KIF11 Associated Disorder

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Purpose:

To clarify the correlation between KIF11 (kinesin family member 11) and clinicopathologic characteristics of non-small cell lung cancer (NSCLC) and identify the prognostic value of KIF11 in patients with NSCLC.

Methods:

For investigating the expression of KIF11 in NSCLC, two tissue microarrays (TMAs: one contained 60 paired NSCLC tissues and paratumor tissues, the other contained 140 NSCLC tissues and 10 normal lung tissues) were constructed, stained, and scored. The Cancer Genome Atlas (TCGA) datasets were used to explore the differential expression level of KIF11 between NSCLC and paratumor. Kaplan-Meier survival curves were plotted and multivariate analysis were carried out.

Results:

The staining of KIF11 mainly distributed throughout the cytoplasm of tumor cells. Its expression was higher in NSCLC than paratumor cells, and similar results were obtained from TCGA datasets. We found that high expression of KIF11 had a significant correlation with lymph node metastases (p = 0.024) and pathologic stage (p = 0.018); that significant difference was not found in any other clinicopathologic characteristic. As univariate and multivariate analysis showed, KIF11 expression was significantly correlated with overall survival time of NSCLC (p = 0.002, p = 0.025, respectively). High KIF11 expression was found to significantly associate with overall survival of stage II-III (p = 0.001) and lung adenocarcinoma (p = 0.036).

Conclusion:

High KIF11 expression predicts poor outcome in NSCLC. KIF11 is expected to be a viable prognostic biomarker for NSCLC.