

Novel classification can lead to new ways to diagnose and treat cancer

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Dr. Chad Creighton is the first author of this work. Credit: Baylor College of Medicine

A novel approach to studying cancer has enabled researchers to group about 10,000 human cancers of 32 different types into 10 classes based on the molecular pathways that drive tumor growth. A better understanding of these pathways can potentially lead to novel ways to diagnose and treat cancer. The study appears in the journal of *Clinical Cancer Research*.

"When we study [cancer](#) at the molecular level we realize that there is not a single [pathway](#) or process that drives all the different types of cancer," said first author Dr. Chad Creighton, associate professor of medicine and member of the Dan L Duncan Comprehensive Cancer Center

division of biostatistics at Baylor College of Medicine.

Past studies have looked at cancers of individual types in detail. Lung cancer studies, for example, have defined molecular-based [lung cancer](#) subtypes that represent different [molecular pathways](#) that have been perturbed and driven lung cancer growth.

"In this study, we wanted to find common pathways across cancers from different tissues," Creighton said. "We used the Cancer Genome Atlas, a publicly available data set that allows us to look at what many types of cancers have in common."

The researchers applied a different computational approach to subtract all tissue-specific differences and identify what pathways remained. They analyzed about 10,000 human cancers of 32 different types and were able to define 10 major cancer groups that they call classes.

Most classes include cancers from different tissues that have in common specific molecular pathways that are altered and potentially driving cancer growth. Then, the researchers identified specific genes that characterize each of those classes to better understand what the pathways do.

Altered pathways

"We found a class that had a very high expression of altered genes that are involved in the immune checkpoint, which refers to [tumor](#) molecules that signal the immune cells in charge of destroying the tumor to leave it alone," Creighton said. "Other classes had altered genes in pathways linked to metabolism or stress."

Another subset had a molecular signature of neuroendocrine tumors, a type of tumors that can be found within a wide range of tissues, but it

has its own unique characteristics and profile.

"We expected that about 1 percent of the tumors would show a neuroendocrine signature, but we found that about 4 percent were showing this," Creighton said. "This represents a substantial number of patients when you consider all human cancers."

Even though the tumors were not originally diagnosed as neuroendocrine tumors, they had a signature of this type of cancer. For the researchers, this finding suggests that there might be a number of neuroendocrine cancers that are being missed.

"We think there is a need for reconsidering what type of markers to look for to identify [neuroendocrine tumors](#)," Creighton said.

Some of the biological pathways identified in this study have been explored in the laboratory setting, for years now.

"An appreciable number of human cancers manifest these pathways that we found to be relevant in the laboratory setting," Creighton said. "We think it is very important to map out the pathways a cancer seems to be using to grow. Knowing this can be the first step in determining how to better target that particular cancer."

More information: Chad J. Creighton et al, Pan-cancer molecular classes transcending tumor lineage across 32 cancer types, multiple data platforms, and over 10,000 cases, *Clinical Cancer Research* (2018). [DOI: 10.1158/1078-0432.CCR-17-3378](https://doi.org/10.1158/1078-0432.CCR-17-3378)

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