First whole-genome lung cancer study set for conference

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A first-of-its-kind study of a patient with lung cancer who never smoked will be presented today by TGen and the Virginia G. Piper Cancer Center at Scottsdale Healthcare at the 14th World Conference on Lung Cancer, July 3-7 in Amsterdam.

Researchers for the first time sequenced the entire DNA and RNA of a patient with metastatic adenocarcinoma of the lung, said Dr. Glen Weiss, the first author of the study, which will be published in a special supplement of the Journal of Thoracic Oncology. Dr. Weiss also is Director of Thoracic Oncology at Virginia G. Piper Cancer Center Clinical Trials, a partnership between TGen and Scottsdale Healthcare that treats cancer patients with promising new drugs.

The patient is a 61-year-old woman who never smoked whose lung cancer had entered her bloodstream and spread to other parts of her body. She had been treated with several types of chemotherapy.

The study, Advanced Never Smoker Adenocarcinoma of the Lung: Report of paired normal and tumor whole genome and transcriptome sequencing, will be presented at the conference today, July 6. The study used Whole Genome Sequencing (WGS), also called Next-Generation Sequencing (NGS), to look at all 3 billion chemical bases of the patient's normal, as well as the patient's tumor, DNA.

The study went further by examining the normal and tumor RNA for whole transcriptome sequencing, which can reveal the possible defects in

how proteins are synthesized. This provided an even more intricate view of the tumors biological make up and what might have led to her cancer.

"Evidently, this is very exciting. Next-Generation Sequencing now offers us the ability to survey the global landscape of cancer," said Dr. John Carpten, Director of TGen's Integrated Cancer Genomics Division and senior author of the presentation.

The results of the patient's sequencing were discussed with her treating oncologist and may be used along with other information to help decide the best course of future treatment.

A review of well-characterized cancer-related genes found that a mutation resided in the TP53 gene, a mutation in the tumor (one base change in the genetic code), and that the mutation was always present in both the DNA and RNA. Such a mutation can halt the creation of tumor suppressor genes and result in the generation of a tumor. Interestingly, the cancer specimen showed no loss of heterozygosity (LOH), in which one side of the DNA's chromosome becomes inactive because of a mutation.

"This observation highlights the complexity of cancer and how different genetic mechanisms can alter a gene. This novel finding would not have been readily determined without the combined DNA and RNA integration approach," said Dr. David Craig, Associate Director of TGen's Neurogenomics Division, and also a senior author of the presentation.

Dr. Weiss said these investigative techniques will be used more often to pinpoint the origins of disease.

"In the future, with improved infrastructure and decreased costs, we anticipate that using NGS techniques will become more commonplace,"

Dr. Weiss said. "NGS has the potential to identify unique tumor aberrations at an unprecedented depth."

The conference is sponsored by the International Association for the Study of Lung Cancer (IASLC), which hosts a meeting every two years.

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