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PROMOTER METHYLATION QUANTIFICATION OF FOUR TUMOUR SUPPRESSOR GENE IN PAPILLARY THYROID CANCER TISSUES

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Endocrine tumours are endocrine system related malignancies like thyroid that is the most common type with mounting trends over the last three decades all over the world. Papillary thyroid cancer (PTC) is making four fifths of all thyroid cancers. Finding some detection markers in order to discriminate malignant from benign one before metastasis could be really important for thyroid cancer patients and clinicians. We determined the quantity of methylation in twelve candidate promoter regions of four tumour suppressor genes using the methylation-sensitive high resolution melting (MS-HRM) assay. Fresh frozen tissues of 57 PTC patients and 45 goiter patients were collected after surgery. DNA was extracted using the DNeasy Blood and Tissue Kit according to the manufacturer's protocol. DNA purity and quantity was determined using a Thermo Scientific™ NanoDrop™ spectrophotometers 2000c spectrophotometer and then stored at -80°C. For bisulfite treatment, DNA from each sample was treated with sodium bisulfite conversion kit. The MS- HRM analyses were run based on the three main steps of Holding, Cycling, and Melt curve. Statistical analyses were done by statistical package for science software (SPSS) version 16.0 and P<0.05 was measured statistically significant. Promoter methylation of four *SLC5A8, RASSF1, MGMT* and *DNMT1*genes has meaningful differences between PTC cases and goiter controls. In spite of the fact that *DNMT1* is a denovo methyl trasferase enzyme its promoter hypermethylation was not as significant as *SLC5A8, RASSF1,* and *MGMT.*

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