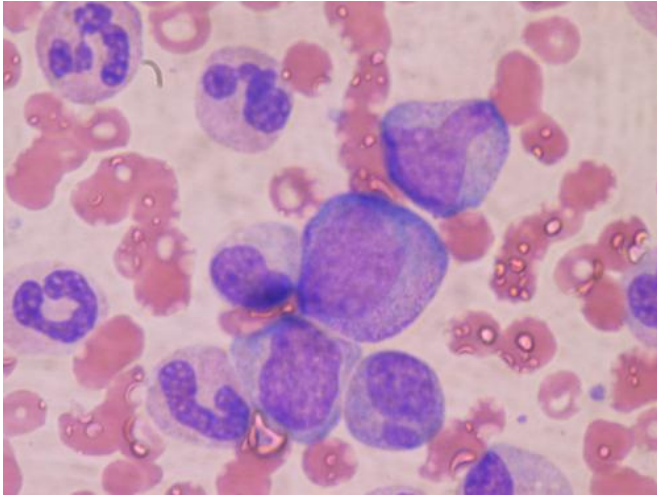# Researchers develop method for separating tissue types in tumor samples

25 October 2019

Hematopoietic precursor cells: promyelocyte in the center, two metamyelocytes next to it and band cells from a bone marrow aspirate. Credit: Bobjgalindo/Wikipedia

A dense web of tissue can surround pancreatic cancer tumors, impeding treatment and sometimes acting as a barrier to the tumor's spread. Researchers want to distinguish cancerous tissue from the surrounding connective tissue and cells known as stroma as well as from immune cells in the tumor's environment in order to drive personalized treatment strategies.

In the journal *Nature Communications*, researchers from the University of North Carolina Lineberger Comprehensive Cancer Center reported they have designed a computational method for separating the different tissues in a particular sample—whether that is stroma in the case of pancreatic cancer, immune cells or cancer cells.

"We developed a way to determine what cellular compartments make up a tumor by deconstructing the tumor's genomic data," said UNC Lineberger's

Jen Jen Yeh, MD, professor of pharmacology and surgery in the UNC School of Medicine, and vice chair for research in the Department of Surgery. "This can help separate out the immune, tumor and stroma microenvironment so that we can better understand the biology of each which can help hone in on clinically important alterations."

Researchers described their method for separating tissue in a sample, which they called DECODER. Using multiple cancer tissue samples from the Cancer Genome Atlas, they demonstrated DECODER could differentiate the common signals across tumors. In addition, they used DECODER to deconstruct samples of pancreatic ductal adenocarcinoma, the most common type of pancreatic cancer, allowing them to see the signals from compartments of immune, tumor or stroma.

Ultimately, the researchers' goal is to separate the tissue in order to further understand the unique biology of a patient's tumor, as well as the tissue that surrounds the tumor.

In previous work, Yeh and her colleagues found the composition of the environment around a tumor is linked to treatment response and patient outcomes. In a study published in *Nature Genetics* in 2015, researchers analyzed how genes are expressed in both the tumor and the stroma and found there are two types of tumor, and two types of stroma.

They envision multiple additional applications for DECODER, including applying their tissue separation method in other tumors to help understand the cancer and the cancer's microenvironment. They are also planning to study whether DECODER can help them identify the cancer for a patient that has a tumor of unknown origin.

More information: Xianlu Laura Peng et al. De novo compartment deconvolution and weight estimation of tumor samples using DECODER,

Provided by University of North Carolina at Chapel
Hill School of Medicine

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