

Researchers develop new method to test for lung cancer

April 1 2008

Researchers from Boston University School of Medicine have developed a new “clinicogenomic model” to accurately test for lung cancer. The model combines a specific gene expression for lung cancer as well as clinical risk factors. These findings currently appear on-line in the journal *Cancer Prevention Research*.

Lung cancer is the leading cause of cancer death in the United States and the world, with more than one million deaths worldwide annually. Eighty-five to 90 percent of subjects with lung cancer in the United States are current or former smokers with 10 to 20 percent of heavy smokers developing this disease.

A previous study by the same researchers reported a gene expression biomarker capable of distinguishing cytologically normal large airway epithelial cells from smokers with and without lung cancer. However, the biomarker has limited sensitivity depending on the stage and the location of the cancer.

Studying current and former smokers undergoing bronchoscopies for suspicion of lung cancer, the researchers compared the likelihood of the subjects having lung cancer using the biomarker, the clinical risk factors and a combination of the two -- clinicogenomic model. They found patients using the clinicogenomic model had increased sensitivity, specificity, positive value and negative predictive value of their cancer compared to the other methods.

“Our data suggests that the clinicogenomic model might serve to identify patients who would benefit from further invasive testing, thereby expediting the diagnosis and treatment for their malignancy,” said senior author Avrum Spira, MD, an assistant professor of medicine and pathology at Boston University School of Medicine.

According to the researchers, it is hoped this prediction model will expedite more invasive testing and appropriate therapies for smokers with lung cancer as well as reduce invasive diagnostic procedures for individuals without lung cancer.

Source: Boston University

Citation: Researchers develop new method to test for lung cancer (2008, April 1) retrieved 26 April 2024 from <https://medicalxpress.com/news/2008-04-method-lung-cancer.html>

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