

Study uncovers possible genetic markers in breast cancer that spreads to the brain

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The Translational Genomics Research Institute (TGen) has uncovered possible genetic origins of breast cancer that spreads to the brain, according to a first-of-its-kind study published in the scientific journal *PLOS ONE*.

The compendium of genetic targets uncovered by TGen now can be used to identify potential new methods of diagnosis and new drug therapies for the estimated 45,000 patients in the U.S. each year whose cancer spreads from the breast to the brain.

The 3-year study is significant since these patients currently have few treatments options—surgery and radiation—and they usually are ineligible for clinical drug trials. Their prognosis is poor, with fewer than 2 percent surviving more than two years

"This is really a significant problem and a huge unmet need. We now want to dig deeper and uncover more specific genomic links and study new ways to treat these patients so we can improve outcomes," said Dr. Bodour Salhia, an Assistant Professor in TGen's Integrated Cancer Genomics Division and the study's lead and co-senior author.

"In this study, we see that breast-brain metastasis retain many features found in primary breast cancer, but we still need to better understand the differences," said Dr. Salhia. "Knowing the key drivers of brain metastasis may lead to preventive measures, as well."

After lung cancer, breast cancer is the second most common cancer that spreads to the brain. Chemotherapy generally has not been used to treat brain cancer, because of the blood-brain barrier that exists between the bloodstream and the cerebrospinal fluid surrounding the brain. However, some small molecule drugs can cross this barrier and form the basis of targeted therapies.

The overall goal of the TGen study was to look at genomic and epigenomic events to understand the causes of [breast cancer](#) brain metastatic lesions, and identify potential new therapeutic targets.

The TGen team performed deep genomic profiling, integrating gene copy number, gene expression and DNA methylation datasets on a collection of 35 breast-[brain](#) metastases samples. The study, Integrated Genomic and Epigenomic Analysis of Breast Cancer Brain Metastasis, published Jan. 29, is the first of its kind to incorporate all of those avenues of inquiry in the study of this disease.

Some of the common genetic alterations identified in the study were gains and losses in chromosome 8, as well as cell proliferation and cell-cycle progression—key mechanisms of cancer caused by genetic alterations—linked to the genes AURKA, AURKB and FOXM1.

"This groundbreaking study sets the stage for more exacting research, using the latest genomic technologies and aimed at developing new therapies that could help the tens of thousand of patients who urgently need our help," said Dr. Nhan Tran, an Associate Professor of TGen's Cancer and Cell Biology Division and the study's other co-senior author.

Provided by The Translational Genomics Research Institute

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