



GENETIC CHANGES AND BIOMARKERS ASSOCIATED WITH DIFFERENT MORPHOLOGICAL AREAS FOUND IN OTHERWISE CONVENTIONAL PAPILLARY THYROID CARCINOMA

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Abstract

Existing literature suggests that conventional Papillary Thyroid Carcinoma (cPTC) with minor proportions of different morphological patterns (such as tall cell/ hobnail) can have aggressive behaviour than expected. This study focuses on establishing molecular profiles of such morphological areas and compare those with the molecular profiles of the background conventional morphological pattern to help in accurate risk stratification of patients with PTC. The presence of the *brafV600E* and the *nrasQ61R* mutations were examined and expression levels of TSHR (thyroid-stimulating hormone receptor) and MnSOD (manganese superoxide dismutase) were analyzed to generate molecular profiles. Formalin-fixed, paraffin-embedded tissue samples were subjected to genotype the *brafV600E* and the *nrasQ61R* mutations using PCR-RFLP assay while quantitative real-time PCR was carried out to quantify the expression levels of TSHR and MnSOD in the test areas containing tall cell, hobnail, and invasive follicular morphology compared to the control areas with conventional morphology. The test and control areas in all the samples tested positive for the *brafV600E* mutation and negative for the *nrasQ61R* mutation. In the quantification of mRNA, all the test areas showed reduced levels of MnSOD and TSHR compared to the control areas. These results indicate the morphological patterns of tall cell, hobnail, and invasive follicular types showing reduced levels of some of the molecular markers associated with aggressive cancer progression. Hence, further studies on analyzing molecular profile to understand the aggressive behaviour of otherwise cPTC would ensure precise diagnosis.

Keywords: *brafV600E*, TSHR, conventional PTC, aggressive behavior, morphological patterns