Etiology and Genetics of Congenital Vascular Lesions

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KEYWORDS

• Malformation • Vascular • Gene • Mutation • Signaling pathway • Inhibitor • Rapamycin

KEY POINTS

- Therapeutic options to treat vascular tumors and malformations are limited. Detection of genetic mutations, inherited or somatic, has opened up the field for understanding the underlying molecular mechanisms.
- RAS/MAPK/ERK signaling is increased because of mutations in *GNAQ* and *GNA11* in congenital hemangiomas and capillary malformation (CM), in *GNAQ*, *KRAS* and *BRAF* in pyogenic granuloma (PG), in *RASA1* in CM-AVM1, in *EPHB4* in CM-AVM2, in *KRIT1* in HCCVM, and in *MAP3K3* in verrucous venous malformations.
- PI3K/AKT/mTOR pathway is increased in hereditary hemorrhagic telangiectasia (HHT) with mutations in *BMP9/10*, *ALK1*, and *endoglin*, in sporadic venous malformations (VM and MVM), and blue rubber bleb nevus syndrome (BRBN), inherited cutaneomucosal venous malformations (VMCM), all with mutations in *TIE2*, and in sporadic VM and lymphatic malformations (LM) with mutations in *PIK3CA*.
- Increased hepatocyte growth factor/c-Met and TGF-ß signaling may occur in glomuvenous malformations (GVM) with mutations in *glomulin*.
- VEGFR1 expression is decreased and VEGF-A/VEGFR2 signaling is increased in infantile hemangioma (IH) with mutations in *TEM8* and *VEGFR2*.

INTRODUCTION

Lesions of the vascular system are the most common congenital and neonatal abnormalities.[1] Vascular malformations of the head and neck region constitute approximately 60% of the lesions and occur approximately in 1 out of 22 children.[2]

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