

Chromosomal gain of 3q and loss of 11q often associated with nodal metastasis in early stage cervical squamous cell carcinoma

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摘要

Abstract

BACKGROUND/PURPOSE: Cervical cancer remains a health problem among women worldwide. Delineation of genetic changes is critical to understanding the molecular basis of tumor progression, as well as for identifying genetic markers for early identification of patients at high risk for a poor outcome. **METHODS:** To provide comparative genomic hybridization data for cervical squamous cell carcinoma in Taiwan, and to gain further insight into genetic markers associated with lymph node metastasis of this disease, we performed comparative genomic hybridization analysis of 30 consecutive cases of cervical squamous cell carcinoma (24 stage IB and 6 stage IIB). **RESULTS:** The results disclosed that higher staged tumors or those with lymph node metastasis had more chromosomal imbalances. The commonly recurrent chromosomal imbalances were gains of 3q (46.7%), 1q (36.7%) and 8q (20.0%) and losses of 11q (36.7%), 3p (33.3%), 6q (23.3%), and 2q (20.0%). The frequencies of these chromosomal imbalances in stage IB and IIB tumors did not differ significantly. However, when compared with tumors without lymph node metastasis, the loss of 11q14-q22 (5/9 vs. 3/21, $p = 0.019$) and gains of 3q11-q22 and 3q26-qter (6/9 vs. 5/21, $p = 0.026$) were significantly more prevalent in tumors with lymph node metastasis. **CONCLUSION:** The results suggest that certain tumor-associated genes residing on 3q and 11q warrant further investigation to elucidate their role in the progression of this disease.