Researchers find malignancy-risk gene signature for early-stage non-small cell lung cancer

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A malignancy-risk gene signature developed for breast cancer has been found to have predictive and prognostic value for patients with early stage non-small cell lung cancer. The advancement was made by researchers at Moffitt Cancer Center in Tampa, Fla., who published their study results in a recent issue of the *Journal of the National Cancer Institute*.

According to corresponding author Dung-Tsa Chen, Ph.D., associate member with the Moffitt Biostatistics program, non-small cell lung cancer (NSCLC) accounts for 80-90 percent of all lung cancers. Patients with NSCLC have a 30-50 percent relapse rate after surgery and a 40-70 percent five-year survival rate. Although adjuvant chemotherapy (ACT) has increased survival rates and has become standard treatment for NSCLC, a proportion of patients do not derive any benefit from it.

"Better prognostic tools have been needed to identify both patients with a high probability of relapse and those who would benefit from adjuvant chemotherapy," said Chen.

He added that the Moffitt researchers are confident that their newly tested malignancy-risk gene signature for NSCLC will provide that tool because their malignancy-risk gene signature is a proliferative gene signature, one associated with both cancer risk and progression.

According to the researchers, their findings suggest a "transferability" of the malignancy-risk gene signature between breast cancer and NSCLC, a "unique feature not seen in other gene signatures derived for various tumor types."

"To the best of our knowledge, our study is the first to show a high consistency of the gene signature on both breast cancer and NSCLC," said Chen. "The gene signature demonstrated a statistically significant association with overall survival and other clinical predictors in NSCLC."

Originally, the malignancy-risk signature gene was designed to distinguish between normal breast tissues and breast cancer tissues by identifying abnormal molecular structure. The Moffitt research team further applied the signature to tissue samples from 442 NSCLC patients in the Director's Challenge Consortium for the Molecular Classification of Lung Adenocarcinoma.

"Additionally, the malignancy-risk gene signature has demonstrated the potential to identify early-stage NSCLC patients who would be likely to benefit from adjuvant chemotherapy," explained Chen. "This malignancy-risk gene signature may provide an additional tool to help identify a subset of patients at high-risk for low overall survival and who may benefit from ACT."

Study results revealed a predictive feature of the malignancy-risk gene signature with an ability to predict overall survival in NSCLC patients. Further, the malignancy-risk gene signature was able to consistently distinguish between low and high malignancy risk groups and correlate the groups by good to poor overall survival rates.

In the future, the researchers plan on carrying out a similar but large study using patient-donated tissue samples from Moffitt's Total Cancer

Care program (www.moffitt.org/totalcancercare), a partnership between patients, doctors and researchers to improve all aspects of cancer prevention and care. Patients participate by donating information and tissue. Researchers use the information to learn about all issues related to cancer and how care can be improved.

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