Local DNA hypermethylation is a potential source of cancer biomarkers. While the evaluation of single gene methylation has limited value, their selected panel may provide better information.

A study aimed to analyze the promoter methylation level in a 7-gene panel in brain tumors and verifies the usefulness of methylation-sensitive high-resolution melting (MS-HRM) for this purpose.

Forty-six glioma samples and one non-neoplastic brain sample were analyzed by MS-HRM in terms of SFRP1, SFRP2, RUNX3, CBLN4, INA, MGMT, and RASSF1A promoter methylation. The results were correlated with patients' clinicopathological features.

DNA methylation level of all analyzed genes was significantly higher in brain tumor samples as compared to non-neoplastic brain and commercial, unmethylated DNA control. RASSF1A was the most frequently methylated gene, with statistically significant differences depending on the tumor WHO grade. Higher MGMT methylation levels were observed in females, whereas the levels of SFRP1 and INA promoter methylation significantly increased with patients' age. A positive correlation of promoter methylation levels was observed between pairs of genes, for example, CBLN4 and INA or MGMT and RASSF1A.

The 7-gene panel of promoter methylation can be helpful in brain tumor diagnosis or characterization, and MS-HRM is a suitable method for its analysis [1].

1)
Majchrzak-Celińska A, Dybska E, Barciszewska AM. DNA methylation analysis with methylation-sensitive high-resolution melting (MS-HRM) reveals gene panel for glioma characteristics [published online ahead of print, 2020 Aug 11]. CNS Neurosci Ther. 2020;10.1111/cns.13443. doi:10.1111/cns.13443