REVIEW ARTICLE

P53 and Brain Tumors: From Gene Mutations to Gene Therapy

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The p53 tumor suppressor gene (TP53) is the most frequently altered gene in human cancer and is also found mutated in several types of brain tumors. Loss of p53 function plays a central role in the development of cancer. The characterization of the biochemical pathways by which p53 alteration triggers tumorigenesis is the foundation for the design of novel therapeutic approaches.

Investigations of the intracellular mechanisms at the origin of p53 tumor suppressive functions have shown that p53 is a transcription factor able to sense a variety of cellular insults and induce a dual response: cell growth arrest/senescence or apoptosis. Less well studied are p53's influences on extracellular events such as tumor angiogenesis, immunology and invasion. Here, we review these findings and specifically discuss their implications for brain tumor genesis, molecular diagnosis and prognosis. Of clinical importance are the findings that brain tumors with wild type (wt) or mutant p53 status may respond differently to radiation therapy and that novel therapeutic strategies using TP53 gene transfer or specifically targeting tumor cells with mutated p53 are being evaluated in clinical trials.

Introduction

p53 is a 53kDa phosphoprotein that has an important function in preventing tumor formation by influencing both the intra- and extra-cellular environment. p53 exerts its tumor suppressive function by sensing cellular damage and integrating this signal into a response where cell cycle arrest and repair mechanisms take place, or where cell elimination by apoptosis or senescence occurs. More recent data show an important role for p53 in angiogenesis and tumor invasion, two fundamental processes in malignancy (reviewed in 56,60).

Biochemically, p53 forms tetramers and is a transcriptional activator of a specific subset of target genes containing a p53 binding domain (Table 1). p53 can also influence cellular functions by interacting with a variety of cellular proteins (Table 2); notably, its interaction with CBF/CBP and TBP inhibits transactivation of genes containing CCAAT and TATA regulatory elements (Table 3).

The variability of pathways in which p53 is involved could constitute an explanation for the high frequency of mutations found at the *TP53* locus in human tumors. Here, we review the molecular and physiological functions of p53 and examine how their loss favors brain tumor development. These findings show the importance of the *TP53* gene in astrocytic tumor formation and allowed the development of therapies for tumor cells with disrupted p53 tumor suppressor pathways.

p53 Function: intracellular effects

The major role postulated for p53 in cells of most human tissues is maintenance of genomic stability; hence its appelation as the "guardian" of the genome. This is accomplished in two ways: either directly by participating in the mechanisms maintaining DNA integrity or, indirectly, by inducing cell cycle arrest, senescence or apoptosis in damaged cells.

p53 and the mechanisms maintaining DNA integrity. p53 may influence genome integrity/stability through

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Genes	Function	P53 binding sequences	References**
A28-RGS14	regulator of G protein signaling		Buckbinder L., 1997, P.N.A.S.,* 4:7868
BAI1	inhibitor of angiogenesis		(80)
Bax	apoptosis promoter	tcACAAGTTa	(78)
		AGACAAGCCT	
CDKN1 (p21)	inhibitor of cyclin dependent kinases	GAACATGTCC	(30)
		cAACATGTTg	
Cyclin G (murine)	cell cycle regulator	AGACcTGCCC	Okamoto K., 1994, EMBO J., 13:4816
		GGGCAAGCCT	
Cytokeratine 8	major component of intermediate type of filament	ctGCcTcCaC	Mukhopadhyay T., 1996, Anticanc. Res., 16:105
DDR protein tyrosine kinase	receptor protein tyrosine kinase		Sakuma S., 1996, FEBS Lett., 398:165
EGF receptor	epithelial growth factor	AGACTAGgCC	Deb SP., 1994, Oncogene, 9:1341
		GAGCTAGCCC	
		GAGCgAGCTC	
EI24 (murine)	unknown function		Lehar SM., 1996, Oncogene, 12:1181
Fas/APO1	inducer of apoptosis		Owen-Schaub LB., 1995, Mol. Cell Biol, 15:3032
GADD45	inhibitor of cell entry in S phase by binding to PCNA	GAACATGTCT	Kastan MB., 1992, Cell, 71:587
		AAGCATGCTg	
GML	GPI-anchored gene	AtGCTTGCCC	Furuhata T., 1996, Oncogene, 13:1965
		AGGCATGTCC	
GD-AIF	inhibitor of angiogenesis		(111)
$HIC-1$	tumor suppressor		Makos-Wales M., 1995, Nat. Med., 1:570
IGF binding protein 3	inhibitor of IGF mitogenic signaling	AAACAAGCCac	Buckbinder L., 1995, Nature, 377:646
		CAACATGCTT	
MDM ₂	p53 inhibitor	GGtCAAGTTg	Oliner JD., 1992, Nature, 358:80
		GGACAcGTCC	
		GAGCTaAGTCc	
		tGACATGTCT	
MSH ₂	DNA-mismatch repair	AGGCTAGTTT	Sherer S.J., (1996), Biochem. Bioph. Res. Comm., 221:722
		AAGtTtcCTT	
Muscle MCK (murine)	ATP generator	tGGCAAGCCT	Weintraub H., 1991, P.N.A.S.,* 88:4570
		tGACATGgCC	Zhao J., 1994, Mol. Cell. Biol., 14:8483
P ₂ XM	ATP-gated ion channel	GAACAAGggC	Urano T., 1997, Canc. Res., 57:3281
		GAGCTTGTCT	
PCNA	proliferating cell nuclear antigen promoter	GAACAAGTCC	Morris GF., 1996, P.N.A.S.,* 93:895
		GGGCATaTqT	
PIG ₁	galectin-7	tAACcTGqTTc	(86)
PIG ₂	quanidinoacetate N-methyl transferarse	ccctcctCCqt	(86)
PIG ₃	quinone oxidoreductase homologue	GAGgccaaCa	(86)
PIG4	serum amyloid A	GTGCggaGgac	(86)
PIG5	normal keratinocyte mRNA	tGGqqccGCaq	(86)
PIG6	proline oxidase homologue	tcctTggaCCt	(86)
PIG7	TNF-a-induced mRNA	ctGggccTgaa	(86)
PIG8	etoposide-induced mRNA	AGctggtTTCc	(86)
PIG9	tax1-binding protein	cGtCccGgagc	(86)
PIG10	actin-binding protein	AGctcacTCCa	(86)
PIG11			
	unknown	AGGCTgtCCag	(86)
PIG12	microsomal glutathione transferase homologue	tGAqTccCTqt	(86)
PIG13	unknown	AGAtgctgdag	(86)
TGFa	growth regulator	GGGCAgGCCC	Shin TH, 1995, Mol. Cell Biol. 15: 4694
		tGcCTAGTCT	
		AGcCAAGTCT	
		tGGCAAGCqq	
TGFb	growth regulator		(31)
TSP-1	angiogenesis inhibitor		(24)
WIG 1	unknown		Varmehziaie S., 1997, Oncogene, 15:2699
WIP-1	nuclear phosphatase		Fiscella M., 1997, P.N.A.S.,* 94:6048
*P.N.A.S.: Proc. Natl. Acad. Sci. USA.			
	**Due to space limitations references in tables are not cited in bibliography unless they appear in article text		

Table 1. Genes transactivated by wild type p53.

several functions: i) cells expressing mutant p53 protein show an increase of spontaneous **intra-chromosomal recombination**, a hallmark of cancer (13, 74). This might be due to loss of wt p53's ability to bind and inactivate Rad 51, a protein involved in homologous recombination (104) (Table 2). ii) p53 interacts through its Cterminal domain with transcription-repair TFIIH-associated factors such as ERCC 2 and ERCC 3 (Table 2) involved in **strand-specific DNA repair** (120). iii) p53 prevents **multiple DNA replication** before mitosis (27), a process that may lead to polyploidy, a regular feature of cancer. The relationship between *TP53* status and genomic ploidy has been examined in a series of 15 low grade astrocytomas that progressed to higher grade gliomas. All the anaplastic recurrences of gliomas harboring *TP53* mutations were non diploid, whereas two out of seven gliomas with intact *TP53* remained diploid (113). Similarly, *TP53* loss preceded genome duplication in a p53-null glioblastoma (3). iv) Lack of p53 results in high frequency of **gene amplification** in normal human fibroblasts when treated with PALA, a drug able to induce cell growth arrest by inhibition of uridine biosynthesis (64). *TP53* mutation, however, is not a prerequisite for DNA amplification. Most glioblastoma which show amplification and rearrangement of the *EGFR* gene express wt p53 and those with mutated forms of p53 rarely amplify *EGFR* (118). Other examples are *MDM2* and *N-MYC* gene amplifications which occur in wt p53 containing astrocytoma (88) and neuroblastoma (49), respectively. v) Correct spindle bipolarity and spindle microtubule assembly are essential to ensure balanced **chromosome segregation** during cell

Proteins	References**				
Viral factors					
Adenovirus 2, 5 & 12 E1B Epstein Barr Virus (EBV) EBNA-5 Epstein Barr Virus (EBV) BZLF1 Hepatitis B Virus X protein Human Cytomegalovirus (HCMV) IE84 Human Herpesvirus 6 (HHV6) orf1 Human Papilloma Virus (HPV) 16 & 18 E6 Simian Virus 40 (SV40) large T antigen	Sarnow P., 1982, Cell, 28:387 Yew PR, 1992, Nature, 357:82 Szekely L., 1993, P.N.A.S.,* 90:5455 Zhang Q., 1994, Mol. Cell Biol., 14:1929 Wang XW., 1994, P.N.A.S.,* 91:2230 Speir E., 1994, Science, 265:391 Kashanchi F., 1997, Oncogene, 14:359 Scheffner M., 1993, Cell, 75:495 Lane DP., 1979, Nature, 278:261				
General transcription factors					
1) TFIID components TAFII31 TAFII40 (drosophila) TAFII60 (drosophila) TATA box binding protein (TBP) 2) TFIIH components TFIIH CSB	Lu H., 1995, P.N.A.S.,* 92:5154 Thut CJ., 1995, Science, 267:100 Thut CJ., 1995, Science, 267:100 Horikoshi N., 1995, Mol. Cell Biol., 15:227 Xiao H., 1994, Mol. Cell. Biol., 14:7013 (120)				
ERCC2 (XPD) ERCC3 (XPB) p62	(120) (120) Leveillard T., 1996, EMBO J., 15:1615				
3) TFIIIB components TFIIIB90	Chesnokov I., 1997, Mol. Cell. Biol., 16:7084				
Transcriptional activators					
CCAAT binding factor (CBF) CBP p300 Sp1 WT1	Agoff SN., 1993, Science, 259:84 Gu W., 1997, Cell, 90:595 Avantaggiati ML., 1997, Cell, 89:1175 Borellini F., 1993, J. Biol. Chem., 268:7923 Maheswaran S., 1995, Genes Develop., 9:2143				
p53 posttranscriptional modulators					
c-Ahl Casein kinase II Redox repair protein Ref1	Goga A., 1995, Oncogene, 11:791 Filhol O., 1992, J. Biol. Chem., 267:20577 Jayaraman L., 1997, Genes Develop., 11:558				
p53 turnover components					
MDM ₂ MDM-X Ubiquitin and conjugating enzymes	Momand J., 1992, Cell, 69. 1237; Oliner JD., 1992, Nature, 358:80 Shvarts A., 1996, EMBO J., 15:5349 Scheffner M., 1993, Cell, 75:495				
Others					
70kD heat shock protein Hypoxia inducible factor 1a p53-BP1 and p53-BP2 p73b Rad 51 S100b Topoisomerase 1	Graeber TG., 1994, Mol. Cell Biol., 14:6264 An W.G., 1998, Nature, 392:405 Iwabuchi K., 1994, P.N.A.S.,* 91:6098 Kaghad M., 1997, Cell, 90:809 (104) Baudier J., 1992, P.N.A.S.,* 89:11627 Gobert C., 1996, Biochem., 35:5778				
*P.N.A.S.: Proc. Natl. Acad. Sci. USA. ** Due to space limitations references in tables are not cited in bibliography unless they appear in article text.					

Table 2. Proteins which interact with p53.

division. p53 interacts with the centrosome during interphase and controls centrosome duplication (17). When spindle assembly is blocked by anti-microtubule agents p53 prevents cell cycle progression (23). In mouse embryonic fibroblasts lacking p53, abnormal centrosome amplification and imbalanced chromosome segregation are observed (32).

Cell cycle arrest/senescence and apoptosis. The second set of mechanisms by which p53 accomplishes maintenance of genomic stability is arrest of the cell cycle and/or apoptosis. Both pathways are induced by DNA damage and have as their ultimate result the repair or elimination of DNA damaged cells. Therefore, these two mechanisms are very important to avoid tumor initiation and/or progression both in the brain and in other human tissues. The decision for p53 whether to act as an apoptosis or cell growth arrest inducer depends on the cell type, its molecular background and the retinoblastoma pathway (39, 40, 85).

a) p53 and cell cycle arrest/senescence. p53 is able to suppress the cell cycle at the G1 and G2/M transitions (2, 63, 103) . In leukemia cells a reversible G1 cell cycle arrest might give time to damaged DNA to be repaired, but in human fibroblasts p53 cell cycle arrest is an irreversible senescent-like process (28, 97). Some studies suggest that p53-induced growth arrest is reversible in human glioma cells (75), but others show that *TP53* transfer induces particular morphological changes reminiscent of a quiescent/senescent cellular state (112).

The main **molecular mechanism** by which p53 induces cell growth arrest is acting as a transcription factor. Many genes involved in cell cycle regulation are induced by p53 (Table 1), but the main effector of the p53-mediated cell cycle arrest is p21, a 21 kDa protein encoded by the *CDKN*1 gene (30) (Table 1). p21 interacts with cyclin-dependent kinase complexes and inhibits their activity, required for cell cycle progression (37). p21 induction through *CDKN*1 gene transfer, or, indirectly, after *TP53* transfer arrests glioma cell growth (51, 112). This was accompanied by loss of tumorigenic capacity in vivo both in peripheral and intracerebral xenograft models (19). However, the absence of *CDKN*1 gene mutations in human glioma (108) suggests that p21 is a growth suppressor rather than a genuine tumor suppressor. Other genes involved in cell cycle control that were found regulated by p53 in human glioma cell lines are PCNA and TGF β (31, 76) (Tables 1 and 3).

b) p53 and apoptosis. Transfer of *TP53* can induce apoptosis in different cell types, including human glioma cells (61). Evasion of the pathways leading to apoptosis is critical for the development of tumors and their restoration holds promise for clinical treatment (reviewed in 56, 60). For example, p21 is an important downstream mediator of p53-dependent cisplatininduced apoptosis (58).

Although different stimuli were shown to induce p53-dependent apoptosis, such as DNA damage, expression of the myc adenovirus E1A proteins and withdrawal of growth factors (reviewed in 56), the **molecular mechanisms** of p53 induced apoptosis are still unclear. In some cases it seems that p53 transactivating function is important to determine cell susceptibility to apoptosis, while in other cases apoptosis is mediated by p53 tran-

Genes	References**				
Viral factors					
Hepatitis B Virus (HBV) X Herpes Simplex Virus (HSV) thymidine kinase Herpes Simplex Virus (HSV) UL9 Human Cytomegalovirus (CMV)	Takada S., 1996, Virology, 216:80 Yuan JN., 1993, Biochem. Biophys. Res. Comm., 191:662 Subler MA., 1992, J. Virol., 66:4757 Subler MA., 1992, J. Virol., 66:4757				
early promoter Human Immunodeficiency Virus (HIV) Type I LTR Human Papilloma Virus (HPV) Types 6, 16 & 18 Long Control Regions	Subler MA., 1992, J. Virol., 66:4757 Subler MA, 1994, J. Virol., 68:103 Desaintes C., 1995, Oncogene, 10:2155				
Human T cell Lymphotropic Virus (HTLV) Type I LTR	Subler MA., 1992, J. Virol., 66:4757				
Rous Sarcoma Virus LTR Simian Virus 40 (SV40) immediate early promoter and enhancer	Subler MA., 1992, J. Virol., 66:4757 Subler MA., 1992, J. Virol., 66:4757 Perrem K, 1995, Oncogene, 11:1299				
Oncogenes					
c-Fos c-Jun b-Myb	Ginsberg D., 1991, P.N.A.S.,* 88:9979 Ginsberg D., 1991, P.N.A.S.,* 88:9979 Lin D., 1992, P.N.A.S.,* 89:9210				
DNA replication associated factors					
DNA polymerase a Polymerase III transcribed templates Topoisomerase Ila	Lin D., 1992, P.N.A.S.,* 89:9210 Chesnokov., 1996, Mol. Cell Biol., 16:7084 Wang Q., 1997, Mol. Cell Biol., 17:389				
Cell cycle associated factors					
Basic FGF Bcl-2 Cyclin A IGF-I receptor IGF-II PCNA	(109) (77) Yamamoto M., 1994, Exp. Cell Res., 210:94 Werner H., 1996, P.N.A.S.,* 93:8318 Zhang L., 1996, Canc. Res., 56:1367 (76)				
Others					
b-Actin Fibronectin Human O6-methylguanine-DNA methyltransferase	Ginsberg D., 1991, P.N.A.S.,* 88:9979 lotsova V., 1996, Cell Growth Diff., 7:629 Harris LC, 1996, Canc. Res., 56:2029				
Hsc70 heat shock protein Hsp70 heat shock protein Interleukine-6	Ginsberg D., 1991, P.N.A.S.,* 88:9979 Agoff SN., 1993, Science, 259:84 Santhanam U., (1991), P.N.A.S.,* 88:7605 Margulies L., (1993), J. Biol. Chem., 268:15096				
Multiple Drug Resistance gene I Nitric Oxide Synthase 2 p53 Rat brain creatine kinase	Chin KV., 1992, Science, 255:459 Forrester K., 1996, P.N.A.S.,* 93:2442 Ginsberg D., 1991, P.N.A.S.,* 88:9979 Zhao J., 1994, Mol. Cell Biol., 14:8483				
Retinoblastoma Serum glucocorticoid-inducible protein kinase	Shiio Y., 1992, P.N.A.S.,* 89:5206 Maiyar AC., 1997, Mol. Endocrinol., 11:312				
VEGF	(115)				
**P.N.A.S.: Proc. Natl. Acad. Sci. USA. ** Due to space limitations references in tables are not cited in bibliography unless they appear in article text.					

Table 3. Genes repressed by p53

scriptional repression activity. Both cases are in agreement with p53's ability to induce the expression of the BAX gene and to repress the Bcl-2 gene (Tables 1 and 3) (77, 78) . Recently, a new model for p53 induced apoptosis was proposed, where p53 transcriptionally induces redox-controlling genes that promote an increase in reactive oxygen species (ROS) (Table 1) which consequently leads to oxidative damage and apoptosis (86).

Other studies using somatotropic progenitors, immortalized by expression of the SV40 T-antigen, show p53 induced apoptosis independent from new RNA and protein synthesis (18). This was confirmed by deletion studies showing that p53-induced apoptosis could be prevented by removal of the N-terminal proline-rich domain of p53, although this did not affect p53's transactivation capacity. This domain likely plays an important role in triggering apoptosis by interacting with other proteins through its Pro-X-X-Pro motifs (93,119). Taken together, all these data indicate that p53 may have separate transcription-dependent and -independent pathways to induce cell death and suggest that the chosen apoptotic mechanism is cell type specific.

Contradictory data have been obtained in the study of p53 involvement in radiation-induced apoptosis in glioblastoma cells. In one study, inactivation of endogenous wt p53 by expression of a dominant negative p53 mutant in U87MG cells prevented apoptosis and made the cells resistant to irradiation (127). In another study, radiation response was shown to depend on p53-induced G1 arrest and p53-independent apoptosis in the same cells (35 .

p53 Function: effects on the microenvironment

p53 and angiogenesis. Angiogenesis is a complex process through which new blood vessels are formed from preexisting ones. Without neovascularization tumors remain small and dormant, a condition where cell renewal is balanced with cell death through apoptosis. Tumor establishment, growth and metastasis occur only with a switch to the angiogenesis phenotype, a state where unbalanced production of activators and inhibitors induces active growth of blood vessels. Both the physiological state of the tumor cells and alterations in specific genes trigger this switch. p53 can affect this process by different mechanisms in different tissues. First, in BT549 human breast carcinoma cells, the reintroduction of a wt *TP53* gene augments the secretion of angiogenesis inhibitor thrombospondin-1 (TSP-1)(24, 116). Second, in cultured fibroblasts from Li-Fraumeni patients the angiogenic switch coincides with loss of *TP53* (24) , which is consistent with the capacity of p53 to induce TSP-1 and repress VEGF expression in these cells (Tables 1 and 3)(115). In contrast, in glioblastoma cell line LN-Z308, p53 is not involved in the regulation of TSP-1 or VEGF (83), but induces the release of an as yet unidentified inhibitor of angiogenesis (111). Recently, a candidate for this activity has been identified (80) (Table 1).

Further data show that mutant p53 can confer an angiogenic gain of function. Experiments made in human glioblastoma cell line U87MG suggest that mutant p53 induces the release of bFGF, whereas wt p53 represses the same factor (Table 3) (109). Finally, in NIH-3T3 cells mutant p53 synergizes with protein

kinase C (PKC) and 12-0-tetradecanoylphorbol-13 acetate (TPA) to enhance VEGF production (52).

p53 and invasion. Astrocytoma of all grades invade surrounding normal brain areas, resulting in difficult clinical management of the patients and high recurrence rates. It has recently been shown that induction of wt p53 in osteosarcoma cells partially reduced their invasive capacity (62). The high frequency of p53 mutations in glioblastoma and the invasive nature of this tumor, certainly warrants examining a potential role for p53 in this process.

p53 and the immune system. The accumulation of either wt or mutated forms of p53 in most human cancers suggests that p53 might elicit immune responses that could be exploited for immunotherapy. The finding of p53 antibodies in sera of tumor patients has demonstrated the presence of a B-cell response to p53 accumulation (67, 96). Such a response constitutes an early way to detect *TP53* mutations in the progression of lung cancer (68). These antibodies were mostly IgG, consistent with a T cell dependent response. A T cell response was also evidenced when p53-derived peptides were used, suggesting that injections of p53 peptides could be a way to enhance immunological recognition and killing of tumor cells by cytotoxic T lymphocytes (CTL)(126). Recent experiments have shown that tumor development could be inhibited by MHC class I restricted CTL responses specific for mutated or wt p53 peptides (73, 92, 114).

These preliminary results should encourage the evaluation of this kind of anticancer immunotherapy for brain tumors.

Another area of interest which has not been explored to date is to evaluate whether cells which have inactivated p53 may have a different susceptibility to immune system recognition than those expressing wt p53.

TP53 mutation spectrum in brain tumors

The specific nucleotides found mutated in genes altered in tumors are the relics of a combined chemical and biological process. They reflect the exposure of some tissues to specific carcinogens and the chemical interactions of these with cellular DNA and repair systems. The mutations that will ensue undergo an indirect biological selection process since only cells in which they confer a growth advantage leading to cancer will survive. Therefore, analysis of the mutation spectrum of such genes can give us some clues to the etiology and molecular pathogenesis of neoplasia (36, 45).

cell lines	origin	induction mode §	TP53 mutations	references		
$EN-1$	type-1 astrocyte	ENU	249: ATC (I) \rightarrow AAC (N)	(43)		
$EN-2$	type-1 astrocyte	ENU	111: TTC $(F) \rightarrow GTC$ (V)	(43)		
$EN-3$	type-1 astrocyte	ENU	229: ATC (I) \rightarrow AGC (S)	(43)		
$EN-5$	type-1 astrocyte	ENU	278: AGT (S) \rightarrow ATT (I)	(43)		
$EN-6$	type-1 astrocyte	ENU	111: TTC $(F) \rightarrow TCC$ (S)	(43)		
$9L*$	unknown	NMU	277: GGG (G) \rightarrow GAG (E)	(5, 10)		
$T9*$	unknown	NMU	wild-type	(22)		
C ₆	unknown	NMU	wild-type	(5, 10)		
RT-2	unknown	ASV	wild-type	(9, 47)		
RG-2 (D74)	unknown	ENU	unknown	(1, 8, 89)		
ENU: N-ethyl-N-nitrosourea, Ş. NMU: N-nitroso-methylurea ASV: avian sarcoma virus * 9L and T9 are subcultures of the same initial cell line propagated independantly (Barth RF (1998) Journal of Neuro-Oncology 36: 91-102).						

Table 4. TP53 mutations in transformed rat glioma cell lines.

TP53 mutation sites. All classes of mutations (deletions, insertions, transitions and transversions) occur in the *TP53* gene. Point mutations which alter p53 function cluster in the hydrophobic central part of the protein (87% in exons 5-8), where many base substitutions alter the protein's conformation and/or its function. This is partially biased due to the fact that most investigators have limited their analyses to exons 5-8. Frame shift and nonsense mutations that truncate the molecule are also situated outside of this region (reviewed in 34). Although more than 250 codons in *TP53* are potential human mutation sites, 25% of all mutations found in human tumors comprise only five of these codons (175, 245, 248, 249 and 273).

Crystallographic analysis allowed to realize that the frequency of *TP53* point mutations decreases at increased distances from the regions involved in p53 DNA binding and that two classes of mutations can be distinguished: mutations of codons directly involved in DNA binding and mutations of residues important for the stable folding of the protein. Two of the most frequently mutated codons (248 and 273) are situated at the large loop 3 and at the β strand loop helix motif, respectively, and are therefore crucial points of p53/DNA contacts, whereas, the hot spot mutation 175 is part of the large loop 2 and has an important role in stabilizing the p53/DNA complex (21) (Figure 1).

TP53 mutations in tumors of the CNS. Analysis of the *TP53* status and overexpression of p53 have been well documented in primary central nervous system (CNS) tumors (Figure 1). Mutations in *TP53* are almost restricted to tumors of astrocytic origin. Currently, the most sensitive protocol for *TP53* mutation detection shows frequencies of 67% in anaplastic astrocytoma,

Figure 1. Representation of all p53 amino acid mutations found in brain tumors as reported by the IARC database: http://www.iarc.fr. The colors of the boxes indicate the tumor type (right hand legend), the letters and symbols in the boxes indicate the type of mutation (left hand legend), black squared boxes indicate the starting site of a frameshift (left hand legend). Mutations at the three hotspot sites (175, 248, 273) are indicated with black columns with a distinctive color and the total number of mutations on the top.On the top left hand legend the particular mutations for each of these are listed. Regions and residues implicated in DNA interaction and protein stability as well as the conserved domains of the protein and the intron/exon boundary sites are indicated (left hand legend).

and 41% in glioblastoma multiforme (106). Mutation frequencies are much lower in oligodendroglioma (13%), medulloblastoma (11%), pilocytic astrocytoma (<5%) and virtually absent in other CNS tumors (reviewed in 54).

The finding of a lower frequency of mutations in glioblastoma (41%) versus anaplastic astrocytoma (67%) lead to hypothesize that glioblastoma was a pathological entity that might be genetically diverse. This idea was reinforced when much lower frequencies of *TP53* mutations (11%) were found in glioblastoma that occured without clinical evidence of a prior less malignant lesion (called *de novo* or primary glioblastoma) as compared to those resulting from the recurrence of a grade II/III astrocytoma (called secondary glioblastoma) (67%) (121). Analysis of other genetic defects in glioblastoma also suggested at least two subtypes (see below). These data also suggested that a large fraction (59%) of glioblastoma occured without the apparent need for a mutation in the *TP53* gene. This result was compatible with several scenarios: i) these glioblastoma develop independently of the p53 pathway, ii) the p53 pathway is altered by alternative mechanisms, iii) wt p53 produced in these cells is functionally inactive and, iv) these tumors have homozygous *TP53* deletions and the wt *TP53* alleles detected derive from non-tumoral cells. The last two issues were addressed by examining *TP53* status and p53 function in glioblastoma cell lines. About 25% have wt *TP53* alleles and express p53 that is transcriptionally competent *in vivo* (110, 112). Cell lines null for *TP53* do occur but are uncommon (3). In conclusion, this suggests that some glioblastoma can occur through a p53-independent pathway or that the need for p53 mutation is bypassed by alterations in other genes of the same pathway. It was demonstrated that amplification of mdm2, a negative regulator of p53 occurs in about 10% of tumors (88). Mutations in $p19^{ART}$, a gene encoding a protein able to downregulate mdm2 may provide a similar effect (128), but this remains to be examined in brain tumors.

The most frequent *TP53* alterations are GC-AT transversions that occur at CpG sites by deamination of 5' methylcytosine and are considered to be spontaneous. There are no brain tumor-specific mutations, the three most commonly mutated codons are in order of frequency: 273, 248 and 175. In other human tumors the most frequently mutated codons are 248, 249 and 175 (reviewed in 15) . Whether this has any meaning is uncertain since there is no data indicating a defined role of specific mutants in brain tumorigenesis.

Clearly, a very interesting question is to determine whether loss of wt p53 biological function is essential for progression from low grade astrocytomas to secondary glioblastoma and if this genetic event is an initial, early or late step during glioblastoma development. In contrast to carcinoma where *TP53* gene mutations occur late during tumor progression, *TP53* mutations occur at similar frequencies in astrocytoma grade II, III and in secondary glioblastoma suggesting that they are an early event in the progression of this tumor type (81, 117). Further analysis in tumor pairs of patients showing malignant recurrence from low grade or anaplastic astrocytoma to secondary glioblastoma showed that most cells of the recurrent tumors harbored mutated *TP53*. These mutations were already present in cells of the primary tumors suggesting that recurrence had occured by clonal expansion of cells with mutated *TP53* (41, 100, 105). Since only a fraction of the cells in the original low grade tumors harbored *TP53* mutations one might conclude that *TP53* is an early progression event rather than "the" initiation event. Such interpretation is complicated, however, with the difficulty of excluding the substantial presence of normal brain in these "diffuse" tumors. Thinking of *TP53* mutation as an early progression event is in accordance with wt p53 function in the cell. In fact, since cells lacking wt p53 should be genetically unstable, they might accumulate additional alterations at an increased rate, facilitating progression to a more malignant stage.

There is also evidence that *TP53* mutation may be "the" initiation event in astrocytoma. Brain tumors occur in patients with germline *TP53* mutations; families with Li-Fraumeni syndrome present an incidence of CNS tumors of 13%, most of which (73%) are astrocytomas (55). Also, a significant fraction of patients with multifocal glioma showed constitutively mutated *TP53* alleles (59). This theory is reinforced by the observation that the pattern of mutations in sporadic and inherited brain tumors is similar. Further evidence derives from spontaneous immortalization of astrocytes derived from *TP53* knockout mice and their subsequent transformation *in vitro* (14, 125). All this information is consistent with *TP53* mutations accompanying astrocytoma initiation/early progression, but does not prove causality. Causal involvement of *TP53* alteration in the disease was provided by functional studies restoring p53 function in cell lines, demonstrating growth arrest or apoptosis as described above. These studies were biased by the use of vectors leading to overexpression of *TP53* and the use of cell lines with mutated p53 derived from de novo glioblastoma (Ishii et al, manuscript in preparation). Stronger evidence for p53 involvement in the transformation of the astrocytic lineage will have to await specific generation of astrocytoma in animals engineered to lack *TP53* alleles in these cells, either through transplantation studies or generation of tissuespecific knockouts.

Carcinogenesis of CNS tumors. Many epidemiology studies have been designed to identify risk factors for brain tumor development. However, the data on noninherited factors are controversial and a specific exposure or causative environmental agent has not been identified yet, with the exception of therapeutic irradiation to the brain (discussed in detail in (25). Only experimental studies in rodents have shown that several classes of chemical carcinogens selectively induce tumors in the CNS. Nitrosourea-derivatives and other alkylating agents are considered as powerful compounds which cause CNS neoplasms in rats after systemic administration. These agents induce the formation of oligodendrogliomas, astrocytomas, ependymomas, primitive neuroectodermal tumors (PNETs) with neural differentiation, and malignant schwannomas (53). This wide variation of histology may indicate that most cell types which construct central and peripheral nervous tissues are susceptible to such carcinogens. The ultimate carcinogen of these alkylating agents is considered to be the methyl or ethyl cation. Interaction of these cations with cellular DNA causes gene mutations leading to malignant transformation of cells. For example, Nethyl-N-nitrosourea (ENU) induces adduct formation on the $O⁶$ position of guanine. This is misrepaired into adenine and causes $G:C\rightarrow A:T$ transitions.

TP53 gene alterations were found in rat glioma cell lines which are transformed by N-ethyl-N-nitrosourea (ENU) (43, 44) (Table 4). All the mutations were located in conserved domains II-V which show 92% homology between human and rat and harbor approximately 95% of *TP53* gene mutations in human tumors. In contrast, spontaneously immortalized and transformed rat type 1 astroglial cell lines showed no alterations in the *TP53* gene (43). This might suggest that cell immortalization may be regulated by gene alterations other than *TP53*, and that *TP53* gene mutation may correlate more with later stages of carcinogenesis. However, as the DNA mutations found in the *TP53* gene were not always compatible with the mechanism of carcinogenesis associated with ENU, other mutagenic factors are not excluded. Furthermore, these results in type 1 rat astrocytes contrast with those obtained with cortical astrocytes of mice where *TP53* nullizygosity was shown to confer immortality (14, 125).

Biological role of mutant p53. Mutant p53 proteins may have different biological activities compared to wt p53. Usually, they have longer half life and may have cytoplasmic as well as nuclear localization (4). Experimental evidence has shown that in general mutant p53 proteins are not able of specific DNA binding and transactivation and have lost the capacity to arrest cell growth. Nevertheless, it is important not to consider all p53 mutants as similar because individual hot spot mutants differ in their properties and may have different behaviors in specific cell types, which might explain why p53 mutation profile differences exist between histological subtypes of cancer. Although there are examples which indicate that these differences are due to exposure to a specific carcinogenic risk (26), at this point we cannot exclude that some p53 point mutations can give tissue specific growth advantages.

It has been shown that heterooligomers between wt and mutant p53 peptidic chains may have an altered conformation which results in a protein tetrameric complex unable to bind DNA and activate transcription. Thus, the presence of a mutant *TP53* allele can have a **dominant negative** effect on the wt allele (102). Nevertheless, it is not possible to predict p53's biological function based only on its conformation. For example, the two "hot spot" DNA contact mutants (248W and 273H) have completely lost p53 biological activity, but maintain wt conformation (82), and heterooligomers between these mutants and wt p53 are, in some cases, able to specifically bind DNA (91). Moreover, the frequent conformational mutant 175H does not seem to be always fully dominant over endogenous wt p53. By induction of mdm2 protein and retention of G1 arrest after irradiation, it was shown that colorectal adenoma cells maintain wt p53 activity when transfected with 175H-p53, but lose it when transfected with 273H-p53 (124). These contradictory data indicate that the dominant effect of mutant over wt p53 could be dependent on the type of p53 mutation as well as on the genetic background of the cell. An issue that has not yet been explored is that cells expressing both mutated and wt *TP53* alleles may contain heterooligomers that lose wt p53-mediated cell cycle control but maintain other biochemical functions mediated by p53.

Some p53 mutants seem to be capable of conferring increased tumorigenicity and metastatic potential on a p53-null background; as an example, it was shown that mutated *TP53* alleles may attenuate p21-mediated growth arrest in glioblastoma cells (51). This **gain of function** of p53 mutants can be achieved by different mechanisms: (i) the ability to stimulate the transcription of several cellular and viral promoters (6, 29, 31, 69, 70, 109, 123); (ii) interaction with cellular proteins p38 and p42 (20); (iii) synergism with protein kinase C in order to induce the expression of the VEGF gene (52); (iv) antagonism of deregulated c-myc-mediated enhancement of apoptosis and decrease in leukemogenicity (65).

Still, there are data that deny the capacity of p53 mutants to confer tumorigenic and metastatic potential. Harvey et al. (38) have shown that a specific mutant *TP53* transgene accelerates tumor development in heterozygous but not nullizygous p53-deficient mice, which indicates the possibility of a dominant-negative effect, but not of a gain of function by mutant p53.

p53 as a prognostic factor for astrocytic gliomas

The limitation of classification based on morphological criteria for glioma has stimulated research for diagnostic and prognostic factors based on molecular analysis. This approach now suggests that two types of glioblastomas exist: type 1 would be characterized by *TP53* gene mutations, would predominantly occur in younger patients and have better prognosis. In contrast, type 2 tumors would show amplification of the *EGFR* gene, loss of heterozygosity on chromosome 10, be commonly found in older age and have poor outcome (118). In a number of cancers, including breast (12,101), lung (46), gastric (72) and colorectal (33), mutation of the *TP53* gene is correlated with more aggressive tumors, a higher rate of metastasis, and worse prognosis. Similar studies were performed on astrocytic tumors, but the correlation between *TP53* gene status and their prognosis is not clarified yet. Here, we will discuss similar studies on astrocytic tumors by focusing on those where *TP53* status was determined by sequencing, since in our opinion p53 immunohistochemistry does not allow reliable *TP53* status determination. Some researchers suggest that *TP53* mutations have no effect on survival of patients with astrocytic tumors (87). Others propose that *TP53* mutation could be an unfavorable factor in childhood malignant gliomas (84), but this is biased by the fact that *TP53* mutations occur almost exclusively in pediatric brain stem gliomas, which are known to have a very poor prognosis. Another group thinks that relative poorer prognosis of gemistocytic astrocytomas as compared to other types of grade II tumors may be linked to their higher frequency of *TP53* mutation (122). In contrast, the existence of *TP53* mutations in recurrent high-grade tumors may indicate better prognosis (113).

From a clinical perspective, postsurgical determination of *TP53* status would be of great importance and could help to establish new treatment strategies for the astrocytic tumors. There is still much controversy as to the therapeutic protocols to be used in these patients. The roles of chemotherapy and radiotherapy remain unclear, both in low- and high-grade astrocytomas (94). Recent studies in human carcinomas, such as colorectal (11), ovarian (90, 98), and acute lymphoblastic leukemia (71), as well as laboratory tests in glioma (50) and other tumor cell lines (66), have shown that mutation of p53 inactivates the p53-dependent apoptotic pathway and induces chemo- and radio-resistance. Replacement of normal p53 function, or stimulation of the apoptotic pathway leads to re-establishment of chemosensitivity (79, 98). Therefore, it has come as a surprise that glioblastoma with wt *TP53* have much poorer prognosis than those with mutant *TP53*. This might be due to the mutation of other genes in the former group making them more radioresistant (107). Since only 35 patients were analyzed in this study it will be important to confirm this finding in larger patient populations.

Gene therapy

Since conventional treatment protocols against astrocytic gliomas have shown their limitations in improving the prognosis of the patients, new strategies are required for a therapeutic breakthrough. The number of these alterations and the quasi-impossibility to target all tumor cells do not give much sense to a pure gene replacement strategy. However, gene therapy acquires a new meaning for cancer therapy if it is used to regulate biological functions. The transferred genes become molecular tools delivering products that stably counterbalance altered physiological equilibriums characteristic to the local tumor microenvironment.

Most current approaches aim to induce selective tumor cell death by apoptosis or senescence after gene transfer (95). With this respect, the wt *TP53* gene appears a suitable candidate for the therapy against the astrocytic gliomas because of its cell autonomous roles in cell cycle arrest after DNA damage, its activation of apoptosis or senescence, and its cell extrinsic potential to induce secretion of anti-angiogenic molecules. Badie et al., used adenoviral vectors to transfer human wt *TP53* genes into established 9L glioma in rat brain. *TP53* gene transduction inhibited tumor growth by 40% and induced cell phenotypic changes *in vitro* (7). Köck et al (57) further investigated the effects of two adenoviruses containing wt *TP53* genes under the control of different promoters on six human glioblastoma cell lines. Growth suppression of human glioblastoma cells *in vitro* and subcutaneous xenografted tumors in nude mice was obtained independently of endogenous *TP53* status in these cells. Apoptosis and tumor regression were only detected when cells were infected with the virus expressing high levels of p53. Tumors regressed to undetectable sizes for 2 months upon 3 intratumoral injections, but recurred 1 month later in 3/5 animals. Li et al (61) also reported that overexpression of p53 protein produced by adenovirus-mediated wt *TP53* gene transfer induces apoptosis of human glioma cells regardless of endogenous *TP53* status. Despite of several advantages, adenoviruses express proteins that trigger immune responses, thereby repeated dosing might be limited. As gene expression may not be permanent, and as glioma cells infiltrate normal brain tissue, repeated delivery of vectors would be necessary for successful therapy.

Unlike viral vectors, DNA-liposome complexes are non-infectious, non-immunogenic, and show low toxicity in vivo. Hsiao et al. injected a liposome-wt *TP53* complex into a cavitary glioblastoma model. This model is created by injecting glioma cells into the peritoneal cavity of nude mice, supposedly mimicking the postsurgical cavity remaining in glioblastoma patients (48). Liposome-DNA complexes penetrated over 20 tumor cell layers and massive necrosis was induced. Tumor cells near the necrotic area expressed exogenous wt p53. Furthermore, mice bearing *TP53* treated tumors survived significantly longer compared to those treated with vector controls (average survival 26 days vs. 15 days). *In vitro*, their study showed that cell growth was inhibited by 54%. Since low efficacy of liposome transfection is the main disadvantage, a number of strategies for enhancing the efficacy have been investigated. (16,48).

In conclusion, reviewing published data revealed that re-introduction of wt *TP53* genes into human glioma inhibit their growth to some degree. However, from a clinical point of view, it is doubtful whether this partial growth inhibition will have a clinical effect on glioma patients by itself, but it could provide useful in combination therapy. The ongoing phase 1 clinical trials with p53 gene transfer will soon address the safety of these treatments. Development of novel gene transfer technology and introducing these new concepts in the clinic will contribute to improved efficacy of this modality in the future, hopefully leading to substantial improvement of the prognosis of patients with CNS tumors.

Viral therapy specific for tumor cells with mutant p53

When an adenovirus infects a cell, p53 gets upregulated due to expression of the viral E1A gene product. p53 increase would normally result in cell cycle arrest or apoptosis, but the virus has evolved a mechanism to circumvent this by expressing the E1B 55kDa protein whose function is to bind and inactivate p53. In tumor cells lacking p53 function, the *E1B* gene is not necessary for viral replication. This feature was exploited to design a new replication-competent adenovirus for cancer therapy. This virus carries an alteration in the *E1B* gene, restricting its replication capacity to tumor cells lacking wt p53 expression. Since virus replication in infected cells induces cell lysis and new virus release, strong antitumor effects were expected.

In vitro, the viruses were 100-fold more toxic to *TP53* mutant tumor cells of a variety of tissues than to normal cells. Anti-tumoral activity against established tumor xenografts in nude mice were also demonstrated after intratumoral or intravenous injection, and this acted in synergy with chemotherapeutic agents. No toxicity to the host animals was observed (42).

Phase I clinical trials are now being conducted to clarify whether specific and non-specific cytotoxic effects might occur. Human patients have an immune system primed with adenovirus and all *in vivo* studies so far were carried out in immuno-deficient mice. The immune system may improve tumor regression by destroying the virus-infected tumor cells, but this might simultaneously reduce virus efficacy. Also, it is not clear whether suppressing the immune system of cancer patients is safe, especially in conjunction with chemotherapeutic agents.

If this virus turns out to be effective in human cancers, it will carry some advantages to treat those malignant gliomas with *TP53* gene alterations since virus spread might reach to deeply invaded tumor cells into the normal brain tissue. This will depend on virus diffusion rate, for virus replication will not occur in normal astrocytes of the infiltrated peritumoral areas.

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