STRESZCZENIE W JĘZYKU ANGIELSKIM

The aim of the doctoral dissertation was to identify a diagnostic panel for papillary thyroid cancer based on genetic testing. In recent years, an increasing incidence of this cancer has been observed, both worldwide and in Poland. Papillary thyroid cancer is the most common malignant tumor of this organ. Also for several years the interest in the research of a molecular biomarker of papillary thyroid cancer has been growing. This biomarker may be miRNA.

The doctoral dissertation consists of a review paper and an original paper. The review paper includes a revision of previous literature on the importance of miRNAs in the diagnosis of papillary thyroid cancer. To date, many authors have attempted to identify specific miRNAs that can assist in the diagnostic process. However, the small size of the study groups, the different research methods used, and the heterogeneous features of the disease prompt further research on the subject at hand.

In the process of preparing the original publication, an attempt was made to identify the diagnostic panel of papillary thyroid cancer using genetic testing. For this study, 41 paraffin blocks containing tumor cells and 39 blocks with healthy tissues were collected from the same patients. The miRNA expression profile was determined in the studied material. A significantly increased expression of 8 miRNAs was observed: miR-146b-5p, miR-221-3p, miR-221-5p, miR-222-3p, miR-34a-5p, miR-551b-3p, miR-15a-5p, miR-31-5p. In contrast, the expression of miR-152-3p and miR-7-5p was significantly decreased. Target gene ontology analysis was also performed and key genes involved in papillary thyroid cancer development were identified.

The diagnostic value of significantly altered miRNAs as biomarkers of papillary thyroid cancer was then evaluated using AUC. The highest AUCs, indicating possible clinical utility in the diagnosis of papillary thyroid cancer, were observed for miR-146-5p (AUC=0.770), miR-551-3p (AUC=0.740), miR-222-3p (AUC=0.720). Using a linear regression model for the panel consisting of miR-152-3p + miR-221-3p + miR-551-3p + miR-7-5p, the AUC=0.841 was obtained. To enhance the reliability of the work, the results were confirmed using RT-PCR.

In conclusion, the expression analysis of miR-152-3p, miR-221-3p, miR-551b-3p and miR-7-5p panel (AUC=0.841) may provide a molecular diagnostic panel useful in the diagnostic process of papillary thyroid cancer.