

Mapping How Cancers Form and Spread

3D maps provide a better understanding of cancer development and progression, which could lead to new prevention and treatment strategies.

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A tumor can contain millions of cancerous cells, many of which may behave and respond to treatments differently. In addition, tumors harbor other types of cells, such as immune cells, which migrate from elsewhere in the body. Tumors can also interact in complex ways with surrounding tissues, known as the tumor microenvironment.

All these factors can influence if, how, and where a tumor grows and spreads. Recent large research projects such as The Cancer Genome Atlas have uncovered many specific genetic changes in cancer cells that can help drive tumor growth. But how these changes emerge and change over time and location in a tumor have remained largely a mystery. Such information is needed to better understand why some treatments don't work in some tumor types and how resistance to treatment develops over time.

In 2018, NIH launched the Human Tumor Atlas Network (HTAN) as part of the Cancer Moonshot initiative. The Network funded research teams across the country to develop new imaging, genetic analysis, and computational tools to map out the workings of single cells within a tumor.

Overall, the network gathered tissue samples from 21 different organ types taken from almost 2,000 people. These included samples from tumors and pre-cancerous growths, and cells from blood cancers like leukemia. The latest results from HTAN appeared on October 30, 2024, in a suite of papers in Nature journals.

In [one of the new studies](#), a team led by Dr. Li Ding from Washington University in St. Louis closely analyzed breast, colorectal, pancreatic, kidney, and uterine cancer samples. They were able to identify distinct substructures, which they called microregions, within many tumors.

They found that cells in different microregions within the tumors often behaved differently. For example, cells closer to the core of tumors used more energy. Cells at the edges of tumors had more interactions with the immune system. In some tumors, different genetic mutations in different microregions could drive tumor growth. Such diversity can pose a challenge for treatment using therapies to target specific mutations. Such differences in tumor cell behavior couldn't be

mapped to the 3D structure of tumors before the spatial mapping techniques developed by HTAN.

“We understood that cancer cells, immune cells, and structural cells were all present in [a] tumor, sometimes protecting the cancer from chemotherapy and immune system attack, but now we can actually see those battle lines,” Ding says. “We now have the ability to see how regions of the tumor differ in 3D space and how the behavior changes in response to therapy or when the tumor spreads to other organs.”

Other papers in the collection provided details about how various cancers develop and spread over time. For example, a team from Stanford University showed that colorectal tumors can contain populations derived from multiple cells that turned cancerous independently, instead of from a single ancestor cell. Other teams tracked how some cancer types first arise, and then later gain the ability to metastasize elsewhere in the body.

A second phase of HTAN now aims to further build on these results. “This work is helping us see and understand tumors in ways we never could before,” says Dr. W. Kimryn Rathmell, director of NIH’s National Cancer Institute. “These resources will spur insights and innovations for years to come.”

This [research summary](#) was published by the National Institutes of Health on November 19, 2024.