

Histological features in pediatric central nervous system tumors with *FGFR* alterations

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Folia Neuropathol 2020; 58 (4): 347-356

DOI: https://doi.org/10.5114/fn.2020.102437

Abstract

Introduction: Identification of genetic alterations in central nervous system (CNS) tumors provides diagnostic and prognostic information and allows identification of potential therapeutic targets. Next-generation sequencing (NGS) technologies currently used for molecular testing are costly and remain largely limited to major academic centers or reference labs. Identification of histologic or immunohistochemical correlates for particular molecular alterations can serve as surrogates and can help triage cases for subsequent NGS-based confirmation. Recently, adult IDH-wildtype adult glioblastomas (GBMs) with fibroblast growth factor receptor (FGFR) gene alterations were reported to show palisading monomorphic cells, delicate arcuate vasculature, and microcalcifications. We explored whether pediatric tumors with FGFR fusion also show these histologic features and whether these features could predict the presence of this gene alteration.

Material and methods: We reviewed pediatric CNS tumors with FGFR-fusions to retrospectively determine the presence/absence of the above-mentioned histological features in fusion-positive tumors.

Results: 10 pediatric tumors with FGFR fusions were identified. Pediatric tumors demonstrated histologic and tumor type diversity, with diagnoses of pilocytic/pilomyxoid astrocytoma, pediatric-type oligodendroglioma, anaplastic astrocytoma, polymorphous low-grade neuroepithelial tumor of the young, rosette-forming glioneuronal tumor, and extraventricular neurocytoma.

Conclusions: Pediatric FGFR-fused CNS tumors demonstrate histologic features similar to their adult counterparts but also exhibit significant morphologic variability. As such, this histologic variability prevents the prediction of FGFR fusion and necessitates molecular testing for the identification of this alteration.

Key words: FGFR, TACC, polymorphous low-grade neuroepithelial tumor of the young (PLNTY), glioneuronal, astrocytoma, fusion testing, next-generation sequencing.

Introduction

In 2016, the World Health Organization (WHO) Classification of Central Nervous System (CNS) Tumors adopted an integrative diagnostic approach incorporating molecular parameters into the classification of CNS tumor entities [14]. Molecular char-

acteristics are likely to play an even more prominent role in the upcoming WHO classification with the possible introduction of several new categories of tumors defined by their molecular signature. In addition to aiding diagnosis, identification of genetic alterations also provides valuable prognostic infor-

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mation and, most importantly, can help in the identification of targeted therapy.

Next-generation sequencing (NGS) technologies are currently the most widely used for identification of molecular alterations in routine clinical practice but require high upfront infrastructure investment and have substantial running costs. The availability of NGS-testing is consequently still largely limited to large academic centers or reference labs. Identification of histologic or immunohistochemical (IHC) correlates can serve as surrogates for molecular alterations and can help triage cases for subsequent NGS-testing in select cases. This strategy has proved useful for IDH-mutant 1p19q-codeleted oligodendroglioma and BRAF V600E-positive epithelioid glioblastoma (GBM), for example [14]. In these tumors, careful histomorphologic examination and IHC studies can reliably select cases likely to harbor the molecular alteration. These can then be confirmed or disproved on targeted molecular testing [14]. Excellent molecular-histologic correlation also exists between BRAF: KIAA 1549 fusion and pilocytic astrocytoma and between MYB:QKI and angiocentric glioma. Many other tumors, however, show poor molecular-histologic correlation. Hence, for each tumor type, it is important to determine if and to what extent molecular-histological correlation exists. If such a correlation is high, it can assist the pathologist in triaging cases for confirmatory molecular testing [13].

Molecular-histologic correlation was recently demonstrated in a subset of adult GBMs when it was shown that adult *IDH*-wildtype adult GBMs with fibroblast growth factor receptor (*FGFR*) gene alterations show palisading monomorphic cells, delicate arcuate vasculature, and microcalcifications [3]. This was confirmed by several subsequent studies [1,2]. Whether *FGFR*-altered tumors show histomorphologic similarity outside of the adult *IDH*-wildtype group is less clear. In this study, we explore whether the histologic features reported for *FGFR*-altered *IDH*-wildtype adult GBMs are shared by pediatric tumors with *FGFR* fusion and if these characteristics can be used to predict *FGFR* fusions in individual cases.

FGFR signaling regulates a variety of cellular pathways including cell proliferation, differentiation, and survival. FGFRs form a family of four highly conserved transmembrane receptor tyrosine kinases (FGFR1-4), and alterations in 3 FGFR genes (FGFR1/FGFR2/FGFR3) have been reported in a variety of

pediatric and adult tumors [4,7,16,17]. Recently, a subset of adult IDH-wildtype GBMs was found to harbor gene fusion events involving FGFR1/FGFR3 with the transforming acidic coiled-coil (TACC) domains of TACC1 or TACC3 genes [3,5,19]. Recognition of this alteration carries particular clinical significance as inhibitors of FGFRs have recently been developed and these could represent a promising therapeutic option for patients with FGFR alterations [5]. Studies have shown that inhibitors of kinase activity can block tumor growth in a preclinical model of gliomas with the TACC3:FGFR3 fusion and clinical response has been documented in a few patients [5]. The TACC gene family includes 3 individual genes, including TACC1, TACC2, and TACC3. TACC domains promote dimerization and constitutive activation of FGFR leading to hyperphosphorylation and constitutive activation of the kinase domain promoting oncogenesis [15,19,23].

Characteristic histologic features reported for FGFR3:TACC3 gliomas in adults include a monomorphic population of small tumor cells with ovoid nuclei, perivascular pseudorosettes, microcalcifications, nuclear palisading, and/or an endocrinoid ("chicken-wire") capillary network [3]. All cases show absence of cytoplasmic IDH1 R132H immunostaining, low p53 nuclear immunolabelling and retained nuclear ATRX expression. The most common cytogenetic alterations include: gain of chromosome 7p/loss of chromosome 10q, absence of EGFR amplification except in rare cases [3,5,9], and frequent CDKN2A homozygous deletion [5,9]. Thus morphology and routine cytogenetic tests can provide clues to the presence of FGFR3 fusions in adult gliomas, the majority of which are GBMs, IDH-wildtype, WHO grade IV [3]. This correlation between histology and the presence of FGFR3:TACC3 alteration is not perfect and molecular testing still needs to be performed to confirm the fusion. While the vast majority of these tumors feature an FGFR3:TACC3 fusion, rare cases showing FGFR3 fusion with a non-TACC3 gene partner (such as *CAMK2A*) have also been reported [9].

Various other pediatric and adult tumors have been reported to have *FGFR* fusions [4,7,17]. While a majority of pilocytic astrocytoma (PA) show *BRAF* fusions or mutations, a small proportion feature *FGFR* fusions [12,16,18,21]. *FGFR1:TACC1* fusion is a frequent event in extraventricular neurocytoma and has been found in up to 60% of molecularly-defined cases [22] with a smaller proportion of cases

showing FGFR3:TACC3 alteration [22], as recently reviewed [1]. Similarly, the recently described tumor termed polymorphous low-grade neuroepithelial tumor of the young (PLNTY) also features FGFR2 and FGFR3 fusions in a large percentage of cases (still other cases are positive for BRAF V600E mutation) [11]. It is noteworthy that many of the histological features described by Bielle et al. [3] in the adult high-grade gliomas with FGFR fusion, such as uniformly small rounded nuclei with conspicuous perinuclear halo, perivascular pseudorosetting, nuclear palisading and calcifications, are also seen in PLNTY, although these are exclusively low-grade tumors [11]. Finally, it is important to realize that FGFR fusions are not exclusive to the central nervous system tumors since FGFR3-TACC3 fusions have been found in non-CNS malignancies including urothelial, breast, endometrial lung and ovarian cancers [10].

We noted that no study has undertaken a direct analysis of the histologic features of *FGFR*-fused CNS tumors in the pediatric population. The purpose of this study is to, for the first time, directly compare histological features of pediatric tumors with *FGFR* fusions and ask whether identification of these histological features might predict which tumors would show the highest yield in terms of identification of fusions and thus allow for triaging of cases for molecular testing of the fusion status, since such testing can be costly, time consuming, and may require send out to a reference laboratory.

Material and methods

We identified CNS tumors with FGFR gene alteration via a retrospective database review of all pediatric patients in the Department of Pathology databases at Children's Hospital Colorado, 2010-present. Fusion testing became available at our institution in 2016; however, some older cases underwent testing at the clinical team's request. For the vast majority of cases (9 out of 10 cases), the initial surgery and subsequent management had been performed at our institution. One case had been biopsied at outside institutions and reviewed at our department for diagnostic consultation. Standard H&E stained sections were examined and the WHO 2016 classification of central nervous system tumors criteria were applied for all diagnoses, with the exception of PLNTY, which followed the diagnostic criteria outlined by Huse et al. [11].

Table I. List of genes tested in ArcherDx Fusion-Plex Solid Tumor Panel

AKT3	EWSR1	NOTCH1	PRKCA
ALK	FGFR1	NOTCH2	PRKCB
ARHGAP26	FGFR2	NRG1	RAF1
AXL	FGFR3	NTRK1	RELA
BRAF	FGR	NTRK2	RET
BRD3	INSR	NTRK3	ROS1
BRD4	MAML2	NUMBL	RSPO2
EGFR	MAST1	NUTM1	RSPO3
ERG	MAST2	PDGFRA	TERT
ESR1	MET	PDGFRB	TFE3
ETV1	MSMB	PIK3CA	TFEB
ETV4	MUSK	PKN1	THADA
ETV5	MYB	PPARG	TMPRSS2
ETV6			

The Archer assay includes gene-specific primers to various exons (and some introns) in the above 53 genes and simultaneously detects and identifies fusions and other mutations associated with the listed genes.

Fusion testing was performed by the Colorado Molecular Correlates (CMOCO) Laboratory in the Department of Pathology at the University of Colorado Denver (UCD). Extracted nucleic acid samples were assessed using the ArcherDx FusionPlex (ArcherDx, Boulder, CO) Solid Tumor library preparation kit followed by sequencing on the Illumina platform [8,13]. This assay uses proprietary Anchored Multiplex PCR (AMP)-based library preparation to detect oncogenic gene isoforms and gene fusions regardless of the identity of the fusion partner. All cases were also tested on ArcherDx VariantPlex (ArcherDx, Boulder, CO) solid tumor panel which tests for mutations in 69 genes, including IDH1 and IDH2. A complete list of genes covered on the fusion and mutational assay has been published previously [8] and provided as Tables I and II.

Clinical data for all cases were collected by review of the patient's electronic medical records on EPIC (Epic Systems Corporation, Verona, WI) and included the age, sex, clinical presentation, pre and post-surgical imaging findings, tumor location, extent of surgical resection, treatment modalities used, and survival.

Results

Ten cases of pediatric/young adult (less than 21 years of age) CNS tumors with FGFR alterations were identified. Of these cases, 6 involved *FGFR1* fusions or tyrosine kinase domain (TKD) duplica-

Table II.	List of	genes	tested	in	ArcherDx	Vari-
antPlex	Solid Tu	mor Pa	nel			

ABL1	AKT1	ALK	APC
AR	ATM	AURKA	BRAF
CCND1	CCNE1	CDH1	CDK4
CDKN2A	CDKN2B	CSF1R	CTNNB1
DDR2	EGFR	ERBB2	ERBB3
ERBB4	ESR1	EZH2	FBXW7
FGFR1	FGFR2	FGFR3	FLT3
FOXL2	GNA11	GNAQ	GNAS
H3F3A	HNF1A	HRAS	IDH1
IDH2	JAK2	JAK3	KDR
KIT	KRAS	MAP2K1	MDM2
MET	MLH1	MPL	MYC
MYCN	NOTCH1	NPM1	NRAS
PDGFRA	PIK3CA	PIK3R1	POLE
PTEN	PTPN11	RB1	RET
RHOA	ROS1	SMAD4	SMARCB1
SMO SRC	STK11	TERT	TP53
VHL			

tions, 1 pediatric patient had *FGFR2* fusion and 3 cases involved *FGFR3* gene alterations. Fusion partners of *FGFR* genes included *TACC1*, *TACC3*, *KIAA1598*, *THAP10* and *INA* genes. Clinicopathologic findings and fusion events are summarized in Table III.

CNS tumors with *FGFR* fusions were negative for co-occurring fusion or mutation events tested on our panels.

The pediatric CNS tumors harboring FGFR fusions in our cohort possessed more diverse histologic and molecular features than those reported for adult high-grade gliomas with tumors. In addition to the 3 FGFR3 fusion cases (with 3 different fusion partners, namely: TACC3, INA or THAP10), 6 cases of FGFR1 structural alterations (3 with FGFR1:TACC1 fusion, and 3 with TKD alterations) and 1 case of FGFR2:KIAA1598 were found. These findings are summarized in Table III. Histologic and radiologic features were similarly varied with cases carrying histologic diagnoses of extra ventricular neurocytoma (n = 1), pilomyxoid astrocytoma (n = 2), pilocytic astrocytoma (n = 1), PLNTY (n = 2), diffuse astrocytoma (n = 1), pediatric-type oligodendroglioma (n = 1), anaplastic astrocytoma with Li Fraumeni syndrome (LFS) (n = 1) and rosette-forming glioneuronal tumor (n = 1)(Table III). In contrast to the adult cases with FGFR fusions, all of which are reported to be GBM, IDH-wildtype, WHO grade IV [3], 9/10 pediatric cases showed

low-grade glioma/glioneuronal histology, with one showing anaplastic astrocytoma histology (Table III).

Despite the diversity in histologic diagnosis, there were unifying features. Pediatric cases in our cohort showed frequent nuclear palisading (Fig. 1A-C), small monomorphic round cells (Fig. 1D-F), frequent calcifications (Fig. 2A-C), thin vasculature (Fig. 2D-F), and a low-grade histology without mitotic figures or elevated MIB-1 (Ki-67) staining (except in case 9, an anaplastic astrocytoma in LFS).

Retrospective review of the histologic features showed four distinct histologic groups as described below.

The first group (n = 3) showed pilocytic or pilomyxoid histology with tumor cells manifesting round to oval nuclei and long fibrillary/piloid processes, prominent perivascular arrangement was seen in two cases with absence of Rosenthal fibers or EGBs hence resembling pilomyxoid astrocytoma (Fig. 1A,B) - and one case was negative for perivascular tumor cell arrangement and positive for Rosenthal fibers (Fig. 1D) – hence consistent with pilocytic astrocytoma. While 2 of these cases showed no recurrence, case 3 with an FGFR1 exon 18:10 fusion has died of disease. In this case, the resection was incomplete owing to the presence of the tumor in an eloquent region (suprasellar/hypothalamic) and the surgery being complicated by parenchymal hemorrhage and brain damage. Whether the poor outcome was due to the FGFR1 exon 18:10 fusion or the sensitive location/incomplete surgical resection remains unclear.

The second group (n=2) consisted of glioneuronal tumors with extensive Cluster of Differentiation 34 (CD34) staining. Both of these cases had small round oligodendroglia-like cells with thin arcuate blood vessels (Figs. 1E, 2A), microcalcifications (Fig. 2A, arrow), and patchy strong CD34 staining, features that are suggestive of PLNTY (Fig. 1E, inset). One of these cases showed *FGFR3:TACC3* and the other *FGFR2:KIAA1598* fusion, similar to what has been previously reported for PLNTY [11]. None of these cases has shown a recurrence in 9-13 months of post-resection follow up.

The third group (n = 3) showed an infiltrative histology (Figs. 1F, 2C-E). These cases had round or oval oligodendrocyte-like or astrocytic cells with variable perinuclear halos (Fig. 1F, 2C, D) and thin arcuate vasculature (Fig. 2D) with one case additionally showing calcifications (Fig. 2C, arrow). Unlike group 2, no CD34 staining was seen in these cases, ruling out PLNTY.

Table III. Clinical and pathologic features of patients with central nervous system (CNS) tumors harboring FGFR structural alterations

Case #	Age (yrs)	Sex	Molecular findings	lmaging findings	Histologic diagnosis	Clinical follow up	Follow up interval
Case 1	1	F	FGFR1 exon 19:10 repeat	Diffusely infiltrating tumor involving bilateral basal ganglia, optic pathways, septum pellucidum, medial left temporal lobe, and brainstem	Diffuse astrocytoma	Died of disease, rapid progression of invasive tumor	15 mth
Case 2	1	М	FGFR1:TACC1	Solid and cystic cervical spinal cord tumor	Pilomyxoid astrocytoma	Negative for tumor recurrence	3 yrs
Case 3	2	F	FGFR1 exon 18:10	Large suprasellar/ hypothalamic mass extending into the right frontal lobe, third ventricle, interpeduncular and prepontine cistern	Pilomyxoid astrocytoma	Died of disease; incomplete resection of tumor followed by intratumoral and parenchymal hemorrhage and subsequent brain damage	9 mth
Case 4	4	M	FGFR1 exon 19:10 repeat	Left thalamic tumor extending into internal capsule, caudate, globus pallidus, midbrain and the medial left temporal lobe	Pediatric-type oligodendroglioma	Died of disease, progressive interval growth of tumor	24 mth
Case 5	6	F	FGFR2:KIAA1598	Right insular cortex cystic and solid mass with haziness to the subjacent white matter	PLNTY	No residual tumor	13 mth
Case 6	9	Μ	FGFR1: TACC1	Acute bleeding at presentation with hyperdense mass of posterior temporal lobe	Extraventricular neurocytoma	Negative for tumor recurrence	25 mth
Case 7	11	F	FGFR3:TACC3	Medial right temporal lobe heterogeneous mass with numerous small cystic components	PLNTY	Negative for tumor recurrence	9 mth
Case 8	16	F	FGFR1: TACC1	Midbrain, dorsal tegmentum and tectum non-enhancing mass	Pilocytic astrocytoma	Negative for tumor recurrence	26 mth
Case 9	19	M	FGFR3:INA	Right frontal lobe non- enhancing lesion with interval growth first identified on screening MRI	Anaplastic astrocytoma in LFS	Negative for tumor recurrence	7 yrs
Case 10	21	F	FGFR3:THAP10	Intraventricular mass, right frontal horn of lateral ventricle	Rosette-forming glioneuronal tumor	Negative for tumor recurrence	8 yrs

 $mth-months, yrs-years, PLNTY-polymorphous\ low-grade\ neuroepithelial\ tumor\ of\ the\ young,\ LFS-Li\ Fraumeni\ syndrome$

Two of these cases showed FGFR1 exon 19:10 repeat fusion and one showed FGFR3:INA fusion; all were IDH1/2 wildtype (tested by IHC as well as mutational analysis) and negative for 1p/19q codeletion (tested by FISH). One of these cases (case 9) occurred in the

context of known history of Li-Fraumeni syndrome and had frankly anaplastic histology. The third case in this group was diagnosed as a pediatric-type oligodendroglioma and was confirmed to be *IDH*-wild-type without 1p/19q codeletion.

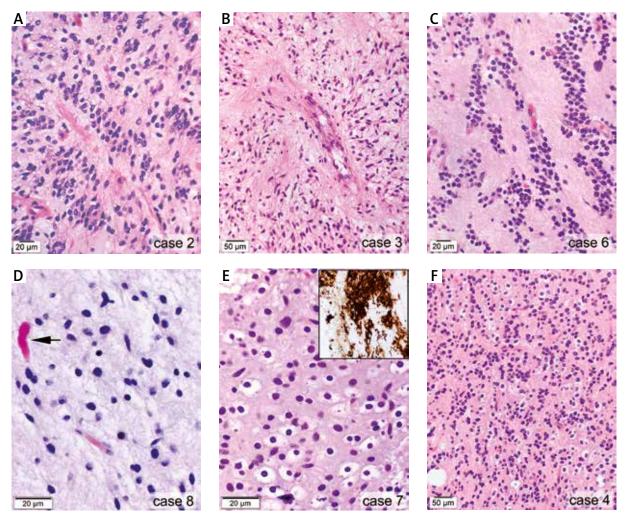


Fig. 1. FGFR altered pediatric central nervous system (CNS) tumors show monomorphic round cells and nuclear clustering: despite histologic variability, majority of cases showed monomorphic round cells and nuclear clustering. A-C) 6 cases with histologic diagnoses of pilomyxoid astrocytoma (A, B), extraventricular neurocytoma (C), pilocytic astrocytoma (D), PLNTY (E) and pediatric-type oligodendroglioma (F) all showing tumor cells with small round monomorphic nuclei. Nuclear palisading/clustering and perivascular arrangement in tumors with histologic diagnoses varying from pilomyxoid astrocytoma (A-B) and extraventricular neurocytoma (C). D) Arrow highlights a Rosenthal fiber. E) Inset shows patchy strong CD34 staining supporting the diagnosis of PLNTY.

Finally, the last group consisted of unique cases (n = 2). One case showed neurocytic rosettes with small round (NeuN+) cells arranged around neurocytic rosettes (Figs. 1C, 2F) and surrounded by microcalcification (Fig. 2B). This case showed *FGFR1:TACC1* fusion and was diagnosed as extra ventricular neurocytoma. The last case (case 10) was consistent with rosette-forming glioneuronal tumor.

It is not clear whether FGFR fusion status effects prognosis in tumors independent of histologic features [18]. Anecdotally, however, we do note that in

our small cohort of 10 pediatric examples, 3 patients with *FGFR1:exon 18 or exon 19* fusions, involving the thalamus, hypothalamus and basal ganglia, died of disease (cases 1, 3 and 4), while the rest are free of disease (Table III). Whether this is due to the surgically sensitive/eloquent nature of midline tumors or the presence of the *FGFR1:exon 18 or exon 19* fusion is unclear.

In summary, most but not all FGFR fused tumors in the pediatric population show at least some characteristic histologic features including small mono-

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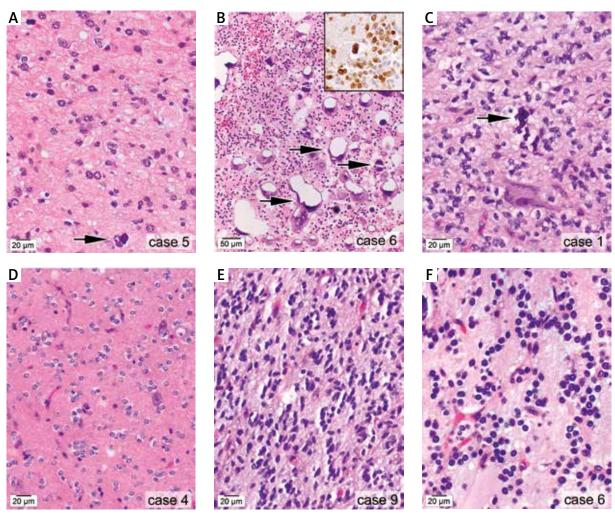


Fig. 2. FGFR altered pediatric central nervous system (CNS) tumors show frequent microcalcifications and delicate arcuate vasculature: A-C) Microcalcifications (arrows) were frequently seen in cases diagnosed as PLNTY (A), extraventricular neurocytoma (B), diffuse astrocytoma (C). Inset in panel B shows NeuN staining confirming the neurocytic differentiation in the extraventricular neurocytoma. D-F) thin delicate arcuate capillary network in cases with histologic diagnosis of pediatric-type oligodendroglioma (D), anaplastic astrocytoma in LFS (E) and extraventricular neurocytoma (F). D) Note the large entrapped neurons with normal cytological appearance and even placement of Nissl substance, excluding consideration of ganglioglioma.

morphic cells, fine arcuate vasculature, and micro-calcification, histologic features that are reported for adult high-grade gliomas with FGFR3:TACC3 fusion.

Discussion

In this study, we report the histological features of pediatric CNS tumors with *FGFR* fusion, adding to the growing literature that these are mostly low-grade glial and glioneuronal tumors. We determine that although the histological features reported by Bielle *et al.* [3] in adult *IDH*-wildtype GBMs are pres-

ent to some degree in pediatric tumors, they are far from uniform and not archetypal enough to allow histological prediction of the fusion for adult gliomas and especially not for pediatric CNS tumors.

Pediatric CNS tumors with FGFR fusions, in contrast to adult high-grade gliomas with this fusion [3], are a more histologically and molecularly heterogeneous cohort, as we and others [4,13] have shown. Thus, the fusion status is more difficult to predict, although certain histological features shared with their FGFR-fused adult counterparts do exist that

can aid in prompting molecular testing. In contrast to adult examples with this fusion [3], pediatric examples have almost exclusively been low-grade, yet, as we have demonstrated, still share overlapping morphological features of monomorphic nuclei, microcalcifications, nuclear palisading, and arcuate vasculature. These features are shared by several types of low-grade tumors and thus result in more diverse diagnoses, such as diffuse astrocytoma, anaplastic astrocytoma, pilocytic and pilomyxoid astrocytoma, PLNTY, neurocytoma, and rosette-forming glioneuronal tumor.

Thus, in pediatric tumors, while we show that FGFR fusions can be suspected based on these histological features in a variety of different WHO 2016 diagnoses, nevertheless, fusion testing is recommended in all pediatric tumors, given the possibility of identifying therapeutically targetable alterations in this age group in order to eschew use of more toxic chemo- and radiotherapies [13]. Of note, while the tumor types in our cohort were mostly lowgrade and thus more aggressive therapies are often not necessary initially after first resection, unfavorable anatomical location may lead to the inability to achieve significant surgical resection and continued tumor growth may contribute to progressive symptomatology at a later time period. Often, some therapy becomes necessary during the course of the disease. Thus, similar to our work with gangliogliomas of the brainstem with BRAF V600E mutation, making them amenable to targeted therapy [6], the situation may arise that targeted therapy is also necessary in FGFR fusion-bearing low-grade pediatric tumors in unfavorable anatomical locations. Indeed, although the number of cases in our study is small, we did observe anecdotally that the only deaths in our cohort of 10 pediatric patients were in those tumors that were located in unfavorable/eloquent anatomical locations (Table III).

Within our cohort, the fusions we encountered parallel those in the literature, as reviewed by Bale [1]. Specifically, the cases of PLNTY showed *FGFR3-TACC3* or *FGFR2-KIAA1598* fusion. Both of these fusions (in addition to cases showing *FGFR2-CT-NNA3* fusion or BRAF *V600E* mutation) have been reported previously in PLNTY [11]. The extraventricular neurocytoma similarly showed *FGFR1:TACC1* fusion which is the most common alteration reported in this tumor [22]. Finally, the single case of rosette-forming glioneuronal tumor in our cohort

showed *FGFR3:THAP10* fusion. It is noteworthy that the largest case series of this rare tumor reported *FGFR1* hotspot mutations in all cases with a majority exhibiting co-occurring *PIK3CA* and/or *NF1* gene mutations [20]. Given the similarities between *FGFR1* and *FGFR3* genes and a shared downstream signaling pathway, our findings are consistent with those of Sievers and colleagues showing activation of mitogen-activated protein kinase (MAPK) pathway in this tumor [20]. We further note that *FGFR* fusions in our study occurred in the absence of any other identifiable fusion or mutation events (for a complete list of genes tested, see Tables I and II).

A recent paper, published during the preparation of this manuscript, shows that the presence of *FGFR* alterations, mostly *FGFR1-TACC1* fusion, in pediatric posterior fossa pilocytic astrocytomas correlate with oligodendroglial morphology, namely small monomorphic cells with round and partly hyperchromatic nuclei, perivascular halos, and calcifications [21]. This and other studies suggest the presence of shared histologic features in *FGFR*-fused tumors.

A major limitation, that might be a consideration, is that this is a single institution study with a relatively small sample size. For each type of *FGFR* alteration, a single or a small set of cases is included. Conversely, however, multi-institution studies looking at histomorphologic features can suffer from inter-observer bias. Hence, one of the strengths of this study is that all cases were diagnosed at a single institution and are more likely to be homogeneous in interpretation of histologic features.

We conclude that while pediatric tumors with FGFR fusions do show monomorphic oligodendrog-lia-like nuclei, arcuate vasculature, and microcalcifications, similar to those described by Bielle et al. in adult tumors, the features are too variable in extent to histologically predict the presence of fusion in pediatric tumors since the FGFR-fusion positive group comprises so many different diagnostic entities, including but not limited to pilocytic astrocytoma, pilomyxoid astrocytoma, PLNTY, extraventricular neurocytoma, rosette forming glioneuronal tumor, and pediatric-type oligodendroglioma.

Our final conclusion is that broad mutational and fusion testing remains necessary for pediatric patients with any glioneuronal CNS tumor, despite the cost and time burdens. We therefore recommend that fusion testing be performed for all pediatric glioneuronal tumors, regardless of histological

features; unfortunately, histological triaging of cases will miss examples with this potentially targetable fusion.

Acknowledgements

This work was supported by the Molecular Pathology Shared Resource of the University of Colorado (National Cancer Institute Cancer Center Support Grant No. P30-CA046934). We thank Lisa Litzenberger for assistance with the figures and Jennifer Platte with editorial assistance.

Disclosure

KDD has received sponsored travel from ArcherDx. All other authors have no conflict of interest to declare. All procedures performed in studies involving human participants were in accordance with the ethical standards of the institutional research board (IRB # 95-500) and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards. This article does not contain any studies with animals performed by any of the authors.

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