

GENETIC ALTERATIONS IN ADULT DIFFUSE GLIOMA: OCCURRENCE, SIGNIFICANCE, AND PROGNOSTIC IMPLICATIONS

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TABLE OF CONTENTS

1. Abstract
2. Introduction
3. Astrocytomas
 - 3.1. Clinical features of diffuse astrocytic glioma patients
 - 3.1.1. Low-grade astrocytomas
 - 3.1.2. Anaplastic astrocytomas
 - 3.1.3. Glioblastoma multiforme
 - 3.2. Genetic alterations and prognostic implications
 - 3.2.1. p53, MDM2, and p14^{ARF}
 - 3.2.2. Platelet-derived growth factor/receptor (PDGF/R)
 - 3.2.3. Chromosome 22
 - 3.2.4. p16, Rb, and CDK4
 - 3.2.5. Chromosome arm 19q
 - 3.2.6. Chromosome arm 11p
 - 3.2.7. Epidermal growth factor receptor (EGFR)
 - 3.2.8. Chromosome 10, PTEN, and DMBT1
4. Oligodendrogliomas
 - 4.1. Clinical features of oligodendroglioma patients
 - 4.1.1. Low-grade oligodendrogliomas
 - 4.1.2. Anaplastic oligodendrogliomas
 - 4.2. Genetic alterations and prognostic implications
 - 4.2.1. Chromosome arms 1p and 19q
 - 4.2.2. p16
 - 4.2.3. Chromosome 10
 - 4.2.4. EGFR
5. Mixed oligoastrocytomas
 - 5.1. Clinical features of mixed oligoastrocytoma patients
 - 5.1.1. Low-grade mixed oligoastrocytomas
 - 5.1.2. Anaplastic mixed oligoastrocytomas
 - 5.2. Genetic alterations and prognostic implications
6. Summary
7. References

1. ABSTRACT

Our understanding of diffuse glioma development and progression has expanded remarkably over the past decade. As the genetic alterations responsible for these tumors are identified, molecular models of glioma pathogenesis are emerging and hold great promise to explain the biologic mechanisms of these neoplasms. Although these models continue to evolve and remain highly simplified, some of the genetic alterations that they encompass appear to be prognostically useful. Among the astrocytic gliomas, age and tumor grade are the most powerful indicators of patient survival, however, a wide range of variability remains, particularly among the low-grade and anaplastic astrocytomas. Recent reports indicate that alterations of the PTEN tumor suppressor gene are independent predictors of overall survival for anaplastic astrocytoma patients, helping to distinguish the cases with behavior resembling their more malignant counterparts, the

glioblastomas. Among the oligodendroglial tumors, alterations of the 1p and 19q chromosome arms have emerged as potentially powerful predictors of overall patient survival and *in vivo* chemotherapeutic response, while alterations of the p16/CDKN2A tumor suppressor gene suggest shorter overall survival. As our molecular models continue to improve, through functional analyses and the identification of additional genetic contributors, we will expand our capacity to more effectively prognose these patients and to design rational therapeutic strategies.

2. INTRODUCTION

Diffuse gliomas exhibit an inherent tendency to progress to more malignant phenotypes and a broad range of clinical behavior. Classification of diffuse gliomas by histologic subtype (figure 1) and malignancy grade (figure 2),

Genetic alterations in adult diffuse glioma

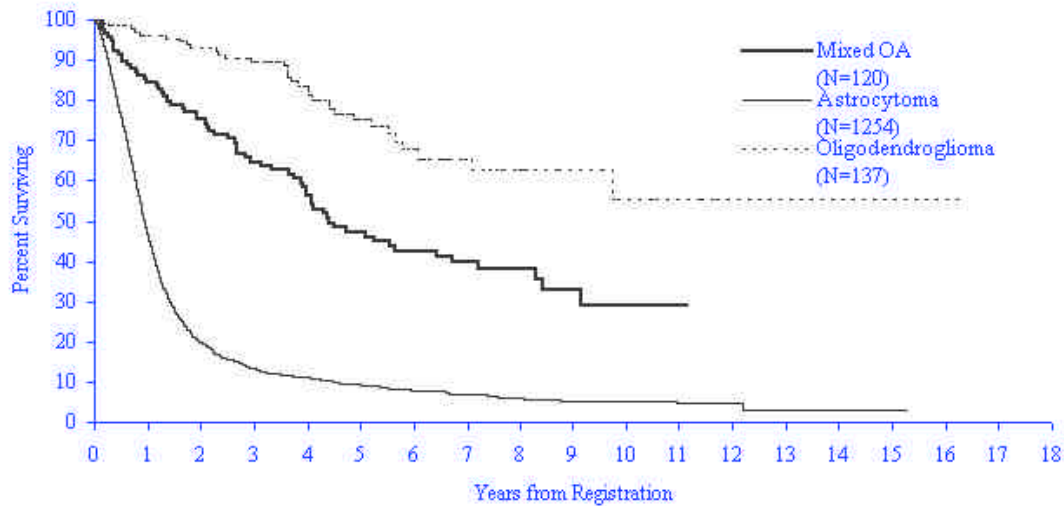


Figure 1. Patient survival by glioma histologic subtype. Data represent 1,511 glioma patients entered on North Central Cancer Treatment Group (NCCTG) therapy trials. Subtype is based on World Health Organization (WHO) guidelines. Log rank p-value <0.0001.

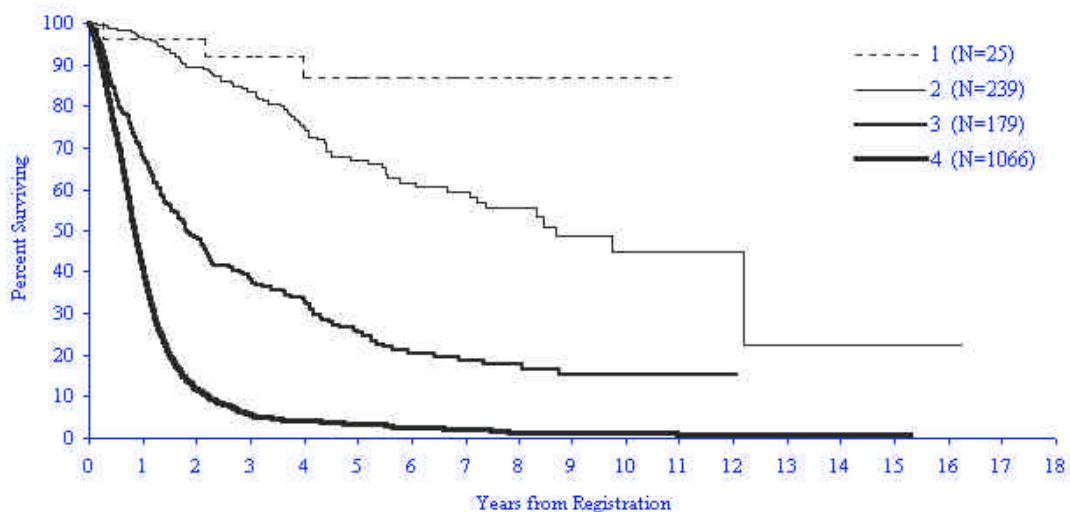


Figure 2. Patient survival by malignancy grade. Data represent 1,509 glioma patients entered on North Central Cancer Treatment Group (NCCTG) therapy trials. Grade is based on World Health Organization (WHO) guidelines. Log rank p-value <0.0001.

in addition to simple clinical variables such as patient age and performance score, remain the gold standards for determining prognosis and treating these patients. However, our abilities to effectively determine the prognosis and to meaningfully stratify diffuse glioma patients for therapy remain limited. Molecular genetic analyses are beginning to provide clinically useful information and promise to extend the capacities of our current approaches. This review provides an overview of the known genetic alterations associated with adult diffuse gliomas and provides discussion of their occurrence, significance, and prognostic implications.

3. ASTROCYTOMAS

Diffuse astrocytic gliomas are defined as tumors consisting primarily of neoplastic astrocytes and comprise approximately 90% of the diffuse gliomas. These tumors represent a continuum from well-differentiated to highly anaplastic lesions and are graded according to histologic features. The current World Health Organization (WHO) criteria (1) for grading astrocytic gliomas notes the presence of nuclear atypia, mitoses, endothelial proliferation, and necrosis, without placing emphasis on any particular feature. According to this system, astrocytomas

Genetic alterations in adult diffuse glioma

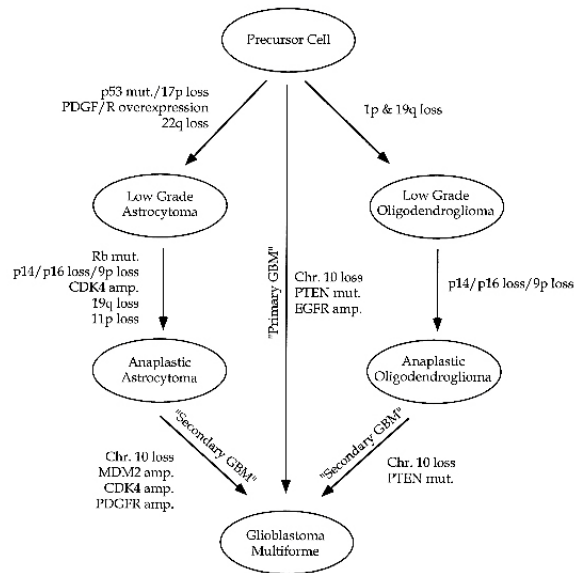


Figure 3. Possible genetic pathways of glioma progression. Histologic subtype and malignancy classifications are based on current WHO guidelines (1).

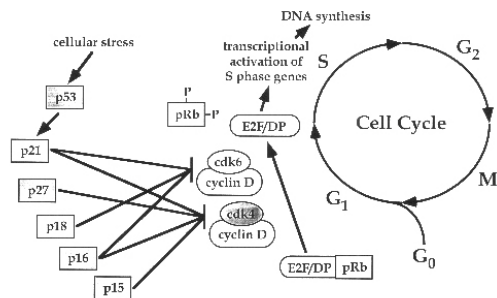


Figure 4. Cell cycle and proteins involved in the regulation of the G₁-to-S transition. Cell cycle inhibitors are squared, and activators are circled. See text for discussion of shaded components. (Modified from De Beeck AO and Caillet-Fauquet P: Viruses and the cell cycle. *Prog Cell Cycle Res* 3:1-19, 1997).

with one of these features are classified as low-grade astrocytomas (grade II), those with two features are termed anaplastic astrocytomas (grade III), and those with either three or four features are termed glioblastomas multiforme (grade IV). Notably, WHO grade I is reserved for special histologic variants of astrocytoma with excellent prognoses following surgical resection. These variants include juvenile pilocytic astrocytoma, subependymal giant cell astrocytoma, and pleomorphic xanthoastrocytoma. Based on their lack of diffusely infiltrating growth and rare capacity for malignant progression, these tumors are not considered among the diffuse gliomas.

The multi-step process of tumorigenesis involves initiation, proliferation, and eventually invasion of the surrounding environment. Astrocytic gliomas, with their inherent tendency to progress to more malignant

phenotypes, have served as powerful substrates for the modeling of these processes, and in this regard, their study has been remarkably productive. Several investigators have studied the genetic alterations associated with the various stages of astrocytoma development and progression and have proposed models to account for these associations (2-7). Possible genetic pathways of glioma progression in relation to known genetic alterations are depicted in figure 3.

3.1. Clinical features of diffuse astrocytic glioma patients

3.1.1. Low-grade astrocytomas

Low-grade diffuse astrocytomas may occur at any site in the central nervous system but favor the cerebral hemispheres and generally afflict patients in the fourth or fifth decades of life. These patients frequently present with seizures and/or symptoms of increased intracranial pressure, and treatment typically involves surgical resection of the symptomatic lesion (8-10). Since the effectiveness of postoperative radiation therapy remains uncertain, some clinicians prefer to reserve its use for recurrent lesions (11-13), and no effective role for chemotherapy has been defined for these patients. The mean survival time following surgical resection is approximately 6-8 years, though there is considerable individual variation, with some cases remaining relatively latent for several years and others progressing rapidly to anaplastic astrocytoma or glioblastoma multiforme (14). Our current capacity to distinguish these latter subsets of patients and to determine the prognosis of low-grade astrocytoma patients in general remains limited and primarily based on clinical features, including patient age, functional status, and extent of surgical resection (15-19). Additional indicators are needed in order to provide more effective prognostic information to these patients and to better design treatment strategies.

3.1.2. Anaplastic astrocytomas

As with low-grade diffuse astrocytomas, anaplastic astrocytomas may occur at any site throughout the central nervous system but most often occur in the cerebral hemispheres. Also similar to the patients with low-grade lesions, anaplastic astrocytoma patients most frequently present with seizures or symptoms resulting from increased intracranial pressure (9, 10). While these tumors may result from progression of a low-grade astrocytoma, they are often diagnosed on first biopsy without indication of a precursor. Surgical resection is generally indicated for these patients, however, since neoplastic cells from these tumors typically migrate away from the main tumor mass, total resection is not possible. Postoperative radiation appears to prolong survival in these patients and is often applied regardless of the extent of resection (20, 21). Recognized overall prognostic indicators include age, functional status, and residual tumor mass (22, 23). The median survival of these patients is two years, and approximately 15% have a five year survival (14). However, providing individual prognosis is difficult, since the latency and rapidity of progression vary considerably, thus affirming the need for additional prognostic markers.

Genetic alterations in adult diffuse glioma

3.1.3. Glioblastoma multiforme

Glioblastomas represent 20-25% of all intracranial tumors and 50% of gliomas (24), most commonly occur in the cerebral hemispheres, and typically afflict patients in the fifth or sixth decade. These tumors may arise from low-grade astrocytomas or anaplastic astrocytomas that have undergone malignant progression, termed "secondary glioblastoma", or they may arise *de novo*, termed "primary glioblastoma" (25) (figure 3). Presenting symptoms of increased intracranial pressure (e.g. headaches, nausea, and vomiting), mental status changes, and motor deficits are common in glioblastoma patients, while seizures are considerably less common (10, 26). Despite their often circumscribed appearance with imaging studies, glioblastomas typically exhibit extensive infiltration of surrounding tissues, making complete resection impossible. Resection is usually indicated, however, for palliative measure, to improve the effectiveness of adjuvant therapies, and to obtain tissue for pathologic diagnosis. Furthermore, retrospective studies suggest that extent of tumor removal correlates with survival (27). Postoperative radiation therapy provides only a modest prolongation of survival, and chemotherapy is only marginally effective and typically used following surgical resection and radiation therapy (20). The effectiveness of newer therapeutic options, such as stereotaxic radiosurgery and interstitial brachytherapy, remains under evaluation (28-30). Median survival is approximately 10 months, with fewer than 20% surviving longer than one year and approximately 5% surviving longer than five years (14). Prominent prognostic factors are simple clinical indicators, including patient age and performance status (23, 31, 32).

3.2. Genetic alterations and prognostic implications

3.2.1. p53, MDM2, and p14^{ARF}

The p53 tumor suppressor gene serves as the "guardian of the genome" by coordinating a complex series of responses to DNA damage (33). Following DNA damage, p53 protein levels are upregulated due to increased synthesis and prolonged stabilization of the protein (34-37). Wild type p53 then induces the transcription of genes that promote cell cycle arrest or apoptosis, including the p21 and BAX genes (38-42). Mutated p53 lacks the ability to induce cell cycle arrest or apoptosis, allowing cells to accumulate mutations and chromosome abnormalities (33, 41, 42). In addition, wild-type p53 has been implicated as a suppressor of angiogenesis, and thus, mutated p53 may also promote neovascularization (43-45).

Mutation of p53 is among the earliest and most frequent events in astrocytic glioma development, occurring in approximately 40% of low-grade and anaplastic astrocytomas (46-48). In glioblastomas, p53 mutation is associated with secondary tumors, which evolved from low-grade or anaplastic astrocytomas, and is rarely observed in primary tumors, which developed clinically *de novo* (49) (figure 3). Thus, while the incidence of p53 mutation in unselected series of glioblastoma is approximately 40%, separately, primary

and secondary glioblastomas exhibit incidences of approximately 10% and 65%, respectively (49).

Based on the apparent capacity of p53 mutations to distinguish primary and secondary glioblastomas, several investigators have hypothesized that these alterations may be prognostically relevant. However, whether searching for p53 gene mutation or p53 protein accumulation, the distinct preponderance of these studies indicates that alteration of p53 is not an independent predictor of astrocytoma patient survival, regardless of histologic grade (31, 46, 47, 50-64). Tachibana *et al.* (47) identified p53 mutation as a strong univariate predictor of prolonged overall survival in a set of 66 similarly treated anaplastic astrocytoma patients. However, after adjusting for the effects of patient age through multivariate analyses, the predictive value of p53 mutation status did not reach statistical significance.

A limited subset of studies do suggest that p53 alterations are of prognostic relevance (65-67). van Meyel *et al.* (65) searched for p53 mutations in 15 low-grade astrocytic gliomas that had progressed to high-grade gliomas, examining both the initial and recurrent tumors. Patients with p53 mutant tumors survived nearly twice as long as those without mutations, and, while there was no significant difference in recurrence-free survival, there was a significant difference in post-recurrence survival. Furthermore, these authors suggested that low-grade tumors that recurred as anaplastic gliomas exhibited p53 gene mutation, while those that recurred as glioblastomas had intact p53 genes. This limited number of cases, however, was selected for recurrence and progression and may not be representative of all low-grade tumors.

Watanabe *et al.* (66) analyzed 144 biopsies from 67 patients with recurrent astrocytoma for p53 alterations and identified mutations in 46 of 67 patients (69%) in at least one biopsy. Among the 28 low-grade astrocytomas studied, the p53 status remained the same in 95% of the cases, irrespective of whether the recurrent lesion had the same or higher grade of malignancy. In addition, progression of low-grade astrocytomas to anaplastic astrocytomas or glioblastomas occurred at similar frequencies in cases with and without p53 mutations. Thus, these authors suggested that p53 alteration is associated with tumor recurrence but not predictive of progression to a more malignant phenotype, in contrast to the findings of van Meyel *et al.* (65). These cases, similar to those studied by van Meyel *et al.*, were selected for recurrence and progression and may not be representative of all low-grade tumors.

Korkolopoulou *et al.* (67) examined p53 expression in 51 astrocytic gliomas, predominantly glioblastomas. These authors reported a statistically significant association between p53 overexpression and disease-free survival on both univariate and multivariate analyses, the latter including correction for age and tumor grade. However, a subsequent study from these authors did not confirm these findings (64).

Genetic alterations in adult diffuse glioma

Loss of p53 function may be mediated through amplification of the MDM2 oncogene (68, 69). MDM2 transcription is induced by p53, and the MDM2 protein binds to and promotes the degradation of p53, thus serving as a negative feedback regulator of p53 (70). MDM2 amplification and overexpression, without p53 mutation, occurs in approximately 10% of glioblastomas and anaplastic astrocytomas (70). Furthermore, both p53 and MDM2 proteins are stabilized through binding of the p14^{ARF} tumor suppressor gene to MDM2 (71). This dual stabilization induces a p53 response, resulting in elevated levels of MDM2 and cell cycle arrest in both G1 and G2/M. MDM2 alterations, as assessed by both gene amplification and overexpression, do not appear to be independent predictors of patient survival (58, 72, 73). The potential prognostic relevance of p14^{ARF} alterations remains to be evaluated.

3.2.2. Platelet-derived growth factor/receptor (PDGF/R)

PDGF, a major mitogen for connective tissue cells and glia, is involved in normal development, especially of the central nervous system, and has been implicated in various pathological processes, including wound healing, inflammation, and neoplasia (74-77). In addition, the PDGF system has been intimately linked to the developing rat central nervous system in which O-2A progenitor cells are stimulated to divide and inhibited from premature differentiation into type-2 astrocytes and oligodendrocytes through PDGF-mediated activation of PDGFRA (78). PDGF occurs as three isoforms of disulfide-linked A- and B-chains (AA, BB, AB) that each bind with different affinities to two different receptors, PDGFRA and PDGFRB (79, 80). Whereas PDGFRA binds all three isoforms with high affinity, PDGFRB only binds the BB isoform with high affinity. These receptors share similar structures and belong to the protein-tyrosine kinase superfamily of growth factor receptors.

Although the mechanism remains unclear, astrocytic gliomas overexpress the components of the PDGF-PDGFR system. Overexpression of PDGFRA mRNA has been identified in all grades of astrocytic gliomas, and overexpression of PDGFRB and PDGFB chain mRNA have been demonstrated in the hyperplastic blood vessels of these tumors (81-83). Thus, these data suggest the presence of both autocrine and paracrine loops in glioma, with activation of A receptors occurring in the glioma cells and activation of B receptors occurring in the intermingled endothelial cells (81). Since elevated levels of PDGFRA mRNA have been found in all malignancy grades of astrocytic gliomas with the highest levels in the most malignant tumors, overexpression of PDGFRA is likely an early event in glial tumor development and related to tumor progression (82, 84). Consistently, amplification of the PDGFRA gene has only been identified in glioblastomas, the most malignant form of astrocytoma (85).

The wide variability in time to progression for low-grade astrocytomas could conceivably be related to the level of activation of growth factors, including those

involved in the PDGF-PDGFR system. In addition, amplification of the PDGFRA and EGFR genes appear to occur in distinct subsets of glioblastomas (85), suggesting different developmental pathways and perhaps different prognoses and optimal therapeutic strategies (86-88). However, no reports to date have specifically addressed the prognostic significance of either PDGFRA expression or gene amplification in these patients.

3.2.3. Chromosome 22

Loss of heterozygosity on chromosome arm 22q occurs in approximately 20-30% of diffuse astrocytomas, regardless of malignancy grade, suggesting the presence of a tumor suppressor gene involved in early astrocytic glioma development (89-93). A recent report by Ino *et al.* (89) has defined two minimal deletion regions on 22q. The incidence of allelic loss of the more proximal region was similar among the histologic grades, consistent with an early event in tumor development. The incidence of allelic loss of the more distal region, however, increased with tumor grade, suggesting that a second tumor suppressor gene mapped to this locus may be associated with tumor progression. This potential dual role of tumor initiation and progression is intriguing and suggests that allelic losses of 22q may have prognostic significance, although such an association remains to be evaluated.

3.2.4. p16, Rb, and CDK4

The mammalian cell cycle is divided into four distinct phases: G1, S, G2, and M (figure 4). A complex system of positive and negative regulators governs cell cycle progression, exerting control at various checkpoints. One of the most critical checkpoints, the transition from G1 to S phase, involves the p16, Rb, E2F, cdk4, cdk6, and cyclin D proteins (figure 4). Under non-replicating conditions, the Rb protein binds to and sequesters key transcriptional factors, including E2F. When the decision is made for the cell to replicate, cyclin D binds to cdk4 and cdk6, forming active kinases that phosphorylate Rb. Phosphorylated Rb then releases the factors that transcriptionally activate the S phase genes, permitting transition from G1 to S phase. The p16 protein is one of the most important regulators of the cdk4-cyclin D complex. p16 blocks the binding of cdk4 to cyclin D, preventing phosphorylation of Rb, arresting the cell in the G1 phase. Inactivation of p16 or Rb or gain of cyclin D1 or cdk4/6 activity all have the same consequence, progression to S phase without regard to genomic integrity.

Release of the G1-to-S checkpoint is a critical step for the development of many human cancers (94), including astrocytic gliomas. Approximately half of all anaplastic astrocytomas and nearly all glioblastomas exhibit inactivation of this checkpoint (95-102). In astrocytic gliomas one of the most frequent mechanisms of abrogating this control is through p16 inactivation which occurs in 33-68% of glioblastoma tumors and in 75-90% of glioblastoma-derived cell lines (98-104). Typically, p16 inactivation occurs through homozygous deletion, though rarer mechanisms include point mutations and 5' CpG island methylation (96, 105, 106). Rb inactivation is the second most common mechanism of abrogating the p16-

Genetic alterations in adult diffuse glioma

cdk4-cyclin D1-pRb pathway in the formation of astrocytic gliomas, occurring in approximately 20-30% of high-grade astrocytomas (95, 96, 107, 108), and amplification of the CDK4 gene is apparent in approximately 10-15% of high-grade astrocytomas (68, 69, 95, 99).

Notably, alterations of p16, Rb and cdk4 are inversely correlated, suggesting that alteration of any one of these components is adequate to sufficiently abrogate the G1-to-S checkpoint (95, 96, 99). However, the Ki-67 index, a measure of proliferative potential, is significantly elevated in high-grade astrocytomas with p16 alteration when compared to those without p16 alteration (109). These observations suggest alteration of p16 may have additional ramifications not encountered with alteration of Rb or cdk4.

Survival analyses have evaluated the prognostic utility of several alterations involving the G1-to-S checkpoint, although the number of studies is limited and not entirely consistent. Nakamura *et al.* evaluated Rb immunostaining in 50 primary anaplastic astrocytomas and identified lack of immunoreactivity as an independent prognostic variable (110). A study by Korkolopoulou *et al.*, however, did not identify Rb immunoreactivity as an independent prognostic indicator when evaluating a set of 48 astrocytic gliomas, predominantly composed of low-grade astrocytomas and glioblastomas (64).

CDK4 gene amplification was examined by Olson *et al.* in 109 astrocytic gliomas, representing all three histologic grades (72). After correcting for the effects of tumor grade and patient age, CDK4 amplification did not emerge as an independent predictor of overall survival. However, expression of p27^{Kip1}, a negative regulator of cdk4 (figure 4), has been suggested to correlate with prolonged patient survival, independent of tumor grade and patient age (73, 111, 112).

Expression of p16 has been evaluated and compared with survival in a set of 80 glioblastomas (58) and in 36 diffuse astrocytic gliomas, spanning all three histologic grades (113). Neither of these studies identified p16 expression as an independent prognostic indicator. Whether homozygous deletion or mutation of the p16 gene provides prognostic information has not been reported.

The general lack of correlation between alteration of the G1-to-S cell cycle regulators and diffuse astrocytic glioma patient survival may be because the Rb, CDK4, and p16 gene products are only portions of larger signaling systems or, simply, because it is universally altered. The potential predictive value of p27^{Kip1} warrants further investigation in prospectively collected patient cohorts.

3.2.5. Chromosome arm 19q

Although the presence of a glioma 19q tumor suppressor gene was first suggested nearly a decade ago (114, 115), this putative gene remains unidentified. Alterations of the chromosome 19 q-arm are of particular importance for several reasons. These alterations have not been reported in other common malignancies (116), and

they are the only known common genetic alteration shared by all three diffuse glioma subtypes (117-119), with gross deletions occurring in approximately 40% of astrocytomas, 45% of mixed oligoastrocytomas, and 75% of oligodendrogliomas (120). In addition, allelic loss of 19q in astrocytic gliomas has been associated with the frequent progression of low-grade lesions to anaplastic astrocytomas and glioblastomas (3, 7, 121). Collectively, these observations strongly suggest that 19q harbors one or more genes important for the pathogenesis of diffuse gliomas and further suggest that this gene may be of importance for glial development and growth regulation.

Multiple investigations have progressively narrowed the 19q common deletion region to an interval within the 19q13.3 cytogenetic band (120, 122-124), and several positional and/or functional candidates for the 19q tumor suppressor gene have been eliminated based on mutational analyses (125-130). The 19q glioma tumor suppressor gene, however, remains to be identified.

Allelic deletion of 19q was not associated with patient survival in a series of 53 glioblastomas analyzed by Smith *et al.* (131). Whether specific alteration of 19q gene(s) provides prognostically relevant information for astrocytoma patients awaits identification of candidate 19q tumor suppressor gene(s).

3.2.6. Chromosome arm 11p

Allelic deletion of the chromosome 11 p-arm occurs in approximately 30% of high-grade astrocytomas and rarely occurs in low-grade astrocytomas (121, 132-135), suggesting the presence of a tumor suppressor gene involved in the malignant progression of astrocytic gliomas. Based on a limited number of mapping studies, the common deletion interval has been localized to a 21-cM region on 11p15.5-pter (133, 134). The c-H-ras gene maps to this interval but has been excluded as a candidate based on single-strand conformation polymorphism analysis (133). Thus, the identity and function of the 11p glioma tumor suppressor gene remain unknown. Allelic loss of 11p has been associated with the malignant progression of astrocytic gliomas (121, 132), but whether these alterations provide prognostically useful information has not been reported.

3.2.7. Epidermal growth factor receptor (EGFR)

EGFR is a transmembrane glycoprotein composed of an extracellular ligand-binding domain, a single hydrophobic membrane-spanning domain and a cytoplasmic tyrosine kinase domain (136). Binding of EGF or transforming growth factor (TGF) to EGFR results in receptor dimerization, autophosphorylation of the receptor itself and phosphorylation of cellular substrates leading to cell division and proliferation (136).

Amplification of the EGFR gene is observed in approximately 40% of all glioblastomas, resulting in overexpression of the EGFR transcript (137-139). In addition, approximately one-third of gliomas with EGFR gene amplification express a mutated variant with constitutive activity (140, 141). Notably, with rare

Genetic alterations in adult diffuse glioma

exception, glioblastomas with EGFR gene amplification also exhibit deletion of chromosome 10, especially 10p (139), suggesting that loss of chromosome 10 precedes EGFR gene amplification in glioma development and may be a prerequisite event for the oncogenic effects of EGFR amplification.

EGFR gene amplification and/or overexpression have been evaluated in multiple series of astrocytic gliomas, and the preponderance of these studies suggests that these alterations are not independent predictors of patient survival (56, 57, 59, 73, 142-148). One of the largest series was studied by Galanis *et al.* (73), who examined 121 astrocytic gliomas for EGFR gene amplification by Southern blotting and did not identify an association between amplification and patient survival by univariate or multivariate analyses. A limited number of studies have suggested an association between EGFR expression and patient survival. However, most of these series are either based on small patient populations (≤ 20 cases) (149, 150) or have studied cases selected based on recurrence or progression (151). Two recent studies have suggested that EGFR amplification may have prognostic relevance in some circumstances. A study from Zhu *et al.* examined EGFR expression in 71 astrocytic gliomas, predominantly anaplastic astrocytomas and glioblastomas and suggested that the percentage of cells positive for EGFR is predictive of patient survival on univariate analysis and after correcting for the effects of patient age and tumor grade (152). While this study is potentially interesting, it stands in contrast to the general consensus of other reports and may simply reflect differences in immunohistochemical approaches.

A recent report by Tachibana *et al.* (47) suggested that EGFR gene amplification may be of prognostic significance after stratifying patients based on age. A collection of 196 high-grade astrocytomas, derived from a series of North Central Cancer Treatment Group (NCCTG) prospective phase III trials, was analyzed for EGFR gene amplification using FISH and PCR. The cohort included 66 anaplastic astrocytomas, 19 mixed oligoastrocytomas, and 111 glioblastomas. Classification and regression tree (CART) analysis revealed that EGFR gene amplification was associated with shorter overall survival among patients less than 40 years of age and was associated with longer overall survival among patients older than 60 years. These opposing effects were negated when CART analyses were performed without age as a parameter. Thus, these data suggest that EGFR gene amplification may have prognostic utility and further suggest that the biological significance of EGFR gene amplification in astrocytic gliomas may be related to patient age.

3.2.8. Chromosome 10, PTEN/MMAC (PTEN), and DMBT1

Deletions of chromosome 10 are the most frequent genetic alteration in glioblastomas, occurring in 60-93% of these neoplasms (99, 114, 139, 153-157). Most cases exhibit loss of an entire chromosome 10, and distinct patterns of deletion on both the long and short arms suggest

the involvement of multiple tumor suppressor genes (157). Recently, a putative tumor suppressor gene, PTEN, was cloned from 10q23 (158, 159) and has proven altered in approximately 30% of glioblastoma tumors and 50-60% of glioblastoma-derived cell lines (158-161), with loss of function occurring through homozygous deletion, point mutation, or loss of expression.

Although PTEN is a dual lipid and protein phosphatase, recent evidence suggests that the biologically relevant targets are probably not proteins, but rather a subset of inositol phospholipids (reviewed in 162). In the phosphorylated state, these phospholipids facilitate the activity of AKT, a serine/threonine-kinase that promotes cell survival and cell cycle entry. Thus, by dephosphorylating the lipids that promote AKT activity, PTEN functions as an indirect inhibitor of AKT.

DMBT1, a member of the scavenger receptor cysteine-rich (SRCR) superfamily, was recently identified from a homozygous deletion at 10q25.3-26.1 in a medulloblastoma cell line (163). Intragenic deletions of DMBT1 have been identified in approximately 25% of glioblastomas and in multiple brain tumor cell lines (163). Members of the SRCR superfamily have been linked to diverse functions, including the initiation of proliferation or differentiation in the immune system or in other tissues (164) and switching of polarity of epithelial cells through mediation of contacts between the extracellular matrix and cell surface proteins (165).

Although two putative glioma tumor suppressor genes, PTEN and DMBT1, have been cloned from chromosome 10, there is evidence for additional contributors. Nearly all glioblastomas with EGFR amplification also exhibit chromosome 10 deletion (139), strongly suggesting a biologic relationship between these alterations. Intuitively, the lost phosphatase activity conferred by PTEN alterations could be prerequisite to enable EGFR amplification to have oncogenic significance, thereby accounting for the close tie between EGFR amplification and chromosome 10 loss. However, EGFR amplification has been demonstrated to occur at similar frequencies among cases with or without PTEN inactivation, suggesting that there may be additional chromosome 10 glioma tumor suppressor genes (161). Mounting evidence suggests that 10p may harbor one of these additional contributors (154-157).

Regarding the prognostic significance of PTEN alterations, Tachibana *et al.* have examined the PTEN coding region by direct sequencing in 196 similarly treated high-grade astrocytic gliomas from patients on NCCTG trials (47). Mutation of PTEN was a strong predictor of shorter overall patient survival in anaplastic astrocytoma patients, independent of patient age. In contrast, mutation of PTEN was neither a univariate nor a multivariate predictor of survival in glioblastoma patients.

Sano *et al.* examined PTEN expression by RT-PCR in 135 diffuse gliomas, including both high- and low-grade astrocytic gliomas and oligodendrogliomas (166).

Genetic alterations in adult diffuse glioma

Multivariate analyses, adjusting for patient age and tumor grade, showed a significantly better prognosis for patients whose tumors expressed high levels of PTEN.

Lin *et al.* (167) examined the PTEN and DMBT1 loci by loss of heterozygosity (LOH) analyses in 26 anaplastic oligodendrogliomas, 31 anaplastic astrocytomas, and 53 glioblastomas. Multivariate analyses, adjusting for patient age and histologic grade (GBM versus non-GBM), showed that LOH at the PTEN locus was a significant predictor of shorter survival. Similar analyses for the DMBT1 locus did not reveal a significant association with survival.

4. Oligodendrogliomas

Oligodendrogliomas are defined as tumors consisting primarily of neoplastic oligodendrocytes and comprise approximately 10-17% of all intracranial gliomas (168, 169). Four-tiered classification systems have been proposed for oligodendrogliomas, including the Kernohan system (170) and one based on the degree of anaplasia proposed by Ludwig *et al.* (171). Neither of these systems, however, consistently produces distinct survival curves (171, 172). The WHO system, a simpler approach, has been advocated as a replacement of the four-tiered systems. WHO guidelines distinguish two types of “pure” oligodendroglioma with distinct survival curves, a low-grade phenotype (grade II) and a more malignant phenotype (grade III), termed anaplastic oligodendroglioma (1). Histologic features that distinguish the latter include high nuclear/cytoplasmic ratios, nuclear atypia, markedly increased mitotic activity, and prominent endothelial proliferation.

It is important to distinguish histologically between oligodendroglial and astrocytic gliomas, since these two tumor subtypes have considerably different clinical courses and optimal therapeutic approaches. Specifically, oligodendrogliomas tend to have a more benign course and are more responsive to treatment than astrocytomas. In addition, genetic and immunohistochemical analyses suggest that these two tumors likely have very different mechanisms of development (114, 173-175), and thus, in order to design more meaningful prognostic markers for these patients and to design more effective and specific treatments, it is critical that these patients are appropriately classified.

4.1. Clinical features of oligodendroglioma patients

4.1.1. Low-grade oligodendrogliomas

Oligodendrogliomas most commonly arise in the fronto-temporal region, though they may develop at any location throughout the neuraxis, in relative proportion to the volume of white matter. These tumors most frequently afflict patients in the fourth or fifth decade of life and often present with seizures, headaches, mental status changes, visual complaints, or focal weaknesses (168-171). For the majority of cases, these tumors grow slowly with an average interval prior to clinical signs of more than one year, regardless of age (176, 177). Although optimal management of low-grade oligodendroglioma has not been

defined, many of these tumors are amenable to complete surgical resection. In addition, a subset of these cases responds to systemic combination chemotherapy with procarbazine, lomustine (CCNU), and vincristine (termed PCV) (178). This chemotherapy may be used as initial treatment followed by surgical resection of remaining tumor or treatment with stereotaxic radiosurgery. Alternatively, surgical resection may be followed by chemotherapy and stereotaxic radiosurgery or external beam radiation (179). Length of postsurgical survival is variable and ranges from five years (50%) to nearly a decade (25-34%) (168, 180-184). Our capacity to provide prognostic information for these patients is limited and primarily relies upon clinical and histologic features, including patient age, preoperative functional status, presence of calcification, and presence of anaplasia (131, 184-189). These factors, however, do not fully account for the considerable variation in clinical behavior observed among these patients.

4.1.2. Anaplastic oligodendrogliomas

As with the low-grade oligodendrogliomas, anaplastic oligodendrogliomas favor the frontotemporal region and have a peak incidence in the fourth and fifth decades. These tumors may develop from a low-grade oligodendroglioma that has progressed to a more malignant lesion, or they may arise *de novo*. The presenting symptoms and imaging studies of an anaplastic oligodendroglioma typically resemble those of the more differentiated oligodendrogliomas, thus requiring tissue for histologic diagnosis. Approximately two-thirds of patients with anaplastic oligodendroglioma respond predictably, durably, and often completely to PCV chemotherapy (190-192). No histologic or clinical parameters have been identified to distinguish the remaining one-third that either responds incompletely or not at all. As with low-grade oligodendroglioma, PCV chemotherapy may precede surgical resection and stereotaxic radiosurgery, or it may be administered after resection and then followed by stereotaxic radiosurgery (179). Overall survival time for anaplastic oligodendroglioma patients is less than 30% of that for low-grade oligodendrogliomas (193). Favorable clinical and histologic prognostic factors include younger patient age, high preoperative functional status, lack of ring enhancement on imaging, and presence of calcification (131, 184-186, 194).

4.2. Genetic alterations and prognostic implications

Oligodendrogliomas are generally thought to develop from molecular pathways distinct from those of astrocytomas (figure 3). While multiple genetic alterations have been identified in astrocytic gliomas and chained together in a logical progression of events, only a limited number of alterations have been defined in oligodendrogliomas, and most of these are observed in both low- and high-grade cases (132). This may reflect the fewer analyses of oligodendrogliomas as compared to astrocytomas, or it may simply indicate that fewer alterations are necessary for the development of oligodendrogliomas.

4.2.1. Chromosome arm 1p and 19q

Allelic loss of 19q occurs in approximately 50-80% of oligodendroglial tumors and with rare exception

Genetic alterations in adult diffuse glioma

involves an entire copy of 19q (117, 118, 120, 195, 196). The incidence of 19q deletion is not significantly different between low- and high-grade oligodendrogliomas, suggesting that this alteration is an early event in neoplastic development (117, 195, 196), in contrast to astrocytic gliomas which typically feature 19q deletion only in high-grade cases (120). Deletion mapping of 19q in oligodendrogliomas is complicated by the rare occurrence of tumors with only partial deletion of 19q. Thus, hypothesizing that astrocytic and oligodendroglial tumors share at least one 19q tumor suppressor gene in common, deletion mapping studies of the oligodendrogloma 19q gene have primarily relied upon astrocytoma samples (120, 122-124).

Deletion of chromosome arm 1p is another frequent event in oligodendrogliomas, occurring in 40-90% of these tumors (120, 195-197). Interestingly, nearly all cases of oligodendrogloma studied with deletion of 1p also exhibit deletion of 19q, suggesting that inactivation of one or more genes on each of these arms is an important event in oligodendrogloma oncogenesis. Deletion mapping of the oligodendrogloma 1p tumor suppressor gene, however, has been complicated by the limited number of cases with only partial 1p deletion (117, 120). A recent report by Husemann et al. identified two distinct deletion regions on 1p, D1S76-D1S253 at 1p36.3 and D1S482-D1S2743 at 1p34-35 (198). Notably, the 1p36.3 deletion interval overlaps the D1S468-D1S1612 deletion interval defined by Smith et al. (120), and narrows the interval to the approximately 5 cM between D1S468 and D1S253.

Deletions of 1p and 19q are of remarkable prognostic utility. Cairncross et al. examined 39 anaplastic oligodendrogloma patients, 37 of which had received PCV chemotherapy (194). Allelic loss of 1p was a statistically significant predictor of chemosensitivity, and combined loss of 1p and 19q was statistically significantly associated with both chemosensitivity and longer recurrence-free survival following chemotherapy. Moreover, Smith et al. have recently demonstrated that the association of 1p and 19q loss with prolonged survival is also evident in low-grade oligodendrogloma patients and that this association may be independent of PCV chemotherapy (131). Importantly, these data need to be confirmed in a larger cohort of prospectively collected patients.

4.2.2. p16

Deletion of the cell cycle regulator p16 is an uncommon event in oligodendrogliomas (199), however, it has recently surfaced as an important prognostic indicator in oligodendrogloma patients. In a study by Cairncross et al. (194), approximately 15% of anaplastic oligodendrogliomas had p16 gene deletion and these patients exhibited significantly shorter overall survival when compared to those patients without this alteration. Furthermore, combined loss of 1p and 19q was inversely correlated with p16 gene deletion, suggesting that oligodendrogliomas may be subgrouped based on these genetic alterations (194).

4.2.3. Chromosome 10

Approximately 25% of anaplastic oligodendrogliomas exhibit allelic loss of 10q while

maintaining intact 1p and 19q chromosome arms, a genetic profile more consistent with an astrocytic, rather than an oligodendroglial tumor (194, 200). Indeed, this may hint that these tumors are actually glioblastomas with prominent oligodendroglial features (200). Allelic loss of 10q, however, is not predictive of survival in anaplastic oligodendrogloma patients (194), contrary to the expected finding if these tumors actually are glioblastomas masquerading as oligodendrogliomas.

4.2.4. EGFR

Although EGFR overexpression is primarily associated with high-grade astrocytomas, several reports implicate its importance in oligodendroglial tumors as well. Increased levels of EGFR expression have been demonstrated in the majority of oligodendrogliomas and are rarely due to EGFR gene amplification (137, 201-204). Based on the approximately equal incidence of EGFR overexpression in both low- and high-grade oligodendrogliomas, this alteration is most likely an early event in oligodendroglial tumor development and not associated with malignant progression of these tumors (201). Whether EGFR overexpression is of prognostic significance in these patients has not been reported.

5. Mixed oligoastrocytomas

Although mixed oligoastrocytomas were first identified by Cooper in 1935 (205), definitive criteria for their diagnosis and classification remain elusive (206). Tumors classified as mixed oligoastrocytomas consist of an eclectic assortment of tumors, ranging from those with distinct regions of oligodendroglial and astrocytic differentiation, to those with an admixture of the two elements. In addition, some cases feature oligodendroglial and astrocytic phenotypic features in the same cells, termed "hybrid" oligoastrocytomas (207). While the classical "pure" astrocytic and "pure" oligodendroglial tumors may be readily distinguished by the trained observer, effective classification of mixed oligoastrocytic tumors is, at best, subjective and remains controversial, even among the most experienced neuropathologists (120). These distinctions are of more than passing academic interest, since diffuse glioma classification has very real implications for patient prognosis and treatment planning. The incidence of mixed oligoastrocytomas has not been well defined, but probably does not exceed 10-20% of supratentorial gliomas (192, 208). Similar to the oligodendrogliomas, WHO guidelines distinguish low-grade and anaplastic subtypes of mixed oligoastrocytomas (1). These two subtypes of mixed glioma are distinguished by the features that separate anaplastic astrocytomas and anaplastic oligodendrogliomas from their respective low-grade counterparts.

5.1. Clinical features of mixed oligoastrocytoma patients

5.1.1. Low-grade mixed oligoastrocytomas

Mixed oligoastrocytomas typically afflict middle-aged patients, with a slight male predominance, and the great majority of these lesions are supratentorial, favoring involvement of the frontal lobe (209, 210). Similar to oligodendrogloma patients, seizures are a frequent presenting symptom for mixed glioma patients (211).

Genetic alterations in adult diffuse glioma

Though optimal management has not been defined for mixed oligoastrocytoma patients, at least a subset appears to be sensitive to the combined PCV chemotherapy regimen (212). Using the WHO classification system, Shaw *et al.* reported a median survival of 6.3 years for low-grade mixed oligoastrocytoma patients (209), although there is considerable variation among studies due to widely differing diagnostic criteria. It is generally accepted, however, that the greater the oligodendroglial component, the more benign the clinical course, since oligodendroglial tumors are typically less infiltrative and thus more amenable to surgical resection (178, 213). Other prognostically favorable clinical and histologic criteria are similar to those of the low-grade astrocytomas and oligodendrogliomas.

5.1.2. Anaplastic mixed oligoastrocytomas

Similar to their low-grade counterparts, anaplastic oligoastrocytomas most commonly affect the middle-aged, favor supratentorial locations, and frequently present with seizures. Optimal treatment remains to be clarified, though study of a limited patient population suggests that these tumors are sensitive to PCV chemotherapy (212). The median survival time is considerable shorter than for the lower grade variant, with one report of 2.8 years and survival rates at 5 and 10 years of 36% and 9%, respectively (209). Another study reported a median survival of only 1.1 years (22). Other prognostic criteria resemble those of anaplastic astrocytomas and oligodendrogliomas.

5.2. Genetic alterations and prognostic implications

The lack of unambiguous criteria for the definition of mixed oligoastrocytomas provides considerable latitude for classifying these tumors and incorporates a heterogeneous collection ranging from those with distinct regions of astrocytic and oligodendroglial differentiation to those with intermingled cells of each type. Furthermore, the widely variable extent of oligodendroglial and astrocytic differentiation in these tumors is not accounted for through current classification schemes (1). This variability, coupled with the relative rarity of these mixed tumors, may account for the paucity of studies focusing on the genetics of mixed oligoastrocytomas.

Most reports indicate that similar genetic alterations are found in mixed oligoastrocytomas as are found in pure astrocytomas and oligodendrogliomas, however, they tend to occur at lower frequencies in mixed gliomas (114, 118, 119, 195, 196). This observation suggests that the mixed oligoastrocytoma histologic type may include at least two subtypes of tumors, those with developmental origins resembling astrocytomas and those with development origins resembling oligodendrogliomas. For example, Maintz *et al.* (119) investigated a large collection of astrocytomas, oligodendrogliomas, and mixed oligoastrocytomas for genetic alterations that occur disproportionately between astrocytic and oligodendroglial tumors, including p53 mutations and allelic loss of chromosomes 1p and 19q. p53 mutations and allelic losses on 1p and 19q were inversely correlated in oligoastrocytomas, suggesting the existence of at least two

different subtypes of oligoastrocytomas based on these alterations, one with p53 point mutations genetically resembling astrocytomas and the other with allelic losses of 1p and 19q genetically resembling oligodendrogliomas.

6. SUMMARY

Our understanding of glioma development and progression on the molecular genetic level has expanded remarkably over the past decade and our ability to use this information for patient prognosis is surfacing. Although age and tumor grade remain the most powerful predictors of patient survival among astrocytic glioma patients, recent reports indicate that alterations of the PTEN tumor suppressor gene are independent predictors of overall patient survival for anaplastic astrocytoma patients, helping to distinguish those cases with behavior resembling their more malignant counterparts, the glioblastomas. The potential prognostic value of EGFR gene amplification in malignant astrocytoma patients stratified by age is intriguing and warrants further investigation. Among the oligodendroglial tumors, alterations of the 1p and 19q chromosome arms have emerged as potentially powerful predictors of overall patient survival and *in vivo* chemotherapeutic response, while alterations of the p16/CDKN2A tumor suppressor gene suggest shorter overall survival. As our molecular models continue to improve, through functional analyses and the identification of additional genetic contributors, we will expand our capacity to more effectively prognose these patients and to design rational therapeutic strategies.

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Genetic alterations in adult diffuse glioma

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