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Cerebral blood volume calculated by dynamic susceptibility contrast-enhanced perfusion MR imaging: preliminary correlation study with genetic profiles in glioblastoma

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PURPOSE: To evaluate the usefulness of dynamic susceptibility contrast-enhanced (DSC) perfusion MR imaging in predicting major genetic alterations in glioblastomas.
MATERIALS AND METHODS: Twenty-five patients (M:F = 13:12, mean age: 52.1 ± 15.2) with pathologically proven glioblastoma who underwent DSC MRI before the surgery were included. On DSC MR imaging, normalized relative cerebral blood volume (rCBV) of the enhancing solid portion of each tumor was calculated by using a dedicated software (Nordic TumorEX, NordicNeuroLab, Bergen, Norway) which enabled semi-automatic segmentation for each tumor. Six major genetic alterations of glioblastomas (epidermal growth factor receptor (EGFR), phosphatase and tensin homologue (PTEN), Ki-67, phosphorylated form of histone H3 (pHH3), O6-methylguanine-DNA methyltransferase (MGMT) and p53) were confirmed by immunohistochemistry and analyzed for correlation with the normalized rCBV of each tumor. Statistical analysis was performed using unpaired Student's t-test and Pearson correlation test.
RESULTS: Normalized rCBVs of MGMT methylation negative group (mean: 9.5 ± 7.5 mL/100 mg) were significantly higher than those of MGMT methylation positive group (mean: 5.4 ± 1.8 mL/100 mg) ($p = .046$). In the analysis of EGFR expression positive group, normalized rCBVs of the subgroup with loss of PTEN expression gene (mean: 10.3 ± 8.1 mL/100 mg) were also significantly higher than those of the subgroup without loss of PTEN expression gene (mean: 5.6 ± 2.3 mL/100 mg) ($p = .046$). Ki-67 labeling index showed significant positive correlation with normalized rCBV of the tumor ($p = .01$).
CONCLUSION: We found that glioblastomas with aggressive genetic alterations tended to have high rCBV in the present study. Thus, we believe that DSC perfusion MR imaging can be a noninvasive radiophenotypic surrogate for genetic alterations which were crucial in predicting the prognosis and selecting the tailored treatment in glioblastoma patients.