MICRONRNAS - MOLECULAR MARKERS FOR DETECTING CANCER IN THYROID NODULES

Serdyukova OS1,2, Veryaskina YA2, Titov S.E.2, Malakhina ES2, Rymar OD1

1 Institute of Internal and Preventive Medicine - branch of Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia
2 Federal State Budgetary Institution of Science “Institute of Molecular and Cellular Biology”, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia

Thyroid nodules are one of the most common pathology of thyroid gland. The prevalence of thyroid nodules varies depending on age of the patients and methods of detection, such as palpation or ultrasonography (US). It varies from 2–6% (palpation) to 19–68% (US), and 8–65% (autopsy) [1]. Despite morbidity level only about 5-10% of such nodules are malignant [2]. Fine needle aspiration cytology of the thyroid nodule is currently the primary diagnostic tool for determining the nature of a thyroid nodule. It is considered as the gold standard for diagnostics of thyroid cancer but in 30 % of cases cytological conclusion is uncertain. Cytological research is not enough to differentiate benign and malignant tumors. The need to improve the effectiveness of fine needle aspiration biopsy findings led to the search for new diagnostic biomarkers and the creation of diagnostic panels on their basis for their application in the diagnostics of uncertain nodules. Determination of molecular markers in the thyroid aspirate will allow to differentiate benign and malignant tumors more accurately at the preoperative stage and to reduce number of inappropriate surgery. Micro(mi)RNAs are endogenous, single-stranded, non-coding RNAs (~ 22 nucleotides) that regulate gene expression by direct degrading of mRNA or suppressing of the post-transcriptional protein translation by bining to the 3' untranslated region (3' -UTR) of the respective target mRNAs. The miRNAs have been reported to regulate 30% of the human genome, and are involved in many cellular processes such as cell proliferation, apoptosis, and development [3]. MicroRNA (miR) expression signatures are proposed to be able to differentiate thyroid cancer from benign thyroid lesions. We selected nine miRs (miR-221, −146b, −187, −199b, −205, −183, −551, −375, -7) to examine the potential use of miRs to supplement diagnostic cytology in cases designated as follicular adenoma (suspicion of follicular carcinoma) (FTC)) and benign nodules.

Materials and Methods. This study was approved by the ethics committee of the Institute of Molecular Biology and Biophysics, Siberian Branch of the Russian Academy of Medical Sciences. MiR expression was measured in thyroid fine needle aspiration (FNA) specimens by quantitative polymerase chain reaction. Gene expression analyses were performed in a training sample set (n=79) to obtain a classification rule to predict FNA cases as benign or malignant. The patients were divided into two groups: benign nodules (n=63) and follicular adenoma (suspicion of follicular carcinoma) (n=16).

Results. A comparative analysis of the expression levels of miRNAs-146b, -221, -375, -205, -187, -199b, -551 -183,-7 between the subgroups of follicular adenoma (suspicion of follicular carcinoma) and thyroid subgroup of benign nodules showed a statistically significant increase of expression level of miRNA-146b 8-fold (p<0.05), miRNA-221 in 3-fold (p<0.05), miRNA-375 4-fold (p<0.05), miRNA-199b 3-fold (p<0.05), miRNA-183 4-fold (p<0.05) in the subgroup of tumors with a diagnosis of follicular adenoma (suspicion of follicular carcinoma) thyroid.

Conclusion. Strong data were collected regarding significance of the determination of molecular markers (miRNA-146b, -221, -375, -205,- 199b, -183) in the thyroid aspirate for differentiation between benign and malignant tumors.

References:

Key words: thyroid, thyroid nodules, molecular markers, FNA, MicroRNA

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DINAMICS OF CYTOCHROME C, BAX AND BCL-2 EXPRESSION IN EXPERIMENTAL DIABETIC CARDIOMYOPATHY

Institute of physiology of NAS of Belarus, Belarus

The most important determinants of myocardial remodeling include cell death [1]. Two ways of cardiomyocytes death – necrosis and apoptosis were identified. Apoptosis is of greater interest due to its possible pharmacological correction. Proteins regulate apoptosis at the level of mitochondria; Bax is proapoptotic and Bcl-2-antiapoptotic.