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Introduction of Novel MicroRNAs as a Diagnostic Approach for Thyroid Cancer

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ABSTRACT

Introduction: According to Global Cancer Statistics, thyroid cancer is responsible for 586,000 cases worldwide, ranking in ninth place for incidence in 2020. It is predicted that in 2023, almost 43,720 individuals in the United States will be diagnosed with this disease, making it one of the most common endocrine malignancies. Therefore, identifying new methods for early diagnosis and better prognosis of this cancer is crucial. MicroRNA expression analysis has gained much attention for detecting various cancers. Bioinformatics is emerging knowledge that is interdisciplinary; thus, it is beneficial to make connections between basic sciences and clinical diagnosis and its implications. The goal of this study was to find significant microRNA genes involved in the pathogenesis of thyroid cancer by applying bioinformatics assay and machine-learning algorithms. We hope these microRNAs could be potential biomarkers for the determination of disease states.

Methods and Materials: RNA expression profiling of thyroid cancer patients was conducted using data from the Cancer Genome Atlas Program database. Additionally, microRNA expression profiling for these patients was performed using information sourced from the microRNA databases. Differential expression analysis utilized advanced machine learning methodologies to identify key diagnostic microRNAs associated with thyroid cancer. Furthermore, the diagnostic implications were evaluated using receiver operating characteristic curves to identify potential biomarkers predictive of patient outcomes. This approach integrates cutting-edge computational techniques with clinical data to enhance our understanding of microRNA-based diagnostics in thyroid cancer.

Results: Results indicated that changes in the expression of hsa.mir.105.1 had a significant role in the pathogenesis of thyroid cancer. Also, the differential expression of both hsa.mir.105.1 and hsa.mir.181b.2, as well as hsa.mir.105.1 and hsa.mir.204, could intensify the progression of thyroid cancer. The evaluation metrics demonstrated the efficacy of the machine learning model, with a minimal mean squared error of 0.005 and a root mean squared error of 0.076, indicating accurate predictions. The R-squared value of 0.93 underscored the model's ability to explain a substantial portion of the variance in the data. The combination of these several hsa.mir markers can be considered diagnostic, with a sensitivity of 0.780 and specificities of 0.881 and 0.966 for the first and second combinations, respectively. Furthermore, the area under the curve values were 0.858 and 0.897, respectively.

Conclusion and Discussion: Through bioinformatics studies and machine learning techniques, a combinational expression analysis of several novel microRNA genes has identified promising diagnostic biomarkers for thyroid cancer. This research enhances our understanding of the pathogenesis of this malignancy. With the potential to detect cancer at its earliest stages, timely treatment could significantly improve patient survival rates.

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