

**Keywords:** O6-methylguanine-DNA methyltransferase; Glioblastoma; Real-time polymerase chain reaction; Temozolomide; Cocarboxin; Bevacizumab; Receptor tyrosine kinase inhibitors

## Introduction

Temozolomide (TMZ) is the only chemotherapeutic agent which has the evidence for the glioblastoma (GB) treatment. Among all other drugs including bevacizumab, it is regarded as the most effective [1,2]. Indeed, temozolomide is a 2-methyl-3-(4-amino-2-methyl-5-imidazolyl)-5-(2-chloroethyl)-3-nitroimidazole-4-carboxamide (ACNU), Bevacizumab, Human epidermal growth factor receptor 2 tyrosine kinase inhibitor (EGFR-TKI), Vincristine, and Carboplatin are used and used for GB treatment in Japan, but the evidence is not clear in the elderly patients for GB treatment [3]. Additionally, the use of Bevacizumab, however, has been not only the evidence of the effectiveness of TMZ, but also the use of Bevacizumab in addition

## Citation:

Ho i al, Tok o, 10 a ien a Na i onal Cance Cen e Ho i al, Tok o; 1 a ien a Shio a Ho i al, In e na i onal Uni e i of Heal h and Welfa e, Yai a; 3 a ien a Ka a aki Ho i al, Hi achi o a; and e ma i n g 1 a ien a Tok o-Ni hi Tok h kai Ho i al, Tok o, Ja an. All of he 55 GB a ien e ce i ed e mo olomide and adia i on a e ge i n a cco dance i h he S oocol [2]. W i en i nfo med con en fo he an i a i on of MGMT mRNA i n mo am le a o i ded b all a ien . RT-PCR ba ed an i a i on of MGMT mRNA (C o Poin of MGMT mRNA i n Gliobla oma) a a o ed b he E hic Commi ee a Tok o Medical Uni e i i n he ea 2005, a Ki a a o Uni e i i n he ea 2002, a he In e na i onal Uni e i of Heal h and Welfa e i n he ea 2012, and a Tok h kai Ho i al i n he ea 2015.

### Real-time polymerase chain reaction based quantitation of MGMT mRNA absolute value

Collec i on of mo am le and an i a i on of MGMT mRNA a e fo med b S e c i al Refe ence Labo a o Co. L d., Hino, Ja an. e me hod ed o an i f he ab ol e al e of MGMT mRNA b RT-PCR a de c i bed e i o l [9]. B i e , he g anidini m hioc ana e- henol-chlo ofo m media ed e ac i on a e fo med i n g I ogen (WAKO J n ak ) fo e ac i n g o al RNA f om e i he 10 mg of f e hl ob a i ned mo am le o ed a 4 C i n QIAGEN RNAla e Ti e P o ec T be (AMBION Inc) o i e f o en a -70 C [10]. F om l g of he e ac ed o al RNA, he com le men a DNA (cDNA) a n he i ed and a b e en l i n c ba ed a 37 C fo 60 min e . e eal- i me ol me a e chain eac i on a ca i ed o i n g a Ta Man Uni e al Ma e Mi (A l i ed Bio em ) com i n g of 120 nM of each i me [11], 200 nM of obe (5- CGA GCA GTG GGA GGA GCA ATG AGA-3), and 2.5 L of each cDNA am le, i h dena a i on a 95 C fo 10 min e and 50 c cle (a 95 C fo 30 econd , 60 C fo 40 econd , and 72 C fo 30 econd ) i n a eal- i me PCR em. e le el of gl ce aldeh de-3- ho ha e deh d ogena e (GAPDH) mRNA e e i on e e ed a a an i a i e i n e nal con ol. U i n g a anda d c e, he e e i on le el of each mRNA a calc la ed. I n o de o ob a i n an e en mo e acc a e an i ca i on, he MGMT mRNA e e i on le el of each am le a no mali ed b he e e i on of he GAPDH gene.

### Statistical analysis

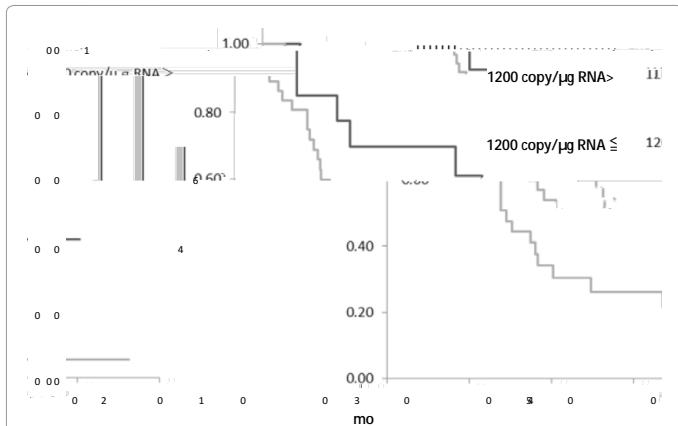
All he a i c i al anal e e e ca i ed i n Mic o o E cel Tok e i So a e. e e o g e i on-fee i al e i od and o e all i al of he 55 GB a ien e e anal ed, and he ca e i h le han 8.1 mon h o g e i on-fee i al and 15 mon h o e all i al e e j dged o be TMZ e i an a cco ding o he e l of B a i n T mo Regi Ja an [12]. e c o o i n e e de e m i ned i n GB ea ed i h TMZ le han 75 and KPS of a lea 60 b ROC anal i . e e c i c i and e n i i i of each c o o i n e e calc la ed. Ka lan- Meie anal i a e fo med o e al a e each i al i me, and he log ank (Man el-Co ) e a con i de ed fo anal i n g he b i na a i able (le han and a lea he c o o i n ). 2- a i led *p* al e a e e o ed. De e m i na i on of he a i c i al i g n i cance of he da a anal i a e a a ob a b i l i le el of 5% ( $p=0.05$ ).

## Results

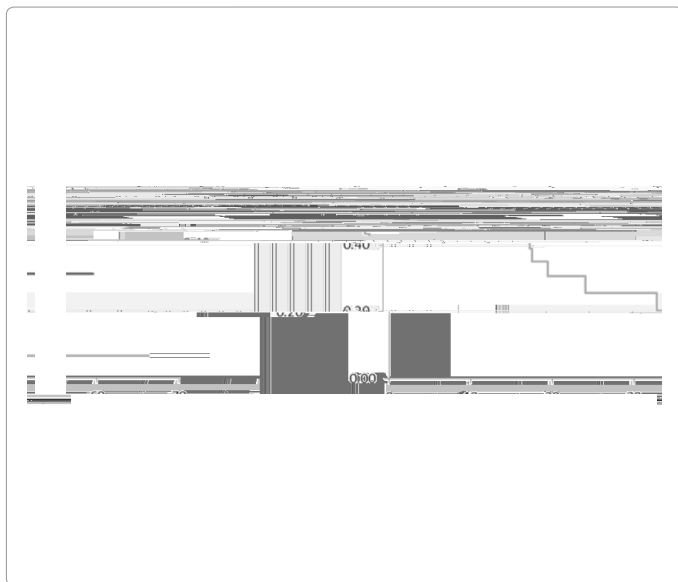
### ROC analysis for selecting candidate cutoff points for MGMTmRNA in GB

e candida e c o o i n i n each GB g o e e calc la ed b aco i e /0371gRNA fe e che ca dida e c o o i n i o a e di n g PFS

ac dida e c o o i n i o a e di n g OS e c i c i i e of a83.6, 7.9()Tj0.208 T T d K69.6%,and e n i i i i e of a39.1, 47.8and 502.2%,ae i e c i i o ]Tj0.077 T T j i m e c].65aach i al 0.5(ome, and he )og ank .5(Man el-Co ) 0.5( o e e d]Tj0.10 T T ed ao e al a e e i na



**Figure 3:** and radiation for GB with less than and at least 1200 copies of MGMT mRNA/ $\mu$ g RNA for overall survival (OS). OS was significantly longer in those who had less than 1200 copies/ $\mu$ g RNA ( $P=0.0189$  by logrank test).



**Discussion**

As mentioned in the introduction section, MGMT is silenced by the methylation of DNA cytosine domain [6]. Methylation of MGMT, which is an immunohistochemical marker for MGMT, is detected by immunohistochemistry, methylation-specific PCR, methylation-specific sequencing, and the absence of MGMT mRNA has been reported [13]. Among the methods, immunohistochemistry and methylation-specific PCR are not fundamentally accurate, and the effect of the methylation level on the prediction and prediction of TMZ therapy, although

Hegi et al. [7], but in the clinical trial of a methylation-specific PCR for the prediction of MGMT methylation. Immunohistochemical detection of methylation in the analysis of MGMT methylation [14]. The analysis of MGMT methylation has high correlation with clinical outcome of alkylating agent. High methylation level is associated with better clinical outcome. Real-time quantitative PCR might not be a reliable method for the prediction of MGMT methylation because the prediction of MGMT methylation is incomplete. Long-term clinical trials [11,16]. Real-time quantitative PCR is a reliable method for the prediction of methylation level, and clinically relevant for the prediction of the outcome of alkylating agent. As described in the introduction, the level of methylation is predicted by immunohistochemistry, PCR and methylation-specific sequencing of MGMT mRNA methylation level based on real-time quantitative PCR and has been reported that the level of MGMT mRNA methylation is negatively correlated with the methylation level of MGMT cytosine [17]. Hence, the level of MGMT mRNA methylation can be a reliable method for the prediction of methylation level.

In fact, methylation-specific PCR is a reliable method for the prediction of methylation level. The level of MGMT methylation based on methylation-specific PCR is a reliable method for the prediction of methylation level of GB. The level of methylation based on methylation-specific PCR is a reliable method for the prediction of methylation level of MGMT cytosine based on methylation-specific PCR and the prediction of methylation level of MGMT cytosine based on methylation-specific PCR. On the other hand, based on SYBR Green method, the level of methylation is negatively correlated with the level of methylation based on methylation-specific PCR and RNA methylation level



**Citation:**

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Motomura K, Natsume A, Kishida Y, Higashi H, Kondo Y, et al. (2011) Benefits of interferon- $\gamma$  and temozolomide combination therapy for newly diagnosed

Identification of regions correlating MGMT promoter methylation and gene

Shen D, Guo CC, Wang J, Qiu ZK, Sai K, et al. (2015) Interferon- $\gamma$  enhances

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