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1: [Neurosurgery](#). 2009 Mar;64(3):455-61; discussion 461-2.



p16 promoter methylation in the serum as a basis for the molecular diagnosis of gliomas.

[Wakabayashi T](#), [Natsume A](#), [Hatano H](#), [Fujii M](#), [Shimato S](#), [Ito M](#), [Ohno M](#), [Ito S](#), [Ogura M](#), [Yoshida J](#).

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OBJECTIVE: Deoxyribonucleic acid (DNA) methylation of tumor origin can be detected in the serum/plasma of cancer patients. The aim of this study was to detect aberrant p16 promoter methylation as a potential diagnostic marker in the serum of patients with diffuse glioma to differentiate between gliomas and, particularly, to differentiate those in the brainstem from others; this was done by using the modified methylation-specific polymerase chain reaction technique. **METHODS:** The methylation-specific polymerase chain reaction was used to detect p16 methylation in the DNA extracted from 20 astrocytic tumors and 20 oligodendroglial tumors and the corresponding serum samples. Serum samples from 10 healthy individuals were used as controls. The association of p16 hypermethylation in the serum DNA of glioma patients with clinicopathological characteristics was analyzed. In addition, the serum DNA in 7 patients with a brainstem tumor (4 gliomas, 1 schwannoma, 1 cavernous angioma, and 1 ependymoma) was analyzed. **RESULTS:** We found p16 methylation in 12 (60%) of the 20 tissues with astrocytoma, but in only 1 of the tissues with oligodendroglioma. Similar methylations were detected in the serum of 9 (75%) of the 12 patients with aberrant methylation in the tumor tissues. No methylated p16 sequences were detected in the peripheral serum of the patients having tumors without these methylation changes or in the 10 healthy controls. Additionally, p16 promoter methylation in the serum was observed in all brainstem astrocytoma cases, but not in other cases. **CONCLUSION:** This assay has potential for use as a serum-based molecular diagnosis technique for diffuse glioma.

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