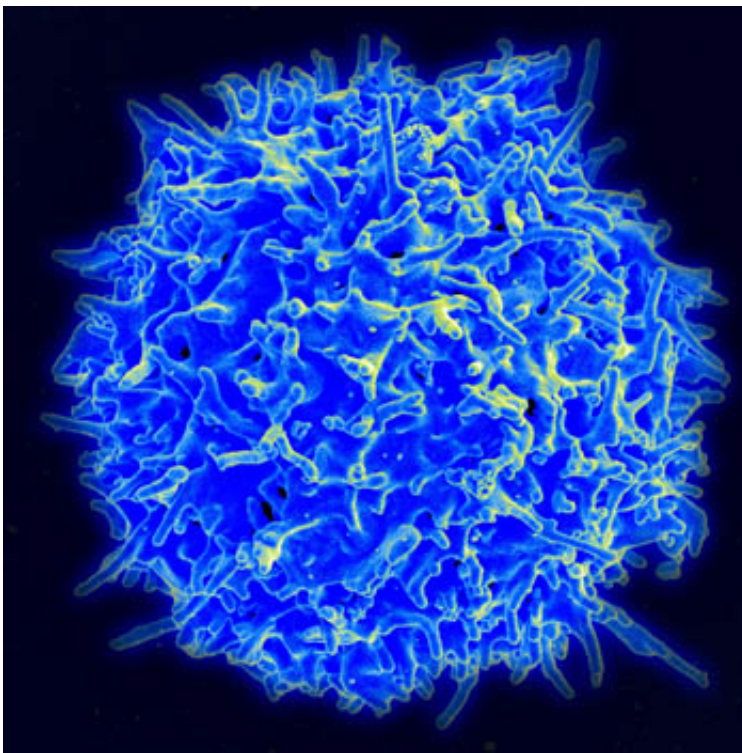# Two teams independently tease out gene expression patterns in tumor-infiltrating lymphocytes using RNA sequencing

June 27 2018, by Bob Yirka

Scanning electron micrograph of human T lymphocyte or T cell. Credit: NIAID/NIH

Two teams working independently of each other have found that it is possible to tease out gene expression patterns in tumor-infiltrating lymphocytes using single-cell RNA sequencing. The first team, based in

Australia, sequenced lymphocytes that had infiltrated breast cancer tumors. The second team, based in China, did the same with lymphocytes that had infiltrated lung cancer tumors and surrounding tissue. Both teams describe their findings and results in the journal *Nature Medicine*.

Lymphocytes are a kind of leukocyte (white blood cell) that tend to exist mostly in the lymphatic system. One particular type is the T cell, which is well known to play a major role in the immune response to foreign material. Cancerous tumors are considered by the immune system to be foreign material, and thus are targeted by T cells and other lymphocytes. Unfortunately, such targeted attacks are not enough to stop many tumors from growing or spreading. In these new efforts, both teams sought to gain a better perspective on which types of immune responses tend to meet with greater success than others. To find out, they conducted single-cell RNA sequencing on lymphocytes involved in such a response—those that had infiltrated tumors.

The team working in Australia focused their study on lymphocytes involved in attacking breast cancer tumors. To that end, they sequenced 6,311 T cells from two major types of breast cancer tumors. Both types of cancer had previously been designated as triple-negative, due to their particular characteristics.

The team in China studied lymphocytes that had infiltrated lung cancer tumors. They sequenced 12,346 single T cells from tumors and from nearby tissue. In their case, the tumors represented 14 distinct types. They also sequenced 8,038 alpha and beta T cell receptors.

In both studies, the researchers report that they were able to tease out gene expression patterns. The team in Australia, for example, found that both the quantity and quality of infiltrating T cells can have an impact on the outcome of tumor progression. And the team in China found they

were able to track migratory effector T cell clones that actually differed from one tissue to the next.

Both teams suggest that their work shows the potential benefits of understanding single-cell genomics of the tumor microenvironment—the possibility of developing new immunotherapy drugs and techniques.

  More information: Peter Savas et al. Single-cell profiling of breast cancer T cells reveals a tissue-resident memory subset associated with improved prognosis, *Nature Medicine* (2018). DOI: 10.1038/s41591-018-0078-7

 Xinyi Guo et al. Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing, *Nature Medicine* (2018). DOI: 10.1038/s41591-018-0045-3

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