



Relationship of *EGFR* DNA methylation with the severity of non-small cell lung cancer

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ABSTRACT. The aim of this study was to study the relationship of *EGFR* DNA methylation with the severity of non-small-cell lung cancer (NSCLC). We enrolled 54 patients with NSCLC between March 2013 and June 2014 from Department of Cardiothoracic Surgery in our hospital. The methylation levels in the promoter region of the *EGFR* gene in cancerous and pericarcinomatous tissue were tested by pyrosequencing. *EGFR* mRNA expression levels were detected by real-time reverse-transcription polymerase chain reaction. The SPSS software was used for data analysis. We found that *EGFR* gene methylation levels showed no significant differences among patients of different gender, age, or smoking status. *EGFR* DNA methylation levels significantly increased ($P < 0.05$) following NSCLC malignancy upgrading, and showed negative correlation with mRNA expression ($P = 0.041$). DNA methylation levels of cancerous tissues were significantly higher compared to the corresponding pericarcinomatous tissues ($P < 0.05$) at stages I, II, and IIIA. The methylation levels at loci 3, 6, 9 among the detected CpG islands were higher in the cancer tissues at each stage ($P < 0.05$). In summary, our

results suggest that the DNA methylation levels of *EGFR* can be used as an important indicator for the stage of cancer tissue malignancy.

Key words: Epidermal growth factor receptor; DNA methylation; Non-small cell lung cancer