Double Negative T Cell Proportion of CD3+ Cells Present in the Thyroid Microenvironment is an Immunogenomic Marker for Predicting Thyroid Cancer

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Thyroid cancer is becoming increasingly relevant in the growing population and has been seeing a greater incidence of diagnosis since the early 1980s. While there has been an increase in diagnosis, there has not been any significant advancement in the quality or sensitivity of screening methods. Current guidelines recommend repeat biopsy in these patients because they lack any guidance if patients continue to yield unclear or contradictory pathology. Current ATA recommendations state that these patients should receive diagnostic surgery which results in the removal of the entire thyroid gland. It is estimated that 60-75% of these surgeries end up removing benign lesions. Yet with the current methods of diagnosis, it is impossible to determine the prognostic status of every thyroid nodule without thyroidectomy for patients with unspecified pathology. We have found a diagnostic profile that lends a greater sensitivity and specificity using the microenvironments of the tumor cells. A fine needle aspirate sample from patients with thyroid nodules was analyzed via flow cytometry. Using this data, we characterized the lymphocytic environment of malignant tumors expressing a large population of T cells which are neither expressing CD4 nor CD8 (CD3+CD4-CD8-) known as double negative lymphocytes (DN T) cells. A profile of >9.14% DNT cells was shown to indicate malignancy with a sensitivity of 96.6% and specificity of 100%. Therefore, measurement of tumor microenvironment cell populations serves as an extremely effective method for thyroid nodule risk assessment. This would be instrumental in cutting back the number of unnecessary surgeries and avoiding excessive patient hardship resulting from surgery or postsurgical care. Clearly, the microenvironment holds significance in the instance of malignant modules, and they reflect the behavior of the tumor. Using High-throughput gene expression analysis, we will analyze the mRNA expression of DN T cells present in the microenvironment. Using the information gathered, we will design a profile of markers that indicate malignancy. Furthermore, our group is working on amplifying DN T cell markers on a PCR-based platform to allow a more economically viable diagnostic test.

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