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EDITORIAL



Medulloblastoma: novel insights into emerging therapeutic targets

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1. Introduction

Medulloblastoma is the most common malignant brain cancer in children, and most frequently arises in the cerebellum [1–3]. Molecular profiling has allowed their classification into four subgroups: Wntless (WNT), Sonic Hedgehog (SHH), Group 3, and Group 4 [4,5]. Although the 5-year survival for medulloblastoma is around 72%, retrospective studies show that long-term outcomes are subgroup-specific. WNT sub-group patients have a better prognosis with a 5-year survival rate of more than 90% [6]. Group 3 and Group 4 medulloblastoma patients have a 5-year survival rate of 40–60% and 75–80%, respectively. The survival of SHH-medulloblastoma patients is defined by the p53 status of their tumors, with p53 mutations (SHH-1) driving down survival to 41%, in contrast to a 5-year survival of 81% in patients with wild type p53 (SHH-2) [6,7]. Based on multivariate analysis, it is accepted that p53 status is the most important risk factor for children with SHH-1 medulloblastoma, with 76% of deaths associated with p53 mutations or loss of function [7]. Despite this intertumoral survival heterogeneity, current treatments for all medulloblastomas include surgical resection, craniospinal radiation therapy, and multiagent chemotherapy. Survival has certainly improved, however, recurrence, metastasis and long-term cognitive deficits due to treatment-related toxicity to the normal brain continue to be major clinical challenges [8]. Therefore, a better understanding of tumor biology will allow a more targeted treatment approach and spare the normal brain. Here, we focus our discussions on molecular differences in tumor vasculature between the medulloblastoma subgroups, and how variability in their structure and architecture may influence survival and therapeutic responses.

2. Molecular basis for medulloblastoma vascular diversity

Tumor vasculature is an important component of the tumor microenvironment and plays a key role in tumor growth and progression [9,10]. Vascular growth in brain tumors has been shown to occur through co-option, angiogenesis, vasculogenesis, and vascular mimicry (VM) [11,12]. Tumor blood vessels are structurally and functionally abnormal [11,13]. Increased endothelial cell proliferation and high angiogenic activity have

been described in other brain tumors [14]. In general, tumor vessels are larger in diameter, have thicker basement membranes, and tend to be tortuous [15,16]. They also exhibit defects in their endothelial cell wall, pericyte coverage, and basement membrane associated with abnormal cell-cell associations and a leaky vascular structure [17]. These characteristics not only uniquely alter tumor growth and progression but also impact permeability to chemotherapy and therapeutic response. Although previous studies have demonstrated that medulloblastoma tumor cells secrete various proangiogenic molecules, a methodical sub-group-specific investigation is somewhat limited [18]. As discussed later, the identification of such angiogenic drivers may allow the design of pharmacological agents to normalize tumor vasculature or even target the tumor vasculature, and although difficult, potentially in a manner that can spare the normal vasculature.

The WNT group of medulloblastomas is driven by ectopic activation of its namesake WNT developmental signaling pathway [19] (Figure 1a). Somatic mutations in the β -catenin gene (*CTNNB1*) occur in a subset of sporadic WNT medulloblastomas [20–22]. Morphologically, the vasculature in WNT medulloblastomas is highly hemorrhagic, thick-walled arterial-type, and also includes numerous small venous and capillary structures lacking an intact blood-brain barrier (BBB) [16,23]. This was captured in a case report of a patient with WNT medulloblastoma which describes the identification of tumor structures with dilated arteriolar vessels with slow flow and lack of venous drainage [23]. Although mechanistic studies are needed in WNT medulloblastomas, work from other systems has implicated β -catenin in the direct regulation of endothelial cell-cell adhesions and maintaining vascular barrier function during embryonic and postnatal development [24,25]. So, it is not entirely surprising that the vascular architecture of WNT-driven medulloblastomas is aberrant. WNT antagonists, WNT inhibitor factor 1, and Dickkopf 1, which can disrupt endothelial cell-cell interaction, are also found at higher levels in WNT MB [26].

Loss of β -catenin expression and activity in endothelial cells has been shown to affect endothelial cell-cell junctions in *CTNNB1*^{-/-} mice and cause increased fragility and permeability during vascular development [27]. Cross-talk between WNT

and NOTCH signaling demonstrated in other systems, and activation of the NOTCH signaling in endothelial cells of patients with WNT-medulloblastomas has the potential to promote vascular sprouting and remodeling of existing arterial and venous networks [28] (Figure 1a). NOTCH signaling is also shown to regulate vascular barrier function and the maintenance of BBB during early and post-natal development by regulating adherens junctions [29]. Non-canonical WNT pathway activation in endothelial cells can also regulate vascular development, which involves a direct β -catenin-mediated upregulation of interleukin (IL)-8 and vascular endothelial growth factor (VEGF) and increased VEGF signaling [30] (Figure 1a). Based on these observations, dysregulation of WNT signaling in medulloblastoma should be expected to affect vascular and BBB integrity, in a similar manner [31]. It is important to note that the above findings may be more relevant to medulloblastoma patients with inherited mutations in WNT/ β -catenin signaling.

In contrast to WNT medulloblastomas, the vasculature in Sonic hedgehog (SHH) tumors, driven by constitutive activation of the SHH developmental pathway, has an intact BBB [16]. It has provided the basis for the assumption that these tumors exhibit a more selective permeability to chemotherapy. Indeed, a recent dynamic contrast enhancement magnetic resonance imaging (MRI) study revealed functional differences in the integrity of the blood-brain tumor barrier (BBTB) and tumor vessel phenotype between various medulloblastoma mouse models [32]. Canonical and non-canonical SHH signaling pathways play important roles in promoting angiogenesis and vasculogenesis [33]. Chemokine signaling through the pro-angiogenic C-X-C motif receptor 4 (CXCR4) and stromal-derived factor-1 (SDF)-1 axis, is upregulated in

SHH medulloblastomas and is associated with poor patient survival [34–36]. Increased hypoxia-inducible factor 1-alpha (HIF1 α) expression, frequently noted in SHH medulloblastomas, may be a likely cause of CXCR4 upregulation in these tumors (Figure 1b) [37]. HIF1 α may also upregulate the expression of VEGF and its cognate receptors, Fms-related receptor tyrosine kinase 1 (*Flt-1*) and, fetal liver kinase 1 (*FLK1*); angiopoietin (*ANG*)-1 and -2 and their receptor tyrosine protein kinase receptor-TIE-2 as well as fibroblast growth factor (FGF) to drive vascular growth, though not demonstrated in SHH medulloblastomas (Figure 1b) [38,39]. Finally, elevation of the pro-angiogenic placental growth factor (PGF) in SHH medulloblastomas was shown to be associated with a surprising lack of effect on vascular growth, although an increase in tumor cell growth was seen (Figure 1b) [40]. Non-canonical SHH signaling pathway activity is also known to affect vascular growth by promoting endothelial cells differentiation and vessel maturation [41].

More recently, the *RE1* Silencing transcription factor (REST), a regulator of neurogenesis was implicated in vascular remodeling in SHH-driven medulloblastomas [42]. A combination of in vitro and in vivo experiments with genetically engineered mice and xenograft models showed that REST elevation in subgroups of SHH medulloblastomas upregulated HIF1 α , PGF, and VEGF expression and increased vascular growth [42,43]. Surprisingly, a REST-dependent increase in the expression of v-ets erythroblastosis virus E26 oncogene homolog 1 (ETS1) and FLT1/VEGF receptor 1 (*VEGFR1*) was also noted in tumor cells, suggesting the existence of an autocrine loop and possibly, VM [42,44]. An in-depth investigation of the mechanisms underlying this phenomenon is needed. In a separate body of work, REST elevation in SHH medulloblastomas was

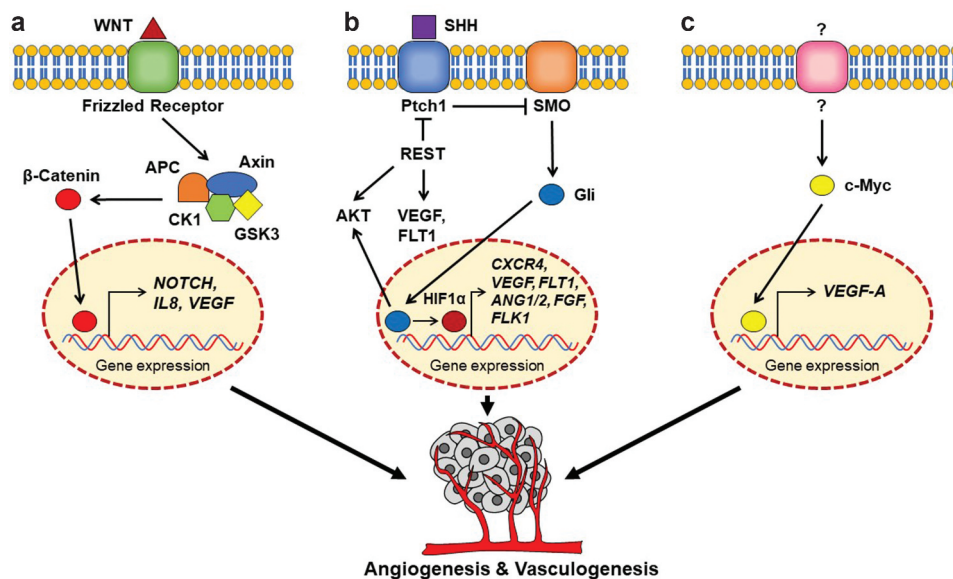


Figure 1. Schematic representation of angiogenic pathways in WNT, SHH and Group 3 medulloblastomas. **(a)** WNT ligand binding to FRIZZLED (Frz) receptor activates downstream signaling and β -Catenin activation, which is known to increase the expression of VEGF either directly [30], or through activation of NOTCH signaling [28]. β -Catenin can also induce IL8 and VEGF expression [30]. **(b)** In SHH medulloblastoma, loss of the tumor suppressor PTCH1 promotes oncogenic Smoothened (SMO) activity and downstream signaling through Glioma associated oncogene (GLI)-1 transcription factor. Gli1 can upregulate HIF1- α and AKT and activate pro-angiogenic CXCR4 signaling. HIF1- α can also directly upregulate the expression of other pro-angiogenic molecules such as VEGF, FLT1, FLK1, ANG1, ANG2 and FGF. REST elevation in SHH medulloblastoma cells has been shown to elevate AKT, FLT1 and VEGF levels [38,39]. **(c)** In Group 3 medulloblastoma, MYC elevation in response to an unknown extracellular signal (?) can upregulate VEGFA expression to promote vascular growth [47].

shown to increase pro-angiogenic AKT signaling [2]. AKT over-expression is known to promote VEGF secretion and upregulate *HIF1a* expression [45,46].

The vascular architecture in Group 3/4 medulloblastomas is not well defined. At the molecular level, Myc elevation, a hallmark of Group 3 medulloblastoma, has been shown to upregulate *VEGFA* expression (Figure 1c) [47]. Group 3 medulloblastomas also exhibit increased expression of Ribonuclease/Angiogenesis Inhibitor 1 (*RNH1*), Secretogranin II (*SCG2*), angiogenic factor with G-patch and FHA Domains 1 (*AGGF1*), and prokineticin 2 (*PROK2*), molecules with known roles in angiogenesis [48]. Finally, the increase in *VEGFA* in Group 3 tumors and its correlation with increased vessel density and poor survival in patients and mouse models, argues for a role for vascular remodeling in disease progression [48]. Information on the molecular characteristics and architecture of Group 4 medulloblastoma vasculature is lacking.

3. Targeting the medulloblastoma vasculature

A systematic molecular group-specific assessment of angiogenesis targeting therapy has not been conducted in medulloblastoma patients. However, a critical review of the published literature on preclinical studies may offer guidance on how this could be facilitated. In WNT medulloblastomas, the increase in the number of tumor vessels and their leaky morphology was associated with responsiveness to the vincristine, which was taken as evidence that a leaky vasculature is a good predictor of therapeutic response [16]. However, work from other groups has suggested that a leaky vasculature can cause spatial and temporal heterogeneity in tumor blood flow along with an increase in tumor interstitial fluid pressure, to disrupt targeted drug delivery [49]. Normalization of tumor vessels by anti-VEGF therapy is proposed as an alternative approach to improve therapeutic efficacy. Indeed, better-targeted delivery of paclitaxel was demonstrated in human xenograft models of ovarian and colon carcinoma [50]. Consistent with these observations, the combination of anti-VEGF and standard chemotherapy was associated with improved survival in patients with colorectal cancer and lung cancer [51,52]. This needs to be explored in brain cancers especially in tumors with leaky vasculature.

WNT and NOTCH pathways regulate vascular growth and inhibition of these pathways either alone or in combination may have potential applications in WNT medulloblastomas. In support of this possibility, preclinical studies with renal cancer cell xenograft models have demonstrated that NOTCH inhibitor (DAPT) and WNT inhibitor (ICG-001) markedly reduced tumor growth likely through an effect on tumor vasculature [53].

Pre-clinical work with SHH medulloblastoma models has shown the feasibility of targeting CXCR4 signaling in mice [34,35,54,55]. These studies employed the CXCR4 inhibitor-AMD3100 either as a single agent or in combination with the Smoothed inhibitor-GDC-0449/vismodegib to demonstrate a significant reduction in tumor burden in the SmoA1 medulloblastoma mouse model [34,56]. However, their effect on tumor vasculature was not investigated. Work by Bai et al. showed that the anti-parasitic agent mebendazole (MBZ)

could inhibit angiogenesis and tumor growth in genetically engineered mouse models of SHH medulloblastomas by inhibiting VEGFR2 signaling [57]. REST-associated chromatin remodelers could also be potential therapeutic targets. Germane to this idea, pre-clinical studies have shown G9a inhibition to block tumor growth in vivo [58]. Histone deacetylase (HDAC) inhibitors such as valproic acid (VPA), vorinostat, and MS275 were shown to reduce levels or target REST activity in vitro [59]. Callegari et al showed the feasibility of targeting REST activity using LSD1 inhibitors [43]. However, a careful investigation of their ability to reduce vascular growth in mouse models remains to be conducted. Such studies would be especially pertinent to patients with SHH (Group 1) tumors, who are typically infants, and where improving chemosensitivity through vascular remodeling may circumvent the need for radiation and prevent late-effects.

In Group 3 and 4 medulloblastoma xenograft models, intratumoral injection of measles viruses expressing the angiogenesis inhibitors endostatin and angiostatin promoted a significant reduction in endothelial cell migration in vitro, and reduced tumor-associated blood vessels and tumor growth in mice [60]. The angiogenesis inhibitor, thrombospondin-1 (TSP-1) showed effectiveness in reducing AKT signaling and metastasis, and promoted chemo- and radio-sensitivity to increase the survival of tumor-bearing mice [61]. MBZ could also reduce vasculature and tumor burden in Group 3 medulloblastoma mouse models.

Clinical evaluation of anti-angiogenic therapy in patients with brain tumors including medulloblastoma has been somewhat focused on the evaluation of the anti-VEGF antibody, bevacizumab. In combination with irinotecan or radiation, bevacizumab promoted an initial antitumor activity in human clinical studies [62–64]. However, tumor recurrence and resistance to bevacizumab were common, and overall survival was not significantly improved [62–64]. However, pre-clinical and clinical follow-up studies are needed to ascertain the molecular basis for this poor response.

4. Expert opinion

The tumor microenvironment, which includes the vasculature, is critical to tumor progression. The vasculature architecture can also influence therapeutic response by modulating the delivery of chemotherapy. Only a few studies have looked at vascular biology in medulloblastoma tumors, although existing studies suggest that neurodevelopmental pathways and chromatin-remodelers may contribute to angiogenic growth in these tumors. Clinical studies with bevacizumab in combination with radiation or chemotherapy have not been very successful. Chromatin remodelers can be pharmacologically targeted, and should be evaluated in pre-clinical models for their anti-angiogenic activity.

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Declaration of interest

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