

ANALYSIS OF GENE AMPLIFICATION IN PAPILLARY THYROID CARCINOMAS

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Thyroid cancer is the most common endocrine malignancy and its rate has been steadily increasing all over the world. Papillary thyroid carcinoma (PTC) represents the most common histological subtype of thyroid cancer, accounting for about 75-85% of the cases. Until now, the mechanisms underlying the tumorigenesis of PTC still remain unclear.

To estimate BRAF and MYC gene amplifications in papillary thyroid carcinomas by FISH analysis and their link with the development of T1 tumor stage and their possible role in etiopathogenesis of this disease through chronic activation of MAPK pathway.

Tumor tissue specimens from 10 female patients with PTC were analysed by immunohistochemistry (CK19 and Ki67) and FISH analysis. FISH probes were applied on 5 µm thick histological sections and covered with glass and sealed with rubber cement. After denaturation at 75 °C for 5 min, hybridisation process at 37 °C during 3 h was done. After washing, DAPI containing mounting medium was applied.

In all tumor nuclei two signals of BRAF and two signals of MYC were found, indicating that gene amplifications were not found in the study group.

Although observed at a low number of patients, amplification of BRAF and MYC genes was not involved in PTC tumorigenesis in the development of T1 tumor stage.

Acta Medica Medianae 2020;59(1):31-35.

Key words: *papillary thyroid carcinoma, gene amplification, BRAF, MYC, immunohistochemistry, T1 tumor stage*