Gene expression microarray technology can be used in the attempt to identify clinically relevant biomarkers of thyroid malignancy.

**OBJECTIVES**

To find new molecular markers that could improve the diagnostics, follow-up protocols, treatment outcome, prognosis and the quality of life of differentiated thyroid cancer patients.

**SUBJECTS AND METHODS**

- Tumor and surrounding normal thyroid tissue samples obtained from patients with differentiated thyroid carcinoma referred for surgery in "C. I. Pahor" National Institute of Endocrinology. All patients signed the informed consent. We analysed 6 cases of classical papillary thyroid carcinoma (cPTC) and 6 cases of follicular variant of papillary thyroid carcinoma (fPTC).

  - **RNA extraction** - RNeasy Mini Kit (Qiagen).
  - **RNA quantification and integrity analysis** - Infinite® 200 NanoQuant (Tecan), 2100 Bioanalyzer (Agilent). Samples with RNA integrity number (RIN) >7 were chosen for microarray gene expression analysis.

  - **Microarray analysis** - Agilent One-Color Microarray-Based Gene Expression protocol, v. 6.6, using SurePrint G3 Human Gene Expression arrays 6x60K v2.

  - **Scanning, data extraction and data analysis** – Agilent High Resolution C Scanner (3 microns resolution), Feature Extraction v. 11.5.1.1 and GeneSpring v.12, respectively.

**RESULTS**

Comparative analysis of tumoral vs normal tissue samples revealed down-regulation of 25 genes and 2 lincRNA (long intergenic non-protein coding RNA 1140 and BROAD Institute lincRNA [XLOC_005062] lincRNA [TCGCONS_00010538]) (p-value <0.05 and fold change ≥ 2) by t-test and Benjamini-Hochberg correction (Table 1).

**CONCLUSIONS**

Gene expression is altered in papillary thyroid carcinoma. Our study identified 3 hyper-expressed genes and 8 genes with low expression in tumoral tissues compared to normal ones. We found a higher dis-regulation of gene expression levels in classic papillary thyroid carcinoma then in follicular variant.

Further studies are undergoing for gene expression data validation by qPCR.

**Bibliography**


