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

Y. Ye¹, D. Wang¹, C. Su¹, T. Rong² and A. Guo¹

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

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

Received August 26, 2009
Accepted October 15, 2009
Published December 23, 2009

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