Prognostic value of genomic alterations in invasive cervical squamous cell carcinoma of clinical stage IB detected by comparative genomic hybridization

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The clinical behavior of invasive cervical carcinoma of clinical stage IB varies considerably in tumors presenting without regional lymph node metastases. The early identification of patients at higher risk for poor outcome may prove useful because these patients would benefit from aggressive adjuvant treatments. In this study, comparative genomic hybridization was applied to evaluate whether genomic aberrations have prognostic significance in cervical carcinoma. Genomic alterations were evaluated in 62 cervical carcinomas of clinical stage IB. DNA sequence losses were most prevalent at chromosomes 4q (53%), 3p (52%), 13q (45%), 4p (44%), Xq (44%), 5q (40%), 18q (37%), and 6q (35%). Several genomic alterations were associated with poor clinical outcome or metastasis. The total number of DNA aberrations/tumor ($P > 0.02$) and the number of DNA sequence losses/tumor ($P > 0.04$) were associated with disease-specific survival. 9p deletions were significantly more frequent in carcinomas with lymph node metastasis than in node-negative tumors ($P > 0.03$). Losses of chromosome 11p ($P > 0.0001$) and 18q ($P > 0.01$) were associated with poor prognosis in cervical carcinomas without lymph node metastasis. These data suggest that inactivation of tumor suppressor genes on chromosomes 9p, 11p, and 18q may play a role in the progression of cervical carcinoma.
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