Recent Molecular Advances in Our Understanding of Glioma

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Abstract

Our molecular understanding of glioma has undergone a sea change over the last decade. In this review, we discuss two recent articles that employed whole genome sequencing to subclassify gliomas vis-à-vis known molecular alterations. We further discuss the relevance of these findings vis-à-vis current treatment paradigms.

Introduction And Background

Diffusely infiltrating gliomas are often persistent and aggressive lesions for which, despite decades of research, long-term control remains elusive. A major development in glioma biology recently pertains to our understanding of its molecular subgroups. These have included divisions into transcriptomal subtypes as well as analyses of glioma molecular evolution [1-5]. While gliomas are known for their genetic heterogeneity which relates to their treatment resistance, it is becoming increasingly apparent that gliomas do fall within distinct molecular subgroups that can generally predict outcomes. As of now, however, treatments based specifically on these molecular classifications have not become mainstream or standardized in the post-Stupp era [6].

Review

Two studies recently published in the New England Journal of Medicine add to this body of knowledge [7-8]. In the first of these, Eckel-Passow, et al. hypothesized that stratification of gliomas based on alterations in the TERT promoter, IDH (including IDH1 and IDH2 mutations), and co-deletion of 1p/19q would identify groups with similar clinical variables, acquired somatic alterations, and germline variants. These alterations were selected for study given their prevalence within glioma, their presence as early alterations in the molecular evolution of glioma, and their strong association with overall survival based on previous clinical studies. Specifically, TERT encodes telomerase which is essential for telomere maintenance (shortened telomeres impede cellular division) and mutations in its promoter are often found in both oligodendroglioma and glioblastoma. As such, telomere maintenance emerges as a common molecular theme across markedly distinct subtypes of diffusely infiltrating glioma. As an aside, TERT is also interesting from the standpoint of aging (telomerase activity usually declines with aging), as one hallmark of glioma is worse prognosis of elderly patients compared to younger patients irrespective of co-morbid conditions [9]. Additionally, evidence has accumulated that the age of glioma stem cells contributes to their overall malignancy, perhaps due to the differing genomic landscape of the aged stem cell versus the younger one [10]. Another mutation investigated in this study was the IDH mutation, which is associated with the accumulation of a metabolite 2-hydroxyglutarate and also associated with improved prognosis [11]. Finally, co-deletion of 1p and 19q was assessed, given its association with chemotherapeutic response and the oligodendroglioma phenotype [12-14].

In this first study, 1,087 gliomas were analyzed and stratified into five groups based on these molecular characteristics and are presented in Tables 1-2. These cases included 317 cases from an initial discovery set and an additional 770 cases over two replication sets, including cases from the Cancer Genome Atlas.

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An interesting takeaway from this data concerns its concordance with what is known about primary and secondary glioblastoma, and age-related features in glioblastoma. For example, in this study, standalone IDH mutations were significantly more frequent in younger patients and seemed to go along with tumor evolution along a secondary glioblastoma pathway. Similarly, patients whose tumors harbored TERT mutations tended to be much older and their tumors also frequently showed EGFR alterations, again more consistent with elderly populations harboring primary glioblastoma. Finally, survival analysis revealed that patients (adjusted for age and grade) harboring TERT mutations suffered worse overall survival compared with the other molecular subgroups. Similarly, patients with triple negative gliomas had poorer overall survival than gliomas with TERT, IDH, or triple positive gliomas. Of note among Grade IV gliomas, the molecular subgroups assigned in this study were not associated with survival differences in multivariate analyses.
This study was important as it found consistent associations between their a priori identified molecular groups and age at diagnosis, survival, patterns of acquired alterations, and germline variants. It also confirmed the importance of the IDH mutation as an important biologic target. Moreover, it showed that IDH mutations are not always favorable. In particular, among patients with a histopathologic diagnosis of glioblastoma, patients with both TERT and IDH mutations had poor overall survival, similar to patients with TERT mutations only. The study also demonstrated a relationship between TERT mutations and germline variants in telomere components (TERC/TERT/RTEL1), which is relevant given interest in telomeres and cancer more generally [15]. Similarly, it was confirmed that SNPs at chromosome locus 8q24 were highly associated with the IDH mutation, which suggests that this region contains a germline alteration that facilitates the development of IDH mutant gliomas.

In a companion study published in the same issue of the June 2015 New England Journal of Medicine, the TCGA Research Network published a whole genome analysis of 293 adult lower grade gliomas and correlated this data with clinical outcomes. In short, their study demonstrated that clinical outcome was better predicted by molecular subclasses dictated by IDH, 1p19q, and TP53 status than by traditional histopathologic diagnosis. Similar to the previous study, the TCGA study found that patients with IDH mutations and 1p19q co-deletions had the most favorable prognosis and a strong histologic correlation with oligodendroglioma. Moreover, this class of patients frequently harbored mutations in CIC, FUBP1, NOTCH1, and the TERT promoter. In contrast, those gliomas with IDH mutations but lacking 1p19q co-deletion had mutations in TP53 as well as ATRX inactivation and were generally associated with astrocytic histomorphology, including those tumors with mixed morphologies. The propensity to achieve gross total resection did not differ by molecular class. Finally, those lower grade tumors without IDH mutations had clinical behavior highly similar to glioblastoma.

Interestingly, the authors queried the genomic data from these gliomas and were able to find clusters within groups related to DNA methylation, gene expression, DNA copy number, and microRNA expression. They then integrated this data with the molecular strata data and histologic subtypes to generate a cluster analysis. Consequently, they were able to show that classifying tumors based on IDH and 1p19q status mapped universally to a specific cluster, whereas histologic designation (i.e., oligodendroglioma, astrocytoma, and oligoastrocytoma) matched one-to-one with a cluster only 63% of the time. This underscores the inability of morphological and other often subjective histological criteria to reflect that broader molecular profile of a particular tumor and suggests that molecular markers are a more reliable way to define clinically relevant diagnostic entities that would be more reflective of their biologic potential. An additional finding was that the background mutational frequency of IDH wild-type tumors was significantly elevated compared to IDH mutant tumors. This was repeated and validated with another genomic analysis approach (OncoSign) that confirmed these findings.

In lower grade gliomas with IDH mutations and 1p19q co-deletion, the authors found frequent mutations in
In this review, we have discussed the importance of two recent studies utilizing whole exome sequencing to understand the molecular evolution, mutational landscape, and clinical behavior of gliomas. The two studies are notable in that they genomically validate the utility of previously reported molecular markers; for example, IDH status and 1p/19q co-deletion are more important prognostically than standard histopathologic diagnosis. This is exemplified by the fact that IDH wild-type infiltrative astrocytomas with a lower histologic grade have a similar prognosis to that of (Grade IV) GBM. Additionally, these studies confirm that lower-grade gliomas with an IDH mutation have either 1p/19q co-deletion or a TP53 mutation, with few gaps or overlaps, reflecting two distinct molecular mechanisms of oncogenesis. This finding supports eliminating the designation "oligodendroglioma", a diagnostic entity of notoriously high inter-observer variability that is often a source of confusion.

Moreover, these studies underscore that the biology of gliomas, when stratified by molecular subgroup, can differ substantially in terms of their molecular evolution, mutational landscape, and clinical behavior. Indeed, the elegance of these studies rests in their power to meaningfully classify gliomas based on a small set of markers that can be queried routinely in the clinic in a way that captures the broader underlying genomic landscape of a tumor, as previous transcriptional studies attempted to do [1-2]. It is also worth noting that these studies confirmed that age plays an important independent prognostic role, particularly in the Eckel-Passow study that mirrored previous clinical papers that prognosticated glioma survival.

These studies also raise important questions and concerns regarding future treatments. For example, what are the practical considerations of developing trials and accruing patients with lower grade gliomas based on molecular parameters? Given the TCGA data especially, should low grade IDH wild-type tumors be treated like glioblastoma initially with adjuvant chemoradiation? Also, does initial surgery/reoperation or "supratotal" resection change the natural history of this disease, and is this response dependent on the molecular strata [10-19]? Finally, while the sampling error in histopathologic diagnosis is a well-recognized problem, can sampling error also lead to misclassification of gliomas on a molecular level, given the genomic heterogeneity of, for example, GBM, and other tumor types [20].

Other questions abound. For example, why do patients with Grade II/III tumors in the Eckel-Passow study with TERT mutations and IDH mutations differ wildly in terms of survival while they co-register fairly well among Grade IV tumors? As alluded to in the study, among lower grade tumors, it is possible that a subset of the TERT/IDH double positives also contain alterations with functional equivalence to that of 1p/19q deletion, without this latter alteration per se. On the other hand, among Grade IV tumors, since there were only 11 TERT/IDH mutant tumors in the Grade IV group, compared to 347 in the TERT-only group, it is possible that this comparison lacked sufficient power to detect a survival advantage. Certainly, this question is worth pursuing. Also, as alluded to by the authors, an open question remains the clinical impact of the cancer methylome in light of recent data, including that of dynamic methylation patterns (TET proteins) in cancer [21-22].

The final question, of course, is the extent to which these analyses reveal clinically relevant distinct entities among diffusely infiltrating gliomas, including GBM. Apart from IDH mutant tumors, the survival curves of glioblastoma in the Eckel-Passow study are very similar, with IDH wild-type tumors performing poorly (particularly the TERT mutant subset). As such, are these molecular strata purely academic or will treatments be devised that take advantage of these molecular differences? Certainly, analysis of long-term survivors based on transcriptional patterns did not show a preponderance of survivors in one transcriptional subgroup versus another in previous studies [23]. It should be emphasized that as molecular markers are increasingly incorporated as diagnostic criteria, the essential principles that dictate the utility of a "diagnostic entity" should be retained; that is, a diagnosis is useful only when it guides treatment decisions and offers prognostic information as specifically as possible. The development of diagnostic schemata is an iterative process with inputs including an evolving knowledge of tumor biology and clinical outcomes. These studies have provided important information that more rigorously classifies these tumors, with hopes that this improved understanding will lead to improved clinical care.

Conclusions

In this review, we have discussed the importance of two recent studies utilizing whole exome sequencing to...
subclassify gliomas. The clinical utility in terms of decision making is yet to become standard, but these studies are an important step towards understanding the fundamental biologic mechanisms that govern gliomas.

### Additional Information

#### Disclosures

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