

PubMed

U.S. National Library of Medicine
National Institutes of Health



Display Settings: Abstract

[Science](#). 2010 Dec 16. [Epub ahead of print]

The Genetic Landscape of the Childhood Cancer Medulloblastoma.

Parsons DW, Li M, Zhang X, Jones S, Leary RJ, Lin JC, Boca SM, Carter H, Samayoa J, Bettegowda C, Gallia GL, Jallo GI, Binder ZA, Nikolsky Y, Hartigan J, Smith DR, Gerhard DS, Fufts DW, Vandenberg S, Berger MS, Marie SK, Shinjo SM, Clara C, Phillips PC, Minturn JE, Biegel JA, Judkins AR, Resnick AC, Storm PB, Curran T, He Y, Rasheed BA, Friedman HS, Keir ST, McLendon R, Northcott PA, Taylor MD, Burger PC, Riggins GJ, Karchin R, Parmigiani G, Bigner DD, Yan H, Papadopoulos N, Vogelstein B, Kinzler KW, Velculescu VE.

Ludwig Center for Cancer Genetics and Therapeutics and Howard Hughes Medical Institute, Johns Hopkins Kimmel Cancer Center, Baltimore, MD 21231, USA.

Abstract

Medulloblastoma (MB) is the most common malignant brain tumor of children. To identify the genetic alterations in this tumor type, we searched for copy number alterations using high-density microarrays and sequenced all known protein-coding genes and miRNA genes using Sanger sequencing in a set of 22 MBs. We found that, on average, each tumor had 11 gene alterations, 5 to 10 times fewer than in the adult solid tumors that have been sequenced to date. In addition to alterations in the Hedgehog and Wnt pathways, our analysis led to the discovery of genes not previously known to be altered in MBs. Most notably, inactivating mutations of the histone-lysine N-methyltransferase genes MLL2 or MLL3 were identified in 16% of MB patients. These results demonstrate key differences between the genetic landscapes of adult and childhood cancers, highlight dysregulation of developmental pathways as an important mechanism underlying MBs, and identify a role for a specific type of histone methylation in human tumorigenesis.

PMID: 21163964 [PubMed - as supplied by publisher]

[LinkOut](#) - more resources