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# Chromosome 17 alterations identify good-risk and poor-risk tumors independently of clinical factors in medulloblastoma.

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### Abstract

Current risk stratification schemas for medulloblastoma, based on combinations of clinical variables and histotype, fail to accurately identify particularly good- and poor-risk tumors. Attempts have been made to improve discriminatory power by combining clinical variables with cytogenetic data. We report here a pooled analysis of all previous reports of chromosomal copy number related to survival data in medulloblastoma. We collated data from previous reports that explicitly quoted survival data and chromosomal copy number in medulloblastoma. We analyzed the relative prognostic significance of currently used clinical risk stratifiers and the chromosomal aberrations previously reported to correlate with survival. In the pooled dataset metastatic disease, incomplete tumor resection and severe anaplasia were associated with poor outcome, while young age at presentation was not prognostically significant. Of the chromosomal variables studied, isolated 17p loss and gain of 1q correlated with poor survival. Gain of 17q without associated loss of 17p showed a trend to improved outcome. The most commonly reported alteration, isodicentric chromosome 17, was not prognostically significant. Sequential multivariate models identified isolated 17p loss, isolated 17q gain, and 1q gain as independent prognostic factors. In a historical dataset, we have identified isolated 17p loss as a marker of poor outcome and 17q gain as a novel putative marker of good prognosis. Biological markers of poor-risk and good-risk tumors will be critical in stratifying treatment in future trials. Our findings should be prospectively validated independently in future clinical studies.

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