Transcriptome Approach to Reveal Novel Prognostic Biomarkers for Thyroid Cancer

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Thyroid cancer (TC) is one of the most common endocrine malignancies worldwide, with 821,214 newly diagnosed cases in 2022. It has the fastest growth rate across all cancers. Despite its prevalence, existing prognostic biomarkers remain suboptimal in clinical settings, particularly in the early identification of high-risk patients. Notably, about 30% of thyroid gland biopsies obtained via fine-needle aspiration remain inconclusive or undiagnosed. This study aims to identify differentially expressed genes (DEGs) associated with poor TC prognosis by integrating wet and dry lab approaches. Four RNA-seq datasets derived from experimental lung metastasis models of papillary (PTC), follicular (FTC), poorly differentiated (PDTC), and anaplastic thyroid cancer (ATC) were analyzed to screen for candidate genes linked to distant metastasis (DM). The TCGA-THCA dataset was then used to validate the candidate genes through bioinformatic analysis. A total of 105 upregulated and 25 downregulated DEGs were consistently identified across all datasets. Subsequent analysis revealed seven genes overexpressed in 13% of PTC samples, significantly associated with poor overall survival ($p < 0.001$). This seven-gene signature has been proposed as a novel prognostic biomarker for risk stratification in distant metastasis (DM), with potential integration into clinical workflows through gene expression profiling of tumor biopsies to identify high-risk patients which may enhance survival outcomes by improving diagnostic precision and enabling earlier, more targeted interventions. This could ultimately reduce the economic and medical burden of TC.

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