Expression of p150 in cervical neoplasia and its potential value in predicting survival

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BACKGROUND: A recently cloned novel p150 protein was found to be overexpressed in human breast carcinoma. To the authors' knowledge, no data on p150 expression in any other human tumors have been published previously. METHODS: To investigate whether the expression of p150 correlated with the clinicopathologic stages of cervical neoplasms or the prognoses of patients with these neoplasms, the authors conducted an immunohistochemical study of archival formalin fixed, paraffin embedded specimens. Seventy-two precancerous lesions (CIN), 75 clinical Stage IB invasive squamous carcinomas, and 20 samples of normal squamous epithelia were included. In addition to p150, the Ki-67 labeling index was assessed as a proliferation parameter. The presence of human papillomavirus was analyzed by in situ DNA hybridization. RESULTS: A significant association of p150 with the grade of atypia in cervical neoplasms was demonstrated. The highest expression of p150 was observed in low grade CIN, with subsequently decreasing expression in high grade CIN and invasive carcinoma. For patients with invasive carcinoma, p150 was significantly correlated with clinical outcome. Patients with high expression of p150 had a better prognosis than those with low p150. Those with regional lymph node metastasis and significant p150 expression had longer relapse free survival than those with insignificant p150 expression. Women whose carcinomas demonstrated vascular space invasion or high microvessel density survived longer when p150 was clearly expressed. p150 behaves as a potential tumor marker during early cervical carcinoma development and is later turned off as cells proceed to more advanced stages of their malignant phenotypes. CONCLUSIONS: p150 is a molecular parameter that might become useful in predicting disease progression and determining the prognoses of patients with invasive cervical carcinoma.
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