Researchers develop new approach to identify 'drivers' of cancer

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UNC Lineberger Comprehensive Cancer Center researchers have developed a new integrated approach to pinpoint the genetic "drivers" of cancer, uncovering eight genes that could be viable for targeted breast cancer therapy.

The study, published online August 24 in *Nature Genetics*, was authored by Michael Gatza, PhD, lead author and post-doctoral research associate; Grace Silva, graduate student; Joel Parker, PhD, director of bioinformatics, UNC Lineberger; Cheng Fan, research associate; and senior author Chuck Perou, PhD, professor of genetics and pathology.

These researchers studied a variety of cancer causing pathways, the step-by-step genetic alterations in which normal cells transition into cancerous cells, including the pathway that governs cancer cell growth rates. A high growth rate of cells, also known as cell proliferation, is recognized to be associated with poor prognosis for breast cancer patients.

Analyzing multiple types of genomic data, UNC Lineberger researchers were able to identify eight genes that were amplified on the genomic DNA level, and necessary for cell proliferation in luminal breast cancer, which is the most common sub-type of breast cancer.

"Using this new computational approach, we were able to take advantage of the rich data resources that exist and identify a number of new potential drug targets for a specific subset of breast cancer patients. This is an important step down the road towards more personalized medicine," said Perou.

In fact, one of the genes identified – CPT1A – is already a target for drug development in lymphoma and could potentially be tested for breast cancer patients as well. Drugs targeting CPT1A have been shown to inhibit human cancer cell line growth in vitro and in mouse models of lymphoma.

This analytical approach used to better understand the drivers of cancers includes a comprehensive and integrated analysis of multiple data types including gene expression data, somatic mutations, DNA copy number, and a functional genomics data set.

While the study focused on identifying genetic drivers for breast cancer, the approach could easily be applied to other tumors types as well. Lead author Mike Gatza added, "While we were able to pinpoint drivers for breast cancer, this approach can and will be applied to other tumor types in the future."

Provided by University of North Carolina Health Care