Tumor and Its Microenvironments Gene Expression in Follicular Lymphoma

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Follicular lymphoma (FL) is the second most common non-Hodgkin lymphoma. For searching the signaling pathways associated with the immune response, the functioning of which is altered in the tumor and its microenvironment, a comparative analysis of transcriptomes of tumor tissue samples from patients with FL was carried out in comparison with control samples of lymph nodes without tumor growth. We identified a total of 997 differentially expressed genes, including 430 upregulated and 567 downregulated genes in tumor samples. Upregulated genes were enriched in the canonical pathway gene sets associated with cell cycle, cellular response to stress, DNA repair, chromosome organization and RNA processing. Downregulated genes were enriched in gene sets related to the immune response. One of the most suppressed signaling pathways in FL controls the activation of T-lymphocytes. Out of the 29 genes involved in the activation of T cells, the expression of which is suppressed in FL, three (*CD28*, *LAT*, *ZAP70*) are involved in signal transduction in anti-PD-1 therapy. Thus, the level of expression of these genes in a patient can potentially be one of the biomarkers that have predictive value in anti-PD-1 therapy in FL.

Keywords: follicular lymphoma, tumor microenvironment, immune checkpoints, PD-1 recepto