Tumori, 93: 473-477, 2007

LOW FREQUENCY OF *p53* AND *k-ras* CODON 12 MUTATIONS IN NON-SMALL CELL LUNG CARCINOMA (NSCLC) TUMORS AND SURGICAL MARGINS

Ozgur Vatan[1], Rahmi Bilaloglu[1], Berrin Tunca[2], Gulsah Cecener[2], Cengiz Gebitekin[3], Unal Egeli[2], Tahsin Yakut[4], and Nur Urer[5]

[1]Department of Biology, Science and Art Faculty; [2]Department of Medical Biology; [3]Department of Thoracic Surgery; [4]Department of Medical Genetics, Medical Faculty, Uludag University, Bursa; [5]Department of Pathology, Hospital of Yedikule Chest Surgery, Istanbul, Turkey

Aims and background: **Lung cancer is one of the most common cancers and has became a predominant cause of cancer-related death throughout the world. The *k-ras* codon 12 mutation, which is the most common lung cancer mutation, is found in 15 to 30% of all lung cancers. Furthermore, the *p53* gene has a very important role in the biological properties of tumor cells, and it is mutated in about 50% of non-small cell lung cancers. Residual tumor cells remain in surgical margins diagnosed as tumor free by histopathological techniques, and they can play a role in forming any local recurrence. Molecular methods may be exploited that are sensitive enough to detect small numbers of tumor cells.**

Methods: **In the present study, we examined *p53* gene mutations and *k-ras* codon 12 mutations from the tumor samples and surgical margins of 34 non-small-cell lung cancer patients. *P53* gene mutations were analyzed by single strand conformational polymorphism analysis, heterodublex analysis and DNA sequencing. *K-ras* codon 12 mutations were analyzed by the mutagenic PCR-restricted fragment length polymorphism method.**

Results: **A *p53* mutation was detected only in primary tumors of 3 out of 34 patients (8.82%). These mutations were clustered in exon 5. Moreover, a *k-ras* codon 12 mutation was detected in both the primary tumor and the surgical margin tissues of 2 out of 34 patients (5.88%).**

Conclusions: **The detected mutation rate was low, in the range given in the literature. We think that different mechanisms related to other genes and individual genetic differences might play a role in cancer formation in our study group. We believe that molecular studies are necessary to identify biomarkers and to determine genetic alterations in histopathologically normal surgical margins.**

Key words: *k-ras* codon 12 mutation, non-small cell lung cancer, p53 mutation, surgical margins.

Acknowledgments: We thank the Society of Investigation and Prevention of Genetic Diseases for technical equipment support.

Correspondence to: Ozgur VATAN, MSc, Department of Biology, Science and Art Faculty, Uludag University, 16059, Bursa, Turkey. Tel +90-224-442-92-56; fax 90-224-442-80-22; e-mail ovatan@uludag.edu.tr

Received November 16, 2006; accepted March 2, 2007.