

Mutation analysis of the *FHIT* gene in bronchoscopic specimens from patients with suspected lung cancer

Gulsah Cecener¹, Berrin Tunca¹, Unal Egeli¹, Mehmet Karadag², Ozgur Vatan³, Esra Uzaslan², and Sahsine Tolunay⁴

¹Department of Medical Biology, Faculty of Medicine, ²Department of Chest Disease, Faculty of Medicine, ³Department of Biology, Faculty of Science and Arts, and ⁴Department of Pathology, Faculty of Medicine, Uludag University, Bursa, Turkey

ABSTRACT

Aims and background. Lung cancer is a leading cause of cancer death worldwide. However, despite recent advances in molecular biology that have revealed various genetic changes in lung cancer, the prognostic outcome of lung cancer patients has improved only minimally. This situation has changed fundamentally with the identification of molecular abnormalities that are characteristic of premalignant changes, such as changes in tumor suppressor genes, loss of heterozygosity at crucial sites, and activation of oncogenes. Inactivation of the tumor suppressor gene Fragile Histidine Triad (*FHIT*) is a frequent genetic change in lung cancer. The aim of this study was to identify *FHIT* gene alterations in bronchoscopy specimens of patients with suspected lung cancer and to determine the molecular relevance, if any, of *FHIT* alterations in the development of cancer.

Patients and methods. Sixty-two patients with suspected lung tumors were screened for variations within exons 5-9 of the *FHIT* gene using intronic primer pairs and single-strand conformation polymorphism and sequencing analysis.

Results. *FHIT* gene alterations were detected in 27 out of 62 bronchoscopic specimens (43.54%). All of these alterations were identified as T to A alteration at position IVS8-17. This intronic variant also was identified in approximately half of control cases (45%).

Conclusions. Our findings showed that the *FHIT* IVS8-17 T to A alteration identified in bronchoscopy specimens from patients with clinically suspected lung cancer is a polymorphism found in the Turkish population. We think that this polymorphism does not affect gene function because it is located in the intron portion of the gene and is present in many cancer patients as well as healthy subjects. We suggest that the *FHIT* gene may be turned off in lung carcinogenesis via other genetic or epigenetic mechanisms rather than mutations.

Key words: lung cancer, bronchoscopy specimen, *FHIT* gene, sequence variant, single-strand conformation polymorphism, DNA sequencing.

Acknowledgments: We thank Prizma and Elips Ltd for their support in supplying the experimental equipment. This research was supported by the Society of Investigation and Prevention of Genetic Diseases.

Correspondence to: Dr Unal Egeli, Department of Medical Biology, Faculty of Medicine, Uludag University, 16059 Bursa, Turkey.
Tel +90-224-2954151;
fax +90-224-4428863;
e-mail egeli@uludag.edu.tr

Received January 24, 2008;
accepted July 29, 2008.