

Fig. 3. Results of an RT-PCR assay showing high levels of IL-6 and IL-1 β mRNA expression. The RT-PCR products were analyzed on a 2% agarose gel and detected using ethidium bromide staining. Lane 1 = RT positive; Lane 2 = RT negative; Lane 3 = water.

dominant. The IgE production requires cytokines, in particular IL-4, and some investigations have revealed an obligatory role of endogenous IL-6 in IL-4—dependent human IgE synthesis.²⁵ A balance between Th1 and Th2 is also considered to be critical in the regulation of IgE synthesis.¹⁵ In this case, the overexpression of IL-6 mRNA as Th2 cytokine was confirmed compared with that of IFNλ as the Th1 cytokine, but IL-4 expression could not be demonstrated. It is not possible to draw a definitive conclusion about the dominant levels of IgE in this patient, and a cytokine class switch from Th1 to Th2 profiles, controlled by a variety of environmental or genetic factors, may be associated with an elevated level of IgE. Furthermore, IL-6 may act on B lymphocytes and accelerate the production of IgE as well as IgG.

More recently, VEGF has also been considered to be involved in the pathogenesis of this disease, especially in the marked vascular proliferation of lymph nodes in the interfollicular space. Vascular endothelial growth factor is a specific mitogen for vascular endothelial cells; it therefore has a central role in angiogenesis and can also accelerate the permeability of the vessels. Moreover, its expression is considered to be induced by IL-6. The results of our cytokine study, performed using RT-PCR and immunohistochemical analysis for VEGF, indicate that VEGF-accelerated vasopermeability induced by IL-6 may play a role, at least in part, in lymphoplasmacyte infiltration, which is one of the histopathological characteristics of a chordoid meningioma, although the mechanism for dominancy of T- or B-lymphocytes within the tumor remains unclear.

Conclusions

Chordoid meningioma must be included in the preoperative differential diagnosis of central nervous system neoplasms featuring anemia, hypergammmaglobulinemia, fe-

ver of unknown origin, or other systemic illnesses. The clinical outcome of a chordoid meningioma featuring Castleman syndrome is favorable following surgical removal of the tumor, as reported previously. The pathogenesis of Castleman syndrome in the case of chordoid meningioma remains unclear, but a complex cytokine network including IL-6, IL-1 β , and VEGF may contribute to the clinicopathological features of chordoid meningioma when associated with this disease.

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IFN-β Down-Regulates the Expression of DNA Repair Gene *MGMT* and Sensitizes Resistant Glioma Cells to Temozolomide

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Abstract

Alkylating agents, such as temozolomide, are among the most effective cytotoxic agents used for malignant gliomas, but responses remain very poor. The DNA repair protein O^{6} methylguanine-DNA methyltransferase (MGMT) plays an important role in cellular resistance to alkylating agents. IFN-\$\beta\$ can act as a drug sensitizer, enhancing toxicity against a variety of neoplasias, and is widely used in combination with other antitumor agents such as nitrosoureas. Here, we show that IFN-B sensitizes glioma cells that harbor the unmethylated MGMT promoter and are resistant to temozolomide. By means of oligonucleotide microarray and RNA interference, we reveal that the sensitizing effect of IFN- β was possibly due to attenuation of MGMT expression via induction of the protein p53. Our study suggests that clinical efficacy of temozolomide might be improved by combination with IFNβ using appropriate doses and schedules of administration. (Cancer Res 2005; 65(17): 7573-9)

Introduction

Gliomas are the most common primary tumors of the central nervous system; they account for 30% of adult primary brain tumors. The prognosis for patients with the advanced glioma, glioblastoma multiforme, is very poor; the mean survival period is 8 to 10 months (1). Alkylating agents are among the most effective cytotoxic agents used for treating malignant gliomas, including glioblastoma multiforme, but responses remain very poor. The most frequent site of alkylation in DNA is the O^6 position of guanine, which forms cross-links between adjacent strands of DNA, leading to cell death. A cellular DNA-repair protein, namely O^6 methylguanine-DNA methyltransferase (MGMT) protein, reverses alkylation at the O^6 position of guanine, thereby inhibiting the lethal cross-linking and bringing about resistance to alkylating agents (2, 3). A number of studies have suggested that MGMT deficiency is closely related to the sensitivity of brain tumors to alkylating agents (4-6). Furthermore, because MGMT protein loss may be a result of promoter hypermethylation, it was reported that methylation of the MGMT promoter in gliomas is a useful predictor of the responsiveness to alkylating agents (7). Temozolomide is a novel alkylating agent that has been currently approved for use in treatment of anaplastic astrocytoma in Europe and the United States. A phase II clinical trial has been organized in Japan. This drug is of significance because it can be administered orally; it

readily crosses the blood-brain barrier and has minimal side effects (8). Before considering the treatment of malignant gliomas with temozolomide, a major obstacle may be the resistance pathway that occurs due to the actions of MGMT. Hence, efficient attenuation of the function of MGMT, which is expressed in ~70% of gliomas (9), either by direct interaction with protein or by indirect means such as the transcriptional control, is required. It could be advantageous if MGMT depletion can be accomplished by a drug that also has antitumor activity, and, therefore, synergistic effects with the alkylating agent may occur. Type I IFNs, including IFN-α and IFN-β, a family of cytokines that elicit pleiotropic biological effects, are widely used either alone or in combination with other antitumor agents such as nitrosoureas in the treatment of malignant gliomas. Among the multiple functions of type I IFNs against human neoplasias, type I IFNs, particularly IFN-β, can act as a drug sensitizer enhancing toxicity against a variety of neoplasias when given in combination with nitrosoureas (10). Therefore, it is of interest to examine whether IFN-B can enhance chemosensitivity of malignant gliomas against temozolomide, the new alkylkating agent; to evaluate the mechanism; and to provide an experimental basis for the rational clinical use of such combinations.

Materials and Methods

Cell lines and reagents. Human glioma cell lines (T98, AO2, SKMG1, U251nu/nu, U251SP, and U251MG) derived from the Memorial Sloan-Kettering Cancer Institute (New York, NY) were maintained at 37°C in a humidified atmosphere of 5% CO_2 in air in Eagle's medium (Nissui, Tokyo, Japan). Medium was supplemented with 10% fetal bovine serum (FBS), 5 mmol/L L-glutamine, 2 mmol/L nonessential amino acids, and antibiotics (100 units/mL penicillin and 100 μ g/mL streptomycin). Human IFN- β and temozolomide were kindly supplied by Toray, Co., Ltd. (Kamakura, Japan), and the Schering-Plough Research Institute (Kenilworth, NJ), respectively. Temozolomide readily discomposes in aqueous solution into DMSO.

RNA interference experiments. The target sequence in p53 and the control nonsilencing sequence are CGGCAUGAACCGGAGGCCCAU and AATTCTCCGAACGTGTCACGT, respectively. These synthetic sense and antisense oligonucleotides were obtained from Qiagen (Hilden, Germany). For the annealing of small interfering RNA (siRNA) oligonucleotides, sense and antisense oligonucleotides were incubated in siRNA Suspension Buffer (Qiagen) for 1 minute at 90°C, followed by 60 minutes at 37°C. siRNA oligonucleotides were mixed with Oligofectamine reagent (Invitrogen, Carlsbad, CA) in Opti-MEM (Life Technologies, Gaithersburg, MD). Cultured cells were washed with medium without serum and added to the siRNA-Oligofectamine mixture, of which the final concentration was 200 nmol/L. Medium with 10% FBS was added 4 hours later.

Determination of cell growth. To compare chemosensitivity of glioma cell lines to temozolomide, the agent (final concentration of 0-1,000 $\mu mol/L)$ was added to the culture medium at 24 hours after aliquots of 2 \times 10 4 cells/well were placed in triplicate wells. Incubation was continued for 72 hours, and the number of viable cells was counted by trypan blue exclusion method. The number was expressed as a percentage of untreated control. The statistical significance of difference was determined by ANOVA using

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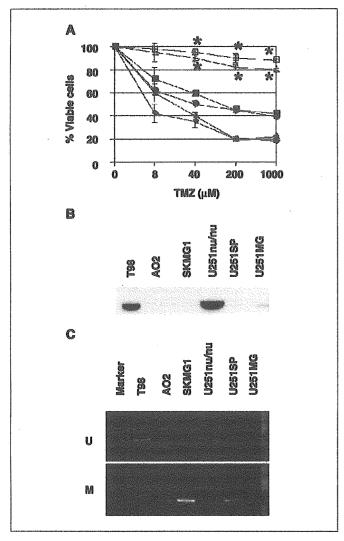
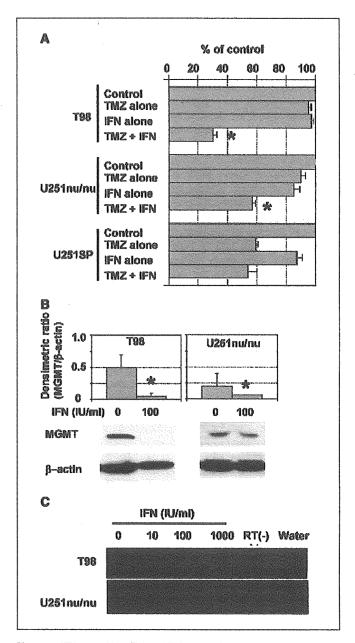


Figure 1. Comparisons among human glioma cell lines. *A*, the antitumor effects of temozolomide against six human glioma cell lines: T98 (□), AO2 (▲), SKMG1 (♠), U251nu/nu (△), U251SP (■), and U261MG (♠). At 72 hours after temozolomide (final concentration of 0-1,000 µmol/L) was added to the culture medium, the number of viable cells was counted. The number was expressed as a percentage of untreated control. *P < 0.05 versus AO2, SKMG1, U251SP, and U251MG at each dose. *B*, Western blot analysis of MGMT in human glioma cell lines. The cell lysate was subjected to Western blotting with anti-MGMT antibody. *C*, methylation-specific PCR analysis of human glioma cell lines. *U* and *M*, reactions for unmethylated and methylated sequences, respectively.

Bonferroni's correction for the multiple comparisons used. For sensitizing assay of IFN- β to temozolomide, IFN- β (100 IU/mL) and temozolomide (100 $\mu mol/L$) were added at 24 and 48 hours after cell inoculation, respectively. The number of viable cells was counted at 96 hours. To examine the effect of siRNA for p53 on the growth of T98 cells treated with IFN- β and temozolomide, either siRNA for p53 or nonsilencing siRNA was transfected as described above at 24 hours after aliquots of 4 \times 10 4 cells/well were placed in triplicate wells. IFN- β (100 IU/mL) and temozolomide (100 $\mu mol/L$) were added at 28 and 48 hours, respectively. The number of viable cells was counted at 96 hours.

Western blot analysis. Cell lysis and immunoblotting were carried out as described (11). Antibodies against the following proteins were purchased: p53 (DO-1: Santa Cruz Biotechnology, Santa Cruz, CA), p21 (EA10: Oncogene Research Products, San Diego CA), MGMT (MT3.1: Neomarkers, Fremont, CA), and β -actin (AC-15: Sigma-Aldrich, St. Louis, MO). Band intensities were quantified by densitometric scanning using the NIH IMAGE program.

Genomic DNA extraction and methylation-specific PCR. Genomic DNA was extracted using the QIAmp DNA Mini kit (Qiagen) following the manufacturer's instructions. DNA methylation patterns in the promoter region of the MGMT gene (Genbank accession no. X_61657) were determined by methylation-specific PCR as previously described (12). Primers for either methylated or unmethylated alleles were 5'-TTTCGACGTT-CGTAGGTTTTCGC-3' (sense) and 5'-GCACTCTTCCGAAAACGAAACG-3' (antisense) or 5'-TTTGTGTTTTGATGTTTTGTAGGTTTTTGT-3' (sense) and



Symbol	Genes	Genbank accession no.	Mean
RBP2	Retinoblastoma-binding protein 2	S66431.1	2.012
PKB	Protein kinase B	X61037.1	2.024
FGF-9	Fibroblast growth factor 9	D14838.1	2.035
Grb14	Grb14	L76687.1	2.035
VCAM-1	Vascular cell adhesion molecule 1 (VCAM-1)	X53051.1	2.035
IL18	Interleukin 18 (IFN-γ–inducing factor)	NM_001562.2	2.047
HOX-11	Homeobox protein (HOX-11)	M75952.1	2.055
bcl-w	Gi 1572492 gb U59747.1 HSU59747 Human Bcl-w (bcl-w) mRNA, complete cds	U59747.1	2.074
IGFBP-5	Insulin-like growth factor binding protein 5	M62782.1	2.081
Clk2	Clk2	L29216.1	2.098
NIK	Serine/threonine protein kinase	Y10256.1	2.106
p68K	p68 kinase	M35663.1	2.112
IGF-II	Human insulin-like growth factor II	M29645.1	2.121
GALNAC4S-6ST	B-cell RAG-associated protein	NM_014863.1	2.128
FGF-10	FGF-10	AB002097.1	2.129
FRA-2	Human fra-2	X16706.1	2.134
FASL	Fas ligand	D38122.1	2.146
PDGF	Platelet-derived growth factor A-chain	A09204.1	2.158
E1A-F	EIA-F	D12765.1	2.163
c-myc	C-MYC	D89667.1	2.167
hTRIP	hTRIP (hTRIP)	U77845.1	2.185
CALM2	Calmodulin 2 (phosphorylase kinase, δ)	NM_001743.3	2.207
PUMP-1	PUMP-1 gene encoding PUMP Bell and binding protein Phy (S2PD2 (PPD/S2PD2))	Z11887.1 U58334.1	2.207
Bcl2 MVV4	Bcl2, p53-binding protein Bbp/53BP2 (BBP/53BP2) MAP kinase kinase 6	U39657.1	2.207
MKK6 [NK3A1	NK3 a1 protein kinase	U34820.1	2.218 2.242
p82	pS2 mRNA induced by estrogen from human breast cancer cell line MCF-7	X00474.1	2.273
PS2 ICAM-2	ICAM-2, cell adhesion ligand for LFA-1	X15606.1	2.276
CREM	Cyclic AMP-responsive element modulator (CREM)	S68271.1	2.289
Humig	Сусис пин чегропоме експени тошшин (Сими) Нитід	X72755.1	2.289
NFATI	Transcription factor NFAT1 isoform C (NFAT1)	U43342.1	2.289
SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated; SFPQ)	NM_005066.1	2.302
N-CoR	Nuclear receptor corepressor	AF044209.1	2,333
IGFBP3	Growth factor-binding protein-3 precursor (IGFBP3)	M35878.1	2.359
IRF-1	IFN regulatory factor 1	X14454.1	2.4
IL-11R	Interleukin-11 receptor	Z38102.1	2.417
hsp70	Heat shock protein 70 (hsp70)	L12723.1	2.424
bcl-3	B-cell lymphoma 3-encoded protein (bcl-3)	M31732.1	2.441
FAS/Apo 1	FAS/Apo 1 mRNA for FAS soluble protein (clone FAS Exo4Del)	Z70519.1	2.471
HSP75	Homo sapiens mitochondrial HSP75	L15189.1	2.481
ICE-LAP6	Cysteine protease ICE-LAP6	U56390.1	2.485
GOS8	Helix-loop-helix basic phosphoprotein	L13463.1	2.487
HEK2	HEK2 mRNA for protein tyrosine kinase receptor	X75208.1	2.493
ERK2	40 kDa protein kinase related to rat ERK2	Z11695.1	2.503
KIAA0347	KIAA0347	AB002345.2	2,504
APAF1	Apoptotic protease-activating factor (APAFI), transcript variant 2	NM_001160.2	2.513
TRA1	Tumor rejection antigen (gp96) 1	NM_003299.1	2.574
TNF	Tumor necrosis factor superfamily member LIGHT	AF036581.1	2,582
FGF-5	Fibroblast growth factor-5 (FGF-5)	M37825.1	2.616
PPAR	Peroxisome proliferator-activated receptor	L02932.1	2.616
TIPM3	Tissue inhibitor of metalloproteinases-3	U14394.1	2.628
Mch3	Mch3 isoform α(Mch3)	U37448.1	2.698
PTPRZ	Protein tyrosine phosphatase ζ-polypeptide (PTPRZ)	M93426.1	2.698
RPGR	Retinitis pigmentosa GTPase regulator (RPGR)	NM_000328.1	2.741
ENO3	Enolase 3, (β, muscle; ENO3), transcript variant 1	NM_001976.2	2.754

Symbol	Genes .	Conhonk	9 h
	Genes	Genbank accession no.	Mea
NFKB1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105; NFKB1)	NM_003998.2	2.761
HRK	Activator of apoptosis Hrk (HRK)	U76376.1	2.774
IFITM3	IFN-induced transmembrane protein 3 (1-8U; IFITM3)	NM_021034.1	2.882
IL15RA	Interleukin-15 receptor achain precursor (IL15RA)	U31628.1	2.918
4MPD2	AMP deaminase 2 (isoform L; AMPD2)	NM_004037.5	2.989
DNAJA I	DnaJ (Hsp40) homologue, subfamily A, member 1	NM_001539.1	3.184
HLA-C	MHC class I HLA-C allele HLA-4	M11886.1	3.265
FN-γ	IFN-γ	X13274.1	3.27
53	p53 cellular tumor antigen	M14694.1	3.30
HLA-B	MHC, class I	NM_005514.4	3.374
CHED	cdc2-related protein kinase	M80629.1	3.686
GADD45	Gadd45	S40706.1	3.694
3PAGI	Bullous pemphigoid antigen 1, 230/240kDa (BPAG1), transcript variant 1e, mRNA	NM_001723.3	3.793
SGF-3	Transcription factor ISGF-3	M97936.1	3.938
TGFR	Transforming growth factor-ftype III receptor	L07594.1	4.34
MC4R	Melanocortin 4 receptor	NM_005912.1	10.82
3. Decrease in	gene expression in T98 cells by IFN-β		
DR3	Death receptor 3 (DR3)	U72763.1	0.5
GST-pi-1	Anionic glutathione-S-transferase (GST-pi-1)	X15480.1	0.5
TSHR	Thyroid stimulatory hormone receptor	M32215.1	0.5
PRDX6	Peroxiredoxin 6	NM_004905.2	0.49
GFBP6	Insulin-like growth factor binding protein 6	M62402.1	0.49
HRR-1	Farnesol receptor	U68233.1	0.49
L8RBA	Interleukin-8 receptor type A	U11870.1	0.49
RPS2	Ribosomal protein S2	NM_002952,2	0.493
COX6C	Cytochrome coxidase subunit Vic	NM_004374.2	0.49
HINT1	Histidine triad nucleotide-binding protein 1	NM_005340.2	0.489
E2F-1	pRB-binding protein	M96577.1	0.483
SKPIA	S-phase kinase-associated protein 1A (p19A; SKPIA), transcript variant 1	NM_006930.2	0.483
4S1	HS1 protein	X57347.1	0.478
PPP2CA	Protein phosphatase 2 (formerly 2A), catalytic subunit, aisoform	NM_002715.1	0.478
G3PD	Glyceraldehyde-3-phosphate dehydrogenase	X01677.1	0.47
/itDR	Vitamin D receptor	J03258.1	0.472
SEC61B	Sec61 ßsubunit	NM_006808.2	0.47
SHC	SHC	X68148.1	0.47
COX6A1	Cytochrome coxidase subunit VIa polypeptide I	NM_004373.2	0.46
PINI	Peptidyl-prolyl isomerase and essential mitotic regulator	U49070.1	0.45
L5Rα	Interleukin 5 receptor a	M75914.1	0.44
RAB	Cellular cofactor	L42025.1	0.43
CD6	T-cell glycoprotein CD6	X60992.1	0.43
VDUFB3	NADH dehydrogenase (ubiquinone) 1 βsubcomplex, 3, 12 kDa	NM_002491.1	0.43
"XN	Thioredoxin	NM_003329.1	0.43
COX4II	Cytochrome coxidase subunit IV isoform 1	NM_001861.2	0.42
MRT	Silencing mediator of retinoid and thyroid hormone action	U37146.1	0.42
RK3	ERK3	X80692.1	0.42
CRB	T-cell receptor βchain	L07294.1	0.42
GALS1	Lectin, galactoside-binding, soluble, 1 (galectin 1)	NM_002305.2	0.41
<i>OD1</i>	Superoxide dismutase 1	NM_000454.2	0.41
OX	ROX protein	X96401.1	0.41
AGI	BCL2-associated athanogene	NM_004323.2	0.40
DC50	Hypothetical protein DC50	NM_031210.3	0.40
THI	Ferritin, heavy polypeptide 1	NM_002032.1	0.39
KRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5	NM_021141.2	0.38

Table 1. (Cont'd) B. Decrease in gene expression in T98 cells by IFN-β Symbol Genbank Mean Genes accession no. GSTOI Glutathione S-transferase w1 NM_004832.1 0.384 Tropomyosin 2 (β) TPM2 NM_003289.1 0.377 CD27L CD27 ligand L08096.1 0.374 PRDXI Peroxiredoxin 1 NM_002574.2 0.372 MAD-3 mRNA encoding IkB-like activity M69043.1 0.369 MAD-3 **CRAFI** CD40 receptor associated factor 1 U21092.1 0.365 Cdk-inhibitor p57KIP2 1122398.1 0.362 KIP2 Ribosomal protein, large, PI NM_001003.2 RPLP1 0.356 AF010309.1. PIG3 Pig3 0.341 GAS Growth-arrest-specific protein L13720.1 0.33 TMSB10 Thymosin, β10 (TMSB10) NM 021103.2 0.322 ME491 Melanoma-associated antigen ME491 X07982.1 0.313 ANXA2 Annexin A2 NM_004039.1 0.29 CollagenaseVCollagenase type IV J03210.1 0.29 S100A2 S100 calcium-binding protein A2 NM_005978.2 0.281 Calcium-activated neutral protease large subunit X04366.1 0.262 calpain FTLFerritin, light polypeptide NM_000146.2 0.239

NOTE: p53-related genes are in bold. The mean was based on three replicate arrays analyzed statistically as described in the text.

5'-AACTCCACACACTCTTCCAAAAACAAAACA' (antisense). All PCRs were done with positive controls for methylated alleles and no DNA control. Human placental DNA was treated *in vitro* with excess SssI methyltransferase (New England Biolabs, Beverly, MA), generating DNA completely methylated at CpG sites, served as the positive control for methylated MGMT, and then the PCR conditions were determined. Each PCR product was loaded onto a 3% agarose gel, stained with ethidium bromide, and visualized under UV illumination.

Reverse transcriptase-PCR. To investigate MGMT mRNA expression, reverse transcription-PCR (RT-PCR) was done using the Superscript first-strand synthesis system for RT-PCR (Invitrogen) as previously described (13). β -actin-specific PCR products from the same RNA samples were amplified and served as internal controls.

Microarray analysis. T98 cells were incubated with 100 IU/mL of IFN- β for 48 hours, and RNA was isolated. Standard Trizol preparation protocol (Invitrogen) and reagents were used for total RNA isolation. RNA amplification and labeling were done using the Amino Allyl MessageAmp aRNA kit (Ambion, Austin, TX). Briefly, after reverse transcription reactions (2 µg total RNA/sample) were preformed, double-stranded cDNA was transcribed in vitro into amino allyl eRNA. The purified and concentrated cRNA (5 µg) was coupled with either Cy3 or Cy5 dyes (Amersham Biosciences). The dyelabeled aRNA was purified from uncoupled dye using Micro Bio-Spin P-30 Tris chromatography columns (Bio-Rad, Hercules, CA) and MicroconYM-30 centrifugal filter devices (Millipore, Billerica, MA). The cRNA was fragmented in fragmentation buffer [40 mmol/L Tris-acetate (pH 8.1), 100 mmol/L potassium acetate, 30 mmol/L magnesium acetate] at 94°C for 15 minutes and purified with Microcon YM-10 (Millipore). Microarrays were preblocked with 1% bovine serum albumin solution. Fragmented cRNA was added to microarrays in hybridization solution and hybridized at 42°C for 16 hours. After this, arrays were washed, scanned at 10 µm pixel size, gridded, and analyzed (GenePix 4000B; Axon Instruments, Union City, CA). Background was subtracted, and the median sum and median ration were calculated. Flagged spots and spots with sum intensity (CH1, CH2) <100 absorbance units were excluded. Data were normalized by trimmed mean at 10% to account for differences in the amounts of RNA labeled or labeling efficiencies.

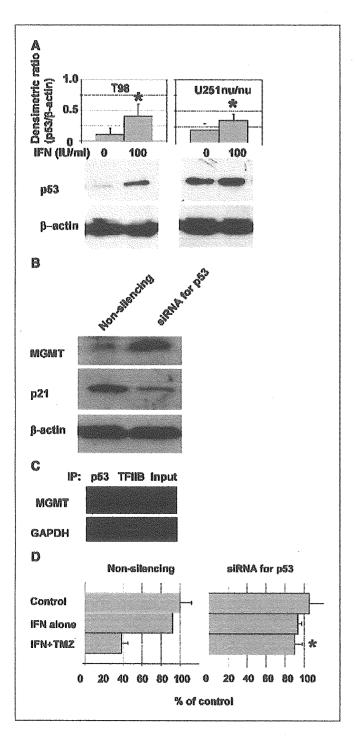
Chromatin immunoprecipitation assay. The chromatin immunoprecipitation assay was done according to the protocol of the manufacturer (Upstate Biotechnology, Lake Placid, NY) with a slight modification. The specific antibodies used for immunoprecipitations were the anti-p53 antibody and a control antibody. After protein-DNA cross-links in the immunoprecipitates were reversed, the purified DNA was analyzed by PCR (35 cycles; 45 seconds at 95°C, 45 seconds at 55°C, 60 seconds at 72°C) with primers that detect the MGMT promoter sequence [5'-GCTCCAGGGAA-GAGTGTCCTCTGC-TCCCT-3' (sense) and 5'-GGCCTGTGGTGGGCGAT-GCCGTCCAG-3' (antisense)] and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter (provided with the kit). The PCR products were visualized on an ethidium bromide gel.

Results and Discussion

Chemosensitivity to temozolomide, MGMT expression, and MGMT promoter hypermethylation of human glioma cell lines. First, we compared chemosensitivity of six human glioma cell lines to temozolomide; T98 and U251nu/nu cell lines were significantly resistant, whereas the other four (AO2, SKMG1, U251SP, and U251MG) showed similar degrees of sensitivity in a dose-dependent manner (Fig. 1A). MGMT expression was not detected by Western blot in the sensitive cell lines (Fig. 1B), and the hypermethylation of MGMT promoter was as assessed by methylation-specific PCR (Fig. 1C), but this was not observed in the T98 and U251nu/nu cell lines. Thus, the results showed that hypermethylation of MGMT promoter could prevent expression of this gene and be associated with chemosensitivity of glioma cells to temozolomide, which was consistent with the results of reported studies (7). Because ~70% of gliomas express MGMT (9), it is essential to suppress the expression or function of MGMT in an efficient manner if treatment with the aid of temozolomide is to be considered.

IFN- β sensitizes resistant glioma cells to temozolomide and down-regulates MGMT expression. IFNs are a family of cytokines

that possess pleiotropic biological effects mediated by a number of responsive genes. IFNs were the first human proteins to be recognized as being effective in cancer therapy (14). Although identified and named for their action to interfere with viral replication, IFNs have immunomodulatory, cell differentiative, antiangiogenic, and antiproliferative effects (15, 16). In the previous studies, we showed that IFN- β has multiple functions relevant to antitumor activity: (a) cytostatic effect on glioma cells, (b) supportive action on the differentiation of CTLs and augmentation of their antitumor immune responses, and (c) behavior as a drug or radiation sensitizer enhancing toxicity against gliomas (10).



To examine whether IFN-β sensitizes T98 and U251nu/nu cell lines that are resistant to temozolomide, the cells were incubated in a culture medium containing IFN-B (100 IU/mL) for 24 hours before the addition of temozolomide (final concentration of 100 μmol/L). As shown in Fig. 2A, whereas IFN-β or temozolomide alone did not suppress cell growth of both T98 and U251nu/nu cells significantly, a combination of IFN-B and temozolomide markedly inhibits the growth. On the other hand, U251SP cell lines that are sensitive to temozolomide, but are resistant to IFN-B did not show the synergistic cytotoxic effect of temozolomide and IFN-β. Consequently, we hypothesized that IFN-β might enhance chemosensitivity due to reduction of MGMT expression and did Western blotting and RT-PCR for MGMT (Fig. 2B and C). It was shown that IFN-B decreased both MGMT protein and mRNA levels of both T98 and U251nu/nu cells at 48 hours after treatment. Thus, IFN-\$\beta\$ decreases MGMT transcription directly or indirectly and sensitizes resistant glioma cells to temozolomide.

Microarray analysis of IFN-β-regulated genes. Because limited information regarding the transcriptional regulation of IFN-β is available, we introduced microarray technology that enables the simultaneous examination of expression of a large number of genes in an experimental condition. This microarray contains 1,300 functionally well-characterized genes involved in various important cellular processes, including the IFN-related pathway, apoptosis, cell cycle, transcription, and immunology. The microarray experiments were repeated thrice about the T98 cell lines that showed the most drastic change of MGMT expression after IFN-\beta treatment. Data analysis identified 71 significantly induced genes and 54 repressed genes in several different categories in T98 cells treated with IFN-B compared with the parental cells. The representative results of these comparisons are reported in Table 1. Some of the alterations in gene expression following IFN-β treatment confirm the involvement of pathways known to be active in this process, and this was anticipated from prior evidence. Consistent with a report that the p53 gene is transcriptionally induced by IFN-B through ISGF3 activation (11), our microarray data showed that the p53 gene and its downstream genes, including bcl-2, FAS/ApoI, and Gadd45, are upregulated in glioma cells treated with IFN-β, suggesting that p53 induction may be a key involved in antitumor action of IFN-B. Thus, we focused on IFN-β-mediated p53 induction. By Western blot, we confirmed that p53 expression level in both T98 cells treated with IFN-B was markedly higher than that in the

Figure 3. IFN-β down-regulates MGMT expression via induction of p53. A, up-regulation of the protein p53 in T98 and U251nu/nu cells by IFN-β. The cell lysate of cells treated with IFN-B (100 IU/mL) was subjected to Western blotting with anti-p53 and anti-β-actin antibodies. The histogram shows the amount of p53 relative to that of β-actin. Columns, mean values from three independent experiments; bars, SD (* P < 0.05). B, RNA interference experiments for p53. After p53 was knocked down by the siRNA specific for p53, Western blotting for MGMT, p21, and β-actin was done. The siRNA with nonsilencing sequence was used as a control. The specific knockdown was confirmed by the diminished expression level of p21, a well-known target gene of p53. C, chromatin immunoprecipitation assay. The protein p53 binding to the MGMT promoter element was examined. Lane 1, PCR amplification of MGMT and GAPDH sequences in immunoprecipitated chromatin fragments with anti-p53 antibody. Lane 2, result of PCR using immunoprecipitated samples with control antibody against TFIIB, the known transcriptional factor of GAPDH. Lane 3, PCR amplification of the total input DNA. D, cancellation of the sensitizing effect of IFN-β by p53 siRNA. T98 cells were treated with the siRNA for p53 or the nonsilencing siRNA before the treatments of IFN-B (100 IU/mL) and temozolomide (100 μ mol/L). Seventy-two hours after, the number of viable cells was counted. *P < 0.05 versus the treatment group with nonsilencing siRNA, IFN-β, and temozolomide.

untreated cells and the similar phenomenon was observed in the U251nu/nu cells as well (Fig. 3A).

IFN-\$\beta\$ down-regulates MGMT expression via protein p53. For >10 years, p53 has been the focus of intensive research. This has led to a plethora of information regarding p53, its biological roles, and its relevance to cancer (17). p53 is primarily a sequence-specific transcriptional activator. It binds to cognate p53-responsive elements within the genome and activates the transcription of genes residing in the vicinity of these binding sites. The proteins encoded by the p53 target genes, whose number is probably in the hundreds, contribute in multiple ways to the biological effects of p53. The biological outcomes of p53 activity include apoptosis, inhibition of cell cycle progression, senescence, differentiation, and accelerated DNA repair. We first confirmed that siRNA for p53 specifically knocked down the protein p53 function by examining the diminished expression level of p21, a well-known target gene of p53 (Fig. 3B). As shown in Fig. 3B, knockdown of p53 by siRNA increased MGMT expression in T98 cells. Therefore, p53 can downregulate transcription of MGMT. To further investigate whether protein p53 directly interacts with MGMT promoter and downregulates transcription of MGMT, we carried out chromatin immunoprecipitation assay. We observed that MGMT promoter, but not GAPDH promoter, coprecipitated with p53. The irrelevant antibody specific to TFIIB, which is a transcription factor of GAPDH, did not coprecipitate with MGMT promoter (Fig. 3C). These findings are in agreement with the previous reports showing that p53 reduces the basal activity of the MGMT promoter, and adenoviral vector-mediated overexpression of p53 reduces MGMT expression (18, 19), although some papers suggested that inactivated MGMT may be linked to cytotoxic effect of alkylating agents and cell signaling events, but was independent of p53 status (20). The reasons for these differences are unclear and may be cell type dependent. Moreover, in cell growth experiments, knocking down of p53 before IFN-B treatment nullified the synergistic inhibitory effect of IFN-B and temozolomide on T98 cell growth (Fig. 3D). Thus, acting together, IFN- β down-regulates MGMT transcription via induction of the p53 expression and sensitizes resistant glioma cells to temozolomide. In conclusion, this report shows that IFN-B is able to decrease MGMT levels in glioma cells via the inhibition of MGMT gene transcription. Moreover, pretreatment of glioma cells with IFN-β markedly enhances chemosensitivity to temozolomide. This suggests that clinical efficacy of temozolomide might be improved by combination with IFN-β using appropriate doses and schedules of administration.

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Multicentric atypical teratoid/rhabdoid tumors occurring in the eye and fourth ventricle of an infant

Case report

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✓ Atypical teratoid/rhabdoid tumors (AT/RTs) are aggressive malignant tumors found in infants and young children. The tumor is characterized by the presence of a rhabdoid cell component in all cases, but the histological origin is still unclear. Recently, germline mutation of the hSNF5/INII gene has been reported in association with AT/RTs.

The authors report a rare case of an intraocular ATRT followed by a fourth ventricular tumor. The results of immunohistochemical studies of the surgical specimens revealed the presence of an AT/RT and from this finding the neural origin was inferred. A novel missense mutation of the hSNF5/INI1 gene was demonstrated by DNA analysis. High-dose chemotherapy with stem cell rescue was effective in treating this patient. The immunohistochemical relationship between rhabdoid cells and the neurogenic zone, which has not been described in AT/RTs, is of great interest in view of the nature of rhabdoid cells.

KEY WORDS • atypical teratoid/rhabdoid tumor • germline mutation • hSNF5/INI1 • subgranular zone • Musashi1 • nestin • pediatric neurosurgery

TYPICAL AT/RTs are aggressive malignant tumors found in infants and young children. The prognosis is poor, despite the use of adjuvant therapy, and many patients die within a year following diagnosis. The tumor is characterized by the presence of a rhabdoid cell component in all cases, variably mixed with other histological patterns including primitive neuroectodermal, mesenchymal, and epithelial components; 26,11,16,17 however, the histological origin is still unclear. Generally, monosomy or deletions from chromosome 22 have been identified in 60 to 90% of the cases. The chromatin-remodeling gene hSNF5/INII has recently been reported to act as a rhabdoid tumor suppressor gene, 18 and a germline mutation of hSNF5/INII has been reported in malignant rhabdoid tumors, termed rhabdoid predisposition syndrome. 15

The locations of AT/RTs vary; most arise in the posterior fossa (52%), followed by the supratentorial (39%), pineal (5%), multifocal (2%), and spinal (2%) areas. ¹⁰ Intraocu-

Abbreviations used in this paper: AT/RT = atypical teratoid/rhabdoid tumor; MR = magnetic resonance; SGZ = subgranular zone.

lar AT/RTs are rare. We report a case involving a neonate who presented with an intraocular tumor followed by an intramedullary tumor in the fourth ventricle.

Case Report

Patient History. This 5-week-old boy had been the product of a normal pregnancy and delivery. He did not appear to have medical problems and did not have a significant family history, but an abnormal left pupil was observed when the child was 2 weeks of age. An ophthalmological examination revealed a lesion appearing as a white mass behind the lens of his left eye. Ultrasonographic biomicroscopy and MR imaging around the orbit demonstrated an intraocular tumor, as demonstrated in Fig. 1. Because of the diagnostic uncertainty and little hope for useful vision, the patient was followed with observation alone; however, his left eye gradually enlarged and his general condition became worse. Ten months after the initial diagnosis, his left eye was enucleated because a histopathological examination revealed this tumor to be a rhabdoid cell tumor.

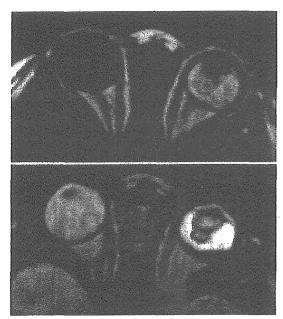


Fig. 1. Preoperative T_1 - (upper) and T_2 -weighted (lower) MR images of the left eye demonstrating a cone-shaped structure connecting the lens and posterior pole of the eye.

Operation. An extensive systemic workup demonstrated a fourth ventricular tumor of approximately 1.5 cm in diameter (Fig. 2). The patient immediately underwent a tumor resection via a suboccipital approach. The tumor was rather soft, relatively vascularized, and attached to the floor of the fourth ventricle. Gross-total resection of the tumor was achieved. Immunohistochemical studies of the surgical specimens from the eye and brain were consistent with AT/RT (Fig. 3, Table 1); DNA analysis revealed a germline hSNF5/INII mutation (Fig. 4).

Postoperative Course. The patient received three courses of cisplatin at 90 mg/m² and etoposide at 300 mg/m², three courses of ifosfamide 9 g/m², carboplatin 1.5 g/m², and etoposide 450 mg/m², followed by two courses of vincristine 1.5 mg/m², nimustine 2 mg/m², and cisplatin 90 mg/m². The patient then underwent myeloablative chemotherapy

with thiotepa 560 mg/m² and melphalan 130 mg/m² with stem cell rescue.^{7,8} At last follow up, the boy had been free from recurrence or new occurrence of tumors for 24 months since the operation.

Histopathological Findings. Routine H & E staining of the intraocular tumor revealed that it consisted largely of necrotic tissues and hemorrhage, and that a small amount of tumor tissue remained. Tumor cells were large, pale, polygonal cells with distinct borders, vesicular nuclei, and moderate amounts of eosinophilic cytoplasm (Fig. 3 upper left), presenting a typical pattern of a rhabdoid cell tumor. The fourth ventricular tumor was composed mainly of poorly differentiated small and hyperchromatic cells resembling those of primitive neuroectodermal tumors and medulloblastomas, and it included rhabdoid cell components (Fig. 3 upper right). Both tumor cells demonstrated diffusely cytoplasmic positivity for cytokeratin AE1/AE3 and CAM-5.2, S100, vimentin, epithelial membrane antigen, and MIC2. Glial fibrillary acidic protein was expressed only in the brain tumor. Desmin, smooth-muscle actin, and HMB45 were not expressed. These results were used to aid in the diagnosis of both tumors as rhabdoid cell tumors. In addition, RNA-binding protein Musashi1 was expressed (Fig. 3 lower left) but nestin was not (Fig. 3 lower right) in both the intraocular and the fourth ventricular tumors; these proteins have been recently reported as markers for neural precursor cells.9,14 The immunohistochemical results obtained with the different markers are summarized in Table 1.

Analysis of DNA. With the informed consent of his parents, genomic DNA was extracted from the peripheral blood of the patient and his parents as well as from the fourth ventricular tumor. Exons 1 to 9 of the hSNF5/INI1 gene were amplified by polymerase chain reaction by using primers and conditions as previously described, 15 and the products of polymerase chain reaction were directly sequenced (Fig. 4). A novel heterozygous missense mutation of the hSNF5/INI1 gene at codon 40 was identified from the peripheral blood of the patient's DNA. This mutation was considered de novo because no mutation was detected in his parents. In addition, the DNA analysis of the brain tumor showed only a mutated allele, suggesting a loss of het-

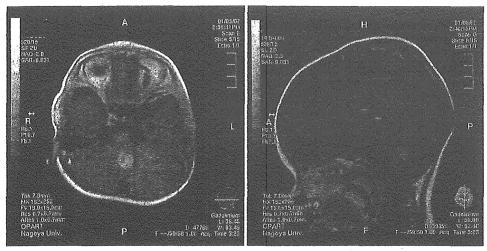


Fig. 2. Preoperative enhanced MR image of the brain demonstrating a fourth ventricular tumor with mass effect.

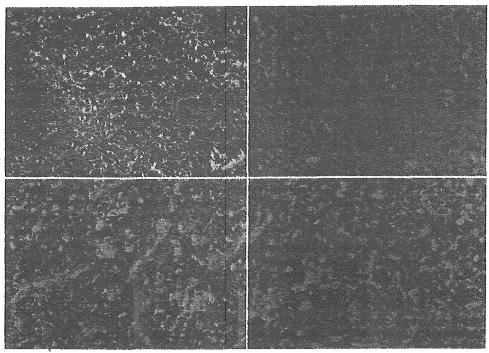


Fig. 3. Immunohistochemical studies demonstrating the intraocular tumor, the tissue of which is composed mainly of hematoma and necrosis, with tumor cells consisting of typical rhabdoid cells (*upper left*). The fourth ventricular tumor with poorly differentiated, small, hyperchromatic cells (*upper right*); the brain tumor with cytoplasmic positivity (*lower left*); the brain tumor specimen with limited positivity in vascular endothelial cells (*lower right*). H & E (*upper left* and *upper right*), Musashi1 (*lower left*), and nestin (*lower right*). Original magnifications × 200.

erozygosity. We could not analyze the intraocular tumor DNA because a limited amount of surgical specimens were available.

Discussion

Intraocular AT/RTs are extremely rare. Until now, there has been only one reported case in the literature of an intraocular malignant rhabdoid tumor that was believed to have metastasized from a renal tumor. The relationship between intraocular and fourth ventricular tumors has not

TABLE 1
Summary of the immunohistochemical findings of the intraocular and brain tumors*

Agent	Intraocular Tumor	Fourth Ventricular Tumor
cytokeratin		
AE1/AE3	+	+
CAM-5.2	+	+
S100	+	+
vimentin	+	+
EMA	+	+
MIC2	+	+
Musashi I	+	
GFAP	-	+
SMA	-	woods.
desmin	_	
HMB45	· <u>-</u>	_
nestin	error .	****

^{*} EMA = epithelial membrane antigen; GFAP = glial fibrillary acidic protein; SMA = α -smooth muscle actin; + = positive; - = negative.

been clearly determined; however, the clinical course of the present case indicates that AT/RTs can possibly arise in the eyeball. Moreover, the germline mutation of hSNF5/INII detected in this patient provides evidence of the multicentric origins of these tumors. The boy was thought to be suffering from a so-called rhabdoid predisposition syndrome, which is most likely to predispose a patient to a variety of cancers.¹⁵

The phenotypic diversity of AT/RT cells is generally observed in tumor tissues; therefore, the histogenesis of AT/ RT remains uncertain. Various cellular origins have been proposed, including neuroectodermal,16 myogenic,17 histiocytic,6 neural,2 and epithelial.11 It may be inferred from these reports that an AT/RT has multiphenotypic characteristics, but the true origin of this enigmatic tumor is unknown. Recent studies involving normal neurons have established that neurogenesis of the brain persists in at least two discrete regions, the subventricular zone of the lateral ventricle⁵ and the SGZ of the dentate gyrus.⁴ Both nestin and the neural RNA-binding protein Musashi1 are expressed in neural stem cells in the subventricular zone.9,14 In contrast, neuronal progenitor cells in the SGZ present with Musashi1 but not nestin. 16 In this case, Musashi1 was expressed but nestin was not in both the intraocular and the fourth ventricular tumors; these results indicate that these tumors might be derived from SGZ. Another hypothesis is that new peculiar cells are the origin for AT/RTs, although we cannot discuss this issue at present. As far as we are aware, this report provides the first documentation of a relationship between AT/RTs and the SGZ.

High-dose chemotherapy with stem cell rescue was effective in this case; however, the prognosis of AT/RTs is

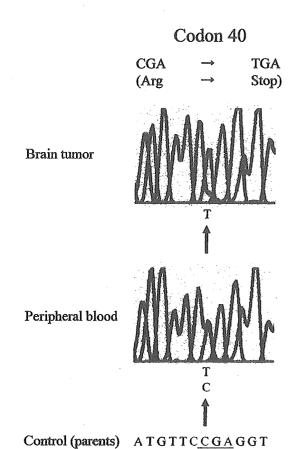


Fig. 4. Analysis of DNA revealing a missense mutation at codon 40 (arrow) in the brain tumor and peripheral blood specimens that predicts truncation of the protein. Control sequence obtained from the patient's parents is demonstrated below.

generally very poor. Even after aggressive surgery and chemotherapy, overall survival rates for children, particularly for those younger than 2 years of age, have been extremely poor, with less than 20% of patients surviving less than 12 months from the time of diagnosis. A variety of different chemotherapeutic agents have been used, but no single agent or combination of agents have been shown to be most effective. Ronghe, et al., 12 recently reported the effectiveness of intensified therapy for AT/RTs. More consideration is needed to develop a new therapeutic strategy for these types of tumors.

Conclusions

We report a rare case of an intraocular AT/RT followed by a fourth ventricular tumor. Immunohistochemical studies indicated the neural origin of these tumors. High-dose chemotherapy with stem cell rescue was an effective treatment in this case.

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THE COMBINATION OF MITOTIC AND KI-67 INDICES AS A USEFUL METHOD FOR PREDICTING SHORT-TERM RECURRENCE OF MENINGIOMAS

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BACKGROUND

The most relevant factor in the progression-free survival (PFS) of patients with meningiomas is the malignant grade. However, using only the current World Health Organization (WHO) definition that does not consider precise quantitative indicators, an unequivocal diagnosis of the malignant grade is difficult. In our retrospective study of the PFS of meningioma patients, we focused on mitoses and the Ki-67 staining index of tumor specimens obtained at the initial surgery.

METHODS AND RESULTS

A total of 349 patients with intracranial meningioma, operated between 1978 and 2000, were followed for a mean of 7 years. According to the mitotic index (MI), we classified them into 3 groups. In Group A (n=326), slide-mounted tumor samples exhibited no mitoses; in Group B (n=15) there were fewer than 4 mitoses, and in Group C (n=8) 4 or more mitoses were seen per 10 high-power fields (HPF). The estimated 5-year PFS rates in Groups A, B, and C were 93%, 10%, and 13% respectively. The mean PFS for Group A was 148 months; in Groups B and C the median PFS was 43 and 16 months, respectively. A Ki-67 staining index (SI) of less than 1% corresponded with no mitosis, while an SI exceeding 5% was indicative of the presence of mitoses.

CONCLUSION

In meningioma patients, no mitoses and/or a Ki-67 SI <1% signals a favorable outcome. An SI >5% or the presence of mitoses, even fewer than 4 in 10 HPF, is suggestive of a short PFS irrespective of other pathologic features. We suggest that in combination, assay of the Ki-67 SI and the MI represents a reliable, quantitative tool for predicting PFS in meningioma patients. © 2004 Elsevier Inc. All rights reserved.

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KEY WORDS

Meningioma, Ki-67 staining index, mitotic index, progression-free survival.

Ithough meningiomas are generally slow-growing, benign tumors, 20% of gross-totally resected meningiomas recur within 20 years [14]. The most relevant factor for progression-free survival (PFS) is their histologic malignant grade: while approximately 7 to 20% of benign meningiomas recur, for atypical- and anaplastic meningiomas the recurrence rates are much higher at 29 to 40% and 50 to 78%, respectively [7,9,11,14,16,24,25]. Thus, while the value of histologic grading is obvious, their objective staging has been hampered by the fact that the World Health Organization (WHO) classification of meningiomas relies heavily on qualitative criteria without taking into account more precise quantitative indicators such as numerical scoring systems.

The mitotic index (MI) is only one numerical criterion of pathologic grades in the WHO classification of meningiomas [14]. For the purpose of diagnosing atypical and anaplastic meningiomas, increased mitotic activity is defined as the presence of 4 or more and 20 or more mitoses per 10 highpower fields (HPF), respectively. Proliferation indices as well as the MI are significantly correlated with tumor-doubling time [14,20] and a Ki-67 staining index (SI) of more than 5 to 10% reflects an increased risk of recurrence as well as a high grade of malignancy [14]. In typical cases with obvious pathologic features of malignancy, increased mitotic activity, and a Ki-67 SI far exceeding the cut-off value, an unfavorable outcome is easily predicted at the time of the initial surgery. However, the prognosis varies in patients with meningiomas that lack

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the typical malignant features and exhibit few mitoses and a Ki-67 SI near the cut-off level.

In this retrospective study of 349 patients with surgically removed intracranial meningiomas, we assessed the correlation between the MI and the clinical outcome represented by their PFS. We paid special attention to the prognostic significance of the presence of any mitotic figures in tumor tissue samples obtained at the time of the initial operation. As we detected a relationship between the Ki-67 SI and the presence of even fewer than 4 mitoses/10 HPF, we now suggest that in combination, these two parameters represent a powerful and quantitative tool for predicting PFS even in some meningiomas that are not easily classified into a benign or atypical type according to the WHO criteria.

SUBJECTS AND METHODS PATIENT POPULATION

Between 1978 and 2000, 426 patients with intracranial meningiomas underwent surgical treatment at Kyoto University Hospital. Their medical records were carefully reviewed and all clinical, laboratory, radiographic, pathologic, and follow-up data were retrieved. Of the 426 patients, 349 were entered into this study because they fulfilled all of the following criteria: 1) they had undergone no previous surgical treatment of their tumors, 2) their postoperative follow-up exceeded 1 year, and 3) they did not have meningeal hemangiopericytoma. Before tumor recurrence, none of the 349 patients had received radiation therapy.

There were 118 males and 231 females; their mean age was 54 years (range 18 to 78 years). Diagnosis was based on hematoxylin-eosin (H&E) staining of tumor samples from the initial surgery; of the 349 meningiomas, 331 (94.8%) were benign, 16 (4.6%) were atypical, and 2 (0.6%) were anaplastic. According to WHO criteria, we made a diagnosis of atypical or anaplastic type based on whether the tumor samples manifested a MI of 4 or more or 20 or more mitoses per 10 high-power fields (HPF), respectively, as well as pathologic findings such as increased cellularity, small cells with a high nucleus: cytoplasm ratio, prominent nucleoli, uninterrupted patternless or sheet-like growth, and foci of necrosis [14].

We used the system of Simpson [28] to record the extent of tumor removal. Accordingly, 118 patients (33.8%) had undergone Grade I resection (complete with excision of the dural insertion), 150 (43.0%) Grade II (complete with coagulation of the dural insertion), 53 (15.2%) Grade III (incomplete, leaving

behind a small amount of tumor tissue), and 28 (8.0%) Grade IV (incomplete, with a large amount of residual tumor tissue). Of the 326 Group A patients, 110 (33.7%) had undergone Simpson's grade I resection, 146 (44.8%) Grade II, 46 (14.1%) Grade III, and 24 (7.4%) Grade IV. Of the 15 Group B patients, 5 (33.3%) had received Grade I resection, 2 (13.3%) Grade II, 4 (26.7%) Grade III, and 4 (26.7%) Grade IV. Of the 8 Group C patients, 3 (37.5%) had undergone Grade I resection, 2 (25%) Grade II, 3 (37.5%) Grade Ill, and none Grade IV. The extent of resection was deduced from the recorded description of the operation and confirmed by inspecting postoperative computed tomography (CT) and/or magnetic resonance (MR) images in the patients' medical records. Other clinicoradiological findings such as perifocal edema, tumor staining, feeding from pial arteries, tumor hardness, arachnoid penetration, tumor demarcation, and tumor location were also confirmed by inspection of the surgical records and/or neuroradiological images.

During a mean follow-up time of 83 months (range 12–253 months), 42 of the 349 patients (12.0%) experienced recurrence; of these, 31 (73.8%) had benign- and the remaining 11 had atypical- or anaplastic meningiomas. The criteria for diagnosing recurrence were the demonstration, during regular follow-up, MR and/or CT evidence of tumor appearance after complete resection, or of regrowth of residual tumors.

ASSESSMENT OF THE MI AND THE KI-67 SI

In all 349 patients, tumor tissues obtained at the first operation were subjected to MI determination. The specimens were fixed with formalin, embedded in paraffin, and tissue samples mounted on slides were stained with H&E. The MI was determined by counting the number of unequivocal mitotic figures in 10 consecutive HPF (\times 400) containing the highest number of mitoses [25].

In 29 of 42 patients with tumor recurrence, the Ki-67 SI of tumor tissues obtained at the first operation was additionally determined. Tissue sections (4 μ m in thickness) were deparaffinized and immunostained using the Ventana NX automated immunohistochemistry system (Ventana Medical Systems, Tucson, AZ). Briefly, the slides were heated in a 750W microwave oven (5 min \times 4) in citrate buffer (pH 6) and then incubated for 1 hour with anti-Ki-67/MIB-1 (Dako, Carpenteria, CA) diluted 1:100 in bovine serum albumin/TBS. Immunoreactions were then performed according to the LSAB method using streptavidin-biotin complex (ABC)-labeled horseradish peroxidase and diaminobenzidine

(DAB). All tissue sections were examined at high-power magnification (× 400). The number of cells stained positively with anti-Ki-67 antibody and the total number of tumor cells were counted in several representative fields containing more than 1000 cells and their ratio was expressed as the Ki-67 SI (%) [20]. In areas with heterogeneous distribution of Ki-67 immunopositive cells, the area containing the largest number of Ki-67-stained cells was considered to represent the proliferative activity of the tumor.

Using the H&E-stained sections, 2 pathologists (NK, YN) independently made the histologic diagnosis and graded the tumors. They inspected H&E-stained or immunostained sections together, using a multi-head microscope, and assigned the MI and Ki-67 SI by consensus. Although they were cognizant of the diagnosis, they made their assessments before accessing any information pertaining to the outcomes.

STATISTICAL ANALYSIS

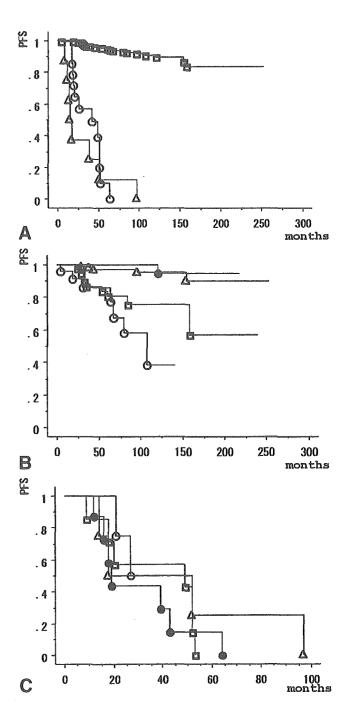
The relationship between the MI and the Ki-67 SI was examined by the Pearson correlation coefficient. In addition, PFS curves were prepared using the Kaplan-Meier method. The log-rank test was employed to determine whether the MI-based classification, the extent of surgical resection, the pathologic diagnosis, and other clinicoradiological parameters were associated in a univariate manner with PFS. Differences were considered statistically significant at p < 0.05.

RESULTS

CLINICAL OUTCOMES AND MI

The 349 meningioma patients were divided into 3 groups according to their Ml. Group A (no mitoses) consisted of 326 patients (322 benign-, 4 atypical meningiomas), Group B (more than 0 and fewer than 4 mitotic figures/10 HPF) of 15 (9 benign, 6 atypical or anaplastic), and Group C (4 or more mitotic figures/10 HPF) of 8 patients with atypical or anaplastic meningioma. There were no cases with 20 or more mitotic figures per 10 HPF.

The 349 patients were followed for a mean of 83 months. As shown in Figure 1A, the estimated 5-year PFS rates in Groups A, B, and C were 93%, 10%, and 13%, respectively. The mean PFS for Group A was 148 months; in Groups B and C the median PFS was 43 and 16 months, respectively. By the log-rank analysis, the difference in PFS between Group A and the other 2 groups was significant (Group A vs. B, p < 0.0001; A vs. C, p < 0.0001; A vs.



(A) Kaplan-Meier curves of progression-free survival (PFS) in patients grouped according to the mitotic index (MI) of surgical tumor specimens. Open squares, Group A (no mitotic figures); open circles, Group B (more than 0 and fewer than 4 mitotic figures per 10HPF); open triangles, Group C (more than 4 mitotic figures per 10HPF). (B) Kaplan-Meier curves of PFS in Group A patients classified according to the Simpson resection grade. Solid circles, Grade I; open triangles, Grade II; open squares, Grade III; open circles, Grade IV. For a description of Simpson grades, see Subjects and Methods. (C) Kaplan-Meier curves of PFS in Group B and C patients classified according to the Simpson resection grade. For symbols, see Figure 1B.

Correlation Analyses of Clinicopathological Factors With Recurrence

	FREQUENCY (%)	Overall Cases	GROUP A	GROUP B	GROUP C	GROUP B+C
Mitoses (+)	7%	< 0.0001	Control of the Contro			
Simpson Grades		< 0.0001	< 0.0001	NS	NS	NS
Simpson I or II	78	< 0.0001	< 0.0001	NS	NS	NS
Perifocal edema on MR images (+)	46	NS	0.009	NS	NS	NS
Hard tumors	48	NS	NS	NS	- NS	NS
Arachnoid penetration (+)	26	NS	NS	NS	NS	NS
Well-demarcated tumors	96	0.01	0.006	NS	NE	NS
Tumor stain on angiograms (+)	75	NS	0.03	NS	NS	NS
Feeding from pial arteries on angiogram	28	NS	NS	NS	NE	NS
Tumor locations		0.03	0.0002	NS	NS	NS
Tumors located on skull base	48	0.01	< 0.0001	NS	NS	NS

Frequency is calculated in overall cases.

Cases with no mitoses, those with 1-4 mitoses per 10HPF, and 4 or more mitoses per 10 HPF are present in each of the 3 groups.

NS = not significant, NE = not examined because of insufficient numbers of cases.

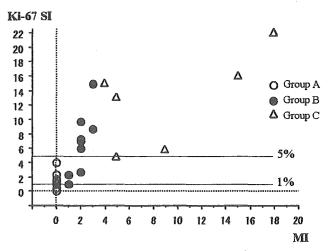
B and C combined, p < 0.0001). Group B and C did not significantly differ with respect to PFS (p = 0.3945).

The frequencies of radiologic, operative, and pathologic findings and their univariate associations are summarized in Table 1. In the analysis of overall cases and of Group A patients, parameters such as the Simpson grade, tumor demarcation, and tumor location contributed to variability in the Kaplan-Meier PFS curves assessed by the log-rank test. In contrast, none of the variables examined significantly affected the PFS curves of Group B and C, nor of Groups B and C combined.

Figure 1B shows the Kaplan-Meier PFS curves for all 326 Group A patients classified according to the Simpson resection grades. The estimated 5-year PFS rates for Simpson Grades I, II, III, and IV were 100%, 97%, 81%, and 77%, respectively; the 10-year PFS rates were 95%, 93%, 76%, and 38%; and the mean PFS was 121, 150, 132, and 85 months. According to the log-rank test, in Group A, the Simpson grade had a significant effect on PFS: the greater the extent of resection, the longer was the PFS and the lower the progression ratio (p < 0.0001). On the other hand, in Groups B and C, the extent of resection had no significant impact on PFS (p = 0.71) (Figure 1C). The estimated 2-year PFS rates for the 23 patients in Groups B and C who had undergone Grade I, II, III, or IV resection were 42%, 50%, 57%, and 75%, respectively; the median PFS was 19, 18, 49, and 6 months. In Group B alone and Group C alone, there was also no significant association of the Simpson's grade with PFS (p = 0.97 and p =0.58, respectively).

KI-67 SI AND MI

In 29 of the 42 patients with recurrence we determined the Ki-67 SI in tumor samples from the initial surgery. The mean Ki-67 SI values \pm SD were 1.5 \pm 1.2 in Group A (n=14), 6.7 \pm 4.3 in Group B (n=9), and 12.8 \pm 6.5 in Group C (n=6). Based on the Pearson correlation coefficient, there was a significant correlation between the MI and the Ki-67 SI ($r=0.81,\ p<0.0001$). Figure 2 shows that all cases with a Ki-67 SI below 1% were from Group A. An SI exceeding 5% was indicative of the presence of mitoses (Groups B and C). Patients from all groups could be found in the 1 to 5% SI range.



Correlation of mitotic index with Ki-67 staining index. Open circles, Group A (no mitotic figures); closed circles, Group B (more than 0 and fewer than 4 mitotic figures per 10HPF); open triangles, Group C (more than 4 mitotic figures per 10HPF).

COMPARISON BETWEEN THE MI AND PATHOLOGIC DIAGNOSIS

The 331 patients with a pathologic diagnosis of benign meningioma manifested an estimated 5-year PFS rate of 91% with a mean PFS of 144 months. On the other hand, in the 18 patients with atypical or anaplastic meningiomas, the estimated 5-year PFS rate was 32% with a median PFS of 52 months. Kaplan-Meier analysis showed that the difference in PFS between benign and atypical/anaplastic meningiomas was significant (p < 0.0001). The Simpson grade had a significant effect on PFS only in the 331 patients with benign meningiomas (p < 0.001); the estimated 5-year PFS rates for Grades I, II, III, and IV were 97%, 95%, 95%, and 90%, respectively; the 10-year rates were 76%, 70%, 80%, and 35%; and the mean PFS was 117, 148, 126, and 82 months.

In Group A, none of the 4 meningiomas designated atypical according to WHO criteria (MI=0) recurred during a mean follow-up of 61 months. On the other hand, all 9 benign meningiomas in Group B recurred after a mean of only 38 months (range 18-64 months), a shorter interval than we expected for ordinary benign meningiomas.

DISCUSSION

Although meningiomas are generally benign, slowgrowing tumors with apparent demarcation, they have a tendency to recur after a period of more than 10 years [14,28]. Putative prognostic factors are age, attachment to intracranial structures (location), the extent of resection [7,8,28], grade of malignancy [9,25], and proliferation indices [6,10-15,17,18,20,21]. The pathologic grade of malignancy has been proposed as the most relevant overall predictor of recurrence [14]. However, there are patients whose tumors are not pathologically identifiable as benign or atypical because the grade of malignancy cannot be unequivocally determined. The WHO classification proposes primarily qualitative criteria for defining grades of malignancy; except for the MI, it does not provide more precise quantitative indicators that could be assessed according to numerical scoring systems. For the purpose of diagnosing atypical meningiomas, the WHO criteria define increased mitotic activity as the presence of 4 or more mitoses per 10 HPF. However, with respect to assigning a malignant grade to meningiomas, the WHO classification system does not consider a finding of fewer than 4 mitoses of importance [14].

Proliferation indices such as the Ki-67 SI are useful for predicting tumor recurrence and survival. While

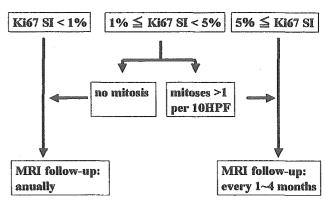
previous studies documented that the Ki-67 SI significantly correlates with the pathologic grade of meningiomas, there is considerable variation in the Ki-67 SI values reported in different studies and by different institutions. In fact, the reported mean values for benign-, atypical-, and anaplastic meningiomas range widely between 0.7 and 3.8%, 2.1 and 7.1%, and 10.9 and 14.7%, respectively [1,10,14,15,21,26,27]. Moreover, some reports suggested significant overlapping of Ki-67 values among various pathologic grades of malignancy [1,6,12,13]. Perry et al [25] who performed statistical analyses of 62 meningioma cases, suggested that a Ki-67 SI of 4.2% represented a threshold and that an SI in excess of 4.2% was indicative of high tumor proliferation activity. Although we agree that values markedly above or below this threshold may signal unfavorable and favorable outcomes respectively, in view of the wide range of reported Ki-67 SI values, we favor the establishment of stricter SI criteria to predict clinical outcomes.

In efforts to develop a system whereby quantitative indicators can be used to predict the PFS of meningioma patients, we performed the current retrospective study. We assessed whether the combination of an MI that confirms the presence of even fewer than 4 mitoses per 10 HPF and the KI-67 SI is of prognostic significance. Surgically removed meningioma tissues in 326 of 349 patients (93.4%) exhibited no evidence of mitosis. In most of the remaining 23 tissue samples the MI was around 4 per 10 HPF; none of the patients had an MI of more than 20. We found that compared to the other 2 groups, in patients with no mitoses (Group A), the 5-year incidence of tumor progression was lower (7%) and the mean PFS longer (148 months), and that the Simpson grade had a significant effect on PFS. Group B (more than 0 and fewer than 4 mitoses) and Group C patients (MI of 4 or more) had higher 5-year recurrence rates at 90% and 87%, respectively, and shorter PFS (median 43 and 16 months, respectively). A Ki-67 SI of less than 1% corresponded with the absence of mitoses in the tumor samples (Group A), while an SI exceeding 5% reflected the presence of mitotic figures (Groups B and C). Therefore, we propose that SI values of 1% and 5% be used as threshold values for predicting favorable and unfavorable outcomes, respectively, in meningioma patients. Patients from all 3 groups were found in the SI value range from 1 to 5%, therefore, a Ki-67 SI in this range is not a reliable, independent predictive indicator of the outcome. Assessment of the Ki-67 SI is relatively easy com**154** Surg Neurol 2004;61:149–56

pared to the calculation of a low MI whose determination is complex. Although the Ki-67 SI alone is generally used for predicting the outcome in meningioma patients, we stress the need for determining the MI, especially in patients whose Ki-67 SI is in the 1 to 5% range.

Patients with atypical and anaplastic meningiomas diagnosed according to the current WHO criteria had higher recurrence rates and shorter PFS than did patients with benign tumors. This finding coincides with the difference we observed in the MI of Group A patients and the MI in Groups B and C. It is important to note that none of the 4 atypical meningiomas in Group A manifested recurrence during a mean follow-up period of 61 months whereas all 9 benign meningiomas in Group B recurred after a mean of only 38 months (range 18-64 months). The time to recurrence of these benign tumors was shorter than we would have expected. In some of our patients the clinical outcome was at variance with the expected outcome based on the malignancy grade determined by WHO criteria. We found that in such patients, the MI reflected the likelihood of short-term recurrence much better than did the malignant grade. In addition, although an MI of 4 or more per 10 HPF is the consensus criterion for atypical meningiomas, our results suggest that a small number of mitoses, even fewer than 4 per 10 HPF, is also an important indicator for predicting the short-term progression of meningiomas.

Atypical and anaplastic meningiomas tend to recur within a short period even after gross total removal. Patients with these meningioma types require repeated operations and some have been treated with postoperative extrabeam radiation therapy (EBRT) although high-grade meningiomas are usually refractory to EBRT [2-4,19,23]. In these meningiomas, stereotactic radiosurgery (SRS) as a boost to EBRT, as salvage therapy after EBRT, or instead of EBRT, has yielded disappointing results. In atypical meningiomas the 5-year local controland 5-year overall survival rates were 32 to 48% and 83 to 95%, respectively; in anaplastic meningiomas they were 0 to 34% and 21.5 to 60% [5,22,23]. As the tumor control rate following SRS was better in patients with small (< 8 cm³) malignant meningiomas [22], we stress that early diagnosis and immediate treatment of small recurrent tumors is imperative for improving the outcomes of patients with atypical and anaplastic meningiomas. We need a method that allows us to predict the PFS in all meningioma patients so that postoperative therapy can be selected on a case-by-case basis.



Proposal schedule of postoperative follow-up MRI based on MI and Ki-67 SI.

CONCLUSION

Our retrospective study of 349 patients with surgically treated meningiomas revealed that numerical scoring systems, i.e., the Ki-67 SI and the MI, determined at the time of the initial operation, make possible the prediction of long or short PFS. Based on our results, we propose that tumors with a Ki-67 SI of less than 1% be followed as benign meningiomas and subjected to annual MRI study (Figure 3). On the other hand, surgical specimens with a Ki-67 SI greater than 5% should be monitored as atypical or anaplastic meningiomas and undergo follow-up MRI study at intervals of a few months. In cases where the Ki-67 SI is between 1 and 5%, we suggest that the MI of tumor tissue samples be carefully determined. If there is no evidence of mitoses, annual MRI study should be performed. However, patients with even a few mitotic figures should be followed by MRI at shorter intervals.

Our retrospective analysis of 349 surgically treated meningioma patients revealed that the presence of mitotic figures in tumor tissues obtained at the first operation correlated with shorter PFS when compared to patients whose specimens contained no mitotic figures. We also determined that the threshold for predicting favorable and unfavorable treatment outcomes with the Ki-67 SI are 1% and 5%, respectively. In meningiomas with a Ki-67 SI between 1% and 5%, the presence of mitoses, even less than 4 in 10 HPF, is indicative of an increased risk for recurrence. The combination of the Ki-67 SI and the MI represents a convenient and quantitative tool for predicting PFS. We posit that in cases where a diagnosis of malignant meningioma is based on current WHO criteria, these combined assays make possible a more precise prediction of the prognosis.

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