenesis (capillary sprouting). ‡Indicates that the factor affects both vascular stenosis and aberrant angiogenesis.

Abbreviations: See [Supplemental Data](#).

according to its relation to MA. As some aspects of MA have been studied more thoroughly than others, some topics receive more attention than others. Despite substantial progress in the study of MA in recent years, much of the literature remains descriptive. Continued basic and clinical research is essential if we are to better understand the etiology of MA, which may result in a further differentiated diagnosis and treatment of patients with MA.

Pathology

MA is related to angioarchitecture and hemodynamics; it involves continuous vascular remodeling, including vascular stenosis and aberrant angiogenesis.^{2,9} Different pathogenetic mechanisms may underlie pathologic vessel changes in MA, and mounting evidence indicates that MA is an acquired proliferative disease of the intima.^{16,151,152}

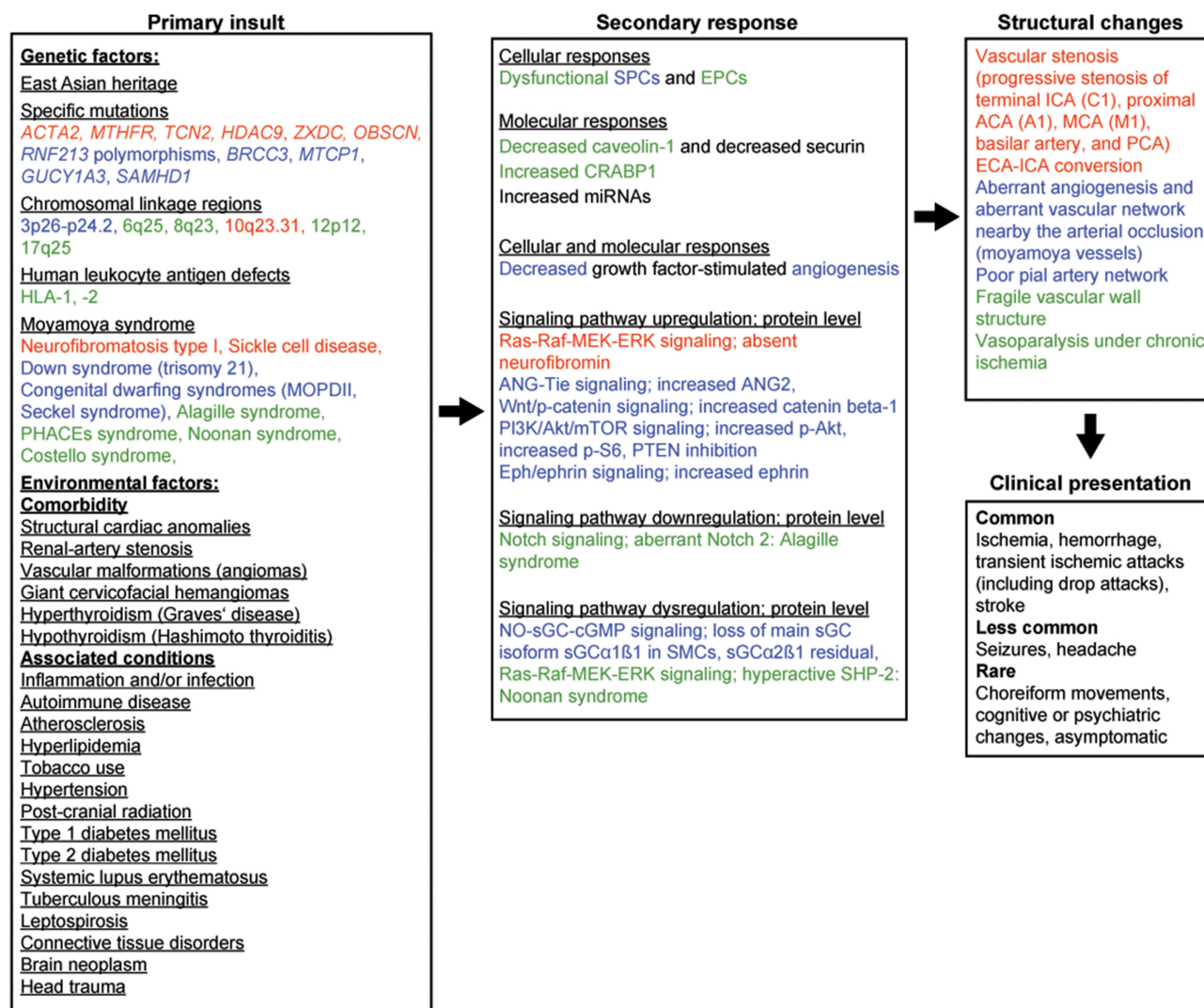


Figure 1 Potential disease mechanisms in MA. Red indicates that the factor affects vascular stenosis (intimal thickening, media attenuation, and internal elastic lamina damage). Blue indicates that the factor affects aberrant angiogenesis (capillary sprouting). Green indicates that the factor affects both vascular stenosis and aberrant angiogenesis.

Notes: Used with permission from Barrow Neurological Institute, Phoenix, AZ, USA.

Abbreviations: See [Supplemental Data](#).

In MA, progressive stenosis involves the supraclinoid ICA, distal ICA bifurcation (C1), and, less frequently, the proximal anterior cerebral artery (ACA) (A1), middle cerebral artery (MCA) sphenoidal segment (M1), the posterior cerebral artery (PCA), and rarely the vertebral artery, posterior inferior cerebellar artery (PICA), and proximal basilar artery (BA).¹⁻³ A significant correlation between the anterior and posterior circulation is present in MA. Hishikawa et al^{9,153} reported that MA stenotic and occlusive ICA lesions ipsilateral to PCA lesions might be significantly advanced compared to ICA lesions ipsilateral to PCAs without lesions. An early and delayed form of interaction between the anterior (ICA, MCA, and ACA) and posterior circulation (PCA) are evident. In early interaction, PCA involvement is correlated with a less

advanced anterior circulation involvement, causing symptoms during childhood. In delayed interaction, PCA involvement is correlated with an advanced anterior circulation involvement, causing adult-onset MA. These findings potentially explain the pathophysiology of the biphasic onset age in MA.⁹ As indicated by Suzuki in 1969,¹⁴ MA converts the cerebral vascular supply from the ICA to the external carotid artery (ECA). “ECA-ICA conversion” may result in intracranial hemorrhage and cerebral ischemia due to inadequate collaterals. Extracranial-intracranial bypass surgery may complement ECA-ICA conversion.^{14,154}

Previous studies demonstrate various associations of MA with atherosclerotic and autoimmune diseases,^{17,151,152,155-158} including a potentially higher autoimmune disease prevalence

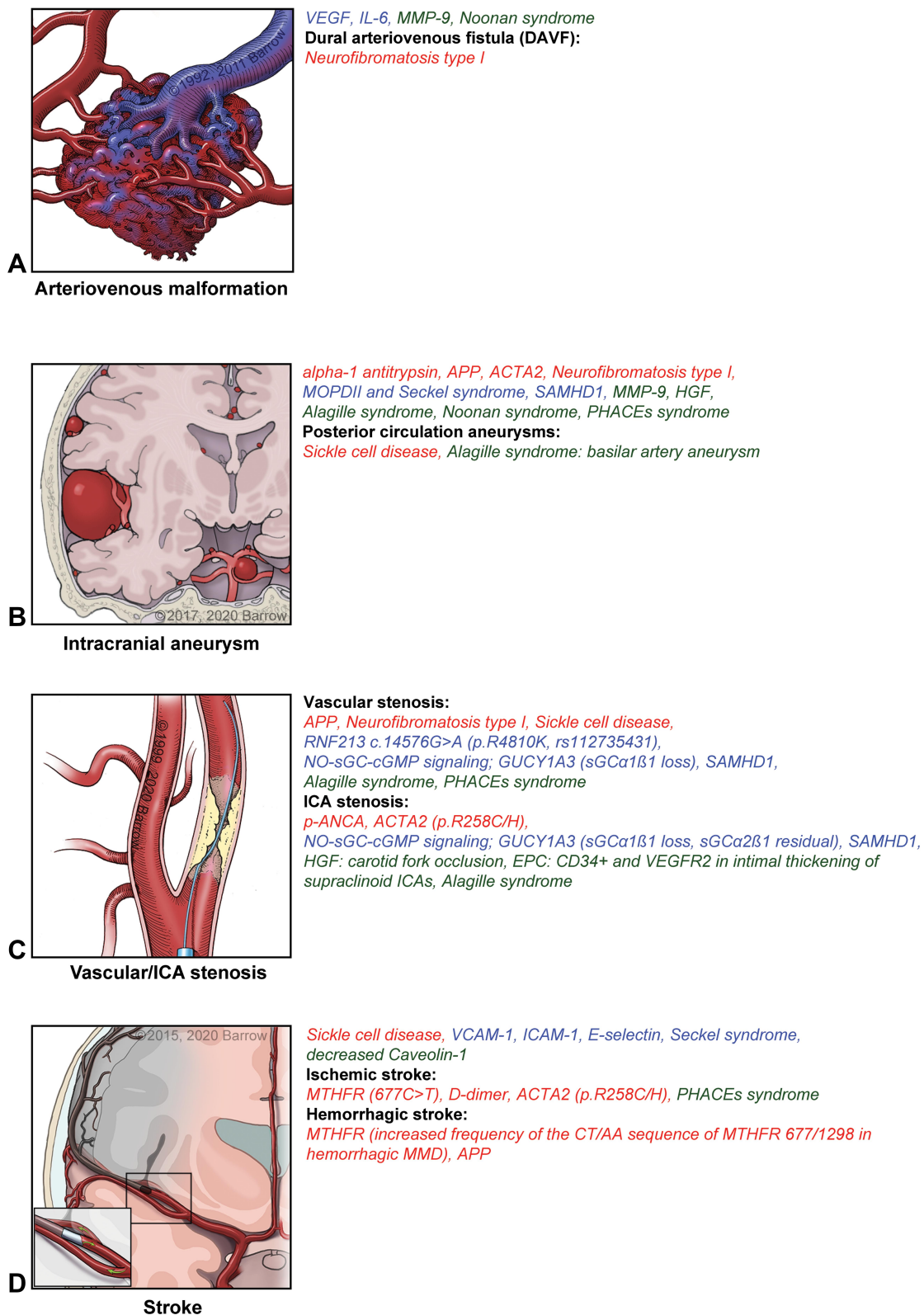


Figure 2 Proteins, cells, genes, and signaling pathways related to cerebral angiopathy characteristics in MA and associated disorders. **(A)** Arteriovenous malformation. **(B)** Intracranial aneurysm. **(C)** Vascular/internal carotid artery stenosis. **(D)** Stroke. Red indicates that the factor affects vascular stenosis (intimal thickening, media attenuation, and internal elastic lamina damage). Blue indicates that the factor affects aberrant angiogenesis (capillary sprouting). Green indicates that the factor affects both vascular stenosis and aberrant angiogenesis.

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Abbreviations: See [Supplemental Data](#).

Intimal thickening and Neointima formation

ACTA2 mutations affecting small muscular arteries: intimal hyperplasia, elastin deficiency; ACTA2 (p.R258C/H): ICA occlusion, HIF-1 α and endoglin overexpression in intimal thickening of the MCA,

MMP/TIMP imbalance: increased MMP-9, decreased MMP-3, decreased TIMP-1, -2: SMC migration and proliferation and intimal hyperplasia, circulating EPCs: intimal thickening of the supraclinoid ICA,

S100A4 protein and immunoglobulin G shown in intimal thickening of the MCA of autopsy specimens

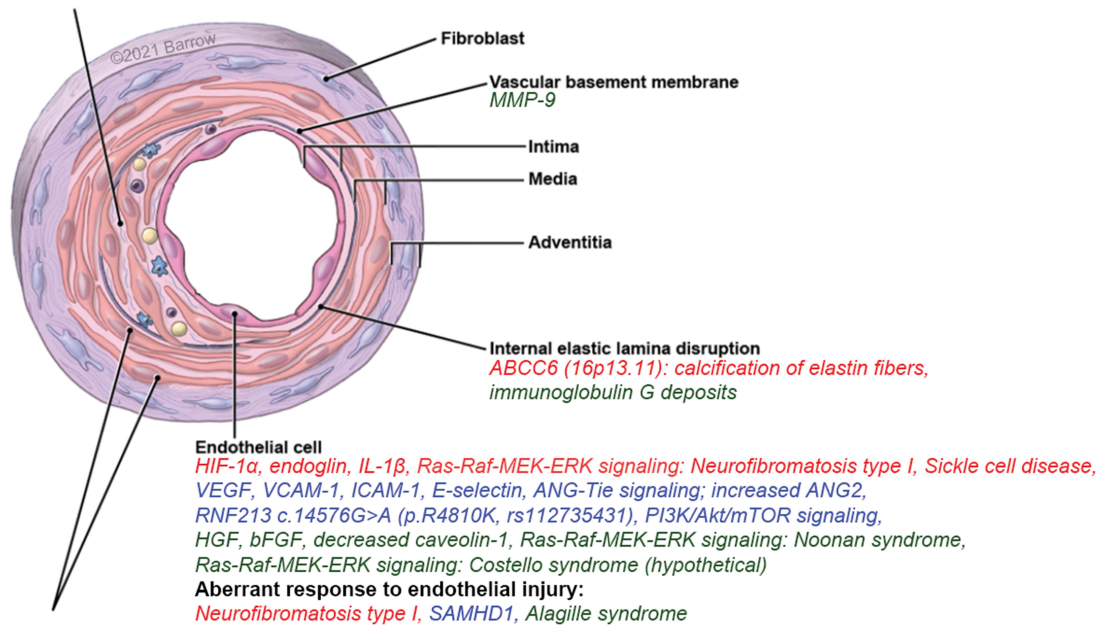


Figure 3 Schematic representation of an artery depicting macroscopic active sites of proteins, signaling pathways, genes, and cells in MA and associated disorders. Red indicates that the factor affects vascular stenosis (intimal thickening, media attenuation, and internal elastic lamina damage). Blue indicates that the factor affects aberrant angiogenesis (capillary sprouting). Green indicates that the factor affects both vascular stenosis and aberrant angiogenesis.

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in unilateral MA.¹⁵¹ The association between MA and a single nucleotide polymorphism located in *PSRC1* (1p13.3), rs599839, previously demonstrated to be associated with coronary artery disease in a European cohort, suggests a common pathophysiological pathway between MA and atherosclerotic disease.¹⁷ Atherosclerotic and juvenile-onset autoimmune diseases are associated with both pediatric and adult MA. Adult-onset autoimmune disease is associated with pediatric MA but not with adult MA.¹⁵⁸ Both pediatric and adult MA are associated with inflammatory disease clusters. In a subset of MA patients, pathologic vessel changes may thus be a sequela of systemic inflammation.^{18,152,158}

Histopathological studies show that vessel occlusion results from a combination of intimal fibrocellular thickening, intimal hyperplasia, luminal thrombosis, noninflammatory lipid deposits, and media attenuation with irregular, tortuous, stratified, ruptured, straight, or multilayered internal elastic

lamina, and a decrease of the outer vascular diameter.^{1,16,17,53}

Intimal hyperplasia is promoted by endothelial proliferation, vascular smooth muscle cell (SMC) proliferation, SMC migration from the media to the intima, angiogenesis, and production of vascular matrix proteins such as elastin, encoded by *ELN* (7q11.23), and collagen.^{17,59} Intimal thickening, which is less prominent in pediatric MA,¹⁵⁹ may result from malfunctioning endothelial and smooth muscle progenitor cells during vascular repair and maintenance.¹³⁵ Vessel exposure to blood constituents may facilitate intimal thickening.⁵ Lin et al¹⁸ showed that the S100A4 protein was detected in the thickened intima and media of the MCA from autopsy specimens and that cerebrovascular SMCs in different parts of the brain showed vacuolar degeneration. These investigators also stated that histopathological findings showed a narrowed lumen due to intimal fibrous thickening without significant inflammatory cell infiltration. Masuda et al¹⁶⁰ in a study of six autopsy

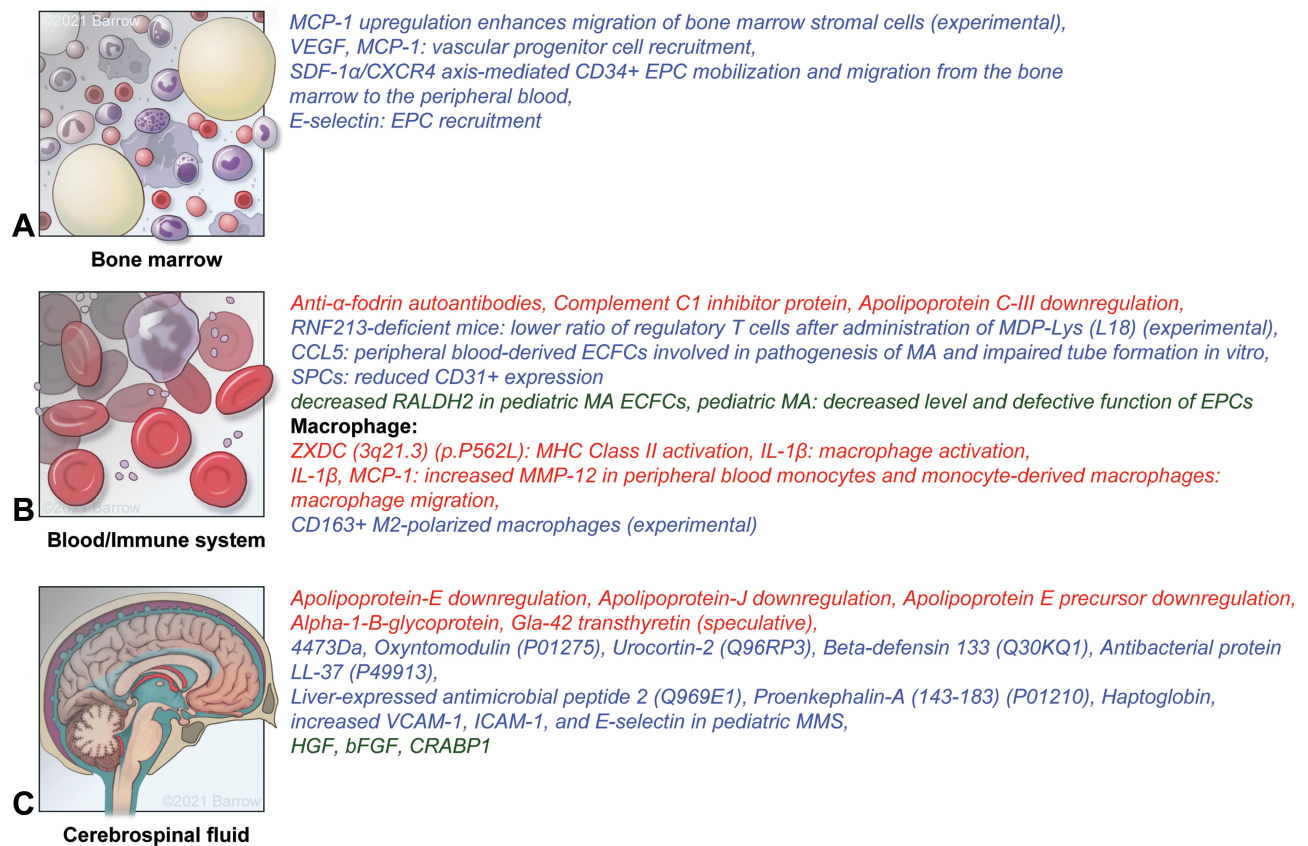


Figure 4 Microscopic active sites of proteins, cells, genes, and signaling pathways in MA and associated disorders. (A) Bone marrow. (B) Blood/immune system. (C) Cerebrospinal fluid. Red indicates that the factor affects vascular stenosis (intimal thickening, media attenuation, and internal elastic lamina damage). Blue indicates that the factor affects aberrant angiogenesis (capillary sprouting). Green indicates that the factor affects both vascular stenosis and aberrant angiogenesis.

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samples of stenotic or occlusive intracranial lesions of MA patients, showed the infiltration of human alveolar macrophage 56-positive cells, presumably macrophages, and ubiquitin carboxy-terminal hydrolase L1-positive cells, presumably T cells. These results should be interpreted with caution as the autopsy samples were obtained from patients with subarachnoid hemorrhage or intracerebral hemorrhage, which may induce inflammation. Detection of macrophage and T cell infiltrates in stenotic segments supports the hypothesis that microthrombi formation may result from chronic inflammation.^{5,160} Aberrant vascular endothelial growth factor (VEGF), transforming growth factor (TGF)- β 1, or matrix metalloproteinases (MMP) may be released in response to inflammatory stimuli or may activate downstream regulators of inflammatory signaling cascades.⁵ A proinflammatory milieu is essential for angiogenesis and collateralization.⁵ Thinning or duplication of the internal elastic lamina creates a neointima, an intimal fibrocellular layer consisting of migrated SMCs.^{17,18} TGF- β and bone morphogenetic protein

4 promote the vascular SMC contractile phenotype, characterized by decreased migration and proliferation. Platelet-derived growth factor (PDGF) induces aspects of the vascular SMC synthetic phenotype, characterized by increased migration and proliferation. A vascular SMC phenotypic switch from a differentiated/contractile to a proinflammatory/promatrix remodeling dedifferentiated/synthetic phenotype causes myointimal hyperplasia, vessel wall degeneration, matrix degradation, and inflammation.^{19,161,162} Subsequent vascular SMC apoptosis leads to a hypocellular vessel wall in intracranial aneurysms with increased susceptibility of rupture.¹⁶¹ Caspase-dependent apoptosis is involved in the disintegration of the arterial wall.¹

Moyamoya collateral vascular networks are usually dilated medium or small muscular-perforating arteries that are regarded as a combination of preexisting and newly evolved vessels.¹ Moyamoya collaterals demonstrate evidence of stress associated with increased flow, an irregular-shaped lumen with intimal thickening or thinning, fibrin deposits in the vessel

wall, a fragmented elastic lamina, attenuated media, and sacular and dissecting intracranial microaneurysms—this stress potentially explains hemorrhagic events in MA.^{1,16,152,163} Other moyamoya vessels are secondarily collapsed with concentric intimal thickening and luminal thrombosis caused by loose fibrous connective tissue, which potentially elucidates the cause of ischemic symptoms.^{1,163}

Moyamoya cortical microvascularization may be characterized by increased microvascular diameter and density, resulting in an increased microvascular surface, accompanied by aberrant microvascular hemodynamics, such as a chronically decreased cortical perfusion and cerebral blood flow, reflecting cerebrovascular hemodynamic insufficiency.^{16,152,164} Vascular anastomotic networks in pediatric MA may be described as a composition of four anastomotic networks with distinct angioarchitectures.¹⁶⁵ Moyamoya basal and cortical vessels may represent either collaterals compensating for reduced cerebral blood flow or aberrant active angiogenic neovascularization occurring before vascular occlusion due to the proliferation of endothelial cells or SMCs.^{16,166}

The pathology of stenotic segments in MA, including coexistence of proliferation and shrinkage and an unknown biology of neovascularization, suggests an aberrant versus a compensatory process that creates a complex MA pathophysiology.¹⁶ Given that several pathologic processes in the formation and potential coexistence of intracranial aneurysms and cerebral arteriovenous malformations (AVM) overlap with MA and MMS—such as vascular stenosis, media thinning, internal elastic lamina damage, angiogenesis, aberrant microvascular hemodynamics, and vascular remodeling—signaling pathways and inflammatory and/or genetic biomarkers may also overlap.^{40,60,72,105,161,167,168}

Genetic Biomarkers of Moyamoya Angiopathy

Specific Mutations Linked to Moyamoya Angiopathy

The E3 ubiquitin-protein ligase RNF213 (RNF213) (14576 G>A) is encoded by ring finger protein 213 (*RNF213*) (17q25.3). *RNF213* encodes a protein-harboring RING (really interesting new gene) finger motif that functions as a RING-class E3 ubiquitin ligase.¹⁶⁹ RNF213 is a cytosolic gene finger protein, with a Walker motif, a structural component of the AAA+ ATPase, and a RING finger domain.^{99,100} Specific mutations in *RNF213* may improve prognosis. The homozygous *RNF213* missense

variant c.14576G>A (p.R4810K, rs112735431) increases susceptibility to MA in East Asians and predicts a severe, early-onset form of MA, including severe ischemia, stenosis, and PCA occlusion.^{2,9,101,102,170} In one study, rs9916351 in *RNF213* showed a stronger genetic effect on early-onset than late-onset MA.³⁷ The *RNF213* p.Arg4810Lys variant causes a classical MA when present in a heterozygous state, but the same variant results in MA and systemic vascular diseases when present in a homozygous state in a gene-dosage-dependent manner. In addition, *RNF213* homozygous patients show a distinctive pattern of diffuse narrowing of the aorta and iliofemoral arteries, along with stenosis of the renal, celiac, or peripheral pulmonary arteries.¹⁷¹ Parallel appearance of the homozygous and heterozygous variant of c.14576G>A demonstrates a variable clinical course and severity of MA in siblings.¹⁰³ In unilateral MA, bilateral progression may be associated with the number of *RNF213* risk alleles.¹⁰⁴ In a genome-wide association study of 785,720 single-nucleotide polymorphisms (SNPs), Kamada et al⁹⁹ compared 72 Japanese MA patients with 45 Japanese controls, resulting in a strong association of chromosome 17q25-ter with an increased risk of MA. The research group confirmed this result through a locus-specific association study with 335 SNPs in the 17q25-ter region. The *RNF213* (p.R4859K, rs112735431) missense variant is linked to an increased risk of MA in Japanese people. *RNF213* polymorphisms rs112735431 and rs148731719 may be associated with MA in Chinese Hans.⁴⁸ *RNF213* mutations are also associated with susceptibility to MA in the Chinese Han population. Ischemic MA is particularly related to the R4810K mutation. Hemorrhagic MA is primarily associated with the A4399T polymorphism. Identification of novel variants in *RNF213* further emphasizes the genetic heterogeneity in MA.¹⁶⁹ In a study using a Chinese population, rs9916351 and rs8074015 in *RNF213* were demonstrated to be significantly associated with MA.¹⁷² The *RNF213* (p.R4810K) variant may predispose individuals of Asian descent living in the United States to MA.¹⁷³ Zhang et al¹⁷⁴ identified 27 rare *RNF213* missense variants in 255 Chinese MA patients not found in 300 healthy controls. No possible disease-causing mutations were identified in *ACTA2*, *BRCC3*, or *GUCY1A3*. In comparison to patients without rare *RNF213* variants, p.R4810K heterozygous patients were younger at diagnosis and showed an increased percentage of familial cases, ischemia, and PCA involvement.¹⁷⁴ Downregulation of Securin by *RNF213* R4810K (rs112735431, G>A) reduces

angiogenic activity of induced pluripotent stem cell-derived vascular endothelial cells from MA patients, suggesting that it may be a promising in vitro model for MA.¹⁷⁵ The MA susceptibility variant *RNF213* R4810K (rs112735431) induces mitotic abnormality and increases genomic instability.¹⁷⁶ Fujimura et al hypothesized that *RNF213* deficiency might cause vulnerability to hemodynamic stress and vascular fragility, leading to MA.¹⁵ In their 2019 review article, Mikami et al¹⁷⁰ hypothesized that *RNF213* may not be directly involved in the pathophysiology of MA, suggesting that inflammation, based on an autoimmune response, may affect *RNF213*, leading to MA progression. To evaluate the role of *RNF213* in the etiology of MA, Sonobe et al¹⁷⁷ generated *RNF213*-deficient mice and investigated whether they developed MA in comparison to wild-type littermates. Their results indicate that a functional loss of *RNF213* did not sufficiently induce MA, suggesting that additional insults, such as inflammation and/or infection, autoimmune disease, ischemia, and radiation, may be required for MA development. The *RNF213* c.14576G>A variant in MA patients may not represent a loss of function mutation. Suppression of vascular remodeling in *RNF213*-deficient mice requires further study.¹⁷⁷ In their 2015 study with homozygous *RNF213*-knockin mice and wild-type littermates, Kanoke et al¹⁷⁸ demonstrated through imaging findings and the anatomy of the circle of Willis that *RNF213* knockin mice did not spontaneously develop MA. The research group suggested that, in addition to genetic factors, multiple secondary insults, eg, environmental factors, may contribute to the onset of MA. Whether the *RNF213* polymorphism in MA is a gain-of function or loss-of-function mutation remains to be elucidated.¹⁷⁸ In 2016, Kanoke et al¹⁷⁹ demonstrated that *RNF213* deficiency and administration of immunological adjuvants such as muramyl dipeptide (MDP)-Lys (L18) or complete Freund's adjuvant did not sufficiently induce MA. The ratio of regulatory T cells after administration of MDP-Lys (L18) was shown to be significantly decreased in *RNF213*-deficient mice, suggesting an involvement of *RNF213* in regulatory T cell differentiation. *RNF213* may compromise immunological self-tolerance, thus contributing to MA pathogenesis.¹⁷⁹

Smooth muscle aortic alpha-actin 2 (*ACTA2*) is encoded by *ACTA2* (10q23.31).^{2,6,16} In 2009, Guo et al⁷³ performed a linkage analysis and association studies, phenotyping 127 individuals of 20 families with heterozygous *ACTA2* mutations and 192 ethnically matched controls,

indicating that mutation carriers may have a variety of premature vascular diseases. Heterozygous *ACTA2* missense mutations may predispose patients to various diffuse and diverse vascular diseases, including familial thoracic aortic aneurysms and dissections, premature coronary artery disease, premature ischemic strokes, and MA.^{73,180} The *ACTA2* p.R258C/H mutation is associated with ICA occlusion and early-onset ischemic stroke.⁷³ The *ACTA2* R179H de novo heterozygous missense mutation is related to an MMS, which might be caused by an autosomal dominant disorder and is associated with early-onset severe cerebrovascular disease due to smooth muscle dysfunction and with nonfamilial MA in European patients.^{2,74,75,181} *ACTA2* mutations have been identified through DNA sequencing of the *ACTA2* gene, according to a previously described protocol.^{180,181} *ACTA2* mutations affecting small muscular arteries cause increased or abnormal vascular SMC proliferation, leading to intimal hyperplasia, occlusive disease, and elastin deficiency. *ACTA2* mutations affecting large elastic arteries result in actin changes that decrease contractility, leading to aneurysmal disease, arterial dilatation, or dolichoectasia.^{16,19,74,75} Cerebral angiopathy characteristics show diverse vascular phenotypes, including a bilateral MMS with proximal ICA ectasia, terminal ICA stenosis, bilateral dolichoectatic ICA, intracranial arteries with a straight course, absence of basal moyamoya collaterals, and potential posterior circulation involvement.^{4,73-75}

Lys-63-specific deubiquitinase BRCC36 (*BRCC3*)/Protein p13 MTCP-1 (*MTCP1*) is associated with MMS, which may be caused by a recessive X-linked disorder. Deletion of *BRCC3/MTCP1* (Xq28) leads to loss of *BRCC3/MTCP1* gene expression. *BRCC3* is a ubiquitously expressed K63-specific deubiquitinating enzyme containing a JAMM (*JAB1/MPN/MOV34* metalloenzyme) domain. *BRCC3* encodes for two protein complexes, the nuclear BRCA1/Rap80/Abraxas/Merit40/*BRCC45* DNA repair complex and cytoplasmic BRISC complex.^{4,119} Cerebral angiopathy characteristics include bilateral anterior MA.⁴

Guanylate cyclase soluble subunit alpha-1 (*GUCY1A3*) is related to an MMS potentially caused by an autosomal recessive disorder. *GUCY1A3* (4q32.1) encodes the $\alpha 1$ subunit of the heterodimeric protein sGC, the primary receptor for nitric oxide (NO). Loss-of-function mutations cause a NO pathway alteration in SMCs. The NO-sGC-cyclic guanosine monophosphate (cGMP) pathway is a key signal transduction pathway controlling vascular smooth-muscle relaxation,

vascular tone, and vascular remodeling. In 2014, Herve et al⁴⁴ suggested that homozygous loss-of-function mutations in *GUCY1A3* may be linked to the loss of the main sGC isoform (sGC α 1 β 1) in SMCs and inadequate response of SMCs to NO. Herve et al stated that the intima-media thickness in carotid arteries of healthy subjects and the neointimal growth in pathological conditions, including moyamoya, are inversely associated with shear stress. In arterial bifurcations, shear stress is modified, and the main function of NO signaling is to normalize shear stress.⁴⁴ Factors specific to a particular vascular territory, such as the residual level of α 2B1 sGC, may explain the predominance of MA at ICA bifurcations.^{4,44} Cerebral angiopathy characteristics include MMS or MA, posterior circulation involvement, isolated MCA and ACA stenosis, and early onset before 5 years of age.⁴

SAM domain and HD domain-containing protein 1 (SAMHDI) (20q11.23) is associated with an MMS potentially caused by an autosomal recessive disorder. *SAMHDI* is involved in cerebral vascular homeostasis and immunoregulation. *SAMHDI* loss-of-function mutations may be associated with intracerebral large artery disease.^{4,74} Cerebral angiopathy characteristics include MA, distal ICA or proximal MCA/ACA stenosis (or both), and saccular aneurysms.⁴

Shoemaker et al³⁶ showed that *ZXD family zinc finger C (ZXDC)* (3q21.3) (p.P562L), a gene involved in MHC Class II activation, was the most enriched variant in White patients and non-*RNF213* founder mutation cases. Using collapsing variant methodology, the research group also showed that *obscurin*, *cytoskeletal calmodulin*, and *titin-interacting (OBSCN)* (1q42.13), a gene involved in myofibrillogenesis, was most enriched in White patients and non-*RNF213* founder mutation cases.³⁶

Another SNP associated with MA, rs2107595 in *histone deacetylase 9 (HDAC9)* (7p21.1), may be involved in large-vessel disease.³⁷

Genetic Associations with Moyamoya Angiopathy

MYMY1 (3p26–p24.2) is associated with moyamoya. Proposed MA genes on chromosome 3 code for von Hippel-Lindau (VHL) disease, suggesting that proteins encoded by *VHL* (3p25.3) are involved in vascular wall homeostasis.⁴⁰ Low oxygen and a mutated *VHL* gene are linked to a decreased ability of the VHL disease tumor suppressor (pVHL) protein to downregulate HIF-1 α , which allows pVHL to dimerize with stable HIF-1 β subunits and cause overexpression of HIF-target genes,

including the genes for VEGF, PDGF-BB, TGF- β , TNF- α , and erythropoietin.⁴¹ Chromosome 6 encodes human leukocyte antigens (HLAs).^{51,52} *HLA1* (6p22.1) and *HLA2* are linked to MA. *HLAB35* (6p21.33) may impact inflammatory and autoimmune processes and have been found in older Korean women with MA.^{1,57} *HLA-DR* (6p21.32) and *HLA-DQ* (6p21.32) genes are associated with familial MA.⁵⁸ The frequency of the HLA allele DRB1*0405 is lower, and that of the DRB1*1510-DQA1*01021-DQB1*0620 haplotype is higher compared to controls. The D6S441 microsatellite marker on chromosome 6q25 showed linkage with MA in 20 affected sibling pairs.⁵¹ Two loci on chromosome 8 encode MA candidate genes, *KLF10* (8q22.3) and *ANGPT1* (8q23.1). *KLF10* is involved in TGF- β 1 expression. *ANGPT1* predominantly acts on Tie2. Receptor-binding cancer antigen expressed on SiSo cells, encoded by *EBAG9* (8q23.2) and E3 ubiquitin-protein ligase UBR5, encoded by *UBR5* (8q22.3), may regulate angiogenesis through VEGF expression.^{52,68} Sakurai et al⁶⁸ provided significant genetic evidence for linkage to chromosome 8q23 and suggestive evidence for linkage to chromosome 12p12. Yamauchi et al⁹³ linked familial MA to chromosome 17q25. Mineharu et al⁹⁷ analyzed large families with an autosomal dominant inheritance pattern of MA and narrowed down the linkage region to chromosome 17q25.3. Based on these results, Liu and colleagues from the same research group¹⁰¹ identified *RNF213* as a major susceptibility gene for MA. In 2008, Mineharu et al⁹⁷ stated that brain-specific angiogenesis inhibitor 1-associated protein 2, encoded by *BALAP2* (17q25.3), interacts with brain-specific angiogenesis inhibitor-1, which might be an inhibitor of basic fibroblast growth factor (bFGF)-induced angiogenesis.⁹⁷ The ss161110142 polymorphism, located in position -1480 from the transcription site of *RPTOR* (17q25), with evidence for linkage to chromosome 17q25, may be associated with MA among East Asians.^{93,96–98}

Neurofibromatosis type I (NF-1) is an autosomal dominant disorder that may be a cause of MMS.⁴ *NFI* (17q11.2) is a tumor-suppressor gene that inhibits cell cycle progression.⁷⁴ Neurofibromin is a regulatory protein involved in blood vessel maintenance and repair that inhibits the Ras-Raf-MEK-ERK pathway.⁹⁴ Loss-of-function mutations in *NFI* cause increased mitogenic signaling, resulting in proliferation and differentiation of endothelial cells and hyperplastic vascular SMCs, leading to vascular wall thickening and stenosis due to absent, dysfunctional, or nonfunctional neurofibromin expression.^{4,19,94,95} NF-1

vasculopathy may be due to failure of the endothelium to suppress increased migration and proliferation of SMCs or due to an altered SMC response to normal endothelial signals.⁹⁵ Cerebral angiopathy of intracranial arteries includes MA, stenosis, occlusion, ectasia, aneurysms, arteriovenous fistula, involvement of the anterior or posterior circulation (or both), and the potential involvement of extracranial carotid or vertebral arteries, with a mean onset age of 5 to 11 years.⁴

Sickle-cell disease is an autosomal recessive disorder, encoded by *HBB* (11p15.4), which may be a cause of MMS. A pain crisis in the disease leads to changes in the formation of factor XIIIa-crosslinked fibrin or fibrinogen, which increases D-dimer levels (a hypercoagulable state).⁸⁰ This hypercoagulable state increases IL-6, E-selectin, and von Willebrand factor, resulting in tissue factor and thrombin generation.⁸⁰ Repeated vascular injury from sickling, abnormal regulation of vasoconstriction, and intimal hyperplasia result in an increased incidence of stroke.^{3,81–83} MMS screening by noninvasive imaging leads to improved neurologic outcomes.^{82,84} Cerebral angiopathy characteristics include distal ICA, proximal ACA or MCA stenosis (or both), moyamoya collaterals, and posterior circulation involvement, with posterior circulation intracranial aneurysms.⁴

Down syndrome (trisomy 21) is an aneuploidy disorder with the karyotype (47, XY + 21) in males, (47, XX + 21) in females, or mosaicism, featuring increased prevalence of autoimmune disorders and autoantibodies, including antiphospholipid antibodies. Chromosome 21 encodes the alpha chains of collagen type VI. Abnormal collagen VI expression is associated with an increased risk of cerebrovascular diseases. Inappropriate expression of proteins encoded by chromosome 21, including cystathionine- β -synthetase, interferon- γ receptor, and superoxide dismutase 1, is linked to structural vascular defects.^{4,116} Cerebral angiopathy characteristics resemble MA.⁴

Posterior fossa malformations, hemangiomas, arterial anomalies, cardiac defects, eye abnormalities, sternal cleft, and supraumbilical raphe syndrome (PHACEs) is a neurocutaneous disorder. The etiology of PHACEs and the pathophysiology of its associated vascular disease are undetermined. A potential cause may be a somatic mutation, affecting vascular development. Aplasia, hypoplasia, steno-occlusive arterial disease, an aberrant circle of Willis, and coexisting aortic arch anomalies lead to arterial ischemic stroke and moyamoya-like vasculopathy. Cerebral angiopathy characteristics include multiple

congenital arterial lesions (eg, dysplasia-hypoplasia-aplasia, aneurysms, and arteries with an aberrant course) and progressive arterial lesions (eg, stenosis, occlusion, and MA).^{4,182,183}

Congenital dwarfing syndromes comprise MOPDII (microcephalic osteodysplastic primordial dwarfism type II) and Seckel syndrome. MOPDII is an autosomal recessive disorder, which may be a cause of MMS. *PCNT* (21q22.3) encodes pericentrin, a centrosomal protein potentially involved in vascular homeostasis. Cerebral angiopathy characteristics involve aneurysms and MA. Seckel syndrome (microcephalic primordial dwarfism) is an MMS with autosomal recessive inheritance, encoded by *ATR* (3q23), *RBBP8* (18q11.2), *CENPJ* (13q12.12-q12.13), *CEP152* (15q21.1), *CEP63* (3q22.2), *NIN* (14q22.1), and *PCNT* (21q22.3). Loss-of-perfusion reserve capacity in hypoperfused brain regions creates tortuous arterial collateral development that results in cerebral ischemia and stroke. Cerebral angiopathy characteristics frequently involve aneurysms and rarely MA.^{4,42,43}

Alagille syndrome is an autosomal dominant disorder that may be a cause of MMS.^{4,25–27} Overall, 94% of cases are due to *JAG1* loss-of-function mutations, 5%–7% are due to deletions incorporating *JAG1*. *NOTCH2* receptor mutations cause less than 1% of cases. *JAG1* (20p12.2) encodes a cell surface protein, protein jagged-1, a ligand for Notch receptors 1, 2, 3, and 4. *NOTCH2* (1p12-p11) encodes the Notch2 transmembrane protein. Kamath et al³¹ suggests involvement of Jagged1 (*JAG1*) and the Notch signaling pathway in vascular development in reference to vascular anomalies in Alagille syndrome, indicating that the vascular anomalies evident in Alagille syndrome may be a direct consequence of a disruption in the Notch pathway. However, their study does not directly show the change of protein levels of *JAG1* in MA.³¹ Cerebral arteries of patients with Alagille syndrome and intracranial hemorrhage show thin-walled vessels with myointimal hyperplasia. Cerebral angiopathy characteristics include unilateral or bilateral MA, other abnormalities of the distal ICA or MCA (stenosis, occlusion, and aneurysm), and basilar aneurysm.^{4,25–34}

Noonan syndrome, an autosomal dominant disorder that may be a cause of MMS, is encoded by *PTPN11* (12q24.13) in 50% of cases, *SOS1* (2p22.1) in 10%–13% of cases, and *RAF1* (3p25.2) in 3%–17% of cases. Rarely involved genes include *KRAS* (12p12.1), *NRAS* (1p13.2), *BRAF* (7q34), and *MAP2K1* (15q22.31). Gain-of-function mutations in these genes activate the Ras pathway and

enhance cellular proliferation.^{4,35} Gain-of-function mutations in SHP-2 phosphatase (*PTPN11*) associated with Noonan syndrome and various childhood leukemias enhance cell migration of endothelial cells, hematopoietic cells, and fibroblasts and in vivo angiogenesis in SHP-2 D61G knockin mice.⁸⁶ Cerebral angiopathy characteristics include MA, AVMs, aneurysms, and hypoplasia of the posterior circulation (BA, PCA, superior cerebellar artery, PICA, anterior inferior cerebellar artery).^{4,35,184,185}

Costello syndrome, an autosomal dominant disorder that may cause MMS, is encoded by *HRAS* (11p15.5) and, less often, *KRAS* (12p12.1). Gain-of-function mutations that affect p.Gly12 or p.Gly13 cause Ras pathway dysregulation, leading to hyperplasia and vascular remodeling.^{4,85} Cerebral angiopathy characteristics include MA.⁴

Molecular Biomarkers of Moyamoya Angiopathy

Vascular Smooth Muscle Enzymes

The serine protease inhibitor alpha-1 antitrypsin, encoded by *Serpin family A member 1* (*SERPINA1*) (14q32.13), is an antiapoptotic factor in vascular SMCs. Increased alpha-1 antitrypsin serum levels, inflammation, and alterations of the alpha-1 antitrypsin gene lead to inhibition of elastase or collagenase, which causes proliferation of SMCs and synthesis of vascular matrix components elastin and collagen; these, in turn, lead to structural alterations of the vascular wall and intimal hyperplasia. Changes in alpha-1 antitrypsin serum levels may be indicative of MA progression, intracranial aneurysm formation, and fibromuscular dysplasia.⁸⁹

MMP-3 (stromelysin-1) inhibits SMC migration. Decreased MMP-3 levels facilitate SMC migration and lead to intimal hyperplasia. The *MMP3* 6A allele and 6A/6A genotype are associated with an increased risk of MA.^{20,78} The MMP-3–1171 5A/6A (rs3025058) single nucleotide polymorphism may be associated with sporadic and familial MA in the Chinese Han population.^{5,79}

The dominant type (GG vs GA+AA) of MMP-9 Q279R (rs17576) may be related to MA.⁶ MMP-9 (gelatinase B) overexpression leads to a decrease in angiotensin level, which degrades the vascular basement membrane and causes extracellular matrix remodeling. This remodeling increases the permeability of the blood-brain barrier, leading to intimal hyperplasia, cerebral ischemia, increased angiogenesis, collateral vessel formation

(moyamoya vessels), and intracranial aneurysm formation and rupture.^{20,39,52,54,122} A paracrine effect on the MA vasculature causes increased MMP-9, leading to pathologic angiogenesis and microhemorrhages.^{5,39,122} Macrophage MMP-9 may be involved in capillary branching in angiogenic revascularization triggered by ischemia (experimental).¹²¹ Sonobe et al¹²³ induced vascular hyperplasia by common carotid artery ligation in *RNF213* knockout mice and their wild-type littermates. The results of this research group suggest that increased vascular expression of MMP-9 and subsequent vascular wall thinning in *RNF213* knockout mice may reflect early distinctive changes in MA, consistent with the proposed constrictive remodeling theory, indicating that the *RNF213* c.14576G>A polymorphism in MA patients may be a loss-of-function mutation.¹²³ Increased serum MMP-9 in MA patients may be associated with spontaneous intracranial hemorrhage and cerebral hyperperfusion syndrome after direct surgical revascularization.^{15,20}

MMP-12 degrades elastin and other extracellular matrix molecules. Increased interleukin (IL)-1 β and monocyte chemoattractant protein-1 (MCP-1) levels increase MMP-12 expression in human peripheral blood monocytes and monocyte-derived macrophages, leading to macrophage and SMC migration.²⁰

Tissue inhibitor of metalloproteinase (TIMP)-1 and TIMP-2 inhibit SMC migration. The vascular injury repair model suggests an MMP/TIMP imbalance as a pathogenic mechanism of MA, which causes increased MMP-9 and decreased MMP-3, TIMP-1, and TIMP-2 levels, leading to SMC migration and proliferation and intimal hyperplasia. In 2010, Kang et al²⁰ compared TIMP2 levels in the CSF between 20 patients and 9 controls. They showed that TIMP2 levels were significantly lower in patients with MA ($p = 0.046$). The G/C heterozygous genotype in the TIMP-2-418 G>C (rs8179090) promoter may be associated with MA. Park et al⁶ observed a significant difference exclusively in 11 familial MA patients, who were not necessarily unrelated individuals. Wang et al⁴⁸ performed an association analysis in 96 MA patients and 96 controls and showed that PDGFRB, MMP-3, or TIMP-2 was not associated with MA in the Chinese Han population. Roder et al¹⁰⁸ also failed to replicate the association in 40 MA patients and 68 controls in the Central European population. Paez et al¹⁸⁶ also denied the association in the Japanese population. Bersano et al stated in their 2016 review article, “Again, conflicting results between studies did not allow any conclusions to be drawn about the

significance of these associations.¹⁸⁷ MMP-2 (gelatinase A) is encoded by *MMP2* (16q12.2). The MMP-2 -1575GA/-1306CC genotype may be a predisposing genetic factor for MA.⁶

The methylenetetrahydrofolate reductase (*MTHFR*) (1p36.22) 677C>T polymorphism is associated with ischemic stroke in children. Homozygous *MTHFR* 677C>T is associated with MA. Recessive *MTHFR* 677C>T and the C677T/A1298C compound genotype are associated with adult MA. The frequency of the CT/AA sequence of *MTHFR* 677/1298 is specifically increased in hemorrhagic MA. rs9651118 in *MTHFR* and rs117353193 in *transcobalamin 2 (TCN2)* (22q12.2) were associated with high-serum homocysteine in MA cases. Tissue enrichment analysis showed that the genes of associated loci were highly expressed in the immune system.^{6,37}

Retinal dehydrogenase 2 (*RALDH2*) is encoded by *ALDH1A2* (15q21.3). Epigenetic suppression of *RALDH2* in pediatric MA is linked to dysfunction of endothelial colony-forming cells (ECFC), which may be reversed by retinoic acid.^{16,90}

Endothelial NO is encoded by *NOS3* (7q36.1). The *NOS3* haplotype a-4b-G is associated with adult-onset MA. Age-specific cerebral angiopathy characteristics may include cerebral ischemia and hemorrhage.⁶

Growth Factors

VEGF is inversely correlated with the number of circulating endothelial progenitor cells.¹³⁷ VEGF receptor (VEGFR)2 or kinase insert domain receptor (KDR) is considered an early marker of endothelial and hematopoietic progenitor cells.⁵ Increased VEGF and PDGF-BB plasma levels may contribute to collateral vessel formation and may be responsible for intracranial microhemorrhages.^{5,20} The *VEGF*634G* allele is associated with MA and defective collateral vessel formation.⁵⁴ The CC genotype of *VEGF*634* and decreased levels of VEGFR1 or flt-1 and VEGFR2 may correlate with synangiosis-induced, favorable postoperative collateral development.^{5,6,55} In 2010, Kang et al²⁰ showed that increased plasma levels of VEGF and MCP-1 in MA patients might be involved in vascular progenitor cell recruitment and collateral vessel formation. Increased angiogenesis in the dura mater may lead to increased VEGF expression in the dura mater.²⁰ Progressive ICA stenosis causes ischemia, leading to the induction of proinflammatory cascades and VEGF expression.^{16,54} VEGF immunoreactivity has been detected in ischemia.⁵ VEGF polymorphisms are associated with

pediatric MA and poor collateral vessel formation.¹⁶ Park et al⁵⁵ showed in a case-control study of 107 Korean MA patients and 243 healthy controls that the 2634CC genotype occurred less frequently in the pediatric MA group, whereas the KDR 2604C/1192A/1719T haplotype increased the risk of pediatric MA. Patients with the CC genotype of VEGF 2634 showed better collateral vessel formation after surgery, suggesting that the VEGF 2634G allele may be associated with pediatric MA and poor collateral vessel formation. In summary, Park et al⁵⁵ suggested that VEGF and KDR polymorphisms may influence MA and the formation of synangiosis-induced collaterals after bypass surgery.⁵⁵ Crosstalk between Notch and VEGF signaling is involved in maintaining physiological angiogenesis.⁵⁶

Endoglin modulates cellular responses to TGF- β 1 signaling. In the intimal MCA, HIF-1 α and endoglin overexpression may lead to intimal hyperplasia.^{59,70,71}

Aoyagi et al¹¹⁷ studied the response of vascular SMCs in MA after PDGF stimulus application and found an alteration in DNA synthesis and proliferation of SMCs compared to controls. In their 1993 follow-up study, Aoyagi et al¹⁸⁸ showed that the diminished cellular response to PDGF is caused by a decreased number of PDGF receptors on SMCs of MA patients. Yamamoto et al⁶³ demonstrated decreased reactivity of replication and migration after a PDGF (PDGF-BB and PDGF-AA) stimulus, suggesting that prolonged exposition of various cytokines caused by delayed repair processes after arterial wall injury due to a decreased PDGF reaction may cause intimal thickening in MA. Kang et al²⁰ demonstrated an 18-fold increase in the PDGF-BB plasma level in MA patients compared to controls, suggesting a compensative mechanism to a systemically decreased amount of PDGFRB receptors. The results by Roder et al¹⁰⁸ on rs3828610, located in the promoter region of *PDGFRB* (5q32), may explain a decreased transcriptional activity and thus a decreased number of PDGFRB receptors.

Hepatocyte growth factor (HGF) is involved in angiogenesis, intracranial aneurysm formation, tumorigenesis, and tissue regeneration.^{5,65} Cerebral ischemia and infection lead to upregulation of HGF and *c-met* protooncogene. This upregulation affects HGF binding to high-affinity *c-met* tyrosine kinase receptor and epithelial and endothelial cells via the *c-met* receptor, leading to activation of tyrosine kinase signaling. This signaling increase stimulates cell growth, vascular SMC migration, extracellular matrix invasion, and morphogenesis, causing intimal

hyperplasia and occlusion of the carotid fork.^{5,66} Endothelial injury alters endothelial barrier properties, which may cause an accumulation of growth factors and cytokines, leading to occlusive changes.^{5,67} HGF has been detected in the ICA tunica media and intima.^{5,67} HGF-induced SMC migration suggests HGF involvement in neointima formation.^{5,63} Increased media HGF is associated with elevated CSF HGF, which is linked to increased angiogenesis, intimal proliferation, and collateral vessel formation (moyamoya vessels).⁶⁷

bFGF is involved in vascular development and dose-dependent increases in angiogenesis or arteriogenesis.^{5,45} bFGF receptor overexpression causes local bFGF expression and release, leading to intimal thickening and angiogenesis.^{20,46} Increased CSF bFGF may correlate with favorable postoperative collateral development in indirect revascularization procedures.^{5,47} bFGF immunoreactivity has been detected in superficial temporal artery endothelial cells and SMCs.⁵

TGF- β is involved in vasculogenesis, angiogenesis, cell growth and differentiation, and extracellular matrix gene expression.^{5,109} TGF- β 1 expression is upregulated in response to shear stress.⁵ TGF- β 1 regulates the expression of IL-1, bFGF, PDGF, and TGF- β by human peripheral blood monocyte chemotaxis.^{5,110} TGF- β 1 overexpression is correlated with increased production of extracellular matrix components (eg, procollagen, collagen, and proteoglycans) and accumulation of elastin synthase in SMCs of MA patients.^{5,111} Elastin synthesis and accumulation via the TGF- β pathway causes intimal and medial hyperplasia and collateral vessel formation.^{5,111,112} TGF- β increase in abnormal vascular growth inhibits HGF expression in vascular SMCs.^{67,113} MA in European patients may be associated with single polymorphisms in *TGFBI* (rs1800471[C/G]) and *PDGFRB* (rs382861[A/C]), and with rs599839, a single nucleotide polymorphism located in the 3' UTR region of *PSRC1* (1p13.3).^{9,17,108} Liu et al¹¹⁴ demonstrated a negative correlation between *TGFBI* polymorphisms rs1800471 and rs1800470 and Japanese MA patients.

Angiopoietins (ANGs) are secreted protein ligands of Tie receptor tyrosine kinases (Tie).^{24,56} ANG1 is encoded by *ANGPT1* (8q23.1), ANG2 is encoded by *ANGPT2* (8p23.1).^{24,69} ANG1 facilitates vascular network maturation, ANG2 initiates neovascularization.¹²⁴ *TIE1* (1p34.2) and *TEK/TIE2* (9p21) are endothelial cell-specific type 1 transmembrane protein receptor tyrosine kinases.²⁴ Tie1-Tie2 heterodimers attenuate signaling from Tie2 homodimers.²⁴ ANG1 is an agonistic paracrine Tie2 ligand that stimulates

Akt-dependent phosphorylation and nuclear exclusion of forkhead box protein O1 (FOXO1) transcription factor.⁸⁷ FOXO1 inactivation decreases the expression of genes involved in endothelial destabilization, apoptosis, and growth control.^{87,88} ANG2 is an endothelial autocrine ligand that acts as a context-dependent weak agonist or antagonist of Tie2.⁸⁷ ANG1-Tie2 signaling regulates proliferation, migration, adhesion, and endothelial cell survival; it also regulates endothelial cell-SMC communication in venous morphogenesis, angiogenesis, vessel maturation and stability, vascular development and maintenance during embryogenesis, inflammation, vascular permeability, and vascular leakage.^{56,125,126} ANG1-mediated Tie2 activation is linked to the maintenance of an endothelial barrier and a quiescent vasculature.¹²⁶ ANG2 activation of Tie2 supports the stable enlargement of normal non-leaky vessels.¹²⁷ ANG2-Tie2 binding is linked to vascular destabilization and sprouting during VEGF-induced neovascularization.^{124,128} The relative ratio of ANG1 versus ANG2 regulates the effect of ANG-VEGF on angiogenesis.¹²⁸ Integrins regulate ANG-Tie signaling.¹²⁵ ANG1 and ANG2 weakly bind integrins, with accentuated integrin effects in low Tie2 expression.^{24,69} Tie2 regulates vascular barrier function.²⁴ Various ANG proteins may induce Tie1 phosphorylation, and Tie1 activation may be amplified through Tie2.¹⁸⁹ Tie1 is involved in maintaining vascular endothelial cell integrity and angiogenic capillary growth, modulating the effects of ANG1 and ANG2 on Tie2 and regulating ANG1-Tie2 signaling.¹²⁵ Tie1 deletion leads to compromised vascular integrity, hemorrhage, and embryo death.⁸⁷ ANG2 acts as a Tie2 agonist in nonpathologic conditions, in the absence of ANG1, and at high levels. In inflammation and at low levels, ANG2 functions as a Tie2 antagonist, promoting vascular dysfunction.^{24,56,69,87,125,127} Blecharz et al analyzed *ANG2* gene expression in MCA lesions obtained from MA patients and atherosclerotic cerebrovascular disease patients. Cerebral endothelial cells incubated with serum of the same patients in vitro were applied. In contrast to the sera of patients with atherosclerotic cerebrovascular disease, the sera of MA patients induced *ANG2* overexpression and secretion, accompanied by the loss of endothelial integrity. The results obtained by the group may identify cerebral endothelial cells as a potential source of vessel-destabilizing factors, inducing plastic and unstable neovascularization and cerebrovascular disintegration in MA, mediated by the autocrine release of the pro-angiogenic cytokine ANG2, thereby elucidating a mechanism that may contribute to cerebrovascular hemorrhagic and ischemic events in MA.¹⁹⁰ Yu et al¹⁹¹ showed that ANG2 may be

involved in the pathophysiology of increased angiogenesis in adult hemorrhagic MA and may also be a prognostic factor of intracranial hemorrhage in adult MA patients. Infection is linked to Tie2 signaling disruption that is related to vascular leakage.²⁴ The A20 binding inhibitor of nuclear factor- κ B (NF- κ B) activation-2 (ABIN-2) is a potential vascular protective protein that acts on Tie2 with antiapoptotic and anti-inflammatory effects on endothelial cells.^{126,129}

Caveolin-1 is involved in endothelial progenitor cell recruitment, inhibits endothelial NOS (eNOS), is critical for VEGF-induced angiogenesis, and may be protective against ischemia/reperfusion injury.^{76,131–133} Some research groups showed an association of *CAVI* with the *RNF213* variant, whereas other groups showed the absence of such an association. Caveolin-1 may be decreased in MA patients with the *RNF213* variant.¹⁶ Bang et al¹⁹² prospectively analyzed clinical data from 139 MA patients, 61 intracranial atherosclerotic stroke patients, and 68 healthy controls, comparing protein biomarkers for caveolae, genetic, angiogenesis, and endothelial dysfunction between MA patients and intracranial atherosclerotic stroke patients. The group used pathological analysis to evaluate whether a certain protein biomarker would mediate the association between genes and MA, suggesting that MA is a disorder of caveolae, potentially related to caveolin-1, involving the regulation of endothelial vesicular trafficking and signal transduction, but may not be related to dysregulation of circulating cytokines or endothelial dysfunction. Chung et al¹⁹³ in a study with 77 consecutive MA patients and 17 patients with intracranial atherosclerotic stroke and no *RNF213* mutation, who served as controls, showed that *CAVI* downregulation induced apoptosis in SMCs, and suppressed angiogenesis in endothelial cells, suggesting that caveolin-1 may be involved in pathological negative arterial remodeling in adult MA, indicating that negative remodeling may be associated with MA symptomatology. In their 2019 review article, Mikami et al¹⁷⁰ stated that caveolin-1 might be involved in MA and inflammation. They reported that caveolin-1 serum levels were shown to be decreased in MA and shown to be markedly decreased in MA patients with the *RNF213* variant. They finally cite that caveolin-1 may be associated with angiogenesis in addition to an association between the caveolin-1/ERK and Wnt/ β -catenin pathways. A decrease in caveolin-1 leads to an increase in eNOS and systemic NO,¹³¹ which alters VEGF-induced ERK activation in endothelial cells.¹³² This alteration increases proliferation and decreases

stabilization, capillary tube formation, and endothelial cell migration.^{16,130,131} Increased endothelial caveolin-1 and VEGF result in decreased angiogenesis in mice.¹³² Aberrant angiogenesis in caveolin-1 gene-deficient mice may be restored by the ablation of eNOS. Caveolin-1 may regulate angiogenesis through multiple pathways, including NO-independent and NO-mediated mechanisms.¹³¹ Absent *CAVI* gene expression, cerebral infarction volume, and ischemic injury increase in mice.^{130,133} Transient decreases in caveolin expression enhance progenitor cell engraftment.⁷⁶

Circulating endothelial progenitor cells (EPCs) reflect mixed conditions of vascular occlusion and abnormal vasculogenesis.^{134,135} Decreased tube formation in EPCs may indicate defects in paracrine function.^{134,135,137} Increased levels of EPCs are associated with aberrant angiogenesis, arteriogenesis, and vascular hyperplasia and may contribute to neovascularization (moyamoya vessels) after cerebral ischemia and MA progression.^{16,134,135,137,139,140} With an inverse correlation between EPCs and VEGF, increased numbers of EPCs may not be entirely mediated by VEGF or granulocyte-macrophage-colony-stimulating factor.¹³⁷ CD34+ cells, a subpopulation of EPCs, have been detected at increased levels with impaired function in the peripheral blood of adult MA patients compared to decreased CD34+ cells with defective angiogenic function in pediatric MA.^{2,16,77,136,139} An inadequate response to vascular progenitor cell recruitment may cause an early-onset severe form of pediatric MA.¹³⁵ Detection of CD34+ cells and VEGFR2 in intimal thickening of supraclinoid ICAs from adult MA patients suggests that EPCs may participate in vascular stenosis.^{135,138} Decreased endothelial progenitor cell-colony-forming units may be associated with early-stage MA or MA progression. Increased endothelial progenitor cell-colony-forming units and outgrowth cells have been demonstrated after revascularization surgery.^{5,134,135} EPCs are associated with increased VEGF, granulocyte colony-stimulating factor, and SDF-1 α .⁵

Vascular smooth muscle progenitor cells (SPC) isolated from the peripheral blood of MA patients demonstrate decreased PDGF receptor- α , major histocompatibility complex, and calponin expression levels, suggesting a defective cell maturation process.^{16,135,141} Increased VEGF causes failure of SPC outgrowth.^{135,141} SPCs of MA patients show irregular tube formation and differential expression of over 200 genes, resulting in reduced CD31 expression.^{2,141} Gene ontology analysis of upregulated transcripts identified ephrin receptor signaling, and analysis of downregulated transcripts

identified cell adhesion, cell migration regulation, innate immune response, enzyme-linked receptor protein signaling pathways, and vessel development.^{135,141}

Transcription Factors

Hypoxia-inducible factor (HIF)-1 α is involved in tissue oxygen homeostasis and helps regulate VEGF, PDGF-BB, TGF, and inducible NO synthase (NOS).^{59,70,71} HIF is a sequence-specific, DNA-binding, heterodimeric transcription factor that binds to hypoxia-response elements and transcriptionally activates genes linked to angiogenesis (eg, VEGF, PDGF), erythropoiesis (eg, erythropoietin), extracellular matrix turnover, and apoptosis.⁷¹ Hypoxia may regulate transcription factors including HIF and NF- κ B in innate and adaptive immune cells.¹⁹⁴ HIF-1 and NF- κ B may be involved in the inflammatory response.^{170,194} The PI3K/Akt signaling pathway may regulate HIF-1 expression.^{170,195} Mikami et al hypothesized that signal transduction pathways may be activated through *RNF213*, triggered by inflammatory cytokines present due to infection or autoimmune diseases.¹⁷⁰ Takagi et al⁵⁹ aimed to clarify the pathogenesis of MA through immunohistochemical analyses of human MCA samples. The research group compared 12 MCA terminal segments (M4) samples obtained at the time of superficial temporal artery (STA)-MCA bypass in MA patients with those obtained from patients with other causes of MCA or ICA occlusion. The group reported that the MCA samples from MA patients showed a thicker intima, higher staining for HIF-1 α in the intima and endothelium, and higher staining for endoglin in the endothelium compared with the controls. TGF- β 3 staining was co-localized with staining of HIF-1 α and endoglin, predominantly in the endothelium.⁵⁹

Adhesion Molecules

Vascular cell adhesion molecule 1 (VCAM-1),^{5,16,20} intercellular adhesion molecule 1 (ICAM-1),^{5,16,20} and E-selectin^{5,16,20} activate leukocytes, causing sticking and rolling of leukocytes along the endothelium before transmigration through the endothelial cell barrier, leading to vascular inflammation.⁵ E-selectin is a molecule on the endothelial surface that binds to β 2-integrin Mac-1 (CD11b/CD18) on neutrophils. β 2-integrin Mac-1 mediates firm adherence of neutrophils to the vessel wall by binding to its endothelial ligand, ICAM-1. E-selectin is involved in endothelial progenitor cell recruitment and angiogenesis.¹⁶ Increased expression of VCAM-1, ICAM-1, and E-selectin

in the CSF in pediatric MA poststroke or with subarachnoid hemorrhage activates leukocytes and extravascular migration, leading to inflammation and neovascularization.¹⁶ Isolated increases in CSF VCAM, ICAM, and E-selectin in pediatric patients with MMS may be associated with immunologic activation.^{5,90,196} Lee et al⁹⁰ compared the gene expression profiles of ECFCs isolated from pediatric MA patients and normal controls. They concluded that the expression of RALDH2 was epigenetically suppressed in ECFCs in pediatric MA patients, which may be critical in their functional impairment. Soriano et al¹⁹⁶ studied CSF and serum samples obtained from 20 MMS patients and 20 patients with congenital spinal deformities. The research group demonstrated increased CSF levels of soluble endothelial adhesion molecules, suggesting that MMS patients may have ongoing central nervous system inflammation and impairment of the blood-brain barrier. These soluble adhesion molecules may be used as indicators of that inflammatory process.

Cellular retinoic acid-binding protein 1 (CRABP1) decreases retinoid activity, which increases growth factor expression that stimulates SMC migration and proliferation, causing neointimal hyperplasia.⁹¹ Increased CSF CRABP1 may be associated with bilateral MA in adults and a postoperative decrease in basal collaterals.^{16,92} Roder et al¹⁰⁸ demonstrated that the two SNPs (rs2280367 and rs3813573) genotyped in the promoter region of *CRABP1* (15q25.1) did not show a significant association with MA.

Inflammation/Coagulation

MCP-1 upregulation enhances migration of bone marrow stromal cells (experimental).²⁰

IL-1 β stimulation of SMCs causes increased expression of prostaglandin E2 and cyclooxygenase-2, endothelial cell and SMC proliferation, macrophage activation, increased vascular permeability, and endothelial dysfunction; these events increase vasodilation and pial hyperemia.^{5,20} Absent *IL-1* and *MCP-1* gene expression reduce ischemic injury in mice.³⁹

IL-6 is involved in the activation of intracellular signal transduction pathways, including the Janus kinase (JAK)-signal transducer and activator of transcription protein (STAT) signaling pathway.⁶¹⁻⁶³ VEGF and IL-6 receptor binding are involved in JAK-STAT signaling pathway activation, which amplifies IL-6 signal transduction and enhances MMP-9, VEGF, and VEGFR2 activation and vascular SMC proliferation.^{60,62} Cerebral oxygen-glucose

deprivation upregulates IL-6 messenger RNA that increases transcription of angiogenesis-associated genes.⁶¹ Increased angiogenesis and extracellular matrix breakdown, initiated in part by IL-6, are associated with vascular instability and AVM rupture.^{60,62} IL-6-mediated endothelial blood-brain barrier disturbances may be decreased by IL-6 receptor inhibition in cerebral microvascular endothelial cells (experimental).⁶⁴ IL-6 inhibits migration of moyamoya SMCs.⁶³ Kang et al²⁰ showed that IL-6 plasma levels were not different between MA patients and controls.

Perinuclear antineutrophil cytoplasmic antibodies (p-ANCA) are associated with inflammation, arterial stenosis, and ICA occlusion.¹⁰⁶ Yanagawa et al¹⁰⁶ describe a case showing bilateral ICA stenosis, moyamoya vessels, and seropositivity of rheumatoid factor and MPO-ANCA, suggesting that immunological factors, inflammation, and vasculitis may be involved in the obstruction and/or stenosis of the ICA.

D-dimer is a potential prognostic biomarker for childhood arterial ischemic stroke and is predictive of stroke recurrence risk and adverse neurologic outcomes.¹⁴²

Roder et al¹⁷ analyzed 40 DNA samples of MA patients and 68 healthy controls from Central Europe and demonstrated a strong association between MA and rs599839, located on 1p13.3 in the 3' UTR region of *PSRC1*, in a Central European cohort. This SNP was described as being associated with coronary artery disease in a European cohort. Stromal cell-derived factor 1 alpha (SDF-1 α) is also known as C-X-C motif chemokine 12 (CXCL12a). Ischemia creates HIF-1-induced expression of platelet-derived SDF-1 α , SDF-1 α plasma levels increase, and SDF-1 α interacts with caveolae-mediated endocytosed C-X-C chemokine receptor type 4 (CXCR4) (fusin or CD184). These interactions cause SDF-1 α /CXCR4 axis-mediated CD34+ EPC mobilization, migration from the bone marrow to the peripheral blood, and peripheral homing, which are associated with increased arteriogenesis and vasculogenesis.^{76,77} Increased SDF-1 α is associated with rapid MA progression.⁷⁷

Fujimura et al¹⁴³ showed that sCD163 serum levels of MA patients were significantly increased compared to controls. CXCL5 serum levels of MA patients were significantly increased compared to controls. The research group observed no differences in both sCD163 and CXCL5 serum levels between each genotype of the *RNF213* polymorphism, variant or wild-type, between MA patients. The group indicated that MA patients

might show an increase in autoimmunity, further elucidating the pathogenesis of MA by the use of CD163+ M2-polarized macrophages. Phi et al¹⁴⁴ showed that peripheral blood-derived ECFCs of MA patients are critical to the pathogenesis of MA and the phenomenon of impaired tube formation in vitro, respectively. The C-C motif chemokine ligand 5 (CCL5) may mediate these interactions. In MA patients, defective ECFCs may direct aberrant recruitment of smooth muscle progenitor cells (SPCs) to critical vascular locations through the action of CCL5.

Immune-Related Factors/Autoantibodies

Protein S100-A4, encoded by *S100A4* (1q21.3), is a marker in the media of vascular SMCs. Hypothetically, it may be linked to the migration of S100A4-positive SMCs into the intima through a broken internal elastic lamina, with potential loss of the contractile phenotype by an endothelial-to-mesenchymal transition. This hypothesized transition may create a proliferation of S100A4-positive SMCs that may cause luminal stenosis with intimal thickening, leading to compensatory small-vessel proliferation. Immunoglobulin G may deposit in the internal elastic lamina and disrupt it.¹⁸ MA may be considered a hyperplastic vascular myopathy, promoting migration and proliferation of SMCs and matrix production.^{18,19}

Ogawa et al¹⁴⁵ showed that the sera of 32 MA patients, who were tested for anti-endothelial cell antibodies through enzyme-linked immunoassays and flow cytometric analysis, contained an increased incidence of anti- α -fodrin autoantibodies, providing further insight into arterial occlusion mechanisms in MA.

Molecules listed in this paragraph were identified by Sigdel et al²¹ via an analysis of 165 significantly elevated autoantibodies in the sera of a multiethnic group of MA patients. Amyloid-beta A4 precursor protein (APP), encoded by *APP* (21q21.3), is associated with an increased risk of hemorrhagic stroke, Alzheimer disease pathogenesis, and DNA damage response/repair.^{21,115} Cerebral amyloid angiopathy in *APP* transgenic mice leads to loss of vascular SMCs, intracranial aneurysms, vessel obliteration, and vasculitis. Extracellular deposition of neuron-derived β -amyloid in the vessel wall disrupts the vessel wall and causes parenchymal hemorrhage.¹¹⁵ Catenin beta-1 is encoded by *CTNGB1* (3p22.1). The Wnt/ β -catenin pathway is associated with angiogenesis, reduced microvessel density, and decreased expression of VEGF and SDF-1.²¹ EGF-like repeat and discoidin I-like domain-containing protein 3 (EDIL3), encoded by *EDIL3* (5q14.3), is involved in

angiogenesis and vessel wall remodeling and development.²¹ EDIL3 mediates adhesion, migration, and proliferation of vascular SMCs via interaction with integrin-receptor $\alpha_v\beta_3$ and may regulate vascular morphogenesis or remodeling during embryonic development.^{49,50} Receptor tyrosine kinase-like orphan receptor 1 (ROR1), encoded by *ROR1* (1p31.3), may be involved in cell migration and cytoskeleton remodeling, potentially explaining the function of ROR1 in neuron development.^{21,22} Adult MA is associated with neuronal impairment.²³ COP9 signalosome complex subunit 1 (GPS1), encoded by *GPS1* (17q25.3), is a component of the COP9 signalosome involved in DNA damage response/repair, which could be compromised in MA.²¹ Stimulated by retinoic acid 13 (STRA13), also known as centromere protein X (CENPX) or MHF2, is encoded by *CENPX* (17q25.3). STRA13 is the DNA-binding component of the Fanconi anemia core protein complex, which is a component of the kinetochore. The Fanconi anemia complex is involved in DNA damage response/repair. Fanconi anemia is a disease associated with MMS.²¹

Biomarker Candidate Proteins

Proteome screening of the CSF and the blood serum in MA patients using mass spectrometry has identified several specific proteins involved in the arteriopathy.²

Rüggeberg et al¹⁴⁶ performed a CSF proteome analysis in 29 White MA patients and 10 arteriosclerosis patients as controls. The research group demonstrated a novel post-translational modification of human transthyretin. Gamma-carboxylation of the Glu-42 (Gla-42), Gla-42 transthyretin, was demonstrated by two-dimensional electrophoresis and subsequent peptide sequencing with ESI-MS/MS. The research group reports that Gla-42 or similar post-translational modifications have not been shown in Asian MA patients so far. Therefore, the pathophysiological relevance of Gla-42 transthyretin in MA patients remains speculative.

Koh et al¹⁴⁷ demonstrated 22 differently-expressed serum proteomes of 6 MA patients and 6 normal controls by matrix-assisted laser desorption/ionization-time-of-flight mass spectrometry and electrospray ionization quadrupole time-of-flight mass spectrometry. Complement C1 inhibitor protein was upregulated (7.23 ± 0.10141 -fold) in MA patients, and apolipoprotein C-III was the lowest expressed protein (0.066 ± 0.05231). Koh et al¹⁴⁷ suggested that complement C1 inhibitor protein overexpression in MA may be related to progressive obstruction of the distal ICA and protection against ischemia.

Masuda et al¹⁶⁰ demonstrated SMC proliferation in occlusive lesions in major intracranial arteries in MA. Koh et al¹⁴⁷ suggested that apolipoprotein C-III downregulation may be biologically protective, reducing the formation of intracranial occlusive lesions.

Molecules listed in this paragraph were identified by Araki et al³⁸ in a pilot study of CSF proteomics via an analysis of CSF samples of 20 MA patients and 12 control patients using surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF-MS). Several CSF proteins with molecular weights corresponding to the 4473-Da peptide are potential biomarkers of vasculogenesis.³⁸ These proteins include oxyntomodulin (P01275), urocortin-2 (Q96RP3), beta-defensin 133 (Q30KQ1), antibacterial protein LL-37 (P49913), liver-expressed antimicrobial peptide 2 (Q969E1), and proenkephalin-A (143–183) (P01210). Aberrant vasculogenesis may be involved in MA.³⁸

Maruwaka et al^{2,149} performed a CSF proteome analysis in 20 MA patients and 17 controls by SELDI-TOF-MS. The research group detected the 4473-Da peptide, a possible prognostic biomarker for antihypoxic response and intracranial inflammation, which is associated with post-operative angiogenesis and favorable postoperative collateral development when found in the CSF of pediatric MA patients.^{2,149}

Hamauchi et al¹⁹⁷ analyzed induced pluripotent stem cell-derived endothelial cells from the peripheral blood of 3 MA patients carrying the *RNF213* R4810K variant and 3 healthy controls, suggesting that downregulation of ECM receptor-related genes may be related to impaired angiogenic activity in endothelial cells derived from induced pluripotent stem cells of MA patients. The upregulation of splicing regulation-related proteins may suggest differences in splicing patterns between endothelial cells of MA patients and controls.

Kashiwazaki et al¹⁴⁸ performed a CSF proteome study in 10 MA patients and 4 controls, using comparative 2-dimensional gel electrophoresis (2D-PAGE) and mass spectrometry. According to the proteome analysis technique, this study demonstrates that the CSF of MA includes 3 downregulated proteins (apolipoprotein-E, apoE precursor, and apolipoprotein-J) and 2 upregulated proteins (haptoglobin and alpha-1-B-glycoprotein). Downregulation of apolipoprotein-E and apolipoprotein-J suggests an involvement of the lipid metabolism in MA pathogenesis. Downregulated apolipoprotein-E may be involved in neurovascular unit dysfunction and neuronal vulnerability

against cerebral ischemia. Downregulated apolipoprotein-J may induce apoptosis of endothelial cells. Haptoglobin overexpression may indicate angiogenesis and/or inflammation in MA. The role of alpha-1-B-glycoprotein in the central nervous system remains to be elucidated.

Implementation and Future Considerations

Future research on MA should carefully consider past studies and current concepts.¹⁵⁰ Continued research into MA pathophysiology and associated signaling pathways may identify new treatment strategies, therapeutic applications, and mechanism-tailored interventions that may halt MA progression.^{4,5,187}

Ideally, biomarkers should assist in the diagnosis, prognosis, and treatment of MA.² Directing future research toward the identification of biomarkers that comprise an MA-specific fingerprint compared to more nonspecific markers of general physiological processes, such as angiogenesis or ischemia, will be essential.² Determining the relationship between any given measurable biomarker and relevant clinical endpoints is essential.^{2,198}

Biomarkers may improve therapeutic efficacy. Studies of cell function may help to predict the capacity for therapeutic angiogenesis. These data could be used to decide between direct or indirect bypass. Measuring circulating peptides may provide additional data to more accurately predict the response to surgery. Changes in biomarker levels may suggest novel therapeutics, such as growth factors, that may modulate surgical collateral growth.^{2,20} Nonsurgical approaches may include the application of trophic factors or chemicals increasing angiogenesis,¹⁹⁹ anti-cancer drugs decreasing SMC proliferation,⁷³ retinoids,^{90,91} increasing caveolin-1 levels,²⁰⁰ and stem-cell therapy compensating for impaired endothelial or smooth muscle progenitor cells.^{16,199} Development of cost-effective, noninvasive screening tests based on biomarkers may revolutionize MA patient care.² Accurate and timely diagnosis of MA may profoundly improve outcomes for MA patients. Neurologic status at the time of treatment critically influences long-term outcomes.^{2,8,201,202} Continued monitoring of at-risk patients with MMS, early referral to neurosurgeons once the arteriopathy becomes evident, considering surgical revascularization in asymptomatic MA patients,²⁰¹ and long-term neurological

and radiological follow-up along with a separate management guideline is advocated to prevent ischemic and hemorrhagic strokes in asymptomatic MA patients.²⁰³ Clinical features, prognosis, outcomes, and risk factors causing ischemic and hemorrhagic stroke in asymptomatic MA patients may be ascertained by prospective multicenter studies, eg, the Japanese AMORE study.²⁰⁴ Biomarker development may also aid in more accurately predicting patients who would benefit from surgery. Data enabling surgeons to prospectively identify the increased probability of posterior circulation stroke or higher risk of contralateral progression in unilateral MA is already employed in clinical practice.^{2,201,205,206} STA-to-MCA anastomosis may decrease the level of endothelial progenitor cells, decrease the formation of moyamoya vessels, halt MA progression, and alleviate headache in ischemic MA by potentially improving perfusion pressure and cerebral circulation.^{12,140} Compared with drug treatment, STA-MCA bypass surgery may significantly lower the risk of postoperative rebleeding and ischemia.¹⁴⁰

In vivo studies and animal models of MA are warranted.¹³⁵ Identification of MA-associated genes may allow the development of moyamoya animal models, essential for preclinical trials. Novel sequencing technologies, such as next-generation sequencing, and high-throughput technologies, such as genome-wide association studies, may accelerate the identification of new familial MA and monogenic MMS.^{4,187} Refining subgroups of MA by mutational genetic analysis, the definition of the function of relevant genes, and evaluation of potential epigenetic factors that serve as important modulators of the MA phenotype are advocated. Identifying protein function from mutated MA-associated genes is a promising area of research. Cell-based biomarkers may provide the best combination of genomic, proteomic, and functional markers of MA.² The study of perivascular cells or pericytes, cells involved in post-injury tissue regeneration, may be a promising approach to elucidate the mechanisms leading to the formation of aberrant collaterals in MA.⁵ Research into the pathophysiological association between MA and inflammation is advocated.¹⁵⁸ Studying levels of circulating biomarkers in relation to the disease stage is another promising path for future research.¹⁶ Establishing separate management guidelines for unilateral and bilateral MA is warranted.¹⁵¹

Clear articulation of strengths and weaknesses of new diagnostic and prognostic capabilities provided by research may avoid unrealistic expectations. Generating consensus on

how best to utilize new data provided by biomarkers will be important.² The relative rarity of MA necessitates collaboration among centers in validating novel candidate proteins. Shared data, multicenter prospective longitudinal, large-cohort, case-control studies, family-based analyses, comparative trials, and close collaboration between the clinical, laboratory, and basic research settings will be essential for generating meaningful results.^{2,5,16,21,84,198}

Ethics

To the best of our knowledge, this manuscript meets all updated current ethics statements.

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