Correlation Between LINE-1 Methylation and MGMT Promoter Methylation in Glioblastomas

Jarin Chindapasirt, M.D., Piyamai Chankate, M.D., Mathawee Aumchaumchaya, M.D., Chinachote Teerapakpinyo, M.D., Iyavut Thaipisuttikul, M.D., Shanop Shuangshoti, M.D. and Virote Sriuranpong, M.D.

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Background: Genome-wide hypomethylation is one of the cancer characteristics. In glioblastomas, hypermethylation of MGMT promoter serves as an important prognostic and a predictive factor for response to alkylating agents. Recent evidence demonstrates that level of genome-wide methylation assessed by measuring level of LINE-1 methylation in glioblastomas is lower compared with those of low-grade gliomas. We hypothesized that there may be a pattern of correlation between the localized methylation in the MGMT promoter and the global DNA methylation in glioblastomas.

Method: We collected 45 formalin-fixed, paraffin-embedded GBM tissues derived from patients treated at the King Chulalongkorn Memorial Hospital during year 2008-2013. We used pyrosequencing technique to determine the percentage of methylation of both LINE-1 and MGMT promoter.

Results: There were 45 GBMs included in this study. The median level of LINE-1 and MGMT promoter methylation were 68.0% and 12.4%, respectively. Fifty-one percent of the tumors was high LINE-1 methylation and 29% was methylated MGMT. There was a trend toward a direct correlation between LINE-1 methylation and MGMT promoter methylation, however, this correlation was not statistically significant (r=0.211, p=0.164).

Conclusion: In limit number of glioblastomas, there is a modest correlation between genome-wide methylation and MGMT promoter methylation status. Low LINE-1 methylation was associated with a trend for better survival. Further studies in larger population are warranted.