Bithalamic Gliomas May Be Molecularly Distinct From Their Unilateral High-Grade Counterparts

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Abstract

Bithalamic gliomas are rare cancers diagnosed based on poorly defined radiologic criteria. Infiltrative astrocytomas account for most cases. While some previous studies reported dismal outcomes for patients with bithalamic gliomas irrespective of therapy and histologic grade, others described better prognoses even without anticancer therapy. Little is known about their molecular characteristics. We reviewed clinical, radiologic, and histologic features of patients with bithalamic gliomas treated at our institution over 15 years. Targeted sequencing of mutational hotspots in *H3F3A*, *HIST1H3B*, *IDH1/2*, and *BRAF*, and genome-wide analysis of DNA methylation and copy number abnormalities was performed in available tumors. Eleven patients with bithalamic gliomas were identified. Their median age at diagnosis was 4.8 years (range: 1 to 15.7). Additional involvement of the brainstem, basal ganglia, and cerebral lobes occurred in 11, 9, and 3 cases, respectively. All patients presented with hydrocephalus. Two-thirds of the patients had a histologic diagnosis of anaplastic astrocytoma. Despite aggressive therapy, our youngest patient, the only one diagnosed before 1 year of age, is the sole long-term survivor. DNA methylation could be performed in seven tumors, all of which clustered with the RTK I 'PDGFRA' subgroup by unsupervised hierarchical analysis of methylation array against a previously published cohort of 59 pediatric high-grade gliomas. Sequencing of hotspots mutations could be done in 10 tumors, none of which harbored *H3F3A* p.K27 and/or the respective DNA methylation signature, and any other hotspot mutations. Amplification of *MDM4* (*n*=2), *PDGFRA* (*n*=2), and *ID2* combined with *MYCN* (*n*=1) were observed in 7 tumors available for analysis. In comparison to the previously published experience with unilateral high-grade thalamic astrocytomas where *H3F3A* p.K27 was

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present in two-thirds of cases, the absence of this molecular subgroup in bithalamic gliomas was striking. This finding suggests that unilateral and bithalamic high-grade gliomas may represent two distinct molecular entities.

Keywords

bithalamic; children; high-grade glioma; infiltrative; molecular characteristics

INTRODUCTION

Thalamic tumors account for approximately 5% of all central nervous system (CNS) cancers in children and consist mostly of astrocytomas with unilateral involvement (4, 17, 19, 23). Bithalamic gliomas represent a rare subset of poorly understood tumors diagnosed based on symmetrical involvement of both thalami (5, 7, 8, 14, 17, 19, 23). Although histologic confirmation is warranted for the diagnosis of bithalamic gliomas since their imaging characteristics overlap with those of other oncologic and non-oncologic entities, (13) some studies have included patients with only radiologic diagnosis (5, 14, 23). Infiltrative low- and high-grade astrocytomas account for most bithalamic gliomas (5, 8, 14, 17, 19, 23). The treatment and prognosis of patients with bithalamic gliomas remains controversial (5, 8, 14, 17, 19, 23). While some studies reported a dismal outcome for patients with bithalamic gliomas irrespective of therapy and histologic grade, (8, 19) others have reported long-term survivors, including patients who underwent only tumor biopsy and/or decompression of hydrocephalus (5, 14, 17, 23).

Very little is known about the molecular characteristics of bithalamic gliomas since suitable tissue for detailed analysis is rarely obtained from small tumor biopsies (1, 27, 28). We conducted clinical, radiologic, and histologic review, and molecular analysis of a cohort of children with bithalamic gliomas. Unlike unilateral high-grade thalamic astrocytomas, (11, 21, 24, 30) bithalamic gliomas lacked *H3F3A* p.K27M mutation and/or the respective DNA methylation characteristics, which suggests that both represent separate molecular entities.

MATERIALS AND METHODS

Following institutional review board approval, we retrospectively reviewed the clinical and radiologic characteristics of all patients younger than 22 years with newly diagnosed bithalamic gliomas treated at our institution from March 1999 until August 1, 2014. We defined bithalamic gliomas as tumors arising bilaterally and completely involving both thalami. Cases with a predominant unilateral involvement and partial spread to the contralateral side and those who developed a bithalamic appearance only at the time of progression were excluded from this analysis. Only patients with diffusely infiltrating gliomas were included in this study and the histologic diagnosis of pilocytic astrocytoma was an exclusion criterion.

Detailed clinical and therapy-related data were collected for all patients. Brain MRIs at diagnosis of suspected cases were selected by a neuro-oncologist (AB) and then independently reviewed by a neuro-radiologist (SNH). A scoring system was used to assess

the extent of gray matter involvement by T_2-weighted and/or FLAIR MRI sequences in the thalami, deep-seated structures (i.e., lentiform nucleus, caudate nucleus, insula, brainstem, and cerebellum), and cerebral lobes as previously described (6). A score of 1 was attributed to involvement of each unilateral structure, the brainstem, and cerebellum. Assessment of the presence of tumor mass was based on T_1- and T_2-weighted/FLAIR signal characteristics independent of the presence of contrast enhancement. All cases underwent histologic review by a board-certified neuro-pathologist (BAO) according to the 2016 World Health Organization (WHO) classification. Immunoreactivity of H3K27M was tested on 4-μm formalin fixed paraffin-embedded (FFPE) sections as previously described using a polyclonal antibody (Millipore, catalog number ABE419, 1:400) (28). Immunohistochemistry of p53 (Zeta Corporation, clone DO-7, 1:200), ATRX (Sigma, catalog number HPA001906, 1:600), and H3K27me3 (Cell Signaling, C36B11, 1:200) were performed according to the manufacturer's specifications.

Molecular Studies

Dual-color fluorescence in situ hybridization (FISH) was performed on 4-μm formalin-FFPE tissue sections. Break-apart and fusion probes for *FGFR1* were derived from BAC clones RP11-246A12 and RP11-118H9 (BACPAC Resources, Oakland, CA). Probes were labeled with either AlexaFluor-488 or AlexaFluor-555 fluorochromes and nuclei were counterstained with DAPI (200ng/mL; Vector Laboratories Inc., Burlingame, CA) for viewing on an Olympus BX51 fluorescence microscope equipped with a 100-W mercury lamp; FITC, Rhodamine, and DAPI filters; 100X PlanApo (1.40) oil objective; and a Jai CV digital camera. Images were captured and processed using the Cytovision v7.3 software (Leica Biosystems Inc, Buffalo Grove, IL).

DNA was extracted from FFPE tissue using the Maxwell® 16 Plus LEV DNA purification kit (Promega, Madison, WI) according to the manufacturer's instructions. DNA was quantified using the Qubit dsDNA BR assay kit (ThermoFisher Scientific, Grand Island, NY).

Targeted sequencing of *BRAF* p.V600, *H3F3A* p.K27, *H3F3A* p.G34, *HIST1H3B* p.K27, *IDH1* p.R132, and *IDH2* p.R172 was performed as previously described (6, 29)

Illumina Infinium Human 450 k Bead Array

Processing and acquisition of DNA methylation data were performed as previously described (6).

Analysis of DNA methylation data was performed using the open source statistical programming language R (18). Files with raw data generated by the iScan microarray scanner (Illumina, San Diego, CA) were read and processed using the *minfi* Bioconductor package as described in the Illumina GenomeStudio software (Illumina, San Diego, CA) (2). Further filtering of the probes was done as previously described (24). In total, 438,370 probes were kept for clustering analysis. To determine the subgroup affiliation of our cohort by methylation array, we used previously published data of DNA methylation in pediatric high-grade gliomas as a reference (n=59; GSE36278) (24). Missing values were imputed using a k-nearest neighbor algorithm (26). We selected the top 10,000 most variable

methylation probes as measured by standard deviation across the combined dataset to conduct an unsupervised hierarchical clustering of bithalamic tumors and 59 reference samples. Samples were then clustered by applying the Ward's method and dissimilarity based on Euclidean distance. Methylation probes in the heatmap were reordered by hierarchical clustering using a similar approach.

We compared the methylation profile of tumors (n=7) in the current manuscript to that of previously published unilateral thalamic high-grade gliomas (n=8) (24). We used the minfi package to obtain normalized M-values for the methylation profile of each tumor (2). For each gene, we used Illumina annotation to identify all probes within the promoter region defined as the area within 1,000 base pairs upstream of the transcription start site. For each gene and tumor, we then computed the average M-value for this promoter region. Next, for each gene promoter region, we used the Welch t-test to compare the average promoter M-values of bithalamic (n=7) and unilateral tumors (n= 8). To address multiple-testing, we used a robust method to estimate the false discovery rate as a function of p-value (16). To gain further biological insight from our study, we used the multi-response permutation procedure (MRPP) to evaluate differential methylation of 9,063 gene-sets defined in the molecular signatures data base (MsigDB; http://software.broadinstitute.org/gsea/msigdb/) with statistical significance determined by 10,000 permutations of group label assignments (15).

Analysis of copy number abnormalities based on the 450 k Infinium methylation array was performed by using the *conumee* Bioconductor package (12). The combined intensities of all available CpG probes were normalized against 12 control samples from normal brain tissue using a linear-regression approach. Probes were combined into genomic bins of 10kb. Bins comprised of less than 10 probes were repeatedly merged with the adjacent bins. Subsequent analysis was performed with default setting in the *conumee* package. Detection of amplification and chromosomal gains and losses was performed by manual assessment of the respective loci for each individual profile following automatic scoring (6, 24).

A logistic regression model to estimate the probability of MGMT promoter methylation from the 450 k methylation array was performed as previously described (3).

Tumor and germline samples from one patient included in this study had already undergone whole exome sequencing as part of the Pediatric Cancer Genome Project (30).

Other Statistical Analyses

Descriptive statistical analyses were used to summarize the demographic and clinical characteristics of the patients. Overall survival (OS) was defined as the interval between date of diagnosis and death. Patients who were alive were censored at the time of last contact. The Wilcoxon rank sum test was used to assess the associations between categorical variables (i.e., gender, presence of tumor mass, and contrast enhancement) and continuous variables (i.e., age at diagnosis, interval from onset of symptoms and diagnosis, and number of gray matter areas affected). The Kruskal-Wallis test was used to test any associations between histologic diagnosis and the same continuous variables. Cox models were used to assess for associations between OS and continuous variables and two-sided log-rank tests were used for categorical variables.

RESULTS

We identified 11 patients (5 [45%] females) with bithalamic gliomas (Table 1). The median age at diagnosis was 4.8 years (range: 1.0 to 15.7). Only one patient was younger than one 1 year at diagnosis. The median latency from onset of symptoms to diagnosis was 30 days (range: 1 to 120 days). Patient 4 had a 24-hour history precipitated by massive intra-tumoral hemorrhage. Most patients presented with signs of increased intracranial pressure. Only two patients had complaints of new pyramidal signs. None of the patients had seizures at presentation.

Figure 1A shows typical MRI characteristics observed in patient 11. All patients presented with hydrocephalus which was decompressed by placement of a ventriculo-peritoneal shunt (n=5) or third ventriculostomy (n=5). Patient 4 had improvement of hydrocephalus following subtotal resection of the tumor. Tumor infiltration of the brainstem and basal ganglia were observed in 11 and 9 patients, respectively (Figure 1B). Patients 8, 10, and 11 had additional involvement of 2, 1, and 2 cerebral lobes at diagnosis, respectively. Distinct tumor masses were observed within the infiltrated thalami in 5 patients, 4 of which enhanced after contrast administration. Patients had a median of 6 (range: 3 to 7) gray matter areas involved at diagnosis.

All patients underwent histologic confirmation (Table 1). The majority of samples analyzed consisted of at least 80% tumor cells. Two-thirds (7 of 11) of the patients had a histologic diagnosis of anaplastic astrocytoma (WHO grade III). Three patients had a glioblastoma (WHO grade IV). Only one patient had a diffuse astrocytoma (WHO grade II; patient 10, Figure 2). All tumors consisted of infiltrative astrocytomas with round to oval nuclear morphology. The tumors lacked specific histologic findings except for one case which demonstrated a small-cell phenotype (patient 4) and another that had scattered multinucleated giant cells (patient 9). Expression of p53 by immunohistochemistry could be assessed in 6 cases, one of which (patient 5) displayed a strong and diffuse pattern suggestive of a mutant *TP53*. While ATRX protein loss was observed in one (patient 4) of 5 cases, mutant H3K27M was not detected in 5 tumors with available tissue (Figure 2). H3K27me3 demonstrated heterogeneous expression in 5 tumors tested.

Molecular Studies

Unsupervised hierarchical clustering of genome-wide methylation was conducted in 7 (64%) tumors for which adequate DNA was available. By comparing to a previously published dataset of pediatric high-grade gliomas, (24) our cohort clustered with the RTK I 'PDGFRA' subgroup (Figure 3 and Table 2). A subgroup representing either *H3F3A* p.K27- or p.G34-mutated tumors was not observed. Only one tumor in the RTK I 'PDGFRA' subgroup displayed MGMT promoter methylation (Table 2).

We observed 364 genes with differentially methylated promoter regions comparing unilateral and bithalamic tumors (estimated false discovery rate of 0.001) (Supplemental Table 1). Thirty-two of these genes exhibited greater methylation in bithalamic compared to unilateral tumors. The remaining 332 genes exhibited greater methylation in unilateral

tumors. The top 100 genes sets that differed between the two groups are presented in Supplementary Table 2.

Sequencing of hotspot mutations was available in 10 (91%) patients. No mutations were observed in *H3F3A* p.K27, *H3F3A* p.G34, *HIST1H3B* p.K27, *IDH1* p.R132, *IDH2* p.R172, and *BRAF* p.V600 (Table 2). *EGFR* and *TP53* mutations were demonstrated in the tumor that had previously undergone whole exome sequencing (30) (Table 2).

Amplification of multiple oncogenes including *MDM4* (*n*=2), *PDGFRA* (*n*=2), *CDK6* (*n*=1), *EGFR* (*n*=1), and a combination of *ID2* and *MYCN* (*n*=1) was observed (Table 2). *FGFR1* fusions were not detected using break-apart FISH probes in 6 tumors with sufficient material. Further confirmation of copy number abnormalities by FISH was not possible due to limited amount of leftover tumor. The most common areas of large gains in 7 tumors were chromosome 7 (71%), 1q (57%), chromosome 2 (43%), 17q (43%), and chromosome 8, 9q, 12p, 13q, and 15q in 28.5% of tumors each. Likewise, the most common areas of large chromosomal losses were 4q (43%), 17p (43%), and 11q, 14q, and 16q in 28.5% of tumors each.

Outcome

Despite aggressive treatment with chemotherapy with or without radiation therapy (RT), (Table 1) only the patient diagnosed as an infant remains alive 7.2 years after diagnosis (Figure 4). Eight patients experienced local disease progression only. Patient 7 experienced massive leptomeningeal spread in his spine following local RT. The pattern of disease progression was not documented in one case. The median OS for all patients was 1 year (range: 0.5 to 7.2 + years). In this cohort, female patients were more likely to have longer intervals from onset of symptoms to diagnosis (median 42 *vs.* 10.5 days; *P*=0.0065). None of the continuous and categorical variables analyzed showed any association with each other or with OS likely due to small sample size.

DISCUSSION

We report for the first time detailed molecular characteristics of one of the largest cohorts to date of patients with bithalamic gliomas. Since this is a rare and poorly defined entity, previous studies contained a maximum of 15 affected subjects, even when reviewing the experience within entire countries (5, 8, 14, 17, 19, 23) (Table 3). The most remarkable molecular finding of our study was the complete lack of *H3F3A* p.K27 and/or the respective DNA methylation signature. The presence of *H3F3A* p.K27 and/or expression of the respective protein have been documented by sequencing or immunohistochemistry in approximately 70% of thalamic high-grade astrocytomas (1, 9, 11, 20, 21, 22, 24, 27, 28) (Table 4). To our knowledge, molecular characteristics of only a few bithalamic high-grade gliomas, one of which harbored the *H3F3A* p.K27 mutation, had been previously reported (1, 27, 28, 30). Since most patients with bithalamic gliomas undergo at most a biopsy, their representation in molecular studies would be assumed to be exceptional. Assuming that 70% of unilateral high-grade thalamic astrocytomas harbor an *H3F3A* p. K27 mutation, (1, 9, 11, 20, 21, 22, 24, 27, 28) our results are substantially different despite the limited sample size (*P*=5.9 x10^{-6}). The absence of other hotspot mutations including *H3F3A* p.G34 in our

patients was not surprising because they predominantly occur in tumors arising in the cerebral cortex (21, 24, 30). In contrast to diffuse intrinsic pontine gliomas, another common pediatric midline CNS cancer, (11, 30) we did not observe hotspot *HIST1H3B* mutations in bithalamic gliomas.

Although our results showed differentially methylated genes comparing unilateral and bithalamic gliomas, (Supplemental Table 1 and 2) including those involved in DNA repair, cell-cycle progression, and apoptosis, no solid conclusions can be drawn from such preliminary data.

Similar to other studies, (11, 21, 24, 30) we observed multiple other amplified oncogenes (i.e., *MDM4*, *MYCN*, *PDGFRA*, and *CDK6*) in our patients. One tumor (patient 7) had concurrent amplification of *MYCN* and *ID2*, a finding recently reported in a subset of supratentorial high-grade gliomas (25).

In contrast to two previous studies, (8, 14) our patients' tumors commonly infiltrated adjacent structures, including the midbrain, basal ganglia, and in a few cases even cerebral lobes. The involvement of cerebral lobes in a minority of cases was reminiscent of gliomatosis cerebri, a condition where typical bithalamic involvement was seen in one-fourth of patients (6). We confirmed that the risk of hydrocephalus is extremely high in bithalamic gliomas.

We acknowledge the bias of the current study since high-grade gliomas accounted for 90% of cases in contrast to previous reports where low-grade gliomas predominated (5, 8, 14, 17, 19). Sampling error of tiny biopsies in such extensive tumors probably accounts for some of this difference. We had already shown that even histologic low-grade bithalamic gliomas portend a dismal prognosis (19). A few previous studies included patients without histologic confirmation, some of which were long-term survivors despite not receiving any anticancer therapy (5, 14, 17, 23). We suspect that some of these patients with better outcomes might have a pilocytic astrocytoma. Pilocytic astrocytomas can display an infiltrative aspect with bithalamic involvement. When patients with thalamic gliomas undergo small biopsies, commonly the only means to differentiate tumors with better or worse prognosis is the presence of suggestive molecular features (e.g., *BRAF* fusion) (10, 20). We removed patients with pilocytic astrocytomas from the current analysis because they represent a separate entity with a potentially better prognosis. Since the radiologic characteristics of bithalamic gliomas overlap with other oncologic and non-oncologic entities, (13) we strongly recommend histologic confirmation before these patients are considered for any anticancer therapy.

The confusion in the definition of bithalamic gliomas accounts for the controversy in therapeutic approaches and outcomes reported for affected patients. While some studies described a terrible outcome for most patients despite treatment with RT with or without chemotherapy, (8, 19, 23) others reported several long-term survivors (5, 14, 17, 23). Unfortunately, conventional methods may not be sufficient to distinguish bithalamic gliomas in clinical practice. The absence of immunoreactivity can rule out *H3F3A* p.K27 mutant

diffuse midline gliomas. However, the heterogenous immunolabeling of H3K27me3 stains was not useful in our diagnostic work-up.

Until the imaging, histologic, and molecular characteristics of bithalamic gliomas are clearly defined, no consensus will emerge about their natural history, best therapeutic approaches, and prognosis of affected patients.

One of the limitations of this study was our inability to perform additional confirmatory or other exploratory molecular analyses due to the lack of further tissue for analysis.

One previous study had speculated that bithalamic gliomas constitute a separate entity based on their unique clinical and radiologic characteristics (8). Although the number of tumors analyzed was limited, the complete absence of *H3F3A* p.K27-mutated tumors among our patients is in stark contrast to other thalamic high-grade gliomas. Therefore, our results suggest that bithalamic gliomas may represent a distinct entity compared to unilateral thalamic high-grade gliomas.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.
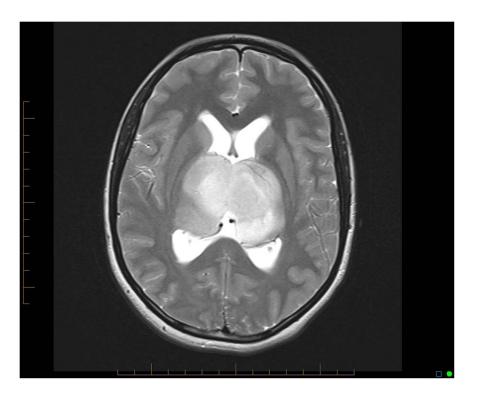
Acknowledgments

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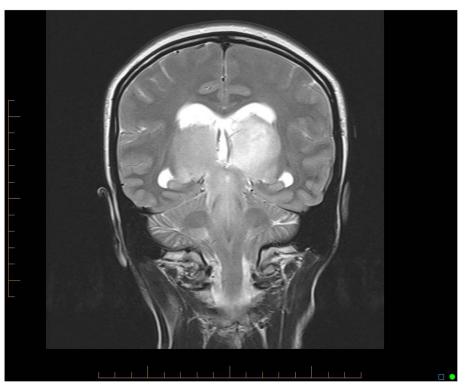
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Figure 1.
Axial T$_2$-weighted brain MRI of patient 11 showing symmetrical bithalamic involvement
(**A**). This patient was also found to have hydrocephalus based on symptoms and enlargement

of lateral ventricles with transependymal flow in their frontal horns. Coronal T$_2$-weighted brain MRI of same patient showing symmetrical bithalamic and midbrain involvement (**B**).
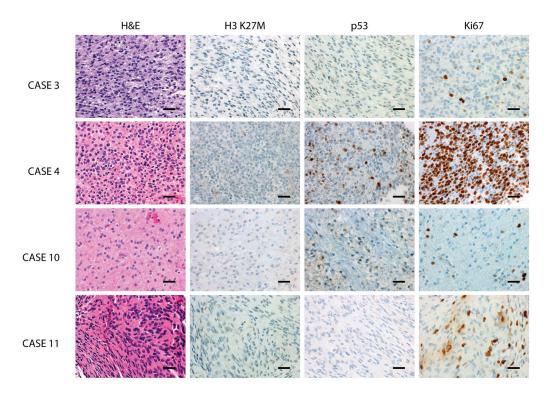
Figure 2.
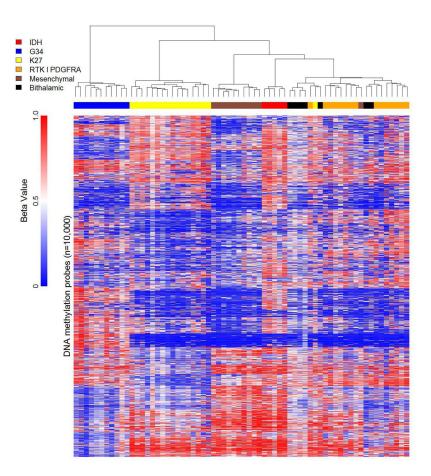Representative histomorphology and immunophenotype of bithalamic gliomas demonstrating infiltrative growth and moderate cytologic pleomorphism. While tumors lacked immunoreactivity for H3K27M, p53 expression was mostly seen in a minority of tumor cells. The proliferative fraction, as assessed by Ki67/Mib-1 immunolabeling, was variable from moderately to very high frequency. The scale bars represent 200 μm.

Figure 3.
Heatmap representation of unsupervised hierarchical clustering analysis of 450 k
methylation array profiles in 7 pediatric patients with bithalamic gliomas in comparison to a
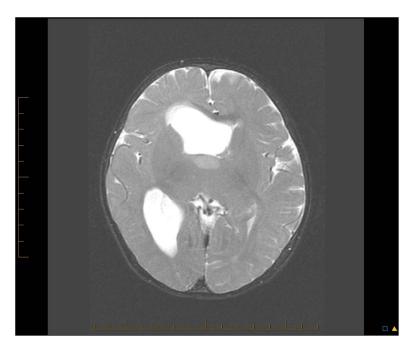dataset of 59 previously published pediatric high-grade gliomas

Figure 4.
Axial T_2-weighted brain MRI of the only long-term survivor (patient 1) at diagnosis. A tumor biopsy was obtained from the T_2 hyperintense anterior portion of the right thalamus.

Table 1

Clinical, radiologic, and histologic characteristics of all patients

Patient No.	Age at Diagnosis (yrs)/Gender	Interval Between Onset of Symptoms and Diagnosis (days)	Race/Ethnicity	No. of Gray Matter Areas Affected	Histologic Diagnosis/Surgery	Therapy	Survival (yrs)
1	1.0/F	120	Caucasian	3	AA/biopsy	Chemotherapy	7.2 +
2	2.4/M	14	Caucasian	3	Glioblastoma/STR	Chemotherapy	0.5
3	2.4/M	21	Caucasian	5	AA/biopsy	RT + chemotherapy	0.8
4	3.3/M	1	Mixed race	4	HGG with small cell features/STR	RT + chemotherapy	1.0
5	4.3/F	60	Hispanic	6	AA/biopsy	RT + chemotherapy	0.75
6	4.8/M	5	African-American	6	GBM/STR	RT + chemotherapy	1.0
7	5.4/M	7	Caucasian	6	AA/biopsy	RT + chemotherapy	1.2
8	9.8/F	35	Caucasian	7	AA/biopsy	RT + chemotherapy	1.5
9	10.7/M	30	Caucasian	6	AA/biopsy	RT + chemotherapy	1.2
10	14.9/F	42	African-American	7	Diffuse astrocytoma WHO grade II/biopsy	RT + chemotherapy	1.75
11	15.7/F	30	Caucasian	5	AA/biopsy	RT + chemotherapy	1.0

Abbreviations: No., number; yrs, years; F, female; M, male; AA, anaplastic astrocytoma; GBM, glioblastoma; HGG, high-grade glioma; WHO, World Health Organization; STR, subtotal resection; RT, radiation therapy

Table 2

Molecular characteristics of evaluable tumors

Patient No.	Methylation Subgroup	MGMT Promoter Methylation	IDH1 p.R132H	H3F3A p.G34	H3F3A p.K27	HIST1H3B p.K27	CDKN2A Loss	Other Relevant Molecular Abnormalities
1	NA	NA	No	No	No	NA	NA	NA
3	RTK I 'PDGFRA'	Methylated	No	No	No	No	No	No
4	RTK I 'PDGFRA'	Unmethylated	No	No	No	No	No	PDGFRA amplification
5	RTK I 'PDGFRA'	Unmethylated	No	No	No	No	No	PDGFRA and EGFR amplification
6[§]	NA	NA	No	No	No	No	No	PDGRFA (structural variation), EGFR G598V (LOH) and TP53 R175H (LOH)
7	RTK I 'PDGFRA'	Unmethylated	No	No	No	No	No	MDM4, ID2, and MYCN amplification
8	NA	NA	No	NA	No	NA	NA	NA
9	RTK I 'PDGFRA'	Unmethylated	No	No	No	No	No	No
10	RTK I 'PDGFRA'	Unmethylated	No	No	No	No	No	MDM4 amplification
11	RTK I 'PDGFRA'	Unmethylated	No	No	No	No	No	CDK6 amplification

Abbreviations: No., number; MGMT, methylguanine methyltransferase; NA, not available; LOH, loss of heterozygosity

[§]Patient whose tumor previously underwent whole exome sequencing

Table 3

Summary of previous series of patients with bithalamic gliomas

Author	Year of Publication	Number of Patients	Median Age at Diagnosis / Range (years)	Histologic Diagnosis	Upfront Therapy	Outcome
Reardon et al	1998	12	NA / 18	LGG: 9; HGG: 3	Not specified	3-year OS=0%
Di Rocco et al	2002	4	8 / 0.25 to 10	DA grade II: 3; astrocytoma grade III: 1	RT: 4	3 patients deceased with median survival of 10 months 1 patient alive after 8 months
Puget et al	2007	9	9.6 (mean) / NA	PA: 1; LGG: 6; HGG: 2	RT: 4	4 patients deceased 5 long-term survivors received no adjuvant therapy (mean F/U of 4.5 years)
Menon et al	2010	7	17 / 5 to 29	DA grade II (6); NC (1)	RT: 7	All patients alive for a median F/U of 1 year (range; 1 to 5 years)
Steinbok et al	2015	10	6.6 (mean) / 1.5 to 14.7	PA: 1; DA grade II: 3; AA: 2; GBM: 3; NC: 1	Chemotherapy: 5; RT: 3	7 patients deceased with median survival of 11.3 months 3 long-term survivors received no adjuvant therapy
Boesten et al	2016	15	7.5 / 2 to 15.1	PA: 2; DA grade II: 9; LGG: 1; NC: 3	Chemotherapy: 3; RT: 3	10-year EFS: 16% ± 13% 10-year OS: 65% ± 13%

Abbreviations: NA, not available; NC, not confirmed; LGGs, low-grade glioma; HGG, high-grade glioma; DA, diffuse astrocytoma; PA, pilocytic astrocytoma; AA, anaplastic astrocytoma; GBM, glioblastoma; RT, radiation therapy; EFS, event-free survival; OS, overall survival; F/U, follow-up

Table 4

Summary of *H3F3A* p.K27 mutations in unilateral high-grade gliomas identified by sequencing and/or immunohistochemistry

Study	Number of Patients	Median Age at Diagnosis (range; years)	% Tumors Harboring *H3F3A* p.K27
Schwartzentruber et al (2012)	6	10.5 (6 to 14)	50%
Sturm et al (2012)	8	11 (6 to 23)	100%
Venneti et al (2013)	**3**	**11.6** (7 to 21.4)	100%
Aihara et al (2014)	18	42 (17 to 78)	55%
Fontebasso et al (2014)	11	11 (6 to 15)	82%
Venneti et al (2014)	7	12 (7 to 21)	71%
Feng et al (2015) §	15	31.7 (mean; 22 to 53)	66.7%
Solomon et al (2015) ¥	23	Adults and children	65%
Ryall et al (2016)	22	10.9 (4 to 17.6)	50%
TOTAL	11**3**		**65%**

§Four patients included had a grade II glioma

¥One of 15 tumors harboring an *H3F3A* p.K27 was a grade 2 glioma. Histologic grade was not provided for 8 tumors.