

Evaluation of *MGMT* methylation status among HUSM glioma patients: A preliminary study

Revathy¹, M., Badrisyah¹, I., Shaharum, S²., Goh W. C.² and Farizan, A^{1,3}

¹Department of Neurosciences, School of Medical Sciences, Universiti Sains Malaysia

²School of Health Sciences, Universiti Sains Malaysia

³Human Genome Centre, School of Medical Sciences, Universiti Sains Malaysia

farizan@usm.my

Abstract

Growing evidences show that understanding the roles of biomarkers has significantly increased our current perception of gliomagenesis, prognostic evaluation, and treatment planning for patients. For instance, identification of the promoter methylation status of *O6-methylguanine-DNA-methyltransferase (MGMT)* gene encodes *MGMT*, a protein with DNA repair activity may improve the efficacy of current standard care in glioma as the methylation status has been recently introduced to be a predictive biomarker for stratification of the treatment plan. To further understand the roles of *MGMT*, the present study aims to evaluate the status of *MGMT* promoter methylation status of glioma patients in HUSM. In this study, 21 samples of paraffin-embedded glioma tissue (FFPE) were obtained based on their grading from Grade II (n = 5), III (n = 4) and IV (n = 12). Subsequently, DNA extraction and methylation status was validated by methylation-specific PCR (MSP) using two pairs of primers specifically targeting the unmethylated (UM) and methylated (M) regions of the *MGMT* gene respectively. MSP results identified high intratumoral heterogeneity of the samples in all grades of the tumours. In Grade II glioma, 20% were M and 80% were both UM and M while in Grade III and IV glioma, 25% were M and 75% were both UM and M. None of the samples exhibited UM status alone of the *MGMT* promoter. Nevertheless, analysis using Fisher's exact test found no statistical association between the *MGMT* methylation status and any of the tested clinicopathological parameters such as tumour grading, age, gender, and race of the patients ($p > 0.05$). Similar to our results, intratumoral diversity of *MGMT* promoter methylation status has also been previously demonstrated in some studies. Besides highlighting the existence of the intratumoral heterogeneity, it may also suggest future challenges for defining personalized treatment based on the epigenetic status of *MGMT*.

Keywords: *MGMT*; MSP; *MGMT* methylation status

*Author for Correspondence