**Effects of Immune Cell Profiling in Cancers**

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**Key Words:**

Cancer cells, tumor cells, breast cancer, heterogeneity, genomic profiling, immune cells, transcriptome analysis, intratumoral, microenvironment, targets

**Individual cell and tumor profiling is used to help aid breast cancer treatment, through gene-targeted therapy. Both articles, discussed below, show that there is a high level of genetic heterogeneity present in cancerous tumors. These tumors, can be analyzed to reveal single cell genomes and characteristics. This reveals the different kinds of cancerous and noncancerous cells that make up the tumor. Different subtypes of the cancers and immune cells were identified, along with their roles in cancer cell development, proliferation, and prevention. By knowing the level and characterization of the heterogeneity in the cancer tissue, researchers helped identify specific targets for treatment, including T cells and Oct-4A. This identification is important because treatment options will broaden and allow for improved prognoses. The results of this study showed 91 % accuracy in relation to subtyping breast cancers. Researchers were able to classify 515 different cells within the tumors and identify 11 different clusters of patterns among them. Overall, the data collected supported the validity of genomic profiling.**

**Introduction**

The article “Stem cell profiling in head and neck cancer reveals an Oct-4 expressing subpopulation with properties of chemo-resistance,” by Reers et al., discusses the potentiality of using stem cell profiling to find subpopulations within oral cancers. In this study, the researchers found that tumors were heterogenic or diverse in cells and cell lines. Within these heterogenous tumors, they were able to identify cancer stem cell markers, the most important marker being Oct-4A. Oct-4A helps in the detection of cancer among subtypes of cancer cells with increased chemo-resistance.

On the other hand, the article “Single-cell RNA-seq enables comprehensive tumour and immune cell profiling in primary breast cancer” written by Chung et al., describes the importance and relevance of tumor and immune cell profiling in finding better treatment options and prognoses for breast cancer. Even though in the past, genomic profiling has been used to characterize and study solid tumors, these researchers chose to use single cell analysis to learn more about the heterogeneity in the cancer tumors, which affect therapeutic outcomes of a treatment. This type of profiling shows both the tumor and surrounded microenvironment (immune cells and tissues), enabling separation of cancerous cells from non-cancerous cells.

The cancerous tumor cells were then divided into 11 clusters with different chromosomal gene expression patterns, allowing for even more separation from the microenvironment surrounding the tumor. With all of this information the scientists discovered that tumor cell properties and heterogeneity need to be resolved at the single-cell level in order to reveal distinct characteristics of tumors and the microenvironment in which they reside. Through this, Chung et al. found four different breast cancer subtypes, “Luminal A, Luminal B, HER2, and triple negative breast cancer,” which each contain their own characteristic mutations and variation patterns. Allowing for the ability to treat each subtype better and more specifically. Through this experiments, the researchers found that there is indeed validity of genomic profiling for specific cell types in breast cancers that can lead to more treatment options and more successful patient outcomes.

**Recent Progress**

The research conducted by Reers et al. and published in 2013, showed the ability of cancer cell-profiling to find different types of cells within cancers as well as different subtypes of the cancers. Therefore, finding potential markers that could lead to an improved understanding of the makeup of the cancer. They identified Oct-4A as an important marker for head and neck cancers but stopped there.

More recently, Chung et al. used a similar technique to profile breast cancer tumors and cells, where they again found many markers, this time including T cells. Through their research they found that these checkpoint targets could lead to new and improved treatment options for those suffering from breast cancer and most likely other cancers. Chung et al. found that their analysis and classification of breast cancer subtypes had 91% accuracy, proving that this type of research is valid and should be used more. Not only does it reveal an even greater understanding of the composition of specific tumors, it helps develop greater treatment strategies that are more likely to succeed.

In addition to the progress that Chung et al. made, there is currently ongoing research to find new immune checkpoint targets in a variety of different cancers. While many of these studies are still in the early stages of their clinical trials, there is hope for successful outcomes. Chung, et al., discusses a continuous need for large scale gene expressing profiling projects, similar to their own, in order to profile entire tumor genomes. By doing so, researchers and oncologists can find even more subgroups, defining characteristics, and target cells within cancers.

**Discussion**

With the technique of single-cell transcriptome profiling and analysis of breast cancer tissue, Chung et al., could clearly define the characteristics of both cancer and immune cells located within the breast tumor. By separating the cancer cells from the non-cancerous cells without preexisting markers, the researchers were able to prove that it is possible to define these populations and find a lack of uniformity within them. In addition, Chung et al. also found that both the innate and adaptive immune systems’ cells had immunosuppressive gene expression, therefore, selecting T cells as potential checkpoint targets due to their role in cancerous tumor cell evasion.

Through both the work of Chung et al. and Reers et al., it was revealed how to discover new target populations for potential treatment options, including the T cell and Oct-4A markers. Through the scientists’ use of transcriptome profiling, they proved that single cell profiling of large, solid tumors is indeed a successful tool in finding cell characteristics and markers. Most importantly, Chung et al. found that single cell gene expression profiling allows for a better understanding of both cancer and immune cells and tissues within their microenvironment. Therefore, leading them to find more effective therapeutic options. The results from their study prove that learning the specific components of “intratumoral heterogeneity,” is of great importance to the field of oncology. If researchers are better able to understand the composition of a non-uniform cancerous tumor, they may identify subpopulations and singe cell markers, leading to more individualized and effective treatment strategies that result in overall improved patient outcomes.

**References**

Chung, W., Eum, H., Lee, H., Lee, K., Lee, H.,

Kim, K., Ryu, H., Kim, S., Lee, J., Park, Kan, Z., Han, W., & Park, W. (2017). “Single-cell RNA-seq enables comprehensive tumour and immune cell profiling in primary breast cancer.” *Nature Communications, 8, 1-12*. doi:10.1038/ncomms15081

Reers, S., Pfannerstill, A., Maushagen, R., Pries,

R., & Wollenberg, B. (2014). “Stem cell profiling in head and neck cancer reveals an Oct-4 expressing subpopulation with properties of chemoresistance.” *Oral Oncology*, 50, 155-162.