

Clinical Research

Comparative Proteomic Profiles of Meningioma Subtypes

Hiroaki Okamoto^{1,3}, Jie Li¹, Alexander O. Vortmeyer¹, Howard Jaffe², Youn-Soo Lee⁴, Sven Gläsker¹, Tae-Sung Sohn¹, Weifen Zeng⁵, Barbara Ikejiri¹, Martin A. Proescholdt⁶, Christina Mayer⁶, Robert J. Weil^{1,5}, Edward H. Oldfield¹ and Zhengping Zhuang¹

¹ Surgical Neurology Branch and ² Protein/Peptide Sequencing Facility, National Institute of Neurological Disorders and Stroke, NIH, Bethesda, Maryland; ³ Department of Neurosurgery, Faculty of Medicine, Saga University, Saga, Japan; ⁴ Department of Clinical Pathology, College of Medicine, The Catholic University of Korea, Seoul, Korea; ⁵ Brain Tumor Institute, Cleveland Clinic Foundation, Cleveland, Ohio; and ⁶ Department of Neurosurgery, Regensburg University Medical Center, Regensburg, Germany

Requests for reprints: Zhengping Zhuang, Surgical Neurology Branch, National Institute of Neurological Disorders and Stroke, NIH, Building 10, Room 5D 37, 10 Center Drive, Bethesda, MD 20892-1414. Phone: 301-534-8445; Fax: 301-402-0380; E-mail: zhuangp@ninds.nih.gov.

Meningiomas are classified into three groups (benign, atypical, and anaplastic) based on morphologic characteristics. Atypical meningiomas, which are WHO grade 2 tumors, and anaplastic meningiomas, which are WHO grade 3 tumors, exhibit an increased risk of recurrence and premature death compared with benign WHO grade 1 tumors. Although atypical and anaplastic meningiomas account for <10% of all of meningiomas, it can be difficult to distinguish them from benign meningiomas by morphologic criteria alone. We used selective tissue microdissection to examine 24 human meningiomas and did two-dimensional gel electrophoresis to determine protein expression patterns. Proteins expressed differentially by meningiomas of each WHO grade were identified and sequenced. Proteomic analysis revealed protein expression patterns unique to WHO grade 1, 2, and 3 meningiomas and identified 24 proteins that distinguish each subtype. Fifteen proteins showed significant changes in expression level between benign and atypical meningiomas, whereas nine distinguished atypical from anaplastic meningiomas. Differential protein expression was confirmed by Western blotting and immunohistochemistry. We established differential proteomic profiles that characterize and distinguish meningiomas of increasing grades. The proteins and proteomic profiles enhance understanding of the pathogenesis of meningiomas and have implications for diagnosis, prognosis, and treatment. (*Cancer Res* 2006; 66(20): 10199-204)