MedicalXpress

How genomic sequencing may be widening racial disparities in cancer care

August 18 2016

Credit: University of Michigan Health System

As scientists learn more about which genetic mutations are driving different types of cancer, they're targeting treatments to small numbers of patients with the potential for big payoffs in improved outcomes.

But even as we learn more about these driver mutations, a new study suggests the science might be leaving racial and ethnic minorities behind.

"Even when studies have a reasonable 'relative' representation of racial and ethnic minorities, the overall 'absolute' number of minorities examined may not be enough to detect small differences in the cancer's genome," says Daniel Spratt, M.D., assistant professor of radiation oncology at the University of Michigan Medical School.

Studies such as The Cancer Genome Atlas project are discovering uncommon genetic mutations in small percentages of patients. This knowledge had led to new cancer treatments targeting these mutations, which has improved outcomes among patients with targetable mutations.

"If you're using this data to identify new mutations and develop new drugs targeting those mutations, then we need to know what mutations are present in patients of different races. Otherwise, we may be unintentionally widening disparities," Spratt says.

For a study published in *JAMA Oncology*, Spratt and colleagues looked at tumor samples studied as part of The Cancer Genome Atlas, a federally funded project to understand the molecular characterization of various cancer types.

The TCGA samples, from 10 different cancer types, were somewhat racially diverse. About 12 percent were African-American, which matches the U.S. population. Only 3 percent were Asian, slightly lower than 5 percent of the overall population, and only 3 percent were Hispanic, much less than 16 percent of the overall population.

But then they looked at the actual number of tumor samples from minorities. Of 5,729 samples, 660 were African-American, 173 were Asian and 149 were Hispanic, compared with 4,389 from white patients.

Researchers analyzed these numbers and determined that there were not enough samples from any minority group to identify a mutation that

would occur in 5 percent of those patients. On the other hand, there were enough samples in nearly every tumor type to detect a mutation occurring in 5 percent of white patients.

Eliminating the noise

What makes it complicated is that all cancers have some mutations in their DNA. But that background noise is not necessarily what fuels a cancer. Without enough samples, researchers can't pick out the dangerous mutations from the background noise.

In many cases, the mutation impacts only a small percentage of patients. For example, only 3 percent of lung cancer patients have alterations in ALK. But multiple FDA-approved drugs exist to improve survival in these particular patients.

"In current practice, we do have drugs aimed at very infrequent alterations," Spratt says. "If we can't detect a mutation present at a lower frequency, we wouldn't be able to develop a treatment against it."

Many studies have demonstrated how cancer behaves differently in different racial and ethnic groups. It's also known that certain cancer types are more common or more aggressive among certain races.

For one example, about 50 percent of Asians with lung cancer have a mutation in EGFR. Studies show the drug gefitinib is effective only in patients with an EGFR mutation.

The study authors suggest more collaborative efforts including industry, government and academia are necessary to collect larger numbers of tumor samples from diverse racial and ethnic groups. As precision medicine becomes increasingly important in cancer treatment, identifying mutations will allow researchers to target and adjust clinical

trials.

More information: *JAMA Oncology*, DOI: 10.1001/gamaoncol.2016.1854