Medical Xpress

Broad genetic testing for advanced lung cancer may not improve survival

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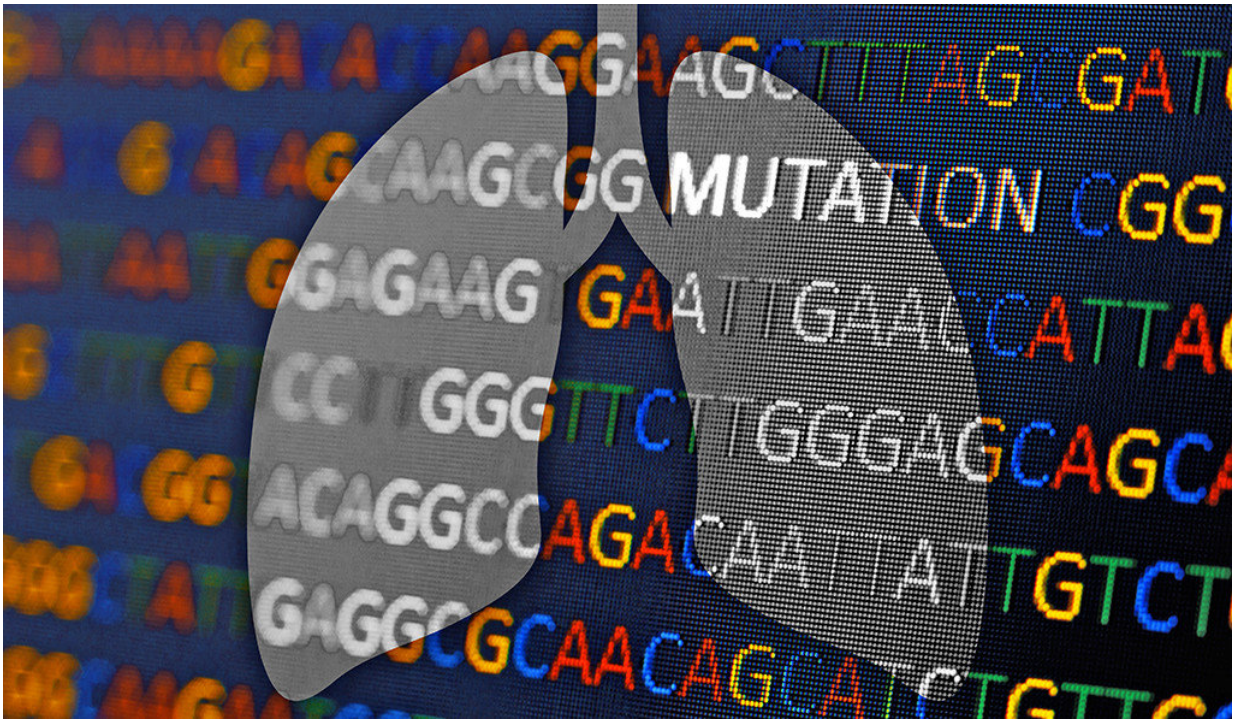

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Testing for dozens of genetic mutations in tumors of patients with a common form of advanced lung cancer did not appear to improve survival compared to routine genetic testing, a study led by Yale Cancer Center (YCC) scientists has found. The research was published in *JAMA*.

Broad-based genomic sequencing (BGS) evaluates numerous genes to identify mutations in tumors of patients with advanced non-small cell lung cancer. If a mutation is found and a drug exists to target the mutation, BGS can help clinicians personalize and treat the disease. However, questions remain about how broad-based testing, which can be costly, compares to more routine testing that focuses on one or two established, treatable genetic mutations.

Researchers analyzed data from Flatiron Health of more than 5,000 patients with advanced non-small cell lung cancer that were treated in a community oncology clinic. The researchers identified patients who received either BGS testing, or routine testing for alterations in two specific genes, EGFR or ALK. They determined how frequently the BGS testing identified specific mutations that guided the choice of therapy and compared overall survival rates for the patients receiving BGS with those receiving routine testing.

The research team found that among patients who received broad-based testing, very few also received a targeted treatment as a result. "The broad-based testing only identified genetic mutations and informed treatment decisions a small proportion of the time, and it's not clear whether the treatments that were provided on the basis of these mutations actually lead to better outcomes," said Cary Gross, M.D., director of Yale's Cancer Outcomes, Public Policy and Effectiveness Research Center (COPPER), professor of medicine, Yale School of Medicine and senior author.

Compared to patients who received routine tests, the BGS group did not have improved survival in the short or long term. "These results could be due to limited targeted therapies at the time period the study was conducted, lack of clinical trial access, cost of new cancer drugs, or insurance denials of off-label drug use," adds lead author Carolyn J. Presley, M.D., who was part of the study team at Yale, but now serves as

a medical oncologist and assistant professor at The Ohio State University. "Our ability to sequence has outpaced our ability to get targeted therapies to patients."

The study also shows while BGS testing is covered by Medicare, the costs of such testing can run thousands of dollars. Even when mutations are identified, there may not be an approved drug available to target them, the researchers said.

However, the study authors note that drug availability and targeting is changing and testing can still have an important role. "Our study shows so many issues that exist with testing, but over the past decade, with science moving so quickly, therapies for patients with advanced non-small cell lung cancer have improved substantially," adds co-author Roy S. Herbst, M.D., chief of Medical Oncology at YCC and Smilow Cancer Hospital. "With more approved availability of new drugs at community sites and clinical trials available at medical institutions like YCC and YCC care centers throughout Connecticut, we are now better able to match more patients with the right drugs and have better outcomes. I hope and expect when this study is repeated in a few years we will see improved outcomes and we now have a baseline from which to build.

Gross adds, "To ensure that new discoveries are able to fulfill their promise, our results suggest further evidence is needed to inform the care of patients with a variety of specific genetic alterations in their tumors before widely disseminating these new paradigms into clinical practice."

More information: Carolyn J. Presley et al. Association of Broad-Based Genomic Sequencing With Survival Among Patients With Advanced Non–Small Cell Lung Cancer in the Community Oncology Setting, *JAMA* (2018). DOI: 10.1001/jama.2018.9824

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