Prediction of O(6)-methylguanine-DNA methyltransferase promoter methylation status in IDH-wildtype glioblastoma using MRI histogram analysis

Xianwang Liu [# 1 2 3], Tao Han [# 1 2 3], Yuzhu Wang [# 3 4 5], Hong Liu [1 2 3], Junlin Zhou [6 7 8]

Affiliations
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Abstract

To evaluate the utility of magnetic resonance imaging (MRI) histogram parameters in predicting O(6)-methylguanine-DNA methyltransferase promoter (pMGMT) methylation status in IDH-wildtype glioblastoma (GBM). From November 2021 to July 2023, forty-six IDH-wildtype GBM patients with known pMGMT methylation status (25 unmethylated and 21 methylated) were enrolled in this retrospective study. Conventional MRI signs (including location, across the midline, margin, necrosis/cystic changes, hemorrhage, and enhancement pattern) were assessed and recorded. Histogram parameters were extracted and calculated by Firevoxel software based on contrast-enhanced T1-weighted images (CET1). Differences and diagnostic performance of conventional MRI signs and histogram parameters between the pMGMT-unmethylated and pMGMT-methylated groups were analyzed and compared. No differences were observed in the conventional MRI signs between pMGMT-unmethylated and pMGMT-methylated groups (all $p > 0.05$). Compared with the pMGMT-methylated group, pMGMT-unmethylated showed a higher minimum, mean, Perc.01, Perc.05, Perc.10, Perc.25, Perc.50, and coefficient of variation (CV) (all $p < 0.05$). Among all significant CET1 histogram parameters, minimum achieved the best distinguishing performance, with an area under the curve of 0.836. CET1 histogram parameters could provide additional value in predicting pMGMT methylation status in patients with IDH-wildtype GBM, with minimum being the most promising parameter.

Keywords: Glioblastoma; Histogram analysis; Magnetic resonance imaging; O(6)-methylguanine-DNA methyltransferase.

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