**Micro RNAs in the core arsenal of Molecular Paradigms in Papillary Thyroid Cancer Modalities**

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**Abstract**

Background:Thyroid cancer is considered to exist among most common cancers and at the same time it is the most recurrent malignancy of the endocrine system. The most frequent type of thyroid cancer is papillary thyroid cancer (PTC), which contributes more than 80% globally & prevalent in females of Eastern and Western Asia, America and Iceland. The genetic elements known as MicroRNAs (miRNAs), endogenous non-coding RNAs operating as post-transcriptional regulators involved in development, proliferation and differentiation. miRNAs are gaining fame as druggable biomarkers and clinical management of neoplasm. The momentous stackeholding of miRNAs by virtue of gene expression variations in the cancer microenvironment has been witnessed in the PTC onset, amplification and apoptosis. The growing body of knowledge highlights the modifiable play at the miRNA level harbors potential in lessening the perpetuation of the disease with safe handlers. The genetic information leads to a big highway which can replace the unified yardstick to tailor PTC with the more targeted personalized disease treatment by monitoring the disease risk and aggression modalities.

Objectives: The study aims to speculate the characteristic involvement of expression level changes in the miRNA genes miRNA-146b and miRNA-181b as tangible biomarkers for papillary thyroid cancer.

Methodology:The present study was conducted on the PTC in Pakistan, a genetically less explored South Asian country. Specimen of cancer tissue, normal samples and multi nodular goiter (MNG) samples from patients were collected. The anthropometric and clinical parameters of patients were recorded after informed consent. Total RNA was isolated and cDNA was synthesized. Gene expression profile for miRNA-146b and miRNA-181b was done by quantitative Real-Time PCR. Relative gene expression was identified as fold change and mutational deregulations were checked through DNA sequencing showing the involvement of these miRNAs in PTC.

Results:The statistically significant relative expression of genes miRNA-146b; 5 to 20 folds and miRNA-181b; 4-60 folds were observed in PTC in comparison to MNG and healthy tissue specimens.

Conclusion: The boosted gene expression of the miRNA genes miRNA-146b and miRNA-181b manifests the plausible misregulations in deployment of these molecular musketeers as foes in PTC. This forged maladaptation of the miRNA-146b and miRNA-181b in the cancer microenvironment may warrant analytically, therapeutically and genetically surmountable miRNA targets for PTC clinical management prevention