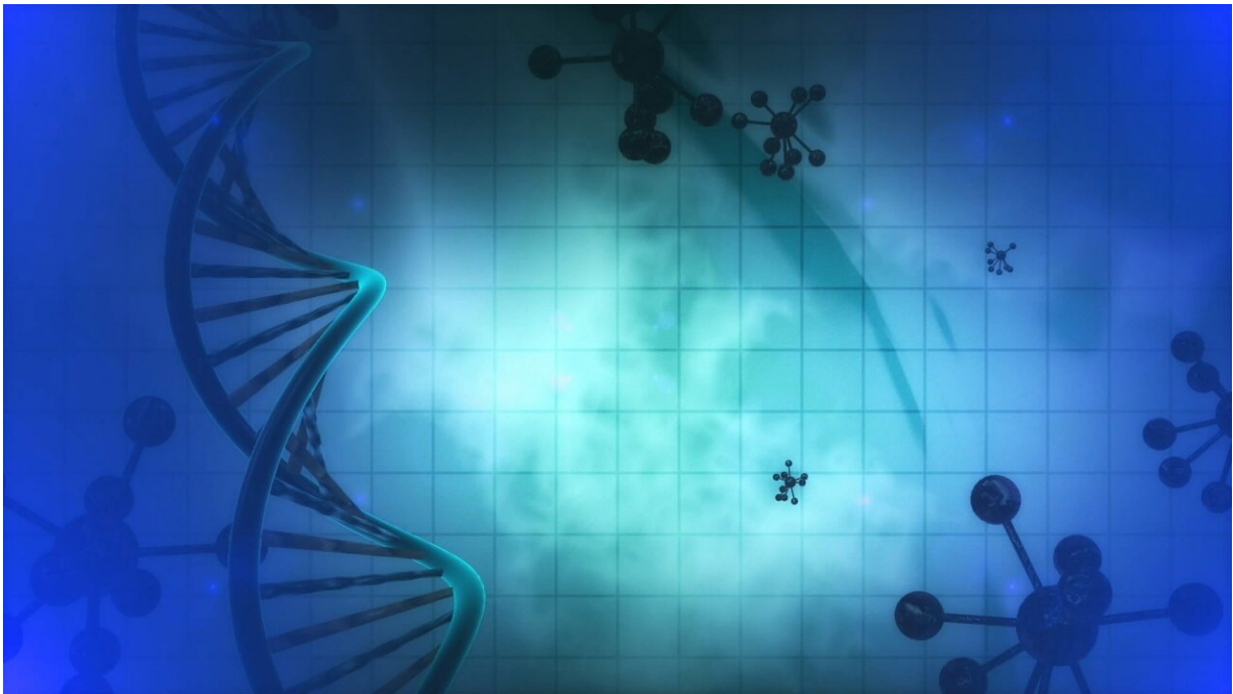


Single-cell RNA sequencing reveals details about individual cells in pancreatic tumors

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Led by the Translational Genomics Research Institute (TGen), an affiliate of City of Hope, and by HonorHealth Research and Innovation Institute, an international team of researchers have described in detail the individual cells that comprise the pancreatic cancer microenvironment, a critical step in devising new treatment options for patients with this aggressive and difficult-to-treat disease.

The study results were published today in the scientific journal *Genome Medicine*, a publication of Springer Nature.

Researchers used a relatively new technique known as single-cell sequencing to genetically identify cell types, and subtypes, that occur in [pancreatic tumors](#), and identify the various [cells](#) in the [tumor](#)'s stroma, a substance surrounding the tumor that can hide the cancer from the body's immune system.

While single-cell transcriptomics has been used previously to study the cellular composition of primary tumor tissues of [pancreatic](#) ductal adenocarcinoma (PDAC), this study also used the technology to profile [individual cells](#) from dissociated primary tumors and biopsies of metastatic tissues, those cancerous lesions that have spread throughout the body from the primary tumor.

This study was carried out in collaboration with investigators from Samsung Medical Center and City of Hope, a world-renowned independent research and treatment center for cancer, diabetes and other life-threatening diseases. Primary tumors and core needle biopsies of metastatic lesions from PDAC patients were sequenced using the Chromium single cell RNA-Seq platform.

"Single-cell transcriptome analysis can offer important clinical insights on individual cell subpopulations and provide clues for developing novel therapeutic strategies for both targeted therapies and immunotherapies," said Haiyong Han, Ph.D., a professor in TGen's Molecular Medicine Division and head of the institute's Pancreatic Cancer Research Laboratory.

"Understanding the diversity and complexity of the PDAC tumor and stromal compartments in individual tumors may help identify unique intervention points and potentially inform treatment and maintenance

strategies for patients with advanced disease," said Dr. Han, the study's senior author.

Distinct [cell types](#) and subtypes were identified in the analysis, including tumor cells, endothelial cells, cancer associated fibroblasts, and immune cells, and the expression levels of various genes in the individual cell populations correlated with patient clinical outcomes.

"Working with our partners and colleagues by utilizing the technology of single cell sequencing, we can continue to learn more about the biology of pancreas cancer. These insights may potentially help us determine more treatment options for our patients," said Erkut Borazanci, M.D., M.S., a medical oncologist and physician-investigator at HonorHealth Research and Innovation Institute, a clinical associate professor at TGen, and one of the paper's authors.

Pancreatic cancer is an aggressive disease that carries a high mortality rate. It is the third-leading cause of cancer death in the U.S., following lung and colorectal cancers. In 2020, the five-year survival rate for pancreatic cancer is only about 10%, though that represents progress from the dismal 6% rate in 2014.

Next, researchers plan to use more advanced single-cell spatial transcriptomics analysis to further investigate the cellular relationships related to survival rates using real-time methods. Broader use of this technology could potentially guide the search for new agents to treat pancreatic cancer.

For more information about pancreatic [cancer](#) research studies at HonorHealth Research and Innovation Institute, please visit HonorHealth.com/research, call 480-323-1364 or email clinicaltrials@honorhealth.com.

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The study, "Single-Cell transcriptome analysis of tumor and stromal compartments of pancreatic ductal adenocarcinoma primary tumors and metastatic lesions," was published in the scientific journal *Genome Medicine*.

More information: Wei Lin et al. Single-cell transcriptome analysis of tumor and stromal compartments of pancreatic ductal adenocarcinoma primary tumors and metastatic lesions, *Genome Medicine* (2020). [DOI: 10.1186/s13073-020-00776-9](https://doi.org/10.1186/s13073-020-00776-9)

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