OHSU publishes huge cancer dataset to advance treatments for AML

Oct 17, 2018, 2:46pm PDT Updated: Oct 17, 2018, 2:50pm PDT
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An OHSU Knight Cancer Research Institute team has published the largest and most comprehensive cancer dataset of its kind, with a goal of accelerating treatments for a rare form of leukemia.

It took researchers more than five years to assemble 672 cancer cell samples from 562 patients.

The samples are from patients with acute myeloid leukemia, or AML, which has a survival rate of only 25 percent beyond five years for newly diagnosed patients. AML isn’t a single disease either, making the search for a cure particularly difficult. The standard of care hasn’t changed in 40 years, according to OHSU.

OHSU is part of a multi-institution collaboration called the Beat AML initiative, sponsored by the Leukemia & Lymphoma Society. Altogether, 11 academic medical centers contributed to the dataset.

The goal is to understand the genomic sequencing and molecular make-up of the samples and how tumors respond to different drugs, said Jeff Tyner, associate professor of cell, developmental and cancer biology in the OHSU School of Medicine and researcher with the institute.

“Our ultimate goal to get new and better therapies to patients,” Tyner said. “A lot of predictions have been made in this dataset about certain therapies that might work
better. We hope there will be clinical trials. Already, we’re starting to see that. I hope that the dataset being out there publicly will allow others to use it in other ways we haven’t thought to do. We hope it will stimulate people to dig into it.”

The clinical information sets the dataset apart from others that were previously published, Tyner said. It can be used to see if a particular gene mutation corresponds with certain drug sensitivities.

OHSU also developed a web browser to help researchers who don’t have advanced computational skills navigate the vast dataset called the Vizome.

“The flood of high throughput, multi-dimensional data has the potential to overwhelm scientists and clinicians, isolating them from knowledge discovery,” said Shannon McWeeney, professor and head of bioinformatics and computational biology, who led development of Vizome.

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