?esearchers identify gene variations that may help predict cancer treatment response

9 August 2013

Researchers at the Moffitt Cancer Center have identified four inherited genetic variants in non-small cell lung cancer patients that can help predict survival and treatment response. Their findings could help lead to more personalized treatment options and improved outcomes for patients.

The researchers analyzed DNA sequence variations in 651 non-small cell lung cancer patients, paying close attention to 53 inflammation-related genes. They found that four of the top 15 variants associated with survival were located on one specific gene (TNFRSF10B). In the study, these variants increased the risk of death as much as 41 percent. The researchers also found that patients with these gene variations had a greater risk of death if their treatment plans included surgery without chemotherapy compared to patients who were treated with chemotherapy following surgery.

"There are few validated biomarkers that can predict survival or treatment response for patients with non-small cell lung cancer," said study lead author Matthew B. Schabath, Ph.D., assistant member of the Cancer Epidemiology Program at Moffitt. "Having a validated genetic biomarker based on inherited differences in our genes may allow physicians to determine the best treatments for an individual patient based on their unique genetics."

Lung cancer is the leading cause of cancer-related deaths in the United States for both men and women. Additionally, non-small cell lung cancer represents more than 80 percent of lung cancer diagnoses.

"Non-small cell lung cancer has an extremely poor five-year survival rate. Only about 16 percent of all patients survive for five years and tragically, only about four percent of patients with late stage disease live longer than five years," explained Schabath. "Part of the difficulty in treating lung cancer is the genetic diversity of patients and their tumors. Using a personalized medicine approach to match the best treatment option to a patient based on his or her genetics will lead to better outcomes."

The researchers noted that there has been no published data examining the association of these four specific variants on cancer risk or outcome, although studies have reported associations with other gene variants in the same gene family as TNFRSF10B.

The study can be found in the July issue of *Carcinogenesis*.

More information: carcin.oxfordjournals.org/cont … rcin.bgt244.abstract

Provided by H. Lee Moffitt Cancer Center & Research Institute