Adding genetic information to risk profile of smokers improves adherence to lung cancer screening

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Researchers have found that adding genetic information to a former or current smoker's clinical risk profile results in a reclassification of their risk for lung cancer in about one in four patients. Preliminary findings from their lung cancer screening feasibility study also suggests that those whose genetic and clinical risk placed them in the highest risk category were more likely to adhere to follow-up computed tomography (CT) scans during screening.

The results of this study, conducted at El Camino Hospital in Mountain View, CA, follows on the heels of the National Lung Screening Trial which enrolled more than 53,000 current or former heavy smokers between the ages of 55 and 74. Those in the CT screening arm of this trial had a 20 percent lower risk of dying from lung cancer if they underwent an annual CT scan of their lungs compared to annual chest x-rays.

Implementation of a successful CT screening program requires that eligible participants be screened in a timely manner. While past studies have demonstrated that participation in lung cancer screening is improved in the context of risk assessment, this is the first study to report on the effects of gene-based risk assessment and screening adherence.

"Outside clinical trials, adherence to screening is typically 50 to 60

percent," said lead investigator Robert Young, MD, PhD, associate professor of medicine and molecular genetics, at the University of Auckland, New Zealand, who will present the results at ATS 2015, May 15 to 20 in Denver. "What our study shows is that risk assessment using personal genetic information is not only of great interest to screening participants, it appears to improve their compliance with screening."

In the community-based study (called REACT), all 157 screening participants agreed to and underwent gene-based risk testing for lung cancer. Young and his colleagues then assigned each participant to one of three risk categories—very high, high and moderate—by combining genetic data with the participant's age, family history of lung cancer and whether they reported having chronic obstructive pulmonary disease, or COPD.

The genetic component represents the net effect of 20 single nucleotide polymorphisms (SNPs) that have been implicated in the development of lung cancer by Dr. Young and other research groups. When present, these SNPs confer either an increased risk of lung cancer (12 susceptibility-related SNPs) or a reduced risk (8 protective-related SNPs). With this personal genetic information, the researchers reclassified 28 percent of the participants: 22 percent were re-assigned to a higher risk category and 6 percent to a lower one.

Overall adherence to the CT screening follow-up protocol was 63 percent. As expected, adherence was greatest in the very high risk category: 71 percent. Those in the high and moderate risk categories both had 52 percent adherence. The difference was significant (71% vs 52%, OR=2.3, P