Preliminary findings about whole-genome sequencing of triple-negative breast cancer presented

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Because cases of Triple-Negative Breast Cancer (TNBC) are so genetically different, whole-genome sequencing is needed to detect the subtle molecular differences that might point to specific treatments for individual patients.

Dr. John Carpten, Ph.D., head of the Integrated Cancer Genomics Division at the Translational Genomics Research Institute (TGen), will deliver that message along with other preliminary findings about whole-genome sequencing of TNBC at the American Association for Cancer Research (AACR) Annual Meeting 2012, March 31-April 4, in Chicago.

"Every TNBC tumor we interrogate is genomically unique," said Dr. Carpten, who is part of an unprecedented and ongoing clinical trial involving the whole-genome sequencing of 14 TNBC tumors. Whole-Genome Sequencing, spells out all of the nearly 3 billion DNA molecules found in human cells, allowing unprecedented scrutiny of patients' genetic codes.

Dr. Carpten will co-chair an AACR panel, Concepts and Challenges in Bringing Next-Generation Sequencing to the Clinic. Dr. Stephen B. Gruber, M.D., Ph.D., M.P.H., and the H. Marvin Pollard Professor of Internal Medicine at the University of Michigan will co-chair. Other panelists include Giselle L. Sholler of the Van Andel Research Institute and Victor E. Velculescu of the Johns Hopkins Kimmel Comprehensive

Cancer Center. The panel is set for 10:30 a.m. EDT April 2 at Chicago's McCormick Place convention center.

TNBC is unlike the nearly 80-90 percent of other breast cancers, which are driven by the hormones estrogen (1), progesterone (2), or too many receptors of the HER2 gene (3). Testing negative for all three means the cancer is "triple-negative."

Estrogen- and progesterone-driven breast cancers can be treated with hormonal therapy, while the drug Herceptin (trastuzumab) targets HER2 receptors.

But there have been no sure-shot treatments developed for TNBC, mainly because these cancers display a startling lack of uniformity, or heterogeneity, in their molecular make up.

"Whole-genome sequencing is enabling us to zero in on the specific challenges presented with each individual TNBC tumor, advancing a 'personalized medicine' approach that helps guide the treatment of each patient," said Dr. Carpten.

Based on mutations uncovered by sequencing, physicians recommend that their patients enter treatment protocols for either existing drugs or for new agents being evaluated in pharma-sponsored clinical trials.

Investigators are sequencing germline and tumor DNA to identify genomic alterations including point mutations, insertions/deletions and structural events such as translocations. RNA sequencing also is performed on the tumors, along with tissue from age- and ethnicity-matched normal breast controls, to obtain insights on gene expression differences.

This clinical study is being conducted in collaboration with US Oncology

Research, with support from Life Technologies Corporation.

"This is among the largest studies of a single tumor type in which whole genome sequencing is being used to identify potential options for targeted treatment," said Ronnie Andrews, president of medical sciences at Life Technologies Corporation. "We are very pleased to help support this study, which is providing key insights into how sequencing can best be used in the clinic."

The theme of the 2012 AACR meeting is "Accelerating Science: Concept to Clinic," reflecting the strides and breakthroughs being made by cancer researchers and the impact they are making on global health. The conference will emphasize the synergy between basic, clinical and translational research that lead to effective cancer therapies and prevention strategies.

Provided by The Translational Genomics Research Institute