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

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Aims and background: Lung cancer is one of the most common cancers and has become 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, heteroduplex 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.