IDENTIFICATION OF RARE CELL TYPES IN LUNG CANCER AND INVESTIGATION OF THEIR USE IN PROGNOSIS

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Cancer is a complex, dynamic and heterogeneous disease. Identification of tumor heterogeneity holds a significant promise not only on tumor classification but also on predicting the prognosis and choosing the right treatment. Therefore, it is essential to investigate tumor heterogeneity in a regular diagnosis procedure.

Tumors contain variety of cell types such as malignant cells, non-malignant cells, immune cells, and rare cells (i.e., dormant cells (DRM) and cancer stem cells (CSC)). [1] All these cell types contribute to the disease progression. For example, dormant cells are major cause of recurrence of cancer because they disseminate from the tumors and enter into a state of cellular dormancy (G0/G1 arrest), and they may start dividing again after a prolonged period of dormancy. [2]

The arrival of single cell RNA sequencing (scRNAseq) provides new opportunities for exploring gene expression profile at the single-cell level. scRNA technique has become favorable for studying the heterogeneous diseases such as cancer. [3]

In this study, rare cell types from single-cell RNA sequencing data [1] were identified by using the Seurat tool [4] in R programing language and single-cell references were determined to analyze bulk data. Bulk data from TCGA [5] were analyzed to find cell type proportions by using the MuSiC tool [6] and survival models were generated to discover whether these rare cell types contribute to the survival time and if they can be used for prognosis. DRM cells negatively affect survival probability of LUAD and LUSC patients over time. These results may indicate that cells in dormant state cannot be detected and eliminated in any treatment applied, and that the disease relapses after a while.

Keywords: Lung cancer, Single-cell RNAseq analysis, rare cells

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