

## INVESTIGATION OF MUTATIONS AND EXPRESSION OF THE *FHIT* GENE IN TURKISH PATIENTS WITH BRAIN METASTASES DERIVED FROM NON-SMALL CELL LUNG CANCER

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**Aims and background:** Brain metastases occur in 20-40% of patients with cancer, and their frequency has increased over time. Lung, breast and skin (melanoma) are the most common sources of brain metastases. Recent studies show that several genes such as *CD44* and *PTEN* have roles in the suppression of metastatic growth. Although it has been determined that there is a relationship between the *FHIT* gene and several primary tumors, its role in the initiation and progression of brain tumors has not yet been entirely explained. Furthermore, it is not known whether the *FHIT* gene has a role in the formation of brain metastases.

**Patients and methods:** The present study investigated mutations of the *FHIT* gene in Turkish patients with brain metastases derived from non-small cell lung cancer (NSCLC). Single-

strand conformational polymorphism and sequencing analysis of the coding exons (5-9) of the *FHIT* gene were performed on 26 tissues. Furthermore, the level of Fhit protein expression of 36 tumor tissues was identified by immunohistochemistry.

**Results:** Using single-strand conformational polymorphism and sequencing analyses, no point mutations of the *FHIT* gene were detected in brain metastases derived from NSCLC. However, it was observed that Fhit protein expression was reduced in 88.9% of subjects.

**Conclusions:** We suggest that the *FHIT* gene may be turned off in brain metastases via other genetic/epigenetic mechanisms rather than mutations.

**Key words:** brain metastases, *FHIT* gene, immunohistochemistry, NSCLC, point mutations.

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