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DNA 'barcoding' enables simultaneous analysis of cancer-related proteins

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New DNA "barcoding" technology developed by researchers at Massachusetts General Hospital allows for simultaneous analysis of hundreds of cancer-related protein markers from patient samples, garnered through minimally invasive methods.

The technology uses antibodies linked to DNA "barcodes" to detect proteins, according to an announcement from MGH. This will allow clinicians to gain more insight into how cancer progresses, and also enable them to show why cancer therapies stop working or are ineffective.

"What this study sought to achieve was to vastly expand the information that we can obtain from just a few cells," said Cesar Castro, M.D., of the MGH Cancer Center, who co-authored a study on the findings published in *Science Translational Medicine*. "Instead of trying to procure more tissue to study, we shrank the analysis process so that it could now be performed on a few cells," he said.

In the past, pathologists could only look at a few protein markers at a time for analysis; now, according to the researchers, they could look at hundreds simultaneously. This is enabled by DNA-barcoded antibody sensing, with the barcodes linked to a type of glue that breaks apart when exposed to light, enabling the barcodes to be detected and quantified. Tested in patients with lung cancer, the technology was able to reflect the differences of cells within single tumors.

"We showed that this technology works well beyond the highly regulated laboratory environment, extending into early-phase clinical trials," Castro, a medical oncologist in the MGH Cancer Center and director of the Cancer Program within the CSB, said. "Ultimately, the implications for this type of technology could be vast. ... By obtaining samples from patients before initiating therapy and then exposing them to different chemotherapeutics or targeted therapies, we could select the most appropriate therapy for individual patients."

In November, IBM and the Baylor College of Medicine began touting software that can mine research papers for clues on the workings of a protein implicated in most cancers.

The software parsed text in 60,000 research articles for clues to the behavior of enzymes called kinases that act on the protein, called p53, and regulate its behavior. It then listed other proteins mentioned in the literature that likely were undiscovered kinases. So far, seven in 10 of its predictions have been

correct.

In May of last year, researchers at Washington University in St. Louis used "powerful algorithms" developed by computer scientists at Brown University to assemble the most complete genetic profile yet of acute myeloid leukemia, Brown announced. The work was part of The Cancer Genome Atlas project, which aims to catalog the genetic mutations that cause cells to become cancerous. Doing that requires sequencing the entire genome of cancer cells and comparing it to the genome of healthy cells.

To learn more:
- read the announcement from Massachusetts General Hospital
- read the study abstract in *Science Translational Medicine*

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