

First genome sequencing clinical trial for triple negative cancer points to new treatments

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Initial results from an ongoing clinical trial, the first designed to examine the utility of whole-genome sequencing for triple negative breast cancer, were reported today during the CRTC-AACR San Antonio Breast Cancer Symposium.

The results indicate activation of targets not previously associated with triple negative disease and could point toward new [treatment strategies](#). Based on [mutations](#) uncovered by sequencing, physicians recommended the women enter treatment protocols for either existing drugs or new agents being evaluated in pharma-sponsored [clinical trials](#).

Triple negative [breast tumors](#), which make up nearly 20 percent of breast cancers, do not respond to treatment with targeted therapies such as [Herceptin](#)[®] (trastuzumab).

Of eleven tumors sequenced to date, each was genomically unique, but commonalities were observed. Some patients displayed amplified genes in the RAS pathway; one patient had amplification of the BRAF oncogene, as well as activation of a growth pathway known as the MEK/AKT pathway. This patient displayed an impressive response to a MEK/AKT inhibitor currently in a phase I clinical study.

"Those results are quite striking considering that these are women with advanced disease," said Joyce O'Shaughnessy, M.D., who presented the

data. "If MEK/AKT activation is found to be present in a substantial fraction of triple negative patients, inhibitors of this pathway could prove a significant tool in fighting this disease."

Dr. O'Shaughnessy is medical director and co-chair of the [Breast Cancer Research Committee](#), US Oncology Research; a practicing oncologist with Texas Oncology; and the Celebrating Women Chair of Breast Cancer Research at Baylor Charles A. Sammons Cancer Center.

"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 John Carpten, Ph.D., director of the Integrated Cancer Genomics Division at the Translational Genomics Research Institute (TGen). "As the field of genomic medicine matures, this study is sure to provide key early insights into how sequencing can best be utilized in the clinic."

More information: The study is titled "Next Generation Sequencing Reveals Co-Activating Events in the MAPK and PI3K/AKT Pathways in Metastatic Triple Negative Breast Cancers."

Provided by The Translational Genomics Research Institute

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