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Lymphocyte migration factors in breast cancer: a transcriptome analysis

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Motivation and Aim: Breast cancer (the overgrowth and breast tissue cells proliferation) is currently documented as one of the most common types of cancer. Immunotherapy is high-potential treatment for many types of cancer, but it is a newly approach for fighting against breast cancer [1], so the prospect of studying this area is steadily growing, as it has been proven that breast cancer is immunogenic tumor. Immunotherapy has become a significant treatment strategy and enhanced the survival of breast cancer patients in the intervening years. Despite the success of this type of treatment, some patients do not respond to therapy or responding patients tend to recrudescence or worsen. The main causes of these adverse effects are complex internal or external mechanisms of resistance. It is also assumed that this is due to the low content (compared to other types of oncology) of tumor-infiltrating lymphocytes (TIL) in malignant tumors [2]. It is highly important to scrutinize the process of infiltration and migration of immune cells in breast cancer in order to improve modern immunotherapeutic interventions. For this reason we use data from the lymph nodes where the maturation of lymphocytes occurs.
Methods and Algorithms: We used open databases to collect transcriptomic data from lymph nodes of donors and patients with breast cancer. The objective was to compare gene expression and identify candidate genes for the analysis of lymphocyte migration in oncology. As a starting point normalization and rank standardization of data from heterogeneous platforms (microarray and RNA-seq) was carried out. In the sequel genes associated with CD4 cell lines were selected where expression differences between normal//control samples were found. With the help of GeneCards, an annotation of functional significance was obtained. The differential expression of the identified genes was tested for the same patients directly in tumor cells in order to obtain an immunological prognosis and obtain data on the migration of lymphocytes from the lymph nodes. Subsequently, these data can be used to develop personalized approaches to the prognosis of immunotherapy in patients with breast cancer, improve response and eliminate relapses.
Results: Immune response markers in oncology – NCAM1 and SIGLEC7 – revealed overexpression in lymph nodes in cancer samples. Proliferation processes, dependent on IL7, turned out to be active, while independent (SLAMF1), on the contrary, are inhibited. CD38, CD98, and SLAMF1 have low expression ranks and are associated with the presence of activated CD4 cells. Genes associated with the CD4+ cell line showed low differential expression in tumor samples from patients.

Conclusion: By the means of transcriptomic analysis, results indicating blocking of some pathways of proliferation of lymphocyte cell lines were obtained, as well as problems of migration into tumor cells. Incomplete picture is spotted: there is a great deal of evidence on reversible cells (eg, peripheral blood) and data on metastasized specimens, but a lack of clean sets from lymph nodes. We consider it promising to study the migration of T cells from lymph nodes for the progress in cancer immunotherapy. This may provide answers to the question of the difference in the patients sensitivity to this type of treatment and palindromia later on.

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