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Combined detection of p53, p16, Rb, and EGFR mutations in lung cancer by suspension microarray

Y. Ye[1], D. Wang[1], C. Su[1], T. Rong[2] and A. Guo[1]

[1]Cancer Center of People's Liberation Army, Nanjing, PR, China
[2]Department of Thoracic Surgery,
Sun Yat-sen University Cancer Center, Guangzhou, PR, China

Corresponding author: D. Wang
E-mail: wangdong_nj001@hotmail.com

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ABSTRACT. Mutations of some contributing factors (p53, p16, Rb, and EGFR) are believed to affect diagnosis and drug resistance of lung cancer. We evaluated the efficacy of a multimarker panel for molecular diagnosis of lung cancer, using a high-throughput suspension microarray. One hundred and twenty-five lung cancer specimens and 30 tumor-free lung tissue samples were assayed by multiplex polymerase chain reaction with specific probes designed to detect hot-spot mutations in p53, p16, Rb, and EGFR. The mutation rates of p53, p16, Rb, or EGFR in the lung cancer specimens were 36.8, 15.2, 11.2, and 18.4%, respectively. Inclusion of four markers elevated sensitivity to 68.0%. The specificity and accuracy of four-marker detection were 90.0 and 72.3%, and the mutation rates of this panel in stage I, stage II and stage III disease were 62.2, 65.9 and 75.0%, respectively. Mutation at p16 occurred more frequently in non-small cell lung cancer (19.3%) than in small cell lung cancer (5.4%); while the mutation rate of Rb was 32.4% in small cell lung cancer versus 2.3% in non-small cell lung cancer. We conclude that simultaneous detection of p53, Rb, p16, and EGFR in a

suspension microarray facilitates rapid diagnosis of lung cancer.

Key words: Lung cancer; Diagnosis; p53; p16; Rb; EGFR

