

Researchers discover new molecular subtype of brain cancer

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A study conducted by a collaborative team led by researchers from the University of Southern California (USC) may lead to better insight into the clinical outcome for some patients with a particularly aggressive type of brain cancer. The research may also provide a framework for development of targeted drug treatments.

The research by The Cancer Genome Atlas (TCGA), published online today in the journal *Cancer Cell*, used epigenomics to determine that tumor DNA methylation profiles were distinctly different in about 10 percent of patients with glioblastoma multiforme (GBM).

"Most GBM patients survive fewer than 15 months, and fewer than 10 percent live more than five years," said Peter W. Laird of the USC Epigenome Center, who led the TCGA team in collaboration with Dr. Kenneth Aldape at M.D. Anderson Cancer Center, Dr. Stephen B. Baylin at Johns Hopkins School of Medicine and many other TCGA consortium members. "With this research, we have identified a subset of patients with a distinct type of GBM that have substantially better clinical outcomes, with a median survival time of more than three years from the time of diagnosis."

Epigenomics is the study of how DNA is packaged and marked to control which genes can be used in a particular type of cell or tissue. The distribution of one of these marks along the DNA, called <u>DNA</u> methylation, is often abnormal in cancer, contributing to the disease process. The characteristic epigenetic profile discovered by the TCGA



team is called G-CIMP (Glioma CpG Island Methylator Phenotype) and was found to occur in much younger patients. G-CIMP tumors have other distinct alterations in their genomic landscape, revealing an interesting association with an acquired mutation in the IDH1 gene.

"Such findings are critical to the detection and treatment of <u>brain cancer</u> based on the genetic or epigenetic profile of each patient's disease," said National Institutes of Health (NIH) Director Francis Collins, M.D., Ph.D. "The depth and breadth of expertise in The Cancer Genome Atlas research network, combined with ever-improving genomic technologies, is generating remarkably detailed insights into cancer."

More information: Noushmehr H., et al., Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma, Cancer Cell (2010), doi:10.1016/j.ccr.2010.03.017

Provided by University of Southern California

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