Single-Cell Analysis Based Identification of Unique Markers and Metastasis Mechanism in Triple-Negative Breast Cancer

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Triple-negative breast cancer (TNBC) is a subtype of breast cancer which has none of the known unique biomarkers of the other subtypes. There is no established targeted treatment for TNBC and rare early diagnosis, which is also metastatic in 46% of cases, leading to poor survival rates in patients. Single-cell analysis maps the genomic information of several cell types from mass patient samples, and can reveal information about overexpressed and unique biomarkers. In this work, R-based detailed analysis was performed on single-cell data from TNBC and non-TNBC patient samples. Data available from repositories such as the GEO (Gene Expression Omnibus) was analyzed to identify two markers CT83 and HORMAD1 (CT46), which were unique, overexpressed biomarkers to TNBC cell types. These markers are cancer/testis antigens, and therefore abnormal to be overexpressed in breast cells. Since the combined presence of CT83 and CT46 was only found in TNBC cancer cells, it was hypothesized that their overexpression drives the EMT metastasis of TNBC. In addition, through AutoDock Vina based molecular drug-docking simulations, this work attempted to perform free-energy calculations and explore the efficacy of various potential drugs. Among these drugs, Olaparib was found to be the most energetically stable in case of both CT83 and HORMAD1, equivalent to the stability of well known drugs of other cancer types. Targeted drugs could help to potentially disrupt or check the activity of CT83 and HORMAD1. This could help to prevent metastasis and spread of TNBC and thus help increase the life expectancy of patients.

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