MicroRNA study provides biomarker for survival in small cell lung cancer

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Researchers at the Translational Genomics Research Institute (TGen), the Van Andel Research Institute (VARI) and the Virginia G. Piper Cancer Center at Scottsdale Healthcare have discovered a biomarker that could help in the treatment of patients with an aggressive type of lung cancer.

Using a particular biomarker, researchers might better predict which patients with small cell lung cancer are resistant to existing drug therapies, and which ones could benefit from new therapies tailored to their specific needs, according to a scientific paper published today in the Journal of Thoracic Oncology.

"There is a need for predictive biomarkers that can aid investigators in designing future clinical trials, to help identify treatments that might be effective for these patients who most likely will be resistance to existing drug therapies, " said Dr. Glen J. Weiss, the paper's senior author and Director of Thoracic Oncology at TGen Clinical Research Services at Scottsdale Healthcare. TCRS is a partnership between TGen and Scottsdale Healthcare that helps bring new therapies quickly to patients at the Virginia G. Piper Cancer Center in Scottsdale.

Nearly 220,000 Americans are diagnosed each year with lung cancer, which is by far the leading cause of cancer death in the U.S., annually killing nearly 160,000 patients.

Of all lung cancer patients, an estimated 33,000 are diagnosed with

SCLC. This is a particularly aggressive disease that usually goes undetected until it is in an advanced stage and treatment options are limited. More than 95 percent of SCLC patients eventually die from the disease.

Researchers from TGen, VARI and the Virginia G. Piper Cancer Center at Scottsdale Healthcare focused on identifying microRNAs, which are single-stranded RNA molecules that regulate how genes and proteins control cellular development. Because microRNAs are so resilient, they are relatively easy to detect in tumor tissue and blood, which is often a limitation for other biomarkers.

"VARI provided bioinformatics support assembling all the different types of data into a cohesive data set for analysis to help identify the miRNA that play a role in the survival of the lung cancer patients," said Dr. David Cherba, a VARI Bioinformatics Scientist.

Researchers profiled 34 tumor samples from patients with a median age of 69. They analyzed each tumor's microRNAs, searching for those that might be associated with cancer survival.

They identified three microRNAs associated with SCLC. But one in particular, identified as miR-92-2*, was "significantly" linked to survival, the paper said.

This microRNA could be used in two significant ways:

- As a predictive biomarker in the development of new treatments for those SCLC tumors that prove to be de novo chemoresistant — possessing properties that render them inherently resistant to existing drug therapies.

- As prognostic biomarkers in the screening of SCLC patients and the design of clinical trials better tailored to their prognosis.

"Our results demonstrate that higher tumor miR-92a-2* levels are associated with chemoresistance and with decreased survival in SCLC patients," said the paper titled MicroRNA 92a-2*, a Biomarker Predictive for Chemoresistance and Prognostic for Survival in Small Cell Lung Cancer Patients.

This was one of the first scientific papers published since the completion of the TGen-VARI alliance and affiliation agreement, announced in February.

"The collaboration that occurred on this project highlights the synergies created by the VARI-TGen alliance," said Dr. Craig Webb, a VARI Senior Scientific Investigator.

Dr. Jeffrey Trent, President and Research Director for TGen and VARI, said the new discoveries could have profound implications for the future of medicine.

"This advanced technology is exciting because of how these microRNA biomarkers could lead to improvements for patients. Hopefully, this will translate to new treatments and improved survival," Dr. Trent said.

The next step in this research should be to attain further validation by analyzing additional independent samples, the paper concludes.

Provided by The Translational Genomics Research Institute

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