

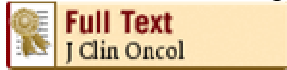


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1: [J Clin Oncol](#). 2009 Apr 1;27(10):1627-36. Epub 2009 Mar 2.



**Outcome prediction in pediatric medulloblastoma based on DNA copy-number aberrations of chromosomes 6q and 17q and the MYC and MYCN loci.**

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**PURPOSE:** Medulloblastoma is the most common malignant brain tumor in children. Current treatment decisions are based on clinical variables. Novel tumor-derived biomarkers may improve the risk stratification of medulloblastoma patients. **PATIENTS AND METHODS:** A model for the molecular risk stratification was proposed from an array-based comparative genomic hybridization (array-CGH) screen (n = 80). Fluorescence in situ hybridization (FISH) analyses for chromosome arms 6q, 17p, and 17q and the MYC and MYCN loci were performed in an independent validation set (n = 260). Copy number aberrations were correlated with clinical, histologic, and survival data. **RESULTS:** Gain of 6q and 17q and genomic amplification of MYC or MYCN were each associated with poor outcome in the array-CGH study (n = 80). In contrast, all patients with 6q-deleted tumors survived. Given these findings, the following hierarchical molecular staging system was defined: (1) MYC/MYCN amplification, (2) 6q gain, (3) 17q gain, (4) 6q and 17q balanced, and (5) 6q deletion. The prognostic value of this staging system was investigated by FISH analysis (n = 260). The addition of molecular markers to clinical risk factors resulted in the identification of a large proportion of patients (72 of 260 patients; 30%) at high risk for relapse and death who would be considered standard risk by application of clinical variables alone. **CONCLUSION:** Genomic aberrations in medulloblastoma are powerful independent markers of disease progression and survival. By adding genomic markers to established clinical and histologic variables, outcome prediction can be substantially improved. Because the analyses can be conducted on routine paraffin-embedded material, it will be especially feasible to use this novel molecular staging system in large multicenter clinical trials.

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