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Gliomes diffus de bas grade de sous type pédiatrique et tumeurs glio-neuronales "oligo-like": caractérisation clinico-pathologique et moléculaire

Alice Metais

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THÈSE D'EXERCICE / UNIVERSITÉ DE RENNES 1
sous le sceau de l'Université Bretagne Loire

Thèse en vue du
DIPLÔME D'ÉTAT DE DOCTEUR EN MÉDECINE

Présentée par

Alice METAIS

Née le 3 mai 1991 à Le Mans (72)

**Challenges in the
diagnosis of
supratentorial tumors
with an
oligodendroglioma-like
component occurring in
children and young
adults**

**Thèse soutenue à la Faculté de Médecine de
Rennes**

le 22 Avril 2021

devant le jury composé de :

Nathalie RIOUX-LECLERCQ

PU-PH, Anatomie et Cytologie Pathologique, CHU
de Rennes / *Présidente du Jury*

Audrey ROUSSEAU

PU-PH, Anatomie et Cytologie Pathologiques, CHU
Angers / *Examineur*

Pascale VARLET

PU-PH, Anatomie et Cytologie Pathologiques, GHU-
Paris Sainte-Anne / *Examineur*

Laurent RIFFAUD

PU-PH, Neurochirurgie, CHU de Rennes /
Examineur

Pierre-Jean LE RESTE

PH, Neurochirurgie, CHU Rennes / *Examineur*

Dominique FIGARELLA-BRANGER

PU-PH, Anatomie et Cytologie Pathologiques, CHU
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A Henri Cardon (1924-2015)

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LISTE DES ABREVIATIONS

BRAF: v-raf murine sarcoma viral oncogene homolog B

cIMPACT-NOW: Consortium to Inform Molecular and Practical Approaches to CNS
Tumor taxonomy – Not Official WHO

CNA: copy number alteration

CNS: central nervous system

CNV: copy number variation

DN: dysplastic neurons

DNT: dysembryoplastic neuroepithelial tumor

EGFR: Epidermal Growth Factor Receptor

FA: fractional abundance

FAM: fluorescein

FFPE: formalin-fixed paraffin embedded

FGFR1-3: fibroblast growth factor receptor 1-3

GG: ganglioglioma

GNE: specific glioneuronal element

GNT: glioneuronal tumor

H3: Histone 3

HEX: hexachloro-6-carboxyfluorescein

HPS: hematoxylin-phloxin-saffron

IDH: isocitrate dehydrogenase

KCTD16: potassium channel tetramerization domain containing 16

KIAA1598: shootin 1

LEAT: long-term epilepsy associated tumors

MAPK: mitogen-associated protein kinase

MC: methylation class

mdPCR: multiplexed digital droplet PCR

MRI: magnetic resonance imaging

MYB: v-myb avian myeloblastosis viral oncogene homolog

MYBL1: v-myb avian myeloblastosis viral oncogene homolog-like 1

NOS: not otherwise specified

NPM1: nucleophosmin 1

NTRK: neurotrophic receptor tyrosine kinase

PCR: polymerase chain reaction

PLGG: paediatric-type low-grade glioma

PLNTY: polymorphous low-grade neuroepithelial tumor of the young

RAS: rat sarcoma viral oncogene homolog

RNA seq: RNA sequencing

RNF130: ring finger protein 130

TACC1-3: transforming acidic coiled-coil containing protein 1-3

TERT: telomerase reverse transcriptase

TKD: tyrosin kinase domain

TNS3: tensin 3

WHO: World health organization

Challenges in the diagnosis of supratentorial tumors with an oligodendroglioma-like component occurring in children and young adults

Alice Métails^{1,2}, Romain Appay^{1,3*}, Mélanie Pagès^{4*}, Catherine Gallardo¹, Karen Silva⁵, Aurore Siegfried^{6,7}, Romain Perbet^{8,9}, Claude-Alain Maurage^{8,9}, Didier Scavarda¹⁰, Frédéric Fina^{1,11}, Emmanuelle Uro-Coste^{6,7}, Laurent Riffaud^{12,13}, Carole Colin³, Dominique Figarella-Branger^{1,3} and contributors of the Biopathology RENOCLIP-LOC network

* Equally contributed

¹APHM, CHU Timone, Service d'Anatomie Pathologique et de Neuropathologie, Marseille, France.

²Service d'Anatomie et Cytologie Pathologiques, CHU Pontchaillou, Rennes, France.

³Aix-Marseille Univ, CNRS, INP, Inst Neurophysiopathol, Marseille, France.

⁴GHU-Paris Sainte-Anne Hospital, Paris University, Paris, France.

⁵Groupe Hospitalier Est, Département de Neuropathologie, Hospices Civils de Lyon, Bron, France.

⁶Department of Pathological Anatomy and Histology-Cytology, Rangueil Hospital, Toulouse, France.

⁷Center for Research in Cancerology, Inserm U1037, University of Toulouse, Toulouse, France.

⁸Institute of Pathology, CHU Lille, Lille, France.

⁹LiNCog, Lille Neuroscience and Cognition, Univ. Lille, Inserm, CHU Lille, U1172, Lille, France.

¹⁰Aix-Marseille Univ, APHM, Institut de Neurosciences des Systèmes, CHU Timone, Service de Neurochirurgie infantile, Marseille, France.

¹¹ID Solutions, Research and Development, Grabels, France.

¹²Department of Pediatric Neurosurgery, Rennes University Hospital, Rennes, France.

¹³INSERM MediCIS, unit U1099 LTSI, Rennes 1 University, Rennes, France.

Biopathology RENOCLIP-LOC network: A. Rousseau (Angers), C. Godfraind (Clermont-Ferrand), C-A. Maurage (Lille), D. Meyronet (Lyon), G. Gauchotte (Nancy), F. Bielle (Paris), K. Mokhtari (Paris), P. Varlet (Paris), E. Uro-Coste (Toulouse), F. Vandebos (Nice), G. Chotard (Bordeaux), F. Escande (Lille), Y. Nicaise (Toulouse).

ABSTRACT

Pediatric low-grade glial (PLGG) and glioneuronal tumors (GNT) are associated with drug-resistant epilepsy and occur in children and young adults. An oligodendroglioma-like component is a frequent feature of ganglioglioma (GG), dysembryoplastic neuroepithelial tumors (DNT) and in the two recently described entities: polymorphous low grade neuroepithelial tumor of the young (PLNTY) and diffuse LGG MAPK-altered. These tumors also share genetic alterations activating the MAPK kinase pathway. Therefore, they represent a diagnostic challenge.

We retrospectively studied 72 supratentorial LGG or GNT tumors with an oligodendroglioma-like component that we reclassified into three groups: GG (presence of dysplastic neurons, n=14), DNT (presence of glioneuronal element n=19) and GNT/PLGG (n=39). Targeted molecular analysis by multiplexed digital PCR (*BRAF*, *FGFR1* mutations and *FGFR1* duplication) found an alteration in 38/72 cases. Among the 34 cases without any alteration, RNA seq revealed a fusion transcript in 9/26. DNA-methylation profiling (n=46) found only 12 cases that displayed a calibrated score > 0.9 (26 %). Non informative calibrated score (> 0.3 and < 0.9) was observed in 26 cases (56.5%). In 8 cases calibrated score was less than 0.3 (17.5%). Unsupervised hierarchical clustering revealed 2 clusters in which GNT/PLGG tumors were equally distributed. LGG/GG cluster was enriched for histologically classified GG, *BRAFV600E*, CD34 expression and LGG GG methylation class (MC). LGG/DNT cluster was enriched for histologically classified DNT, *FGFR1* alterations, CD34 negative tumors and LGG DNT MC. Seven tumors fulfill diagnostic criteria for PLNTY. A decisional algorithm for histomolecular diagnosis of GG, DNT, PLNTY and LGG MAPK-altered is suggested.

Our study highlights the challenges in the diagnosis of supratentorial tumors with an oligodendroglioma-like component occurring in children and young adults and shows that these tumors belong to two major groups of biological relevance although four entities are currently recognized within this spectrum of tumors by WHO CNS5 classification.

INTRODUCTION

In 2016, the World Health Organization (WHO) classification of tumors of the CNS introduced for the first time molecular markers for the diagnosis of some entities (1). Accordingly, three major genetic alterations i.e. *H3* K27M mutation, *IDH* mutation and 1p19q codeletion stratify diffuse astrocytic and oligodendroglial tumors (2–4). As an example, both *IDH*-mutation and 1p19q codeletion are required to perform a diagnosis of oligodendroglioma and the terminology used for these tumors is now “(anaplastic) oligodendroglioma, *IDH*-mutant and 1p19q codeleted”. However, gliomas, lacking *IDH* mutation or *H3* alterations, encompass a wide range of tumors that might display heterogeneous histological features, distinct genetic alteration and clinical behaviour according to the age of the patient. In 2016 a “pediatric box” was included in the chapter oligodendroglioma, *IDH*-mutant and 1p19q codeleted to describe a subgroup of gliomas recorded as “oligodendroglioma lacking *IDH* mutation and 1p19q codeletion (paediatric-type oligodendroglioma)” (1). These tumors mainly occurred in children and adolescents and carry a good prognosis (5–7). The molecular landscape of these tumors has been recently described. Their tumorigenesis is driven by activation of the RAS-mitogen-activated protein kinase (RAS/MAPK) pathway, related to key genetic alterations in this signaling pathway (8–11). The cIMPACT-NOW group (*the consortium to Inform Molecular and Practical Approaches to CNS Tumor taxonomy*), has provided from a few years a forum to evaluate and recommend proposed changes to future CNS tumor classification (12). According to cIMPACT-NOW update 3, the terminology “diffuse astrocytic glioma, *IDH*-wild type with molecular features of glioblastoma, WHO grade IV “ was introduced to describe a group of diffuse gliomas *IDH* wildtype appearing in elderly subjects associated with an aggressive clinical course and molecularly defined by gain of chromosome 7 and loss of chromosome 10 or *TERT* promoter mutation or *EGFR* amplification (13). This consortium has recently pointed out the molecular similarities between benign diffuse gliomas occurring in children and young adults and some other circumscribed gliomas and glioneuronal tumors, therefore introducing the concept of paediatric-type diffuse gliomas (14). They define this group as a WHO grade II infiltrating glioma with astrocytic and/or oligodendroglial differentiation, low or absent mitotic activity, absence of necrosis or microvascular proliferation and recurrent genetic alterations such as *BRAFV600E* mutation, *MYB* or *MYBL1* rearrangement, *FGFR1* alteration (15). The cIMPACT-NOW update 6 summarized the conclusions of the cIMPACT-Utrecht meeting and provide diagnostic

principle recommendations for the future CNS tumor classification and grading (16). Hence, the WHO CNS5 classification will change all WHO CNS tumor grades to Arabic numerals and diffuse gliomas will be divided into adult-type and pediatric-type (either low-grade or high-grade). Four tumor types are recorded in the group of pediatric-type diffuse low-grade gliomas: diffuse astrocytoma, *MYB* or *MYBL*-altered, angiocentric glioma, polymorphous low-grade neuroepithelial tumor of the young (PLNTY) and diffuse low grade glioma, MAPK-pathway-altered. Although diffuse astrocytoma, *MYB* or *MYBL*-altered, angiocentric glioma are characterized by an astrocytic component (17–19), polymorphous low-grade neuroepithelial tumor of the young (PLNTY) (20–25) and a subgroup of diffuse low grade glioma, MAPK-pathway-altered are characterized by a prominent oligodendrogloma-like component. This pattern is also shared by some glioneuronal tumors especially dysembryoplastic neuroepithelial tumor (DNT) and ganglioglioma (GG) (26). All these entities display genetic alterations in the MAPK-pathway. Although some recurrent genetic alterations are more frequent in some entities than in others it is obvious that two of them: the *BRAF* V600E mutation and *FGFR1* alterations have been reported in all of them and therefore diagnosis might be tricky in some cases.

Here we report a series of 72 supratentorial tumors occurring in paediatric setting and young adults characterized at histology by an obvious oligodendrogloma-like component associated or not with some characteristic pathological features leading to three major groups: ganglioglioma (GG, presence of dysplastic neurons), dysembryoplastic neuroepithelial tumors (DNT, characterized by the occurrence of the specific glioneuronal element) and a mixed group: glioneuronal tumors/pediatric low grade gliomas (GNT/PLGG). We performed careful clinic-pathological analysis, targeted molecular analysis by multiplexed digital PCR (*BRAF* mutation, *FGFR1* mutation and *FGFR1* duplication) and in a subset of cases DNA methylation profiling and RNA sequencing in order to define the most relevant pathological and molecular features of each group that could be instrumental in routine diagnostic practice to reach an integrated diagnosis according to the new CNS5 classification of brain tumors. Moreover, our results are discussed in line with the new entities recorded in the classification: the PLNTY and the group of diffuse low-grade gliomas, MAPK-pathway-altered.

MATERIALS

Tumor samples from 113 patients (from Rennes University Hospital, Marseille University Hospital, Lyon University Hospital, Lille University Hospital, Nice University Hospital, Grenoble University Hospital, GHU-Paris Sainte-Anne and Bordeaux University Hospital) operated on for a supratentorial tumor with a pathological diagnostic of dysembryoplastic neuroepithelial (DNT, simple, complex and non-specific form), ganglioglioma (GG), or glioneuronal tumor or paediatric-type low-grade glioma not otherwise specified (GNT/PLGG-NOS). Written informed consent to participate in this study was provided by the participants' legal guardian/next of kin. This study was reviewed and approved by the Aix-Marseille University ethics committee (2019-25-04-003). None of these cases displayed *IDH* mutation. All tissue samples were centrally reviewed (DFB, RA, AM) (Figure 1). Only tumors presenting with an oligodendroglioma-like component, associated or not with dysplastic neurons or a specific glioneuronal element (floating neurons in mucoid matrix) and one available formalin-fixed-paraffin embedded (FFPE) block were retained for further analysis, resulting in 72 cases effectively included in the study. Clinical and radiological data were retrospectively collected for each case. Clinical data included gender, tumor location, symptoms, age at first symptoms, age at surgery, extent of surgical resection, follow up (including date of last follow up and date of surgical excision for relapse if any), second resection if any. The delay between first and second resection was also recorded. Imaging was available for 59 patients. Minimal imaging data consisted in at least MRI report and if available significant FLAIR and T1 with gadolinium injection MRI sections.

METHODS

Pathological analysis and immunohistochemistry

Samples were stained with hematoxylin-phloxin-saffron (HPS) according to standard protocols. For each case the following pathological features were searched for and scored as present or absent: infiltrative growth pattern, nodular growth pattern, specific glioneuronal element (GNE), dysplastic neurons (DN), piloid features, papillary features, rosette features, cytoplasmic vacuolization aspects, nuclei clustering, Rosenthal fibers, eosinophilic granular bodies, calcification, inflammation, siderophagous infiltrate, meningeal involvement, microvascular proliferation.

Immunohistochemistry was performed on Benchmark Ventana autostainer (Ventana Medical Systems SA, Illkirch, France) for OLIG2 (6F2, Dako®), CD34 (QBE10, Roche®), Neurofilament (2F11, Menarini®), Ki67 (MIB1, Dako®). In 36 cases BRAF immunostaining (VE1, Eurobio-Spring®) was also performed.

DNA extraction and quantification

DNA was extracted from each tumor samples (n=72) using the IDXTACT-mag-FFPE kit (ID-Solutions, Grabels France) coupled to the automaton (IDEAL-32, ID-Solutions) as per the manufacturer's directions. DNA was qualified and quantified using DNA calibrated by an external standard range using the IDQUANTq kit (ID-Solutions) and the Mic® quantitative PCR instrument (Bio Molecular Systems, Queensland, Australia). If necessary, the DNA was diluted or concentrated (Vivacon 500, Sartorius Göttingen, Germany) in order to be able to perform a dPCR test sample of 8 µL of DNA in between 1 to 5 ng of DNA, and to have 250-500ng in 8µL. Technical steps for DNA extraction were performed in La Timone University hospital (Marseille) by CG. When insufficient DNA amount was extracted, additional sections were utilized. Post-scrapping Hematoxylin-phloxin-saffron staining sections were systematically examined to ensure tumor cell content.

Multiplexed droplet digital PCR

BRAF V600E mutation, *BRAF* exon 14 duplication, *FGFR1* N546K and K656E mutations and *FGFR1* duplication were assessed for every patient of the cohort by multiplexed droplet digital PCR (mdPCR) as previously described (27–29). Technical steps for mdPCR were performed in La Timone University hospital (Marseille) by CG. Briefly, 8 µL of DNA comprising 1 to 5 ng and 13 µL of PCR mix (comprising uracil N-glycosylase (UNG), ready to use) were used for each mdPCR assay. A similar amplification program (50°C 2 min; 95°C 10 min; 40 x 95°C 30 sec- 60°C 1 min; 98°C 10 min) was used for all targets. The QX200 Droplet Digital PCR System (Bio-Rad) was used for the qualitative and quantitative analyses. The cut-off values and detection thresholds were set up as previously described (27–29). *BRAF* V600E mutation was targeted using 100% FAM labelled probe. *BRAF* exon 3, used as reference, was targeted using 100% HEX labelled probes. *BRAF* exon 14 was targeted using a mixture of both FAM and HEX labelled probes. *FGFR1* N546K and

K656E mutations were targeted using 100% FAM labelled probe, *FGFR1* exon 16 was targeted using 100% HEX labelled probes and *FGFR1* exon 8, used as reference, was targeted using a mixture of both FAM and HEX labelled probes. Fractional abundance (FA) and copy number variation (CNV) were calculated as described by Appay et al. 2020 (29).

Methylation analysis

Samples containing up to 250 ng DNA were selected for DNA methylation profiling. Technical steps were performed in La Timone University hospital (Marseille) by CG. DNA bisulfite conversion was processed using the ZymoEZ DNA methylation kit (Zymo research, USA), then treated with FFPE DNA Restore kit (Illumina, San Diego, CA, USA) and DNA clean and concentrator-5 (Zymo research, USA). The standard quality controls confirmed DNA quantity/quality and bisulfite conversion. The DNA was then processed using the Illumina Infinium HumanMethylation EPIC Bead-Chip array (Illumina, San Diego, CA, USA) according to the manufacturer's instructions. The iScan control software was used to generate raw data files from the BeadChip in IDAT format, analyzed using GenomeStudio version 2.0 (Illumina, San Diego, CA, USA) and were checked for quality measures according to the manufacturer's instructions.

Data processing

The .idat files were uploaded to the online CNS tumor DNA methylation classifier (11b4 version) at <https://www.moleculareuropathology.org> and a report for every tumor was generated, providing prediction scores for methylation classes (MC) and chromosomal copy-number plots. The calibrated scores were integrated to the histopathological findings according to the recommendations from Capper *et al.* (30,31). A methylation class (MC) associated with a calibrated score > 0.9 was relevant for diagnosis. A max-score between 0.3 and 0.9 was considered potentially useful but integrated with caution. No MC was given for a calibrated score less than 0.3.

Additional analyses were performed in R studio (v4.0.2). Raw signal intensities were obtained from .idat files using the minfi Bioconductor package (v1.34.0). Background correction and dye-bias correction were performed on each sample. Filtering criteria

of probes were removal of probes targeting X or Y chromosomes and removal of probes containing single nucleotide polymorphisms. Hierarchical clustering was performed using the Complex Heatmap package (2.4.3). Clustering of beta values from methylation arrays was performed based upon Euclidean distance with a ward algorithm. Methylation heatmap shows only the most variable probes ($SD > 0.20$). Tumors with a calibrated score for control tissue methylation classes were excluded.

RNA extraction and targeted RNA sequencing

Cases without alteration detected by mdPCR and for whom enough material was remaining underwent RNAseq analysis in Toulouse University Hospital (EUC, AS, YN) (32). RNA was extracted from two 8 microns thick FFPE material sections approximately, using the high Pure FFPE RNA Isolation Kit (catalogue # 06650775001, Roche diagnostics, Boulogne-Billancourt, France) according to the manufacturer's instruction.

The RNA concentrations were measured on a Qubit 4 Fluorometer (# Q33238, Thermo Fisher Scientific, USA) with the Invitrogen Qubit RNA BR Kit (# Q10210, Thermo Fisher Scientific). The percentage of RNA fragments >200 nt (fragment distribution value; DV200) was evaluated by capillary electrophoresis (Agilent 2100 Bioanalyzer). A DV200 $>30\%$ was required to process the next steps of analysis. NGS-based RNA sequencing was performed using the Illumina TruSight RNA Fusion Panel on a Nextseq550 instrument according to the manufacturer's instructions (Illumina, San Diego, CA, USA). This targeted RNA sequencing panel covers 507 fusion-associated genes, to assess most known cancer-related fusions. The TruSight RNA fusion panel gene list is available at https://www.illumina.com/content/dam/illumina-marketing/documents/products/gene_lists/gene_list_trusight_rna_fusion_panel.xlsx.

7690 exonic regions are targeted with 21 283 probes. Libraries were prepared according to Illumina's instructions of TruSight RNA fusion Panel kit. STAR_v2.6.1a or Bowtie softwares were used to produce aligned reads in relation to the Homo sapiens reference genome (UCSC hg19) (33). Manta v1.4.0, Tophat2 and Arriba tools were used for fusion calling (34).

Statistical analysis

Categorical variables were presented as frequencies and percentages, continuous variables as median and range or mean and standard deviation. The Fisher exact test was used to compare qualitative variables. Statistical tests were two-sided, the threshold for statistical significance was $p = 0.05$. Statistical analysis was done using XLSTAT software Version 2020.1.01 (Addinsoft, Paris, France).

RESULTS

Clinicopathological data

Seventy-two patients presenting with tumors with an oligo-like component were retained for further analysis after centralized histopathological review (figure 1). These include 39 women and 43 men (sex-ratio 1.43). Mean age at surgery was 18.4 +/- 12.4 years with 2 cases of infants (age ≤ 1 year) (2.8%), 42 cases of paediatric patients (age ranging from 1 year to 18 years) (58.3%) and 28 cases of adult patients (age above 18 years) (38.9%). Most of the cases ($n = 63/72$; 87.5%) had epilepsy, starting at a mean age of 15.5 +/- 10.9 years. Few cases presented neurological deficit ($n = 3$; 4.2%). Forty-nine cases had gross total resection (68%), 12 had biopsy or partial resection (16.7%) and information regarding surgical resection was not available for 11 patients (15.3%).

All tumors were supratentorial, most frequently localized in the temporal lobe ($n=44$; 61%), 12 in the frontal lobe (16.6 %), 4 in the parietal and 3 in the occipital. In 9 cases the tumor was localized in two or three lobes including the temporal lobe in 7/9. Altogether the temporal lobe was involved in 51 cases (70.8 %). Forty tumors demonstrated a cortical or cortico-subcortical localization (56%). Low signal T1 was observed in 40 cases (56%). High signal FLAIR was observed in 47 cases (65%). Contrast enhancement was observed in 30 cases (42%), edema in 5 cases (7%) and bubbly or cystic aspect in 31 cases (43%).

Follow-up data were available in 63 cases (87.5 %), with a median follow-up of 31.1 months [0-229.4 months]. Nine patients experimented recurrence associated with a second surgical resection, with a median time of 61.9 months [5.3-213.3 months] between the two interventions. No patient died. No patient had oncologic adjuvant therapy (radiotherapy or chemotherapy).

Among the 72 cases reviewed, 52 were initially diagnosed as DNT (either simple, complex or “non-specific form”, 72 %), 11 as GG (15%) and 9 as GNT/PLGG-NOS (13%). Central review board (DFB, RA, AM) reclassified each tumor in three groups: GG (presence of dysplastic neurons), DNT (presence of the specific GNE) or GNT/PLGG (oligodendroglioma-like component only associated or not with neuron-like component). Thus, 14 cases were reclassified as GG (19.5%), 19 cases were reclassified as DNT (26%) and 39 as GNT/PLGG (54.5%). In the whole cohort, infiltrative growth pattern was observed in 41 cases (57%) and nodular pattern was observed in 31 cases (43%). Meningeal involvement was observed in 21 cases (29%). Calcifications were recorded in 21 cases (29%), eosinophilic granular bodies in 16 cases (22%), Rosenthal fibers in 3 cases (4%), cytoplasmic vacuolization in 4 cases (5.5%), nucleus clustering in 7 cases (10%), inflammatory infiltrates in 14 cases (19%), piloid features in 12 cases (17%), papillary features and rosette features in only 1 case (1.4%), siderophagous infiltrate in 7 cases (10%), and microvascular proliferation in 7 cases (10%). All tumors expressed OLIG2 and demonstrated residual axons with neurofilament staining. Mitotic activity was inconspicuous and Ki67 proliferation index was low (mean: 2.4% +/-3%). Extravascular CD34 immunostaining was present in 33 cases (46%).

Multiplex digital PCR

mdPCR was performed in all cases and demonstrated at least one alteration in 38 cases (53%) whereas no alteration was observed in 34 cases (47%). *FGFR1* alteration only was observed in 18 cases (25%) including 13 cases with *FGFR1* exon 16 duplication and 5 cases with *FGFR1* mutations. *BRAF* V600E mutation only was recorded in 18 cases (25%). Surprisingly, 2 cases presented with *FGFR1* exon 16 duplication associated to a *BRAF* V600E mutation. In these cases, BRAFV600E mutation was confirmed by immunohistochemistry. For further analyses these cases were grouped together with those demonstrating BRAF mutation only. Moreover, 6 additional cases presented with a BRAF duplication. In three cases, BRAF duplication was the only molecular alteration recorded, whereas in three other cases, it was associated with *FGFR1* exon 16 duplication. For further analyses these 3 cases were grouped together with those demonstrating *FGFR1* exon 16 duplication only.

Correlation between histopathological diagnosis, clinico-pathological and molecular data

No difference in age, sex, tumor location, and tumor recurrence was recorded between the three groups of patients (DNT, GG and GNT/PLGG). The results are summarized in Table 1.

We did not observe statistical difference regarding the pattern of growth (infiltrative *versus* nodular) within the three groups. Although calcifications were more frequent in GNT/PLGG group (15/39) than in GG (4/14) or DNT (2/19) it was not statistically significant ($p = 0.084$). In contrast, presence of eosinophilic granular bodies ($p = 0.034$), inflammation and CD34 immunostaining ($p < 0.0001$) were more frequent in GG group than in the two other groups. *BRAF* V600E mutation was more frequent in GG (10/14) than in GNT/PLGG (10/35) or DNT (0/19) ($p < 0.0001$). In contrast, occurrence of *FGFR1* mutation or duplication was not statistically different within the three groups of patients ($p = 0.247$). These results are summarized in Table 2. At last, extravascular CD34 expression was strongly associated with *BRAF* V600E mutation (among the 32 cases with CD34 expression, 19 displayed *BRAF* V600E mutation whereas only 1/36 cases negative for CD34 demonstrated *BRAF* V600E mutation) ($p < 0.0001$).

DNA methylation profiling

Results were obtained in all cases ($n = 46$; 64%). However only 12 cases displayed a methylation class (MC) associated with a calibrated score > 0.9 (26 %). Among them we recorded 3 cases with a MC concordant with pathological diagnosis (confirmatory), 4 cases with a MC inconsistent with pathological diagnosis (control tissue) and for 5 cases the diagnosis was refined: 5 GNT/PLGG were reclassified as LGG DNT (3 cases) (Figure 2) or LGG GG (2 cases).

Non informative calibrated score (> 0.3 and < 0.9) was observed in 26 cases (56.5%). At last in 8 cases MC score was less than 0.3 (17.5%) and no MC could be assigned.

Targeted RNA sequencing

Among the 34 cases without alteration found by mdPCR, 26 were eligible for targeted RNA sequencing. One had technical failure (FFPE block older than 8 years). Twenty-five were analyzable. A fusion transcript was found in 9 cases: one *FGFR1-TACC1*,

two *FGFR2* fusions (*FGFR2-INA* and *FGFR2-KIAA1598*) (Figure 3), two *FGFR3-TACC3* fusions (Figure 4, Supplementary Figure 1), two *BRAF* fusions (*RNF130-BRAF* and *NPM1-BRAF*), and two *NTRK2* fusions (*KCTD16-NTRK2* and *TNS3-NTRK2*) (Supplementary Figure 1). Except for *NPM1-BRAF* fusion all other fusions have been previously reported in primitive brain tumors, with proven or predicted activation of the MAPK pathway (11,35). The results are summarized in Table 3.

Unsupervised clustering analysis based on DNA methylation data revealed two main clusters: LGG/ganglioglioma and LGG/DNT

Unsupervised hierarchical clustering based on 34 tumors (8 DNT, 5 GG and 21 GNT/PLGG) included in the present series revealed two major clusters (Figure 5). The first one comprised all the cases histologically classified as DNT as well as 2 GG and 11 GNT/PLGG, while the second one includes 3 GG and 10 GNT/PLGG. *FGFR1* alterations, recorded in 7 cases (mutation, duplication and fusion), were exclusively observed in cluster 1 whereas 7/9 cases harboring the *BRAF* V600E mutation were found in cluster 2. Cluster 2 was enriched in cases demonstrating CD34 expression (9/13 (%)) while only 4/21 of the cases (%) from the cluster 1 showed CD34 expression. Age and sex distribution were in similar range in both clusters. Although the temporal location was the most frequent in the whole cohort, it was obvious that large tumors and tumors located outside the temporal lobe were more frequently observed in cluster 1 (10/21, %) than in cluster 2 (3/13, %). In addition, all cases showing relapses (4 cases) were found in cluster 1. All cases (n = 15) with a max-score for the LGG DNT methylation class (range 0.33 to 0.98) fell into the cluster 1 whereas cluster 2 encompasses all cases (n = 3) with max-score >0.9 for the LGG GG methylation class as well as 4/5 cases with a low max-score for LGG GG (range 0.31-0.89). Therefore, we named cluster 1 LGG/DNT and cluster 2 LGG/GG. Importantly, the cases classified at histology as GNT/PLGG were equally distributed in the two clusters. Among the two cases classified at histology as GG and belonging to the cluster LGG/DNT, one case match with the methylation class LGG PA, subclass hemispheric PA/GG and the other showed a max score (0.86) for LGG PA. These two cases expressed CD34 and demonstrated *BRAF* V600E mutation.

Diagnostic testing algorithm for supratentorial tumors with an oligodendroglioma-like component occurring in children and young adults

According to our results we suggest the following algorithm to improve and facilitate diagnosis of supratentorial tumors with an oligodendroglioma-like component occurring in children and young adult (Figure 6). First careful pathological examination should search for GNE or DN. Tumors showing GNE can be classified as DNT and those with DN as GG. In these cases, search for molecular alteration is not required. When these pathological features are lacking it is mandatory to search for *FGFR1* mutations and/or duplication and *BRAF* V600E mutation. Cases demonstrating *FGFR1* alteration can be classified as diffuse LGG MAPK pathway-altered. In cases lacking *FGFR1* alteration and *BRAF* V600E mutation search for fusion activating MAPK pathway is required. In both cases harboring *BRAF* V600E mutation and cases demonstrating fusion, presence of calcification and CD34 expression should prompt to the diagnosis of PLNTY whereas the remaining cases fulfill criteria for diffuse LGG MAPK pathway-altered. In all cases DNA-methylation profiling might help tumor classification but it is of utmost importance to perform this technique in cases lacking GNE, dysplastic neurons and the molecular alterations described above. Moreover, DNA-methylation profiling could rule out another diagnosis. This is summarized in Figure 6.

According to our algorithm, 7/72 cases were classified as PLNTY, 16/72 as GG, 16/72 as diffuse LGG MAPK pathway altered, and 23/72 as DNT. Finally, 10/72 cases remained unconcluded because techniques could not be performed (5/10) or did not provide additional information (5/10). For these last ones, no fusion was detected, and no MC could be assigned. Indeed, one had a calibrated score < 0.3, two had a max score of respectively 0.31 and 0.32 for LGG GG MC, and two had a max score of respectively 0.64 and 0.72 for LGG DNT MC.

DISCUSSION

Glioneuronal tumors including DNT and GG are characterized by the presence of a glial component that may resemble fibrillary astrocytoma, oligodendroglioma or pilocytic astrocytoma and a neuronal component characterized by the GNE in DNT and dysplastic neurons (also named dysmorphic ganglion cells) in GG. In some cases, the glial component is made of monomorphous oligodendroglioma-like cells only. Oligodendroglioma-like component might be the unique neoplastic cells in some diffuse low-grade glioma MAPK pathway-altered and in PLNTY (14,16). These two tumor types, that will be included in the WHO CNS5 tumor classification as new entities, lack characteristic pathological features although calcifications and CD34 expression are common in PLNTY. Besides, DNT, GG, diffuse low-grade glioma MAPK pathway-activated and PLNTY belong to the group of long-term epilepsy associated tumor (LEAT) (36) and share in common, in addition to refractory epilepsy, supratentorial location, young age, indolent behavior and genetic alterations causing activation of the MAP kinase signaling pathway (14,22). Unsurprisingly, the differential diagnosis between these four tumor types remains difficult. Although DNA-methylation profiling has emerged as a powerful molecular tool to classify CNS tumors (30,31) some authors have pointed out its less accurate value to decipher challenging diagnoses among low grade glial and glioneuronal tumors (37,38). In accordance with these last studies, DNA-methylation profiling of the cases included in the present work provides disappointing results. Only 12/46 cases tested displayed a methylation class with a calibrated score of diagnostic value (>0.9) and among these, 4 cases showed a MC of control tissue. In 26 cases however, although the MC was associated with a calibrated score under the threshold value for diagnosis (<0.9), it provides consistent results for LGG and in 8 cases no MC could be assigned (calibrated score <0.3). Importantly, in none of the cases included in the present series, the MC pointed to other tumor types than LEAT tumors suggesting that the cases were accurately selected. It is likely that the low tumor cell density of the tumors analyzed as well as normal tissue included in the specimen subjected to DNA-methylation profiling might explain in part the low methylation scores observed in our series, since macrodissection was not performed. Nevertheless, in all cases the tumor represented at least 40% of the specimen. Another limitation of DNA-methylation profiling in LEAT tumors is represented by the wide range of MC for LGG tumors. In our series, four MC were observed including LGG DNT, LGG GG, LGG PA, LGG PA, subclass hemispheric PA/GG, highlighting the commonalities between

all these tumors. Moreover, there is no MC assigned yet by the 11b4 version of the Heidelberg classifier for PLNTY nor LGG MAPK pathway-activated entities. In spite of these limitations it was obvious that unsupervised clustering provides an overview of emerging subgroups among tumors. Our analysis recognized two main clusters of tumors that we named LGG/GG group and LGG/DNT group and classified all the cases diagnosed at histology as GNT/PLGG into these two main groups. This is in accordance with two previous studies focusing on LEAT tumors (26,39). In one study that comprised 43 GG, 18 DNT and 37 so called “glioneuronal tumors of uncertain histologic type” (GNT NOS) two tumor groups were recorded after DNA-methylation profiling: group 1 contained 19 GG, 1 DNT and 1 GNT NOS whereas group 2 encompasses 2 GG, 8 DNT and 6 GNT NOS (39). In the other study that included 5 DNT, 8 GG and 7 “diffuse glioneuronal tumors”, cluster 1 comprised all the DNT whereas the other tumors belonged to cluster 2 (26). Of interest one study underlined the oligodendroglioma-like component found in 11/43 GG, 17/18 DNT and 16/37 GNT NOS (39). Although it remains overlap between clinic, pathological features among the two tumor groups: LGG/GG and LGG/DNT, it is obvious that some specificities especially regarding pathogenic mutations in *BRAF* and *FGFR1* distribution occur in each group highlighting their biological relevance. The LGG/DNT group contains all tumors with a pathological diagnostic of DNT (by using strict pathological criteria) and all tumors displaying *FGFR1* alterations. Although we and others have previously reported BRAFV600E mutation in DNT (26,40,41), other studies failed to find this alteration in these tumors (15,42). These discrepant results likely rely on marked inter-observer variability in making DNT diagnosis (26,36). Among *FGFR1* alterations, duplication of the tyrosine kinase domain (TKD) is relatively unique to DNT (15,27,42). Although *FGFR1* alterations characterize the LGG/DNT group it is obvious that some typical DNT (on both pathological criteria and MC LGG DNT) are devoided of this genetic alteration. Therefore, *FGFR1* alteration is not required for DNT diagnosis but its occurrence in a supratentorial tumor with an oligodendroglioma-like component should point towards DNT and in the absence of the characteristic GNE, to the diagnosis of diffuse low-grade glioma MAPK pathway-altered (14). In contrast to *Qaddoumi et al.* who recorded *FGFR1* alteration in up to 93% (39/42) of LGG with an oligodendroglial phenotype, a large part of the cases included in the present study that share the oligodendroglioma-like component do not harbor *FGFR1* alteration and belong to the LGG/GG group (15). This group is enriched in cases demonstrating *BRAF* V600E mutation. Again this alteration is not

specific and is encountered in many tumor types (including LGG and high grade glioma) but is a common feature of GG and PLNTY (22,36). *BRAF* V600E mutation in contrast to *FGFR1* alteration is strongly associated with CD34 expression (26,39)(present study). In GNT/PLGG tumors with a major oligodendroglioma-like component, careful attention must be paid to tumors demonstrating CD34 expression and calcifications to perform a diagnosis of PLNTY. In our series 7 tumors fulfill these criteria. They include 5 cases with *BRAF* V600E mutation, and two cases with *FGFR2* fusion (*FGFR2-INA* and *FGFR2-KIAA1598*). Interestingly the present case presenting *FGFR2-INA* fusion share with the previous reported cases same pathological features: oligodendroglioma-like component, CD34 expression and calcifications (43). In the present study we also observed two cases with *FGFR3-TACC3* fusion classified at histology as GG for one and PLGG/GNT for the other. One case showed CD34 expression but no calcification and the other the reverse; therefore, they do not fulfill all criteria for a PLNTY. Importantly the case with intraventricular location displayed numerous chromosomal copy number aberrations (CNAs) and relapsed in contrast to the other. *FGFR3-TACC3* fusion has been previously reported in LGG including PLNTY (20,22,25,44), and one malignant transformation of a PLNTY is on record (44). Since *FGFR3-TACC3* also characterized a subset of malignant diffuse glioma in adults (45), we strongly encourage to follow carefully LGG harboring this fusion. In keeping with previous reports (39,41,46) we record in our series frequent CNAs, the most frequent being gains at chromosome 5 and 7. At last we recorded in our series *NPM1-BRAF* fusion which has not been previously reported in LGG. The auto-inhibitory N-terminal domain of *BRAF* is lacking in the predicted *NPM1-BRAF* fusion protein and various studies have shown that *BRAF* fusions promote MAPK pathway activation by effectuating loss of this domain (47). The *NPM1-BRAF* fusion encompasses almost all of the coding sequence of *NPM1*, coding for nucleophosmin 1, a nucleolar phosphoprotein implicated in several pathways including mRNA transport, chromatin remodeling and genome stability. Recurrent *NPM1-HAUS1* fusions have been reported in acute myeloid leukemias with a similar breakpoint in *NPM1* exon 11 (48). To prove the oncogenicity or specificity of this new *NPM1-BRAF* fusion is beyond the scope of this descriptive study.

To conclude, our study highlights the challenges in the diagnosis of supratentorial tumors with an oligodendroglioma-like component occurring in children and young adults. It shows that these tumors belong to two major group of biological relevance

although the WHO CNS5 classification recognized four entities within this spectrum of tumors. We also suggest a step by step algorithm to achieve the histomolecular diagnosis.

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TABLES

Clinical features	DNET	GG	GNT/PLGG
Gender (<i>n</i> = 72)	12M/7F	9M/5F	22M/17F
Age at surgery (years) (<i>n</i> = 72)	13.3 [4.0 -32.9] (<i>n</i> = 19)	14.8 [0.3-36.6] (<i>n</i> = 14)	14 [0.8-57.2] (<i>n</i> = 39)
Tumor location (<i>n</i> = 72)	Frontal (<i>n</i> = 6) Temporal (<i>n</i> = 10) Other (<i>n</i> = 3)	Frontal (<i>n</i> = 1) Temporal (<i>n</i> = 12) Other (<i>n</i> = 1)	Frontal (<i>n</i> = 5) Temporal (<i>n</i> = 22) Other (<i>n</i> = 12)
Recurrence (<i>n</i> = 63)	1 (<i>n</i> = 16)	2 (<i>n</i> = 14)	6 (<i>n</i> = 33)
Median time between first surgery and recurrence (months) (<i>n</i> = 9)	126.9 (<i>n</i> = 1)	160.5 [107.7-213.3] (<i>n</i> = 2)	52.6 [5.3-70.0] (<i>n</i> = 6)
Median follow-up (months) (<i>n</i> = 62)	36.9 [0.1-126.9] (<i>n</i> = 16)	35.7 [2.3-229.4] (<i>n</i> = 14)	22 [0-126.3] 23 (<i>n</i> = 32)

Table 1: Summary of clinical features

DNT: dysembryoplastic neuroepithelial tumor; GG: ganglioglioma; GNT/PLGG: glioneuronal tumor / paediatric type low-grade glioma; M: male; F: female

Histological and molecular features	DNET (n = 19)	GG (n = 14)	GNT/PLGG (n = 39)	Fisher exact test p value
Specific glioneuronal element	100% (19)	0% (0)	0% (0)	p < 0.0001
Dysplastic neurons	0% (0)	100% (14)	0% (0)	p < 0.0001
Infiltrative growth pattern	37% (7)	78% (11)	56% (22)	p = 0.059
Nodular growth pattern	63% (12)	21% (3)	44% (17)	p = 0.059
Calcification	11% (2)	29% (4)	38% (15)	p = 0.084
Eosinophilic granular bodies	5% (1)	43% (6)	23% (9)	p = 0.033
Inflammation	0% (0)	57% (8)	15% (6)	p < 0.0001
CD34 extravascular immunostaining	11% (2)	86% (12)	49% (19)	p < 0.0001
BRAFV600E mutation	0% (0)	71% (10)	26% (10)	p < 0.0001
FGFR1 alterations (mutation + duplication)	42% (8)	7% (1)	23% (9)	p = 0.247
FGFR1 mutation	21% (4)	0% (0)	2% (1)	p = 0.103
FGFR1 duplication	26% (5)	14% (2)	21% (8)	p = 1.000
Fusion transcript	0	1	8	

Table 2: Summary of histological and molecular features

DNT: dysembryoplastic neuroepithelial tumor; GG: ganglioglioma; GNT/PLGG: glioneuronal tumor / pediatric type low-grade glioma

Transcript fusion	BP partner A	BP partner B	Diagnosis	Age at diagnosis (years)	Tumor location	Growth Pattern	Calcifications	Eosinophilic granular bodies	Inflammation	CD34	Recurrence	Follow-up (months)
FGFR1-TACC1	exon 17	exon 2	GNT/PLGG	4.6	Temporal	Nodular	-	-	+	-	-	21.6
NPM1-BRAF	exon 7	exon 11	GNT/PLGG	5.9	Occipital	Infiltrative	-	-	-	-	NA	NA
RNF130-BRAF	exon 3	exon 9	GNT/PLGG	11.3	Temporal	Nodular	+	-	-	-	-	3.5
FGFR2-KIAA1598	exon 16	exon 7	GNT/PLGG	9.2	Parietal	Nodular	+	+	-	+	NA	NA
FGFR2-INA	exon 17	exon 2	GNT/PLGG	3.1	Temporal	Infiltrative	+	-	-	+	+	46.9
FGFR3-TACC3	exon 17	exon 12	GG	14.8	Temporal	Infiltrative	-	-	-	+	-	37.9
FGFR3-TACC3	exon 17	exon 10	GNT/PLGG	5.1	Intraventricular	Infiltrative	+	-	-	-	+	125.5
TNS3-NTRK2	exon 17	exon 10	GNT/PLGG	44	Temporal	Infiltrative	-	-	-	-	-	0
KCTD16-NTRK2	exon 3	exon 14	GNT/PLGG	5.6	Frontal	Nodular	-	-	-	-	+	69.1

Table 3: Clinical and histological features of patients presenting with a fusion transcript

GG: ganglioglioma; GNT/PLGG: glioneuronal tumor / paediatric type low-grade glioma; NA: not available.

FIGURES

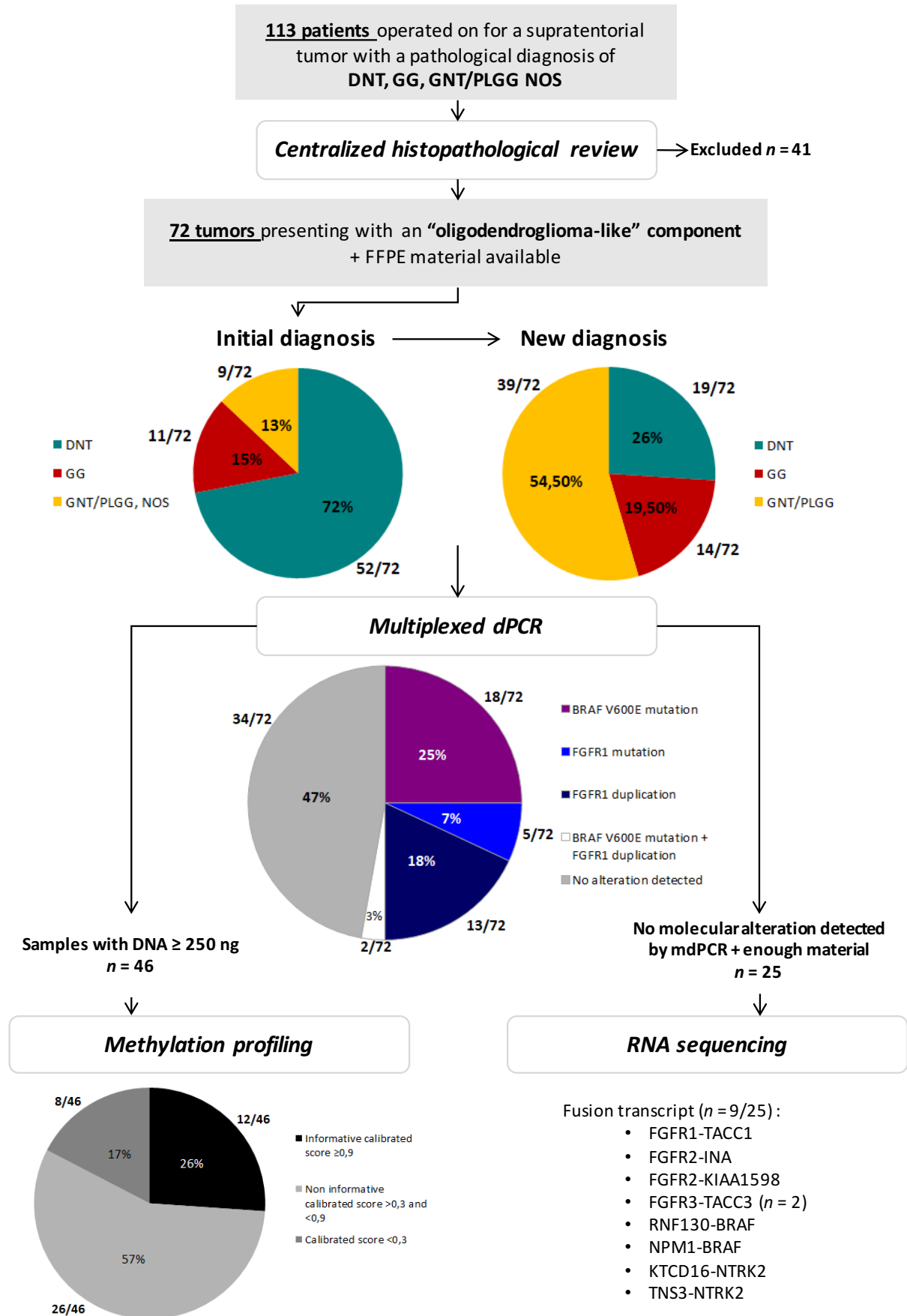


Figure 1: Workflow of the study

Figure 1: ddPCR: digital droplet PCR; DNT: dysembryoplastic neuroepithelial tumor; FFPE: formalin-fixed paraffin embedded; GG: ganglioglioma; GNT/PLGG NOS: glioneuronal tumor / paediatric type low-grade glioma not otherwise specified; GNT/PLGG: glioneuronal tumor / paediatric type low-grade glioma; mddPCR: multiplexed digital droplet PCR.

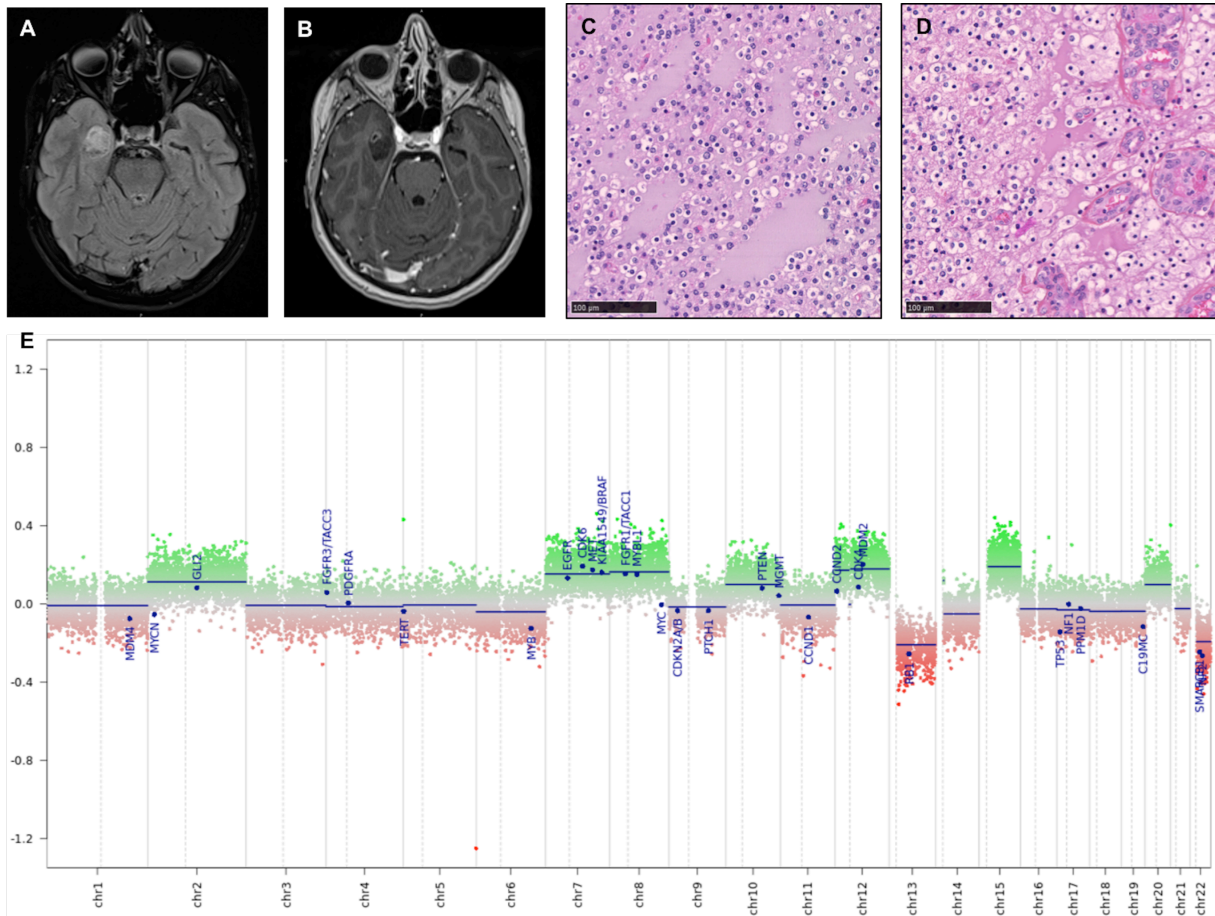


Figure 2: Tumor from a 14 years old female patient, without genetic alteration detected, with a final diagnosis of DNT after DNA-methylation profiling.

The tumor was located in the right temporal lobe and displayed bubbly cystic changes on MRI, associated with focal contrast enhancement (A: FLAIR MRI section, B: T1 with gadolinium injection). Histologically, there was an oligodendroglial-like component associated with pools of mucin without floating neurons (C: HPS section, scale bar: 100 μ m). Vasculature showed microvascular proliferation (D: HPS section, scale bar: 100 μ m). Methylation profiling classified the tumor in LGG DNT with a calibrated score of 0.96. CNV profile was imbalanced (E: CNV plots).

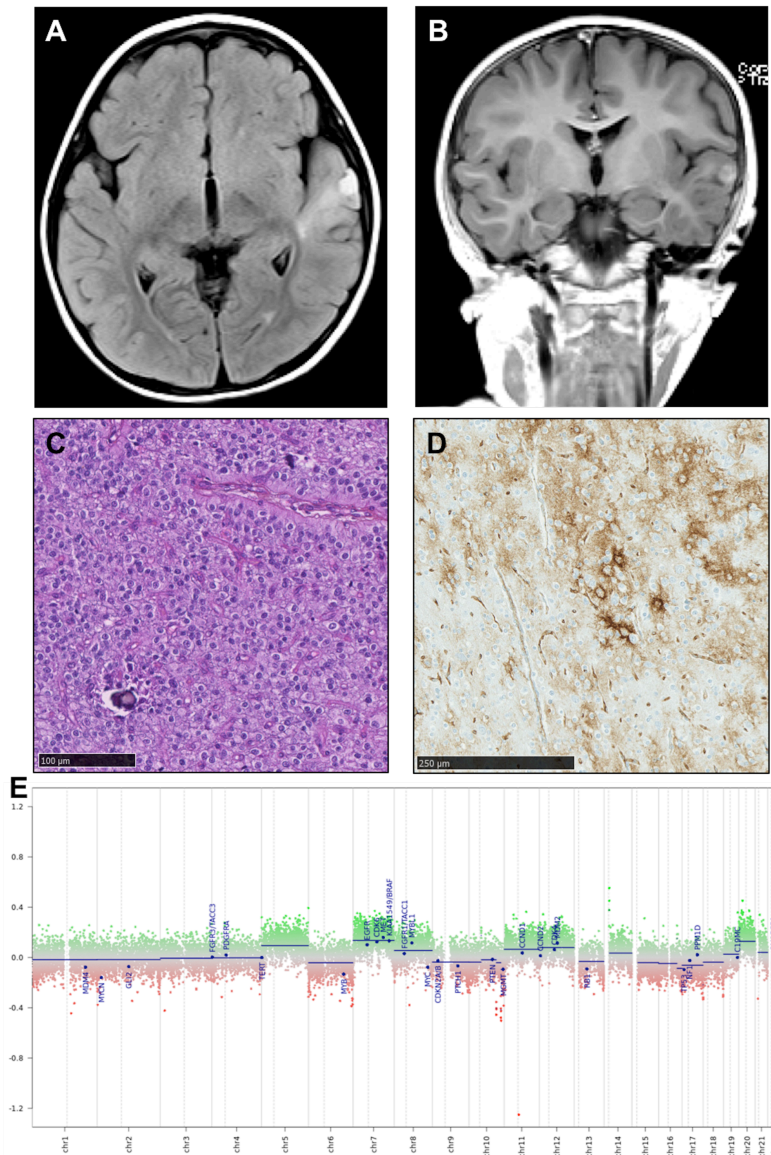


Figure 3: Tumor from a 3 years old female patient, with *FGFR2-INA* fusion, definitively classified as PLNTY.

The tumor was peripherally located in the left temporal lobe, appearing in high signal FLAIR with a nodular contrast enhancement (A: FLAIR MRI section, B: T1 with gadolinium injection). Histologically, there was oligodendrogloma-like with microcalcifications (C: HPS section, scale bar: 100 μ m), and extravascular CD34 expression (D: CD34 immunostaining, scale bar: 250 μ m). Although methylation profiling classified this tumor as LGG GG, with a calibrated score of 0.96, we classified the case as PLNTY in the absence of dysplastic neurons. CNV profile was imbalanced (E: CNV plots).

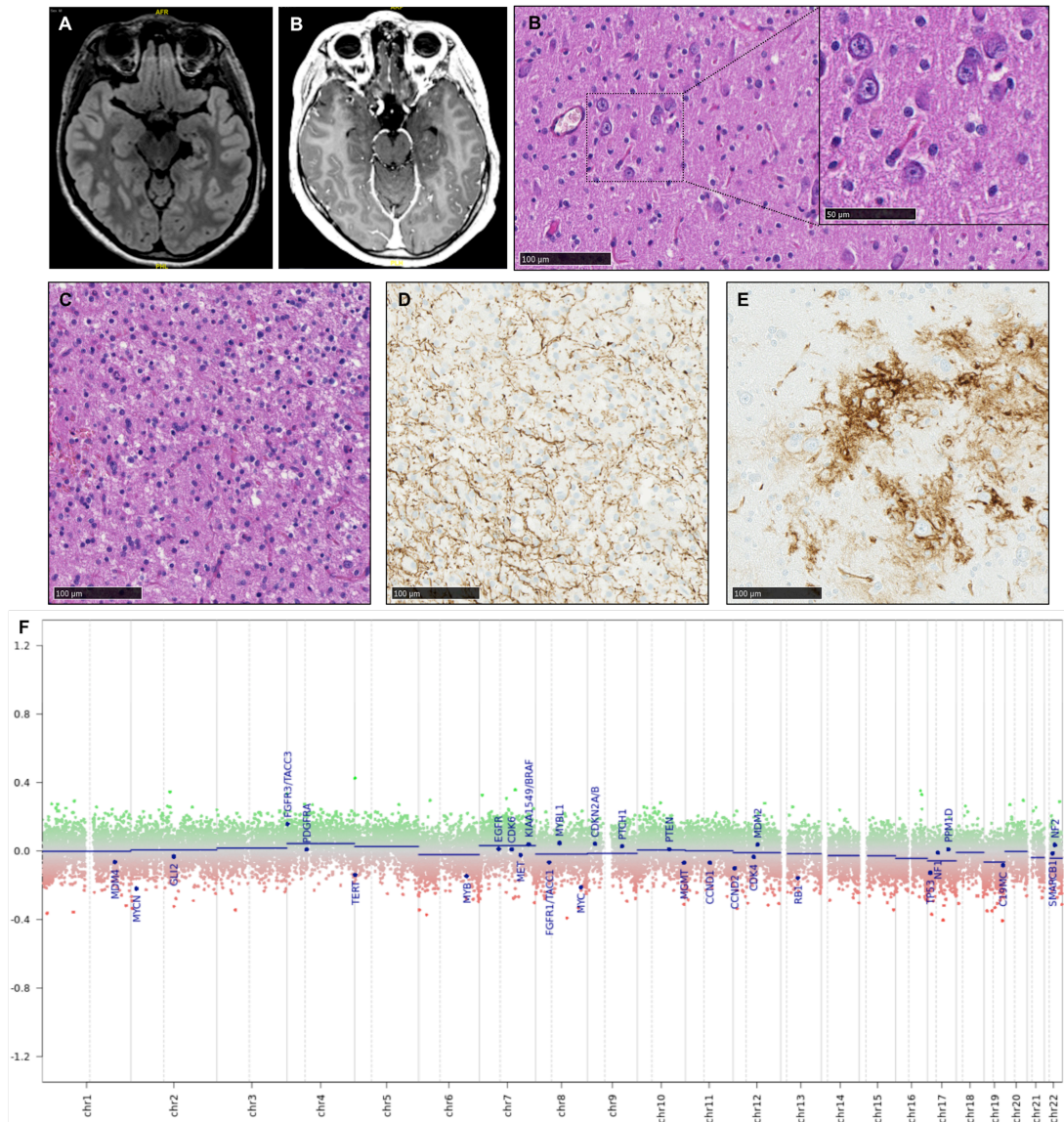


Figure 4: Tumor from a 15 years old male patient, classified as GG associated with a *FGFR3-TACC3* fusion.

The tumor was located in the right temporal lobe, displaying bubbly cystic changes and focal contrast enhancement (A: FLAIR MRI section, B: T1 with gadolinium injection). Histologically, the tumor demonstrated dysplastic neurons (B: HPS section, scale bar: 100 μ m and 50 μ m in the zoom box) an oligodendrogloma-like component (C: HPS section, scale bar: 100 μ m). Immunohistochemistry highlighted an infiltrative growth pattern (D: neurofilament immunostaining, scale bar: 100 μ m) and demonstrated extravascular CD34 immunostaining (E: CD34 immunostaining, scale bar: 100 μ m). Methylation profiling classified the tumor as LGG GG with a calibrated score of 0.89. CNV profile was balanced (F: CNV plots).

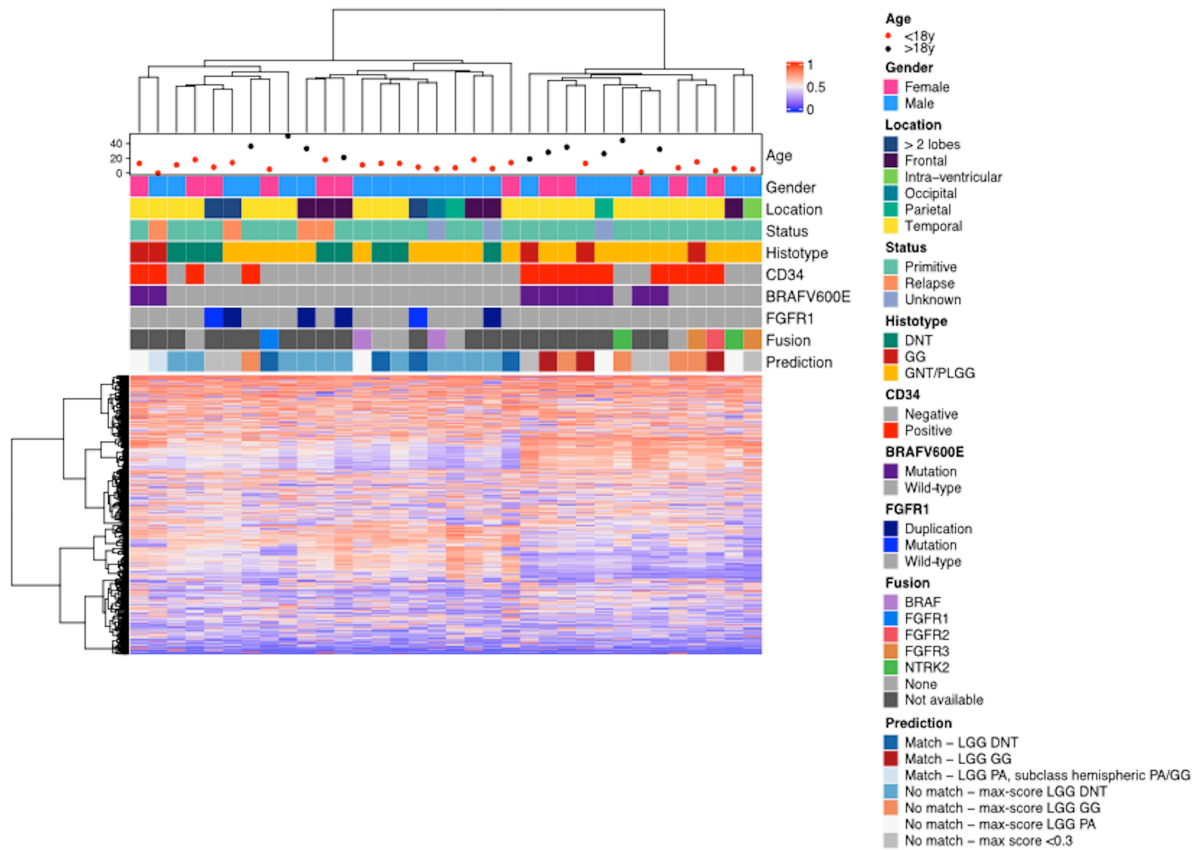


Figure 5: Unsupervised hierarchical clustering

Unsupervised hierarchical clustering revealed two groups. The first one, named LGG/DNT, was enriched in cases classified at histology as DNT (except for 2 GG), CD34 negativity and *FGFR1* alterations. The second one, named LGG/GG, was enriched for cases classified at histology as GG, CD34 positivity and *BRAFV600E* mutation.

DNT: dysembryoplastic neuroepithelial tumor; *GG*: ganglioglioma; *GNT/PLGG*: glioneuronal tumor/paediatric-type low-grade glioma; *LGG DNT*: methylation class low-grade glioma, dysembryoplastic neuroepithelial tumor; *LGG GG*: methylation class low-grade-glioma, ganglioglioma; *LGG PA*: methylation class low-grade glioma, pilocytic astrocytoma; *LGG PA, subclass hemispheric PA/GG*: methylation class low-grade-glioma, pilocytic astrocytoma, subclass hemispheric pilocytic astrocytoma/ganglioglioma.

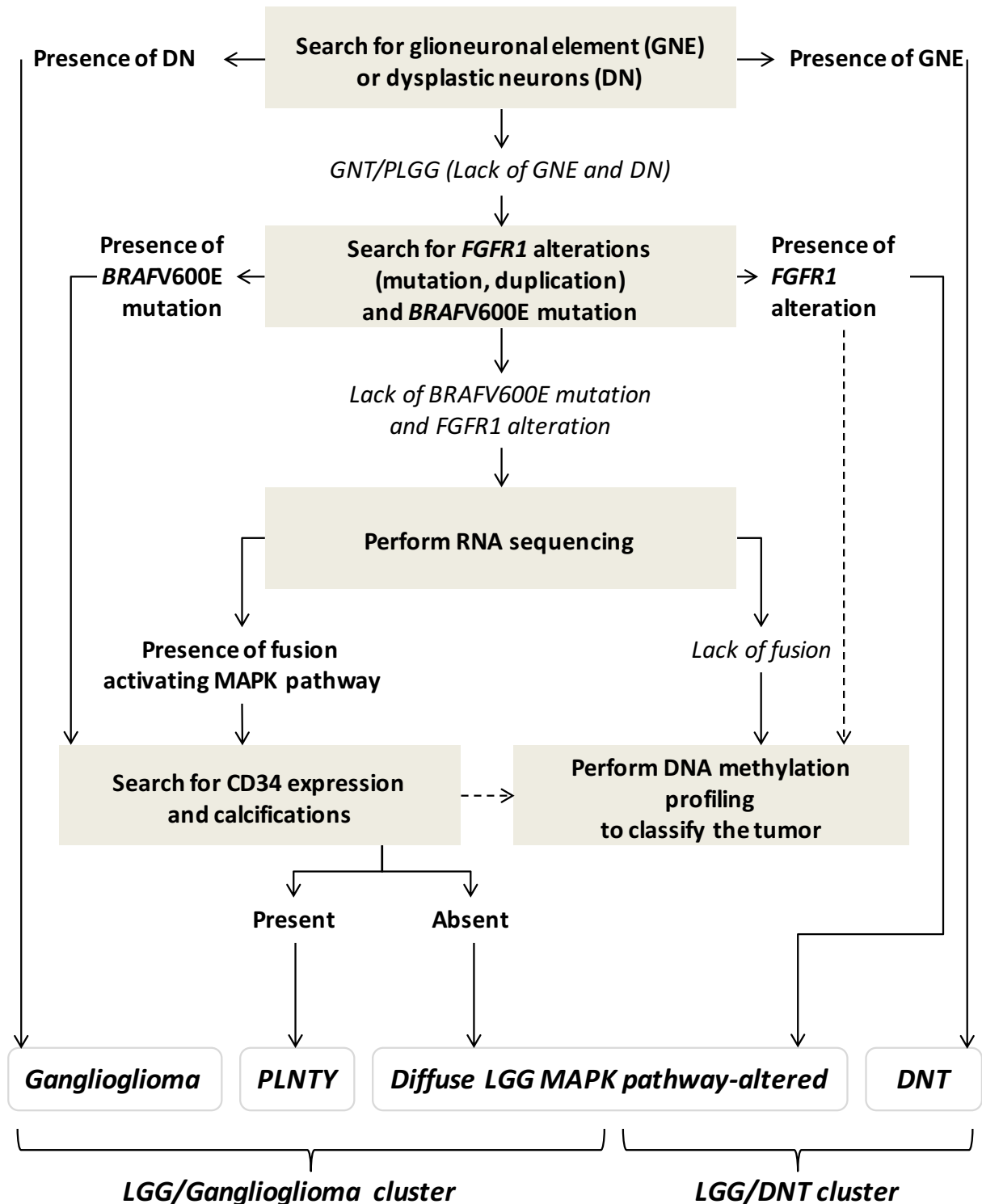
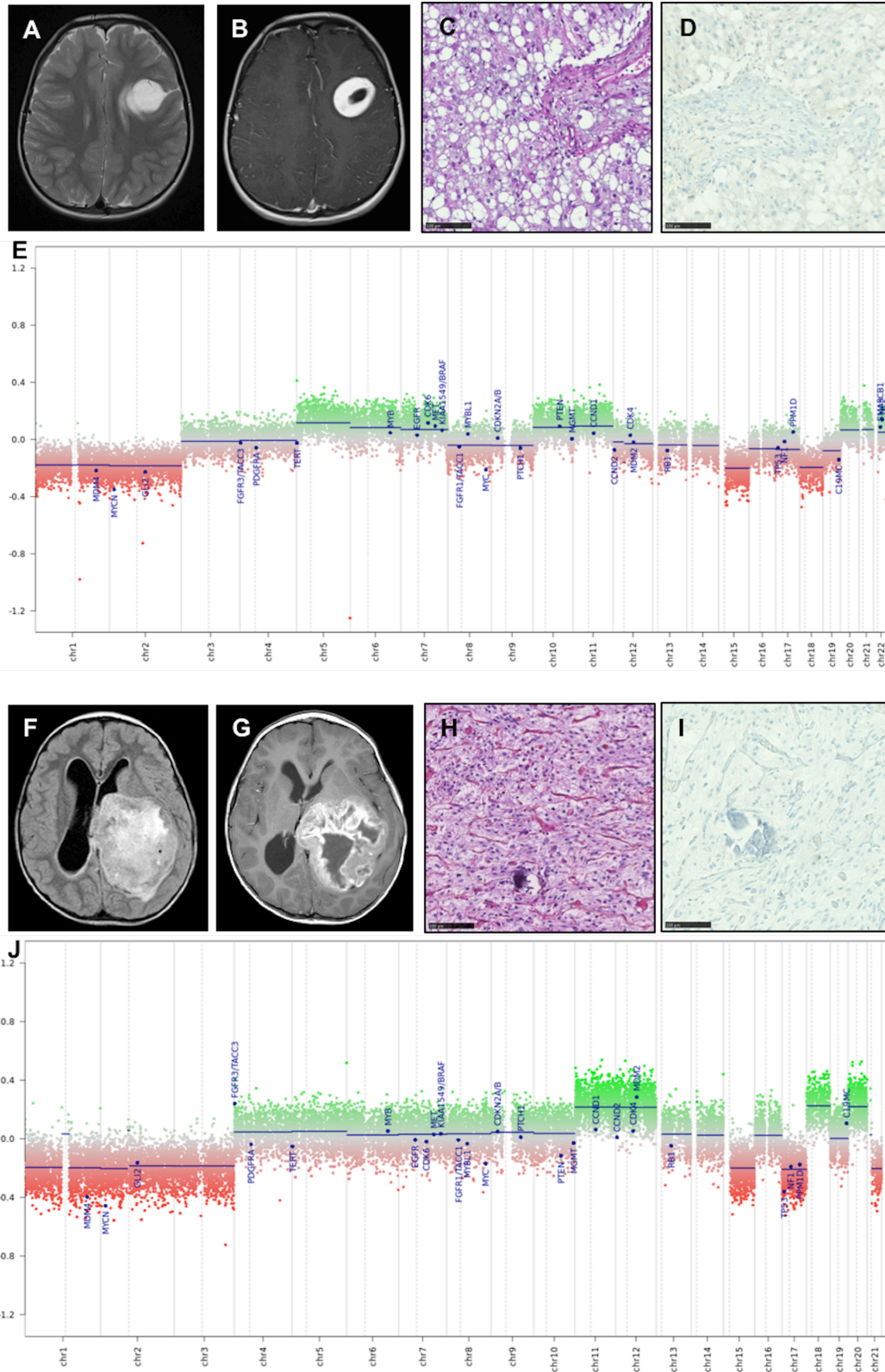


Figure 6: Proposed decision tree

DN: dysplastic neurons; DNT: dysembryoplastic neuroepithelial tumor; GNE: specific glioneuronal element; LGG: low-grade glioma; LGG/DNT: low-grade glioma/dysembryoplastic neuroepithelial tumor; PLNTY: polymorphous low-grade neuroepithelial tumor of the young.

SUPPLEMENTARY FIGURES



Supplementary figure 1: Cases of a 3 years old male with a *KCTD16-NTRK2* fusion (A-E) and a 5 years old male with a *FGFR3-TACC3* fusion (F-J), both definitively classified as diffuse MAPK pathway altered gliomas.

Supplementary figure 1: For the first case (A-E), the tumor was located in the left frontal cortex with contrast enhancement (A: FLAIR MRI section; B: T1 with gadolinium injection MRI section). At histology, there was a circumscribed oligodendroglioma-like lesion with massive calcifications (C: HPS section, scale bar: 100 μ m; D: neurofilament immunostaining, scale bar: 100 μ m) and negative for CD34 (not shown). Methylation profiling found a max score of 0,55 for LGG PA methylation class. CNV profile was imbalanced (E: CNV plots). The second case (F-J) presented as a massive intraventricular tumor, partially cystic with contrast enhancement (F: FLAIR MRI section, G: T1 with gadolinium injection MRI section). At histology there was a circumscribed oligodendroglioma-like lesion with microcalcifications and a hyaline stroma (H: HPS section, scale bar: 100 μ m; I: neurofilament immunostaining, scale bar: 100 μ m) and CD34 immunostaining was negative (not shown). Methylation profiling could not assign a methylation class (calibrated score < 0.3). CNV was imbalanced (J: CNV plots).

METAIS, Alice – Challenges in the diagnosis of supratentorial tumors with an oligodendroglioma-like component occurring in children and young adults

45 feuilles., 7 illustrations., 3 tableaux, 30 cm.- Thèse : (Médecine) ; Rennes 1; 2021 ; N° .

Les gliomes diffus de bas grade de sous-type pédiatrique (PLGG) et les tumeurs glioneurales (GNT) atteignent préférentiellement les enfants et les jeunes adultes et sont à l'origine d'une épilepsie pharmaco-résistante. Histologiquement ces tumeurs sont souvent caractérisées par la présence d'un contingent glial « oligo-like », en particulier dans les gangliogliomes (GG), les tumeurs dysembryoplasiques neuro-épithéliales (DNT) ainsi que dans deux entités récemment décrites : les tumeurs neuro-épithéliales polymorphes du sujet jeune (polymorphous neuroepithelial tumor of the young, PLNTY) et les gliomes diffus de bas grade avec altération des MAPK kinases. De plus ces tumeurs ont en commun des altérations moléculaires activatrices de la voie des MAPK kinases. De part ces caractères communs les PLGG et GNT sont particulièrement difficiles à classer. Dans le but de mieux caractériser ces tumeurs, nous avons réalisé une étude rétrospective multicentrique portant sur 72 prélèvements chirurgicaux et biopsiques de tumeurs gliales et glio-neurales de localisation supratentorielle de bas grade réalisés entre 2002 et 2020. Dans tous les cas une relecture anatomopathologique centralisée a permis de classer ces tumeurs en trois grands groupes : DNT (présence d'une composante glioneuronale spécifique, n = 19), GG (présence de cellules ganglionnaires dysplasiques, n = 14) et GNT/PLGG (n = 39). Trente-huit cas sur les 72 analysés présentait une altération moléculaire détectée par PCR digitale multiplexe (mdPCR) (mutation *BRAFV600E*, mutations et duplication de *FGFR1*). Parmi les cas 34 cas ne présentant pas d'altération, 9/26 avaient un transcrit de fusion détecté par RNAseq. Quarante-six cas ont pu être analysés par profil de méthylation, parmi lesquels 12 avaient un score de méthylation supérieur à 0,9 (26%). Un score non informatif (entre 0,9 et 0,3) était retrouvé dans 26 cas (56,5%). Pour 8 cas le score de méthylation était inférieur à 0,3 (17,5%). Le clustering hiérarchique non supervisé a montré l'existence de deux groupes entre lesquels les GNT/PLGG se répartissaient équitablement. Le groupe LGG/GG réunissait la plupart des tumeurs classées histologiquement en GG, avec une mutation *BRAFV600E*, une positivité du CD34 et dont le profil de méthylation répondait à la classe de méthylation LGG GG. Le groupe LGG/DNT réunissait les DNT, avec altération de *FGFR1*, une négativité du CD34 et répondant à la classe de méthylation LGG DNT. Sept cas ont été reclassés en PLNTY. La démarche diagnostique a été résumée dans un algorithme.

Cette étude souligne la difficulté à bien classer les tumeurs supratentorielles oligo-like chez les sujets jeunes. Enfin, bien que quatre entités soient actuellement définies pour ce type de tumeurs par la 5^{ème} classification de l'OMS, nos résultats indiquent qu'elles se répartissent en deux groupes biologiquement distincts.

Rubrique de classement : ANATOMIE ET CYTOLOGIE PATHOLOGIQUES

Mots-clés : paediatric-type low-grade glioma, glioneuronal tumor, dysembryoplastic neuroepithelial tumor, polymorphous low-grade neuroepithelial tumor of the young, diffuse glioma MAPK pathway altered, long-term epilepsy associated tumor

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Président : Mme le Professeur Nathalie RIOUX-LECLERCQ

JURY : Assesseurs : Mme le Professeur Dominique FIGARELLA-BRANGER (directeur de thèse)

Mme le Professeur Pascale VARLET

Mme le Professeur Audrey ROUSSEAU

Mr le Professeur Laurent RIFFAUD

Mr Pierre-Jean LE RESTE