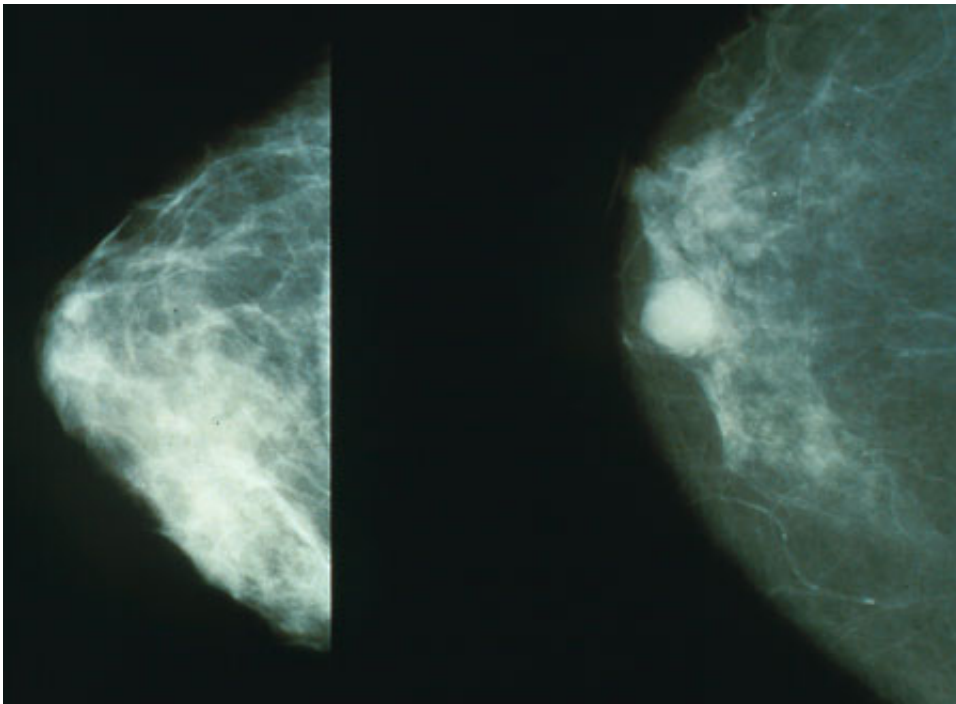


Researchers identify biomarkers of response to treatment in invasive breast cancer

December 8 2016



Mammograms showing a normal breast (left) and a breast with cancer (right).
Credit: Public Domain

Why do some breast cancers respond to treatment while others resist it? A study led by researchers at the University of North Carolina Lineberger Comprehensive Cancer Center may provide insight into this important question.

The [researchers](#) report at the San Antonio Breast Cancer Symposium

that they have identified biomarkers they believe can be used as part of a larger model to predict how patients with HER2-positive operative breast cancer will respond to the targeted treatment trastuzumab, commercially known as Herceptin, and chemotherapy.

"We're trying to find biomarkers for resistance to trastuzumab treatment and chemotherapy," said the study's first author Maki Tanioka, MD, PhD, a postdoctoral research associate at UNC Lineberger. "What's the cause of response? What's the cause of resistance? That's what we are trying to identify in this genomic study."

Tanioka and his colleagues analyzed multiple biologic features of cancer cells from 213 patients treated for HER2-positive breast cancer through a National Cancer Institute cooperative group clinical trial, CALGB 40601. The biologic features included multiple kinds of genetic information such as DNA mutations, DNA copy number and RNA gene expression data. The researchers found that certain gene signatures, and either having too many, or too few, of certain genes were predictive of whether patients responded to treatment, and that combining those two features was the most effective method of predicting response.

Examining features like mutations, amplifications or deletions of genes in tumor cells, the overall subtype of the tumor, as well as indicators of immune responses helped the researchers predict response. The researchers also determined that amplification of a specific chromosome, and a particular gene called MAPK14 on that chromosome, may be a predictor of sensitivity to treatment, while deletions of other genes predicted resistance.

The researchers say the next step is to identify another set of data to validate and broaden their findings.

"HER2-positive [breast cancer](#) is genomically heterogeneous," Tanioka

said. "Therefore, we need a model that incorporates all these different [features](#). We are actively seeking a set of patient data that we can use to validate the biomarkers we have identified so we can create a comprehensive predictive model of response to allow us to better tailor [treatment](#)."

Provided by UNC Lineberger Comprehensive Cancer Center

Citation: Researchers identify biomarkers of response to treatment in invasive breast cancer (2016, December 8) retrieved 23 April 2024 from <https://medicalxpress.com/news/2016-12-biomarkers-response-treatment-invasive-breast.html>

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