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## Circumscribed/non-diffuse histology confers a better prognosis in H3K27M-mutant gliomas

Drew Pratt<sup>1</sup>, Siva Kumar Natarajan<sup>1</sup>, Adam Banda<sup>1</sup>, Caterina Giannini<sup>2</sup>, Pankaj Vats<sup>3</sup>, Carl Koschmann<sup>4</sup>, Rajen Mody<sup>4</sup>, Arul Chinnaiyan<sup>3</sup>, and Sriram Veneti<sup>1</sup>

<sup>1</sup>Department of Pathology, University of Michigan, Ann Arbor, MI, USA

<sup>2</sup>Laboratory Medicine and Pathology, Mayo Clinic, Rochester, Minnesota, USA

<sup>3</sup>Michigan Center for Translational Pathology, Ann Arbor, MI, USA

<sup>4</sup>Department of Pediatrics, University of Michigan School of Medicine, Ann Arbor, MI, USA

Diffuse midline gliomas harboring a recurrent H3 lysine 27-to-methionine (p.Lys27Met, H3K27M) constitute a recently defined pathologic entity with a particularly poor prognosis. They mainly occur in midline structures, such as the pons and thalamus of children and young adults, and are highly infiltrative [2]. More recently, case reports have described the H3K27M mutation in circumscribed (non-diffuse) gliomas, many of which are low-grade (e.g., pilocytic astrocytoma, ganglioglioma) [1, 3–5] (additional references are provided in Online Resource 1). Because of the rarity of these tumors, it is unknown whether they carry the poor clinical outcome ascribed to H3K27M-mutant infiltrating gliomas of the midline. Here, we address this gap in our knowledge by performing an integrated meta-analysis on collated clinical and pathologic data from published studies, data repositories, and collaborative efforts.

A systematic search of the literature was performed from 2012 to November, 2017. Tumors were categorized based on diagnosis, location, histologic grade, growth pattern, and H3K27M mutation status. IDH 1/2-mutant diffuse gliomas were excluded to avoid bias arising from the good prognosis attributed to this mutation. Circumscribed gliomas included pilocytic astrocytoma, ganglioglioma/glioneuronal tumor/ganglion cell tumor, pleomorphic xanthoastrocytoma, and ependymoma. Data from The Cancer Genome Atlas (TCGA) (<http://cancergenome.nih.gov/>) was obtained through the cBioPortal and PedcBioPortal for Cancer Genomics. Factors extracted included age, sex, overall survival, tumor location, histopathologic diagnosis and WHO grade. Patient samples were then cross-referenced across studies to filter out duplicate data. Cases were also acquired from our in-house sequencing efforts and through collaboration with the Mayo Clinic in Rochester, Minnesota. Co-occurring mutations were also documented. The endpoint extracted from all data sources was overall survival (OS). Survival functions were estimated using the Kaplan-Meier method and differences analyzed with the Log-rank (Mantel-Cox) test using GraphPad

Corresponding Author: Sriram Veneti, MD, PhD, Department of Pathology, University of Michigan, Ann Arbor, MI 48104, Phone: (734) 763-0674, [sveneti@med.umich.edu](mailto:sveneti@med.umich.edu).

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Prism software (version 7). The Cox-proportional hazards model was used to calculate hazard ratios (HR) using SPSS (version 24, IBM). All studies were approved by ethics committees at the respective institutions. See Online Resource 1 for further details of the methods.

Among published studies and through institutional collaboration, we identified 28 cases of H3K27M-mutant circumscribed gliomas (grade I: n=19; grade III, n=9). Histopathology included pilocytic astrocytoma (n=7), ganglioglioma (n=10), anaplastic ganglioglioma (n=3), glioneuronal tumor (n=1), anaplastic glioneuronal tumor (n=1), ganglion cell tumor (n=1; Fig. 1a–d), anaplastic ependymoma (n=3), and circumscribed glioma, not further specified (n=2) (see Online Resource 2 for references and case details). Strikingly, more than 96% (n=26/27 cases with location provided) of H3K27M-mutant circumscribed gliomas occurred within the midline, including the brainstem (n=7), thalamus (n=5), cerebellum (n=2), spinal cord (n=8) and other midline regions (peduncle, posterior fossa, midline-not further specified; n=4) (Fig. 1g). Of the remaining two cases, one was reported in the cerebrum, while the location was not specified for the other. H3K27M mutations occurred in *H3F3A* (n=21), *HIST1H3B* (n=1), *HIST1H3C* (n=1), and five cases were detected by immunohistochemistry. Information on co-occurring somatic mutations were available in 50% (14/28) of cases. The most frequent alteration was *BRAFV600E* (n=7) mutations followed by *ATRX* (n=3), *FGFR1 N546K* (n=2), and *NF1* (n=2) (see Online Resource 2). Copy number alterations were reported in chromosomes 13 and 17 in two tumors.

Survival information was available for 21 cases (grade I: n=14; grade III: n=7). Univariate analysis of these tumors demonstrated poor OS compared to H3-wildtype circumscribed gliomas (n=59; grade I: n=51; grade III: n=8) (Log rank,  $p<0.0001$ ), but a significantly improved OS compared to H3/IDH-wildtype (Log rank,  $p=0.025$ ) and H3K27M-mutant diffuse gliomas (Log rank,  $p<0.0001$ ) (Fig. 1e). This association remained significant after matching tumors for grade (grade I, Log-rank,  $p<0.0001$ ; Fig. 1f) and treatment (chemotherapy and/or radiotherapy, Log-rank,  $p<0.0001$ ; Supp. Fig. [Online Resource 3]). Cox regression analysis with age, sex, grade, and mutation status included as covariates showed the H3K27M mutation remained an independent predictor of OS (HR, 5.980; 95% CI, 1.839–19.445;  $p=0.003$ ; Fig. 1h).

These results confirm that the poor prognosis of the H3K27M mutation also extends to circumscribed gliomas. While H3K27M-mutant circumscribed gliomas show poor survival compared to H3-wildtype circumscribed gliomas, prognosis remains significantly better than both H3K27M-mutant and H3-wildtype diffuse gliomas. This has important implications regarding the current WHO grading of H3K27M-mutant diffuse gliomas, which are uniformly labeled as grade IV. However, we note that an important limitation to our study is the relatively short follow-up duration, largely owing to the rarity of these tumors. We also show that H3K27M-mutant circumscribed gliomas show a similar predilection for midline regions. Our data suggest that midline circumscribed gliomas should be routinely tested for H3K27M mutations.

## Supplementary Material

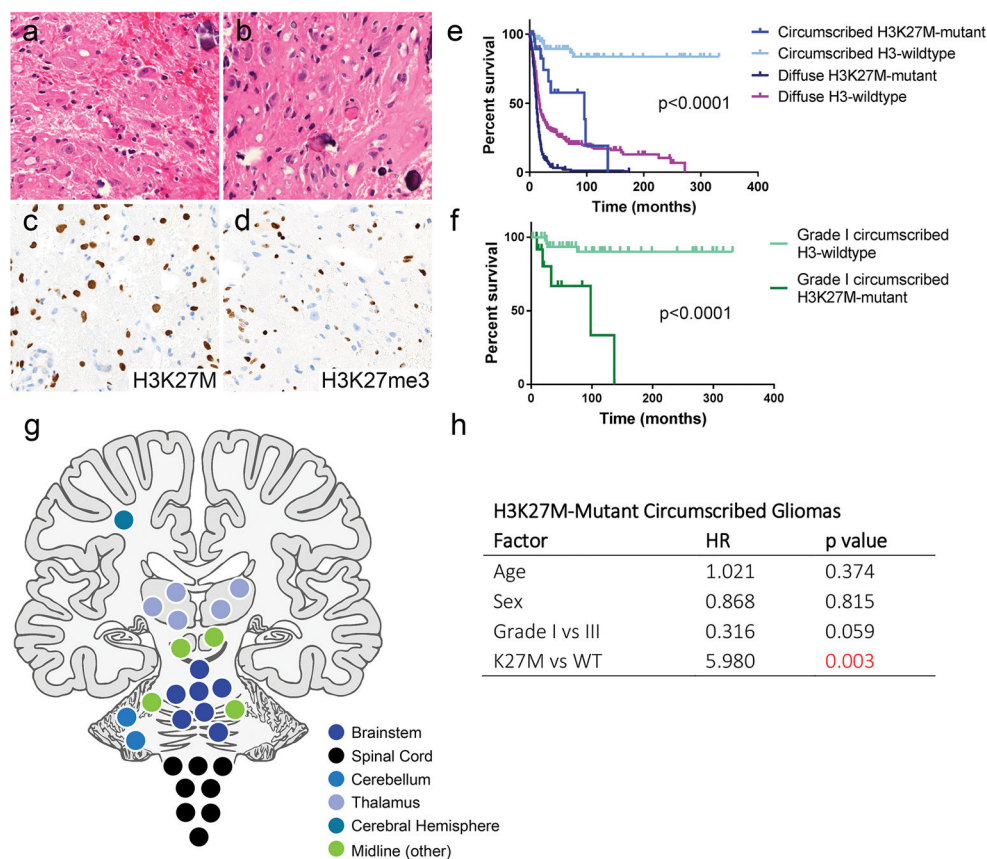
Refer to Web version on PubMed Central for supplementary material.

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**Fig. 1.** Histopathology, localization, and survival analyses in H3K27M-mutant circumscribed gliomas.

**a–d.** Representative histology of a ganglion cell tumor (**a–b**, H&E) with nuclear expression of the H3K27M mutant protein (**c**) and concurrent loss of H3K27me3 (**d**)

**e.** Kaplan-Meier estimation shows stratification of overall survival based on growth pattern and H3K27M mutation status (circumscribed glioma H3-wildtype, n=63; circumscribed glioma H3K27M-mutant, n=21; diffuse glioma H3/IDH-wildtype, n=550; diffuse glioma H3K27M-mutant, n=432).

**f.** H3K27M mutation demonstrated a worse prognosis compared to H3-wildtype tumors in grade I-matched circumscribed gliomas.

**g.** Locations of H3K27M-mutant circumscribed gliomas.

**h.** Cox regression analysis.