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MGMT parameters as favorable prognostic factors in glioma patients

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Background: O-6-methylguanine-DNA methyltransferase *(MGMT)* gene promoter methylation and its subsequent loss of protein expression has been identified to have a variable impact on clinical outcome of glioma patients indicated for chemotherapy with alkylating agents (Temozolomide). The present study aimed to investigate methylation status of *MGMT* gene and *in situ* protein expression in malignant glioma patients of different histological types to analyze the clinical outcome using alkylating drugs and radiotherapy.

Methods: Sixty-three cases of glioma were evaluated for *MGMT* promoter methylation by methylation-specific PCR (MS-PCR) and protein expression by immunostaining (IHC).

Results: *MGMT* gene methylation was detected in 38 (60.3%) cases and loss of protein expression was found in 36 cases (60%). Methylation status of *MGMT* and loss of protein expression showed very high concordance and significant association ($p<0.0001$). Both *MGMT* parameters showed a significantly higher OS and PFS (log rank p=.000). Multivariate Cox regression analysis showed both *MGMT* methylation and loss of protein as significant independent prognostic factors in glioma patients with Hazard Ratio as 3.27 (95% CI; 0.96-10.73; p=0.048) and 7.17 (95% C.I; 2.01-25.5; p=0.002). Interestingly concordant *MGMT* methylation and lack of protein showed better response in patient subgroups treated with TMZ therapy as against those without ($p<0.05$).

Conclusion: We found the merits of prognostication of *MGMT* parameters, methylation as well as loss of its protein as favorable predictive factors for using TMZ therapy for better survival. We conclude both parameters of *MGMT* should be considered to benefit the glioma patients put on TMZ therapy.

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