Genome-wide data can classify gliomas into subtypes

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(HealthDay)—Genome-wide data can help classify subtypes of gliomas, according to two studies published online June 10 in the *New England Journal of Medicine*.

Daniel J. Brat, M.D., Ph.D., from Emory University Hospital in Atlanta, and colleagues performed genome-wide analysis of 293 lower-grade gliomas from adults. They identified concordant classification of three robust, nonoverlapping subtypes of lower-grade gliomas; the subtypes were captured more accurately by *IDH*, 1p/19q and *TP53* status than histologic class. The most favorable clinical outcomes were seen for patients with an *IDH* mutation and 1p/19q codeletion. Nearly all gliomas with *IDH* mutations and without 1p/19q codeletion had *TP53* mutations and inactivation of *ATRX* (94 and 86 percent, respectively).

Jeanette E. Eckel-Passow, Ph.D., from the Mayo Clinic in Rochester,

Minn., and colleagues defined five glioma molecular groups with the use of three genomic alterations: *TERT* promoter mutation, mutations in *IDH*, and 1p/19q codeletion. Tumors were scored for the markers in 1,087 gliomas, and correlations were assessed using 11,590 controls. The researchers found that the mean age at diagnosis was lowest and highest among patients with gliomas with only *IDH* mutations and only *TERT* mutations, respectively (37 and 59 years, respectively). Among patients with grade II or III gliomas, but not those with grade IV gliomas, molecular groups were independently associated with survival.

"The groups had different ages at onset, overall survival, and associations with germline variants, which implies that they are characterized by distinct mechanisms of pathogenesis," Eckel-Passow and colleagues write.

More information: Abstract - Brat
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