Researchers take step toward bringing precision medicine to all cancer patients

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Researchers from the University of Michigan Comprehensive Cancer Center and Thermo Fisher Scientific have developed and tested a new tool that searches for the most common genetic anomalies seen in cancer. The assay demonstrates the ability to make gene sequencing easier over a large volume of samples.

"We have a lot of experience at the University of Michigan in applying sequencing in this area. One of the main challenges we've found is that doing the analysis is a major bottleneck. Our goal is to find a way to

make the process easier to scale to a larger volume," says Scott A. Tomlins, M.D., Ph.D., assistant professor of pathology and urology at the University of Michigan Medical School.

Tomlins is the senior author on a paper published in *Neoplasia* that describes the new assay, called the Oncomine Comprehensive Assay, a research use only test developed by Thermo Fisher Scientific.

The researchers sifted through a database of more than 700,000 tumor samples and identified the most common genetic variants across cancer types. They then filtered the list to include those variants associated with FDA-approved drugs, referenced in clinical guidelines, or associated with investigational therapies in clinical trials.

The researchers evaluated the panel on more than 300 tissue samples, including more than 100 that had also been tested by routine clinical genomic testing. The assay confirmed the previously identified genetic changes. It also identified additional relevant variants in the tissue samples.

The new assay completes sequencing more quickly and for less money than current sequencing platforms. It also can be used with a large range of tumor sample types, including small biopsies and archived tissue samples. In the future, this may mean that patients would not always need to undergo a fresh biopsy in order to identify a potential treatment strategy, as is currently necessary with more comprehensive sequencing approaches.

"One of the real challenges of personalized medicine is the idea that we're going to find a truly actionable target for every patient. What we're finding is that's not always the case, particularly when we look at samples from patients who have failed multiple lines of standard therapy," Tomlins says. "The future of personalized medicine will mean

knowing early in the disease course what genetic variant drives a patient's tumor. Then we would be able to put them on the best treatment path as soon as possible.

"The result of this study is that we can now help clinical researchers overcome challenges that had prevented the routine use of next-generation sequencing to identify and prioritize relevant gene variants," said study co-author Dan Rhodes, Ph.D., vice president of oncology strategy at Thermo Fisher Scientific. "As we have demonstrated, it is now possible to apply a highly scalable, targeted sequencing approach to detect relevant cancer variants, opening the door for routine clinical applications in the near future."

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