NSCLC, locally advanced

DNA METHYLATION OF TUMOR SUPPRESSOR GENE IS A PREDICTOR OF PATHOLOGIC COMPLETE RESPONSE IN STAGE IIIA (N2) NSCLC PATIENTS TREATED WITH NEOADJUVANT CCRT FOLLOWED BY SURGERY

J.H. Kim
Thoracic Surgery, Dongnam Institute of Radiological & Medical Sciences, Busan, KOREA

Aim: The aim of this study was to evaluate the clinical implications of DNA methylation of tumor suppressor gene in pathologic complete responders in stage IIIA (N2) NSCLC patients treated with neoadjuvant CCRT followed by surgery.

Methods: Methylation-specific multiplex ligation probe amplification (MS-MLPA) was used to analyze the DNA methylation status of 36 tumor suppressor genes in 15 stage IIIA (N2) NSCLC patients who were treated with neoadjuvant CCRT followed by surgery between October 2011 and January 2014. FFPE (formalin-fixed, paraffin-embedded) tissue samples obtained from 15 paired pre-CCRT lung biopsy and post-CCRT surgically resected tumor specimens were used. Factors predictive of pathologic CR were evaluated using logistic regression. Pre-treatment methylated DNA number less than 2, the ratio of unmethylated DNA after neoadjuvant CCRT and difference between pre-, posttreatment SUV max of primary tumor and mediastinal lymph node were analysed.

Results: The median follow-up time was 17.4 months. One patient had recurrence at mediastinal lymph node. Factor predictive of pathologic complete response after neoadjuvant CCRT followed by surgery was pre-treatment methylated DNA number less than 2 (p = 0.03) in stage IIIA (N2) NSCLC patients. The change of the ratio of unmethylated DNA after neoadjuvant CCRT (p > 0.6) of the paired samples and difference between pre-, posttreatment SUV max of primary tumor and mediastinal lymph node were not a predictive factor of pathologic CR (p > 0.15).

Conclusions: These results suggest that pre-treatment methylated DNA number less than 2 is a predictor of pathologic complete response in stage IIIA (N2) NSCLC patients treated with neoadjuvant CCRT followed by surgery. And we think that an analysis of the correlation between DNA methylation status and the long-term survival and recurrence rate is needed in these patients.

Disclosure: All authors have declared no conflicts of interest.