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Major gaps exist in patient understanding of genomic test results, Lung-MAP study shows

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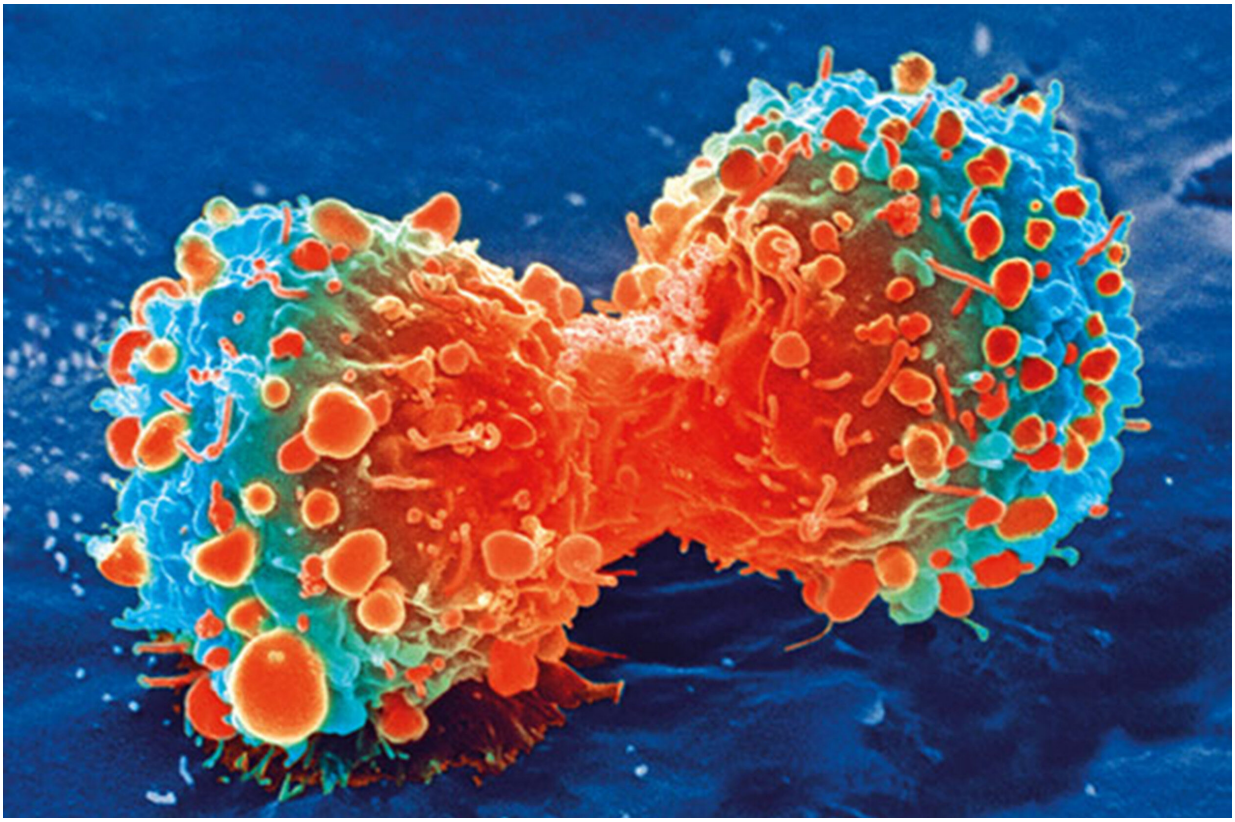

Cancer cell during cell division. Credit: National Institutes of Health

A majority of cancer patients don't understand key aspects of the genomic test results they receive as participants in biomarker-driven clinical trials, according to a first-of-its-kind pilot study conducted under

the Lung Cancer Master Protocol (Lung-MAP).

In a September 9 presentation at the World Conference on Lung Cancer in Barcelona, Lung-MAP investigator Joshua A. Roth, Ph.D., MHA will report results of his research conducted as part of Lung-MAP, the first lung cancer precision medicine trial supported by the National Cancer Institute, (NCI) part of the National Institutes of Health (NIH).

Roth, an assistant member of the Hutchinson Institute for Cancer Research Outcomes (HICOR) at the Fred Hutchinson Cancer Research Center, said most patients in his study showed serious gaps in knowledge about the potential uses of gene sequencing results provided in Lung-MAP and other precision medicine trials. In biomarker-driven cancer trials, patients receive genomic testing that detects DNA mutations in cancer cells, known as somatic mutations, which are typically found in tumor tissue samples. Precision trials may also include germline testing, which detects inherited DNA mutations, changes typically detected in blood or saliva.

Both kinds of genetic information are cornerstones of the precision medicine revolution in cancer research. This "precision" approach uses patients' genetic information to match them to a trial treatment that is more likely to be effective—extending or improving their lives and sparing them from potentially costly and painful treatments that aren't likely to improve their health.

Among the 123 participants who took part in a 38-item telephone survey devised by Roth, 86 percent correctly knew that their test results would be used to select their treatment regimen on the Lung-MAP trial. Another 83 percent also reported that they received enough information about their tests to understand the benefits of enrolling in the trial.

In Lung-MAP, patients receive somatic testing of mutated cells found in

their cancer tumor. They do not get germline testing for inherited mutations. In Roth's survey, patients were asked about both kinds of tests. Only 9 percent correctly knew that the somatic testing they had could not predict if a family member was at increased risk of getting cancer. And only 12 percent correctly knew that their results can't predict their own increased risk of getting other diseases.

"Given the public conversation about precision medicine, and the sharp increase in biomarker-driven cancer clinical trials, it's clear that lot of people don't really understand these complex trials and the testing that drives them," Roth said. "We need to learn more about the public's knowledge gaps so we can fill them."

Roth's study is the first to investigate the attitudes on tumor genetic testing in cancer clinical trials. He plans to analyze additional findings from his Lung-MAP study and present those at the 2020 American Society of Clinical Oncology Annual Meeting, held every spring in Chicago.

Lung-MAP is the first major NCI cancer trial to test multiple treatments, simultaneously, under one "umbrella" design. Lung-MAP is also a groundbreaking public-private partnership, one that includes the National Cancer Institute and its National Clinical Trials Network (NCTN) including SWOG Cancer Research Network, Friends of Cancer Research, the Foundation for the National Institutes of Health (FNIH), Foundation Medicine, pharmaceutical companies which provide their drugs for the study, and several lung cancer advocacy organizations.

Provided by SWOG Cancer Research Network