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LETTER TO THE EDITOR

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Disseminated diffuse midline gliomas, H3K27-altered mimicking diffuse leptomeningeal glioneuronal tumors: a diagnostical challenge!



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Diffuse midline gliomas (DMG) are divided into four subtypes depending on their molecular characteristics, and/or location: DMG, H3.3 K27-mutant; DMG, H3.1 or H3.2 K27—mutant; DMG, H3-wildtype, with EZHIP overexpression and DMG, *EGFR*-altered [1]. Leptomeningeal dissemination at diagnosis has been variably reported depending on the series (up to 42%) [2]. Very little genetic and epigenetic data is available for those disseminated cases, with one case harboring a concomitant *FGFR1* mutation [3] and another a 1p deletion [4]. Consequently, their relationship with diffuse leptomeningeal glioneuronal tumors (DLGNT), remains unclarified.

Herein, we describe the histopathological, neuroradiological and molecular (including DNA-methylation profiling) features of three initially disseminated H3K27altered tumors with glioneuronal features including two cases with an associated MAPK pathway alteration.

The cases concerned three females, aged 14, 13 and 40-year-old (see Additional file 1: Table S1). At the initial diagnosis, in all cases, the tumors were disseminated with supra-tentorial and infra-tentorial leptomeningeal

¹ Department of Neuropathology, GHU Paris Psychiatrie Neurosciences, Sainte-Anne Hospital, 1, rue Cabanis, 75014 Paris, France Full list of author information is available at the end of the article infiltration. An intraparenchymal mono-thalamic involvement was observed in cases 1 and 2; case 3 did not present any intraparenchymal involvement, until the end of the follow-up (Fig. 1). A leptomeningeal biopsy was performed in all cases. Histopathologically, all tumors presented a glioneuronal immunophenotype, and, one of them also had numerous microcalcifications (Fig. 2 and Additional file 2: Table S2). A 1p deletion was evidenced in case 1 and therefore a diagnosis of DLGNT was suggested (Fig. 2D). NGS sequencing showed a FGFR1 N546K mutation (case 1), a BRAF V600E mutation (case 2) and a H3F3A K27M mutation (case 3). The DNA-methylation profiling classified cases 1 and 3 as DMG, H3K27-altered, subtype H3K27M/EZHIP overexpressing (calibrated scores 0.99 and 0.82 respectively) and case 2 as DMG H27K27-altered, subtype EGFR-altered (calibrated score 0.95) (Additional file 3: Fig. S1). Complementary analyses found a loss of H3K27me3 (in all cases), an EZHIP overexpression (cases 1 and 2) (Fig. 2), but no EGFR alteration (all exons were tested by whole exome sequencing, and an amplification was ruled out by FISH analyses) was evidenced. Case 1 received several lines of chemotherapy and craniospinal radiation therapy but passed away 16 months after the initial diagnosis, whereas the case 2, treated by chemotherapy and targeted anti-BRAF therapy, is still alive with a stable disease, 7 months after the initial diagnosis. The patient 3 received chemotherapy



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and craniospinal irradiation but died 4 months after the diagnosis.

DLGNTs are glioneuronal tumors molecularly defined by a chromosome arm 1p deletion and a MAPK pathway alterations [1]. Contrary to what their name suggest, they can present a parenchymal component, which can include a thalamic location, with or without leptomeningeal involvement [5]. The already published H3K27M-mutant cases with a disseminated radiological presentation (including a case with a 1p deletion) raises the question of a potential overlap between DLGNT and DMG [3, 4, 6]. However, those cases did not have DNA-methylation analysis, and their relationship to DMG, H3 K27–altered remains open in the last version of the World Health Organization classification [1]. Herein, we present three initially disseminated leptomeningeal tumors, including one case with a 1p deletion



Fig. 2 Histopathological and molecular features. Case #1 **A** A glial proliferation with oligo-like features and one microcalcification (HPS, magnification × 400). **B** Diffuse expression of Olig2 (magnification × 400). **C** Diffuse synaptophysin immunoreactivity without true neuropil islands (magnification × 400). **D** 1p deletion by FISH analysis (green signal for 1q25 and orange signal for 1p36, magnification × 400). **E** EZHIP overexpression in all tumor cells (magnification × 400). Case #2 **F** A glial proliferation with astrocytic features (magnification × 400). **G** Diffuse expression of Olig2 (magnification × 400). **H** Diffuse synaptophysin immunoreactivity without true neuropil islands (magnification × 400). **H** Diffuse synaptophysin immunoreactivity without true neuropil islands (magnification × 400). **I** Loss of the trimethylation H3K27me3 in tumor cells (magnification × 400). **J** EZHIP overexpression in all tumor cells (magnification × 400). **G** Diffuse synaptophysin immunoreactivity without true neuropil islands (magnification × 400). **I** Loss of the trimethylation H3K27me3 in tumor cells (magnification × 400). **J** EZHIP overexpression in all tumor cells (magnification × 400). Case #3 **K** A high-grade glial proliferation with several mitoses and necrosis (magnification × 400). **L** Immunoreactivity for neurofilament in a subset of tumor cells (magnification × 400). **N** Loss of the trimethylation H3K27me3 in tumor cells (magnification × 400). **O** H3K27M immunopositivity in all tumor cells (magnification × 400). Black scale bars represent 50 µm

and two with *BRAF/FGFR1* mutations, classified as DMG using DNA-methylation profiling. Like patients with DMG-H3K27 mutant with concomitant *BRAF* or *FGFR1* mutation, the two current disseminated cases H3K27-altered (one with EZHIP overexpression) with a MAPK mutation were older than classical DMG and histologically presented a glioneuronal immunophenotype and /or microcalcifications [7, 8]. The case 2, classified as DMG, H3K27-altered (*EGFR*-mutant) proven by DNA-methylation analysis,

represents the first example of a disseminated presentation of this typically bithalamic tumor type [9]. Another particularity of this case was its having a *BRAF* V600E mutation without an *EGFR* alteration (as 20%, 8/40 of all published cases), representing the second example of this discrepancy between genetic and epigenetic results (the first being reported as unilateral thalamic) [9]. Gliomas with concomitant mutations of H3K27M and *BRAF/FGFR1* are supposed to be associated with a better prognosis than other DMG, H3K27-altered according to some publications [7, 8]. As a result, it can be suggested that these molecular alterations (MAPK and H3K27M/EZHIP alterations) confer a different biological behavior, with a metastatic phenotype and/ or a slower local progression ultimately allowing the development of disseminated lesions. Arguing for this hypothesis, a previously published monothalamic tumor classified as ganglioglioma, H3K27M- and *BRAF* V600E-mutant presented secondary leptomeningeal dissemination 7 years after the initial diagnosis [10]. Further data is needed to understand this disseminated phenotype in detail.

In summary, we showed that despite the histopathological and molecular overlaps with DLGNT, DMG, H3K27altered may be found to have, in exceptional cases, an initial disseminated radiological presentation.

Supplementary Information

The online version contains supplementary material available at https://doi. org/10.1186/s40478-022-01419-3.

Additional file 1. Table S1: Summary of clinical data of cases from current series.

Additional file 2. Table S2: Summary of histopathological and molecular data of cases from current series.

Additional file 3: Fig. S1. Methylation-based t-SNE distribution. t-distributed stochastic neighbor embedding (t-SNE) analysis of DNA methylation profiles from the investigated tumors alongside selected reference samples. Reference DNA methylation classes: diffuse midine glioma H3 K27M mutant/EZHIP overexpressing (DMG_K27), diffuse midline glioma *EGFR_*altered (DMG_EGFR), glioblastoma, *IDH* wildtype, H3.3 G34 mutant (GBM_G34), pediatric glioblastoma, IDH wildtype, subclass *MYCN* (GBM_pedMYCN), glioblastoma, *IDH* wildtype, subclass *MYCN* (GBM_pedMYCN), glioblastoma, *IDH* wildtype, subclass RTK1 (GBM_ RTK1), glioblastoma, *IDH* wildtype, subclass RTK2 (GBM_RTK2), pediatric glioblastoma, *IDH* wildtype, subclass RTK2 (GBM_PedRTK2), g

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Author contributions

ATE, AS, MG, SB, JB, P, JG, VDR and NB compiled the MRI and clinical records; ATE, AS, EUC, AM, FC, AE and PV conducted the neuropathological examinations; ATE, AS, EUC, YN, DC and PV conducted the molecular studies; ATE, AE, LH and PV drafted the manuscript; all authors reviewed the manuscript.

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Declarations

Competing interests

The authors declare that they have no conflict of interest directly related to the topic of this article.

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