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IDH mutation status and role of WHO grade and mitotic index in overall survival in grade II–III diffuse gliomas

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Abstract

Diffuse gliomas are up till now graded based upon morphology. Recent findings indicate that isocitrate dehydrogenase (IDH) mutation status defines biologically distinct groups of tumors. The role of tumor grade and mitotic index in patient outcome has not been evaluated following stratification by IDH mutation status. To address this, we interrogated 558 WHO grade II–III diffuse gliomas for *IDH1/2* mutations and investigated the prognostic impact of WHO grade within IDH-mutant and wild-type tumor subsets independently. The prognostic impact of grade was modest in IDH-mutant [hazard ratio (HR)=1.21, 95% confidence interval (CI)=0.91–1.61] compared to IDH-wild type tumors (HR=1.74, 95% CI=0.95–3.16). Using a dichotomized mitotic index cut-off of 4/1000 tumor cells, we found that while mitotic index was significantly associated with outcome in IDH-wild type tumors (log-rank $p < 0.0001$, HR=4.41, 95% CI=2.55–7.63), it was not associated with outcome in IDH-mutant tumors (log-rank $p = 0.5157$, HR=1.10, 95% CI=0.80–

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Conflict of Interest

The authors declare they have no conflict of interest.

1.51), and could demonstrate a statistical interaction ($p < 0.0001$) between IDH mutation and mitotic index (i.e. suggesting that the effect of mitotic index on patient outcome is dependent on IDH mutation status). Patient age, an established prognostic factor in diffuse glioma, was significantly associated with outcome only in the IDH-wild type subset, and consistent with prior data, 1p/19q co-deletion conferred improved outcome in the IDH-mutant cohort. These findings suggest that stratification of grade II–III gliomas into subsets defined by the presence or absence of IDH mutation leads to subgroups with distinct prognostic characteristics. Further evaluation of grading criteria and prognostic markers is warranted within IDH-mutant versus IDH-wild type diffuse grade II–III gliomas as independent entities.

Keywords

diffuse glioma; IDH; 1p/19q; outcome; WHO grade; pHH3

Introduction

Diffuse gliomas are common and variably aggressive primary central nervous system tumors, currently stratified by the World Health Organization (WHO) into three malignancy grades: II, III and IV. Glioblastoma (WHO grade IV) is generally classified as a diffuse glioma of astrocytic morphology with microvascular proliferation and/or necrosis. For WHO grades II and III diffuse gliomas classification is based on morphologic determination of cell type (i.e. astrocytic, oligodendroglial, mixed morphology). Determination of grade (II versus III), is made primarily on the basis of tumor proliferative activity (mitotic activity), along with additional criteria of increased cellularity and nuclear atypia. Additional factors, such as microvascular proliferation and tumor necrosis play a role in the grading of oligodendroglial and oligoastrocytic tumors [41]. Regarding proliferative activity in diffuse glioma, there is flexibility in the interpretation of the proposed WHO grading criteria, without strict criteria for delineation of mitotic figure cut-offs to distinguish grade II from grade III tumors. This can result in a great deal of interobserver variability in the determination of grade [62]. This consideration has become relevant for clinical practice because current treatment guidelines [46] and ongoing clinical trials [62] are primarily stratified by glioma morphology and WHO grade.

Isocitrate dehydrogenase (IDH) mutations and 1p/19q co-deletion have proven significant prognostic and predictive (1p/19q co-deletion) biomarkers that greatly impacted the field of neuro-oncology [29,7,8,63]. IDH mutations precede 1p/19q co-deletion [67], are associated with younger age, and are prognostic in most WHO grade III and IV diffuse gliomas [21,26,72,69,59,68,65,4] but their prognostic impact in low-grade diffuse glioma (WHO grade II) has not been completely clarified [24,45,34,44,1,50,28,20]. Additional signature lesions within the IDH-mutated grade II–III gliomas include mutations in *ATRX* (common in 1p/19q non-co-deleted tumors) and *TERT* promoter (common in 1p/19q co-deleted tumors) [32,33,31,70]. There is evidence that grade II and III diffuse gliomas are comprised of molecularly distinct subgroups based on the presence or absence of IDH mutations [17,73]. On the other hand assessment of IDH mutational and 1p/19q co-deletion status in diffuse glioma is becoming routine in clinical practice and efforts are made to find a way to

integrate molecular and morphological information [42]. From a clinical stand-point and despite investigation of molecular signatures in diffuse glioma, the impact of the conventional WHO grade and mitotic index in low grade and anaplastic diffuse glioma following IDH molecular stratification is not established, and further efforts to integrate IDH mutational and 1p/19q status in a clinical context may improve stratification of patient risk groups.

The main purpose of this study was to evaluate the role of tumor grading in predicting patient outcome in grade II and III diffuse gliomas stratified by IDH mutation status. To accomplish this we interrogated a large cohort of low grade and anaplastic diffuse gliomas to ensure that molecularly-defined subsets could be represented in a robust fashion. Since tumor proliferative activity is a key component of WHO grading criteria to distinguish grade II from grade III gliomas, we also investigated the prognostic role of mitotic index [13] within IDH-mutant and wild-type tumor subsets.

Materials and Methods

Data collection

The study protocol was approved and carried out in accordance with institutional review board guidelines. Formalin-fixed paraffin embedded tissues from primary (non-treated) diffuse gliomas that were WHO grades II and III were retrospectively identified and collected from the files of our institutions: 485/558 cases were obtained from the pathology files at MD Anderson Cancer Center and 73/558 cases were obtained from the VU University Medical Center. Some of the cases from VU University Medical Center/The Netherlands have been previously published in another context [66]. The cases were selected based on sufficient tissue availability (i.e. to provide adequate material for immunohistochemical and molecular testing) and availability of clinical information (i.e. duration of follow-up). Patients with gliomatosis cerebri were not included. Patients with stereotactic biopsies were not included. Slides stained with hematoxylin and eosin (H&E) were reviewed and the diagnosis was confirmed for all cases.

The following data were collected: age (at initial histopathological diagnosis), date of initial surgery, histological subtype of diffuse glioma (astrocytoma, oligodendroglioma, mixed morphology), WHO grade (as per original pathology report confirmed with H&E central review per current 2007 WHO grading criteria), survival status (alive or dead), and date of death or date of last follow-up. Overall survival (OS) was calculated by extracting the date of initial surgery (tissue diagnosis) from the date of last follow-up or death. Data sets are provided in Online resource 1.

Immunohistochemistry

As an initial step for IDH mutational assessment, immunohistochemistry with the anti-IDH1-R132H mutation specific antibody was utilized for sample interrogation. Immunohistochemistry was manually performed with anti-IDH1-R132H mouse monoclonal antibody (Dianova, Hamburg, Germany, clone H09, dilution 1:200) and anti-pHH3 (Ser 10)

rabbit polyclonal antibody (Cell Signaling Technology, MA, USA, catalog#9701L, dilution 1:100) as previously described [51]. All controls were appropriate.

Phospho-HH3 mitotic index (number of pHH3-positive mitotic figures per 1000 tumor cells) was calculated as previously described [13]. Briefly, we selected the best tissue section for each case as the one with the highest tumor density, the lowest amount of inflammation, and the lowest percentage of normal brain. If still present in selected best tissue sections, inflammation-rich areas were avoided for mitotic index assessment. Two experienced neuropathologists (AO, KDA) manually counted mitoses per 1000 tumor nuclei in the highest mitotically active foci. We only counted nuclei accompanied by chromatin condensation, the signature of a mitotic cycle. The uniformly stained positive nuclei and the finely speckled stained nuclei were not counted, as these findings are not part of the mitotic cycle [23]. When discrepant findings were observed [i.e. no mitoses in an anaplastic diffuse glioma which occurred in 21/296 (7%) or mitoses in a grade II diffuse glioma which occurred in 218/262 (83%)] the controls and the original H&E were reviewed and the mitotic index was confirmed.

IDH sequencing and 1p/19q analysis

All cases that were negative for the *IDH1-R132H* mutation by immunohistochemistry were interrogated by targeted sequencing for *IDH1* exon 4 (codon 132) and *IDH2* exon 4 (codons 172). Sanger sequencing was performed at the MD Anderson Cancer Center Genomics Core Facility. Some of the cases (those obtained via VU University Medical Center) had been previously analyzed and reported for 1p/19q analysis using low-pass whole genome sequencing [66]. Analysis for 1p/19q was performed on MD Anderson samples using either fluorescent in situ hybridization or quantitative microsatellite analysis as previously described [43,47,71].

Data mining and statistical analysis

To define the best mitotic index cut-off that best separates the data classification and regression tree analysis was performed (Statistica, v. 11, StatSoft, Inc., Tulsa, OK, USA). Survival analyses were performed using Kaplan-Meier, log-rank, and Cox proportional hazards methods (Statistica, v. 11, StatSoft, Inc., Tulsa, OK, USA; JMP Pro v. 11.2.0, Sas Institute Inc., NC, USA). Findings were considered statistically significant at $p < 0.05$.

Results

We included 558 patients with low grade (WHO grade II (n=262)) and anaplastic (WHO grade III (n=296)) diffuse gliomas. Patient age ranged from 17.4 to 78.4 years overall. Adjuvant treatment data was available for 439 patients, of which 281 received radiation and 236 received chemotherapy. One hundred and eighty seven patients received either radiation or chemotherapy, 165 patients received both, and 87 did not receive adjuvant treatment. Morphologically, after central review 235 tumors had astrocytic features, 11 had mixed oligoastrocytic, and 312 had oligodendroglial histology. As expected, in the whole group tumor grade was associated with patient outcome (Fig. 1a). This finding did not hold true when the cases were stratified by astrocytic/mixed histology (Fig. 1b), but only when

stratified by oligodendroglial histology (Fig. 1c). Using both IDH1-R132H-specific immunohistochemistry followed by targeted sequencing for *IDH1* non-canonical (non *IDH1-R132H*) and *IDH2* mutations, 475 tumors (85.12%) were IDH mutated, and in the remaining 83 cases (14.87%), an IDH mutation was not detected. A summary of the IDH mutation results is presented in Table 1. The age distribution in IDH-wild type tumors was between 19.0–78.4 years (median = 45) and in IDH mutated tumors was between 17.4–74.2 years (median = 37). As expected, IDH-mutant tumors were clinically less aggressive than IDH-wild type tumors (Fig. 1d).

Two hundred and twelve tumors were 1p/19q co-deleted, representing a subset of the IDH-mutant tumors. Consistent with the literature, 1p/19q co-deletion was associated with improved outcome (Fig. 1e). When the two molecular signatures were combined, patients with IDH-mutant and 1p/19q co-deleted tumors performed best (median OS=15.86 years, range=0.02–23.98) compared to those with IDH-mutant and 1p/19q intact tumors (median OS=10.88 years, range=0.02–30.06) and to those with IDH-wild type and 1p/19q intact tumors (median OS=2.35 years, range=0.02–19.84) (log-rank $p < 0.0001$). For distribution of IDH mutations and 1p/19q co-deletions among morphological subtypes see Online resource 2.

To date, the role of tumor grade/tumor proliferation on patient survival has not been well characterized in grade II–III gliomas after accounting for IDH mutation status. To evaluate the role of histologic grade/tumor proliferation rate within cases stratified by IDH status, the IDH-mutant ($n=475$) and IDH-wild type ($n=83$) tumors were considered separately. Among the 475 IDH-mutant tumors, comparison of outcome based on WHO grade (II versus III) showed no statistically significant difference on log-rank analysis ($p=0.1739$), with a small effect size of WHO grade on survival. Cox analysis revealed a hazard ratio (HR) of 1.21 (95% confidence interval (CI)=0.91–1.61) and median OS of 12.41 years (range=0.08–30.06) in the grade II tumors versus 13.35 years (range=0.02–26.77), in the grade III tumors (Fig. 2a). Survival analysis in the IDH-wild type cohort (Fig. 2b) showed a statistically significant difference in outcome based on WHO grade ($p=0.0507$), and with a larger effect size with a hazard ratio of 1.74 (95% CI = 0.95–3.16) and median OS of 4.82 years (range=0.24–12.07) for WHO grade II versus 1.97 years (range=0.02–19.84) for WHO grade III tumors.

To further characterize these results, we quantified the mitotic index (mitoses per 1000 tumor cells) using pHH3 immunostaining. We used a mitotic index cut-off of 4 as previously described [13] to distinguish low-proliferative (mitotic index = 0–4) from high-proliferative (mitotic index > 4) tumors. This cut-off value was also confirmed by classification and regression tree computational analysis (details in Online resource 3). With the use of the mitotic index, an overall finding similar to WHO grade was observed, with no statistical difference between high- versus low-proliferative tumors in the IDH-mutant subset (Fig. 2c) [HR = 1.10, 95% CI=0.80–1.51 and median OS 12.99 years (range=1.41–21.78) for high-proliferative versus 12.76 years (range=0.02–26.77) for low-proliferative tumors]. In contrast, the effect size of mitotic index on IDH-wild type tumors was more substantial (Fig. 2d), with a HR of 4.41 (95% CI = 2.55–7.63) and median OS of 1.49 years (range=0.24–11.34) for the high-proliferative tumors versus 8.28 years (range=1.01–19.84)

in the low-proliferative tumors. To formally evaluate the prognostic effect of tumor proliferation and IDH mutation status on patient outcome, we tested for the presence of statistical interaction, which on Cox proportional hazards multivariate analysis, was present (Table 2).

To further characterize relationships between relevant co-variables and patient outcome, Cox multivariate analysis was performed (for multivariate analyses with WHO grade and adjuvant treatment see Online resource 4). When the entire cohort was examined, IDH mutation status, 1p/19q co-deletion status, mitotic index, and age at initial diagnosis were all statistically significant (Table 3). This held true after adjustment for adjuvant treatment (Online resource 4, Table S4.1) The finding that older patient age is significantly correlated with poorer patient outcome is a consistent finding in glioma. To evaluate this in subsets defined by IDH mutation status, Cox multivariate analyses were performed independently in the IDH-mutant and wild-type cohorts. In the IDH-mutant cohort, mitotic index was not a significant predictor of outcome ($p=0.3535$) (Table 4) and only a borderline significant predictor of outcome after adjustment for treatment ($p=0.0566$) (Online resource 4, Table S4.2.A), while a much stronger predictor in the IDH-wild type cohort ($p=0.0010$) (Tables 5 and S4.3.A). Interestingly, patient age was not independently predictive of survival in the IDH-mutant cohort (Tables 4 and S4.2) but was significantly correlated with outcome in the IDH-wild type cohort (Tables 5 and S4.3). To illustrate this graphically, Kaplan-Meier curves demonstrated no statistical difference in older versus younger patients (using an age cut-off of 40) in IDH-mutant cases (Fig. 3a, median OS= 13.36 years (range=0.02–30.06) for younger patients and 12.76 years (range=0.02–23.98) for older patients). In contrast, IDH-wild type tumors showed a striking difference in OS (median OS=11.34 years (range=1.52–19.84) for younger patients and 1.35 years (range=0.02–13.18) for older patients (log-rank $p<0.0001$) (Fig. 3b). To further test these findings, similar analyses were performed on the subgroup of IDH-mutant and 1p/19q non-co-deleted cohort of tumors ($n=264$). In this subset, mitotic index, WHO grade, and age were not statistically correlated with patient survival (details in Online resource 5). Based on these findings along with mitotic index results in Tables 3–5, results show that the prognostic effect of mitotic index in the overall glioma cohort is primarily driven by the effect limited to the IDH-wild type cohort.

Taking the findings together and in context, two clinical groups can be defined in the IDH-mutant cohort, based on the presence or absence of 1p/19q co-deletion. In the IDH-wild type cohort, clinical groups are defined by proliferative activity, here defined using a mitotic index cut-off of 4. These findings define 4 clinical-pathologic groups of low grade and anaplastic diffuse glioma, as shown in Fig. 3c.

Discussion

In this study we investigated the prognostic value of tumor proliferation and patient age in low grade and anaplastic diffuse glioma stratified by IDH mutation status. We evaluated patient outcome as related to initial tumor grade, and found that the effect of grade (II versus III) on patient outcome was small in the IDH-mutant subset of tumors as compared to the IDH-wild type subset of tumors. Recognizing that tumor grade is subject to interobserver

variability, as well as the fact that, in large part, the distinction of grade II versus grade III diffuse gliomas is based primarily on mitotic activity, we further evaluated mitotic index as related to patient outcome.

We used a cut-off of 0–4 versus >4 immunohistochemistry-confirmed mitoses per 1000 tumor cells to define two groups, based on our prior experience [13] and confirmed this cut-off using classification data mining methods (Online resource 3).

Similar to the findings using WHO grade, the impact of mitotic index was small in the IDH-mutant cohort relative to the IDH-wild type cohort. A significant statistical interaction could be discerned suggesting that the prognostic impact of mitotic index groups, so defined, was conditional on IDH status. Verifying past literature, we found that 1p/19q co-deletion was restricted to a subset of the IDH-mutant tumors [36] and within this subset offers further prognostic value [10,16,20,24]. Interestingly, the impact of patient age, a long-known prognostic marker in glioma, also varied based on IDH mutation status, and was pronounced only in the IDH-wild type subset.

For some time the WHO grade and the morphological subtype (oligodendroglial vs. astrocytic) have been the principal pathologic prognostic factors for patients with grade II–III diffuse gliomas [41]. Additional clinical variables like patient’s age [53], Karnofsky score to assess patient’s performance status [3], tumor size [12,53], and the extent of surgical tumor resection [39,27,57,58], added prognostic value for these patients. To date, the WHO grade and the morphological subtype are the primary criteria for treatment stratification [46]; however the current diagnostic criteria for diffuse gliomas [41] can be subjective, significant interobserver variability having been reported in both mitotic figure assessment and call, and in morphological subtyping [14,62,35,2]. There is a critical need for more objective criteria to define prognosis and guide therapy for patients with II–III grade diffuse glioma.

Several molecular biomarkers have emerged to characterize subgroups of diffuse glioma. Since 1994, when combined loss of 1p and 19q was identified in oligodendrogliomas [54], the field has made significant progress. Today several mutually-exclusive molecular signatures have been well-characterized for groups of astrocytomas (mutations involving *TP53* and *ATRX*) and for oligodendrogliomas (1p/19q co-deletion, mutations involving *CIC* and *FUBP1*) [5,26,30,70,56,32] in adults. Both molecular tumor categories have a common denominator: mutations involving IDH [26,70,30,36].

IDH mutations quickly emerged as powerful prognostic biomarkers, challenging current concepts by overcoming histology in certain instances [21,44]. They changed the view on gliomagenesis by highlighting the critical role of epigenetic regulation [25,61]. IDH mutations are responsible for the glioma-CpG island methylator phenotype (G-CIMP) associated with a proneural genetic signature [49]. They have been proven to be acquired early in tumor formation [67,28] and retained following treatment or tumor recurrence/progression [28,38], becoming the molecular signature for secondary glioblastomas [48].

Pathologic grading of diffuse gliomas is performed to stratify patients into clinical risk groups, as a means to tailor therapy based on estimated clinical aggressiveness. Mitotic

activity is an important criterion to distinguish grade II from grade III diffuse gliomas. Microvascular proliferation and necrosis may play a role in distinguishing oligodendroglial and oligoastrocytic grade II versus grade III gliomas as well (according to the most recent, i.e. WHO 2007 classification the presence of necrosis in mixed gliomas even leading to a diagnosis of glioblastoma with oligodendroglioma component, WHO grade IV)[41]. The finding that the grade II and III gliomas are in fact composed of at least two distinct biologic subtypes, defined by IDH mutation status, raises questions regarding the role of conventional grading/tumor proliferation rate on patient outcome within IDH-mutant versus IDH-wild type tumors.

In this study we investigated the prognostic value of WHO grade, mitotic index, and patient age in grade II and III diffuse glioma stratified by IDH mutation status. We found, consistent with prior studies, that IDH-mutant tumors comprised the majority of the cohort and further, that the IDH-mutant subset had an improved outcome compared to IDH-wild type tumors. With that as a background, we compared the role of tumor grade and outcome in IDH-mutant vs. wild-type tumors and found a larger effect size of tumor grade on outcome among the IDH-wild type tumors, compared to IDH-mutant tumors. To further characterize this result and acknowledging that the distinction of grade II from grade III is based largely on mitotic activity, we used mitotic index and found an analogous result. Inspection of the Kaplan-Meier curves among the IDH-mutant tumors for tumor grade (Fig. 2a) and mitotic index (Fig. 2c) with the curves for the IDH-wild type tumors (Fig. 2b and 2d) shows that the relationship between tumor grade/proliferation and outcome is related to a substantial degree upon the IDH mutation status. This finding was confirmed by demonstrating statistical interaction between mitotic index and IDH status (Table 2) (i.e. the prognostic effect of tumor proliferation on outcome depends on IDH mutation status).

Morphologically identical gliomas have distinct molecular signatures, expression signatures, and prognostic features [18]. By molecular profiling of 101 grade II–III astrocytomas, Gorovets et al identified molecular subgroups of gliomas mainly stratified by IDH mutation status. Significant molecular differences were reported between IDH-mutant and IDH-wild type gliomas [17]. IDH-mutant gliomas were associated with *TP53* mutations, *PTEN* promoter methylation, gains of 8q, and defined two distinct subgroups based on transcriptional profiling. These two distinct subgroups, called neuroblastic and early progenitor-like, showed mature neuronal signatures and developmental pathway signatures respectively and provided potential evidence of glioma cells originating from subventricular zone progenitors as previously shown [37,60]. The *TP53* mutations associated to the early progenitor-like subtype, which also showed additional chromosomal copy number aberrations (7p, 15q gains; 13q, 9p23, 19q, 4q34.3, 11p, 12q21.33 losses). IDH-wild type gliomas exhibited *EGFR* amplification, *PTEN* loss accompanied by 7p gain, 9p and 10q loss, signatures characteristic of primary glioblastoma. Similar to primary glioblastomas, PI3K/AKT pathway was activated in IDH-wild type tumors [11,52,17]. This subset of IDH-wild type gliomas defined a third highly heterogeneous transcriptional subgroup, suggestively called pre-glioblastoma. Importantly the authors did not find survival differences among WHO grades within molecular subgroups and the latter were more predictive of OS compared to the WHO grade [17].

Yan et al, on a cohort of 225 diffuse gliomas of all WHO grades also identified three distinct prognostic molecular subclasses based on gene expression profiles. The subgroup that lacked IDH mutations, although enriched with primary glioblastomas (71), contained a substantial number (24) of grade II and III diffuse gliomas [73].

Our data show that IDH, followed by 1p/19q testing, can be reliably integrated as a first approach toward risk stratification (Fig. 1e) and this is consistent with data reported by others [16,20,10,24]. With the established predictive value for 1p19q for chemotherapeutic benefit [6,9,8,64,63], and potential predictive value for IDH mutations [10,15], this paradigm holds the potential to be extremely important for the management of patients with grade II and III diffuse gliomas.

In our study, following IDH stratification, only 1p/19q was prognostic in IDH mutated grade II–III gliomas after adjustment for tumor proliferation, age, and adjuvant treatment. Interestingly in our cohort tumor proliferation and age were prognostic only in IDH-wild type gliomas, but not in IDH-mutant gliomas, suggesting that the overall effect is attributed only to the IDH-wild type tumors. This effect seems relatively strong, given the minority of IDH-wild type tumor samples in our cohort (n=83) compared to IDH-mutant samples (n=475). In our cohort IDH-wild type tumors had the lowest median OS, of only 2.35 years and due to the lack of IDH mutations we speculate that these tumors share the biology of primary glioblastoma, with clinical behavior that is distinct from IDH-mutant glioma and approaches that of grade IV IDH-wild type tumors [52,48,25,55,26,17,73]. Further molecular characterization for commonly described molecular markers of primary glioblastoma [52,11] is needed to prove this suspicion. Also, it remains to be seen if other morphological components traditionally used in grading of diffuse gliomas (i.e. microvascular proliferation and necrosis) still carry additional prognostic information (besides mitotic activity) in the IDH-wild type, 1p/19q non-co-deleted subgroups of grade II and III diffuse gliomas. Additional markers are needed to distinguish favorable from unfavorable grade II–III IDH-mutant gliomas, and in this regard, one clue comes from a recent study on grade II gliomas which suggests that distal loss of 10q is a late onset event and a marker for reduced overall survival [66].

Limitations of this study are its retrospective nature with potential selection bias due to tissue and clinical data availability; we lack data on the extent of resection and clinical performance status, both important predictors of outcome in diffuse glioma, but difficult to accurately assess retrospectively. In this study only a small percentage of mixed oligoastrocytomas is present [11/558 (2%)]; this diagnostic category was only sparingly used at MD Anderson, the major source for the cases; therefore we caution the reader for this additional selection bias to not draw conclusions on this particular morphological category but rather to integrate the molecular signatures in the histological context. An additional bias was possibly caused by the choice of only a single block per case for mitotic index, which can of course vary within the tumor. Even with these limitations, a comparison of IDH-mutant and IDH-wild type tumors, examined in similar fashion, yielded different relationships of grade and mitotic index on patient survival and at minimum, our results suggest that independent confirmation is warranted.

Although pHH3 immunohistochemistry raises practical issues, there are several advantages to assess mitotic activity. On top of the antibody's known increased sensitivity and specificity for mitotic figure detection [23,22,19,13,40], the mitotic index (per 1000 glioma cells) is, in concept, favored over a per-10 high power fields assessment, since tumors vary widely in cellularity. At some institutions this method is part of routine practice, complementing the assessment of the MIB-1/Ki-67 index (also measured as a true index, rather than on a high power field basis). Additional experience is required to more fully evaluate its clinical utility in daily practice.

A major strength of the study is the cohort size (n=558), allowing us to examine the existence of at least two distinct biological molecular subgroups of grade II and III glioma: IDH mutated and IDH-wild type, each likely encompassing several distinct prognostic molecular subgroups [17]. Based on these findings we suggest that the concept of tumor grading, as a means of defining clinical risk groups, be further examined independently for IDH-wild type versus IDH-mutant grade II–III diffuse gliomas. In addition, consistent with ongoing efforts to integrate IDH mutation status within WHO tumor classification guidelines [42], it is hoped that this study will spur further effort into the identification of factors that control clinical behavior among diffuse gliomas, acknowledging that IDH-mutant and IDH-wild type low and anaplastic grade diffuse gliomas are biologically and clinically distinct.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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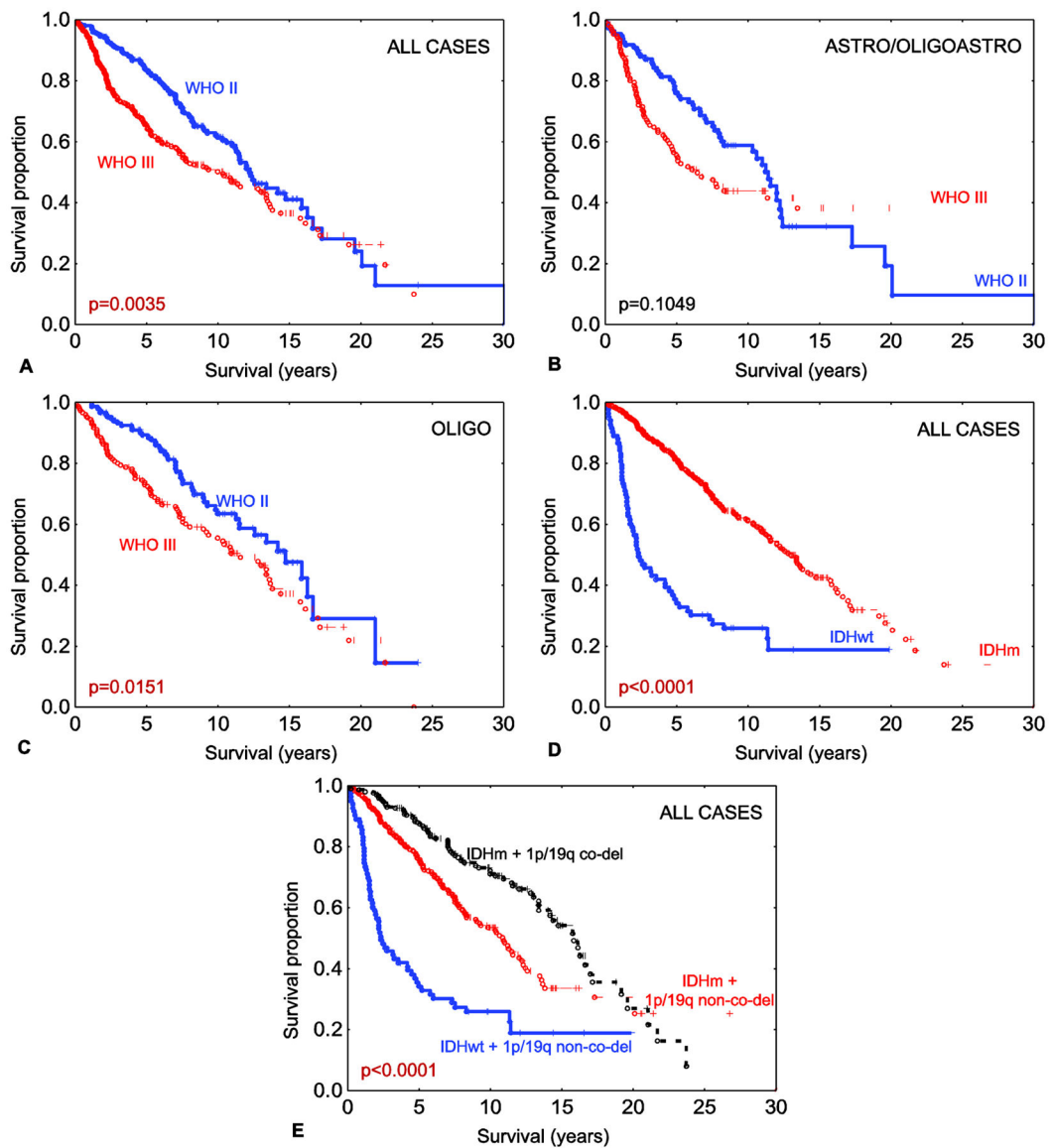


Fig. 1. Overall survival among all 558 grade II–III diffuse gliomas stratified by WHO grade (a). Overall survival among all 246 astrocytic gliomas and gliomas with mixed morphology stratified by WHO grade (b). Overall survival among all 312 oligodendroglial gliomas stratified by WHO grade (c). Overall survival among all 558 grade II–III diffuse gliomas stratified by IDH mutation status (d). Overall survival among all 558 grade II–III diffuse gliomas stratified by combined IDH mutation and 1p/19q co-deletion status (e). Legend: co-del – co-deleted; IDHm - IDH-mutant; IDHwt – IDH-wild type; non-co-del – non-co-deleted. Note: all reported p values are log-rank.

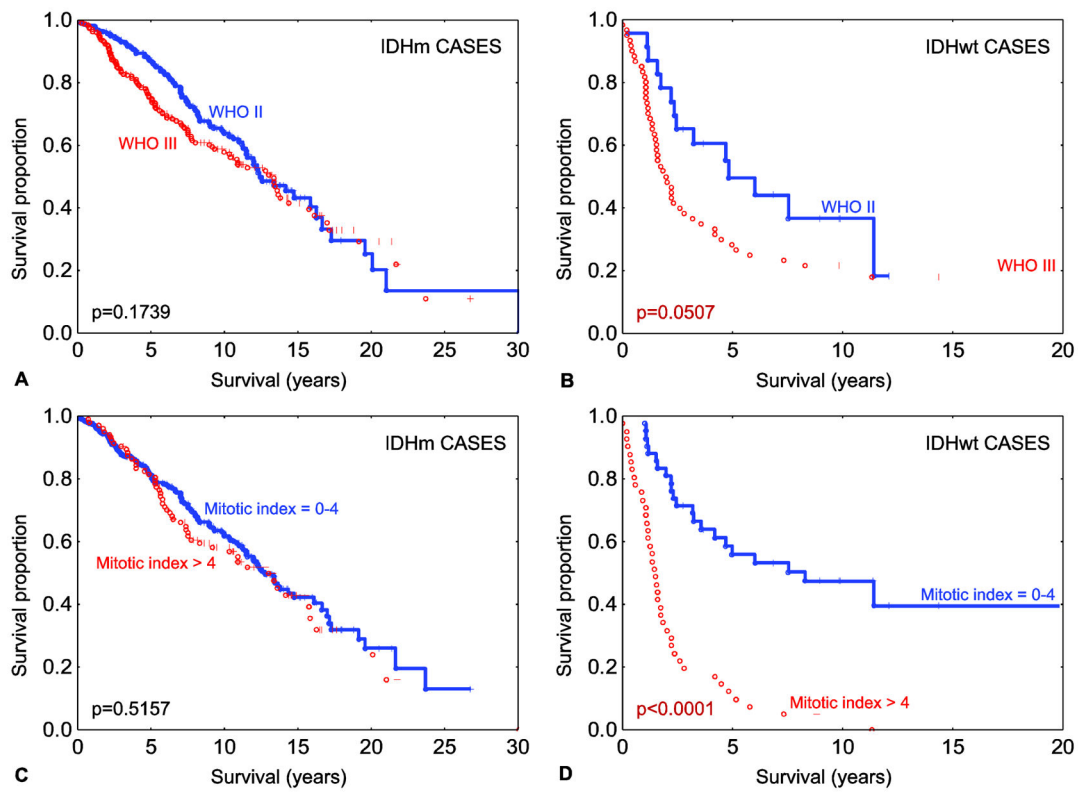


Fig. 2. Overall survival among IDH mutated diffuse gliomas (n=475) stratified by WHO grade (a). Overall survival amongst IDH-wild type diffuse gliomas (n=83) stratified by WHO grade (b). Overall survival amongst IDH mutated diffuse gliomas (n=475) stratified by mitotic index subgroups (c). Overall survival amongst IDH-wild type diffuse gliomas (n=83) stratified by mitotic index subgroups. Legend: IDHm - IDH-mutant; IDHwt – IDH-wild type. Note: all reported p values are log-rank.

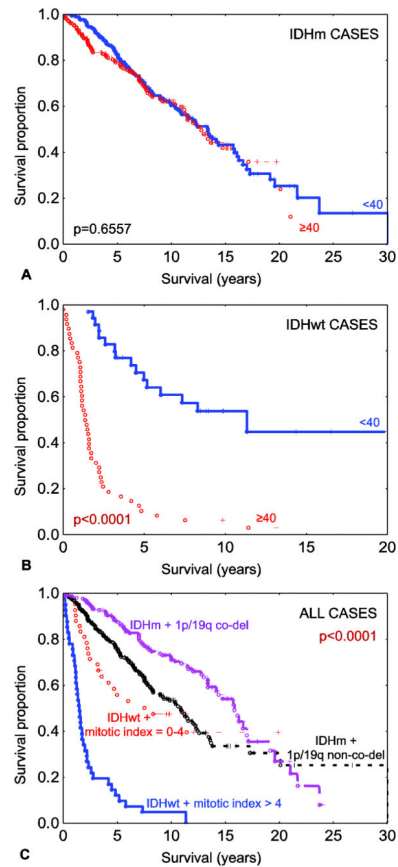


Fig. 3. Overall survival among IDH mutated diffuse gliomas (n=475) stratified by age groups (in years) (a) and overall survival amongst IDH-wild type diffuse gliomas (n=83) stratified by age groups (b). Overall survival among all 558 grade II-III diffuse gliomas stratified by combined IDH mutation, 1p/19q co-deletion status and mitotic index subgroups (c). Legend: co-del – co-deleted; IDHm - IDH-mutant; IDHwt – IDH-wild type; non-co-del – non-co-deleted. Note: all reported p values are log-rank.

Table 1

Summary of IDH mutations identified.

IDH1/IDH2 protein-coding change identified	# (% total)	# (%) in 1p/19q non-co-deleted tumors	# (%) in 1p/19q co-deleted tumors
IDH1			
p.R132H	434 (77.77)	243 (56.00)	191 (44.00)
p.R132C	14 (2.50)	4 (28.58)	10 (71.42)
p.R132G	12 (2.15)	12 (100.00)	0 (0.00)
p.R132S	9 (1.61)	5 (55.55)	4 (44.44)
IDH2			
p.R172K	6 (1.07)	0 (0.00)	6 (100.00)

number of events.

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Table 2

Cox multivariate analysis to test for interaction between mitotic index and IDH mutation status on overall survival.

Variable	p-value	95% CI
Mitotic index high vs. low	<0.0001	3.58–10.32
IDH status mut vs. wt	0.0265	0.38–0.94
Mitotic index-IDH interaction term	<0.0001	0.10–0.34

CI - confidence interval, mut – mutant, N/A-not applicable, wt – wild-type.

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Table 3

Cox multivariate analysis on all 558 diffuse glioma.

Variable	p-value	Hazard Ratio	95% CI
IDH status (mutvswt)	<0.0001	0.38	0.28–0.52
1p/19q status (codel vs non-codel)	<0.0001	0.53	0.40–0.71
Mitotic index (high vs low)	<0.0001	1.70	1.31–2.19
Age	<0.0001	1.03	1.02–1.04

CI: confidence interval, codel – co-deleted, mut mutant, wt – wild-type.

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Table 4

Cox multivariate analysis on all 475 IDH-mutant diffuse glioma.

Variable	p-value	Hazard Ratio	95% CI
1p/19q status (codel vs. non-codel)	0.0002	0.57	0.42–0.77
Mitotic index (high vs. low)	0.3535	1.16	0.85–1.59
Age	0.1243	1.01	0.99–1.03

CI: confidence interval, codel – co-deleted, mut – mutant, wt – wild-type.

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Table 5

Cox multivariate analysis on all 83 IDH-wild type diffuse glioma.

Variable	p-value	Hazard Ratio	95% CI
Mitotic index (high vs. low)	0.0010	2.73	1.50–4.96
Age	<0.0001	1.05	1.03–1.06

CI: confidence interval

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