1055 IMMUNE CELL SUBTYPES ASSOCIATED WITH THE LEVEL OF TUMOR-INFILTRATING LYMPHOCYTES IN BREAST TUMOR MICROENVIRONMENT

[1]Su Min Cha*, [1,2]Jeong-Han Seo, [2,3]Jung-Wook Park, [2]Hee Jae Lee, [1,2]Hee Jin Lee. *[1]University of Ulsan College of Medicine, Seoul, South Korea, Republic of; [2]NeogenTC Corp., Seoul, South Korea, Republic of; [3]Sungkyunkwan University, Seoul, South Korea, Republic of*

Background The level of tumor-infiltrating lymphocytes (TILs) is a predictive and prognostic factor for improved clinical outcomes in breast cancer. To identify immune cell subtypes associated with the level of TILs, we compared composition of immune cells between breast cancers with high or low level of TILs using single cell RNA sequencing (scRNA-seq).

Methods The scRNA-seq was performed with dissociated and CD45+ sorted cells from 21 breast tumor tissues. Among them, 12 samples with high TIL (≥ 40%, n=6) or low TIL (≤ 2%, n=6) were compared. Standard procedures were performed by the Seurat package in R. T cells, B cells, monocytes, and dendritic cells (DCs) were separated using the Azimuth package. Differentially expressed genes (DEGs) were computed according to the level of TILs for pathway analysis using ReactomePA package (p value < 0.05, abs(log2 fold change) ≥ 1).

Results The proportion of T cells (60.6% vs 41.8%) and B cells (9.8% vs 3.9%) in the high TIL group were higher than the low TIL group. Monocytes (16.3% vs 29.3%) and DCs (4.6% vs 4.5%) in the high TIL group were lower or not different. In each immune cell type, cell subtypes and clusters were compared by proportion in the high and low TIL groups. T cell subtypes showed no difference between the high and low TIL groups. However, B cells, monocytes, and DCs had different composition of cell subtypes between the high and low TIL groups [B intermediate (22.2% vs 35.8%), B memory (14.2% vs 36.6%), plasmablast (57.1% vs 19.1%), cDC2 (54.5% vs 66.7%), pDC (39.0% vs 27.8%), and 4 monocyte clusters (11.1% vs 19.6%, 12.7% vs 20.1%, 18.8% vs 13.8%, and 14.9% vs 7.5%)]. DEGs derived from differential subtypes between the high and low TIL groups were used for pathway analysis. Upregulated pathways including interleukin and interferon signaling pathways in the high TIL group were shared by several immune subtypes.

Conclusions Composition of immune cell subtypes and their signaling pathways were different between breast cancers with the high or low level of TILs. Further researches for better understanding and modulation of immune cell subtypes associated with high level of TILs are needed to heighten the level of TILs in breast cancer microenvironment.

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