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Aurora kinase A (AURKA) expression is a prognostic marker in patients with colorectal cancer

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Background & Aim: Aurora kinase A (AURKA), also known as STK15/BTAK, is a member of a serine/threonine kinase family that plays important role in mitosis and maintenance of chromosomal stability. This study evaluates the clinical significance of AURKA expression in colorectal cancer.

Methods: Expression of AURKA protein was evaluated by immunohistochemistry in 151 patients with colorectal adenocarcinoma using tissue microarray blocks. We then analyzed relationship between clinicopathological characteristics and AURKA expression. Also we assessed the prognostic significance of various clinicopathological data on progression-free survival(PFS).

Results: AURKA expression was detected in 45% (68/151). The positive staining of AURKA was more often detected in the colorectal adenocarcinoma with male patients ($P=0.035$) and distally located tumor ($P=0.021$). Progression-free survival of the patients with AURKA positive was shorter than those with AURKA negative ($P=0.001$). Univariate analysis demonstrated that AURKA expression ($P=0.001$), age ($p=0.034$), lymphatic invasion ($P=0.001$), perineural invasion ($P=0.002$) and TNM stage ($p=0.013$) were variables affecting PFS. In a multivariate analysis for PFS, a Cox proportional hazard model confirmed that AURKA expression was an independent and significant prognostic factor in colorectal adenocarcinoma (hazard ratio, 3.944; $P=0.001$).

Conclusions: AURKA could serve as an independent factor to predict a poor prognosis in colorectal cancer.

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TLR9 is a risk factor of postoperative radiotherapy in patients with lung cancer

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Lung cancer is one of the most common types of malignant tumor in the world. In this study, we analyzed the association of Toll-like receptor 9 (TLR9) expression with clinical pathological characteristics in patients with lung cancer. The lung cancer specimens and medical records of 63 cases with surgery in Jinshan hospital from March 2007 to December, 2011 were retrieved. TLR9 expression in cancer tissue was determined by immunohistochemistry. Among these cases, 36 patients received the postoperative radiotherapy. The TLR9 expression associated with clinical pathological characteristics in patients with lung cancer was analyzed by Kaplan-Meier survival analysis and multivariate Cox regression analysis. TLR9 was not detectable in normal pulmonary tissue, but was expressed in lung cancer tissue with the positive rate of 68.3% (43/63) and appeared in the cytoplasm of cancer cells. The expression of TLR9 was significantly increased in patients with the later T stage of tumor and lymph node metastasis ($P < 0.05$). By analyzing the survival of 36 cases who had postoperative radiotherapy, we found that TLR9 expression was significantly associated with the disease-free survival (PFS) and overall survival (OS) in patients with postoperative radiotherapy ($P < 0.05$). This association was significantly affected by lymph node metastasis and histological type (squamous cell carcinoma or adenocarcinoma) ($P < 0.05$). With Cox multivariate regression analysis, TLR9 expression and lymph node metastasis were independent prognostic risk factors on the survival of patients with postoperative radiotherapy. In summary, TLR9 may be a survival marker of postoperative radiotherapy in patients with lung cancer.

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