Breast cancer study confirms importance of multigenerational family data to assess risk

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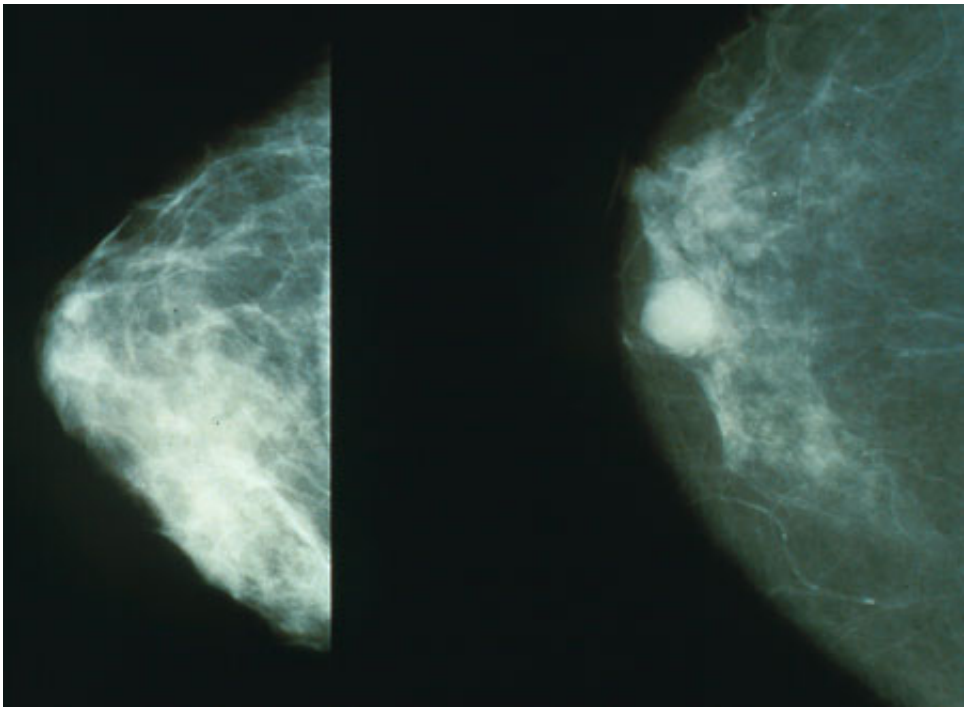

Mammograms showing a normal breast (left) and a breast with cancer (right). Credit: Public Domain

A team of researchers led by Columbia University Mailman School of Public Health Professor Mary Beth Terry, Ph.D., evaluated four commonly used breast cancer prediction models and found that family-history-based models perform better than non-family-history based models, even for women at average or below-average risk of breast cancer. The study is the largest independent analysis to validate four

widely used models of breast cancer risk and has the longest prospective follow-up data available to date. The findings are published online in *The Lancet Oncology*.

Dr. Terry and colleagues used the Breast Cancer Prospective Family Study Cohort composed of 18,856 women from Australia, Canada, and the U.S. without breast cancer, between March 1992 and June 2011. Women between the ages of 20 to 70 were selected for the study who had no previous history of bilateral prophylactic mastectomy or ovarian cancer, and whose family history of breast cancer was available. The researchers calculated 10-year risk scores for the final cohort of 15,732 women, comparing four breast cancer risk models which all vary in how they use information regarding multi-generational and genetic information as well as non-genetic information: the Breast and Ovarian Analysis of Disease Incidence and Carrier Estimation Algorithm model (BOADICEA), BRCAPRO, the Breast Cancer Risk Assessment Tool (BCRAT), and the International Breast Cancer Intervention Study model (IBIS). A second analysis was conducted to compare the performance of the models after 10 years based on the mutation status of the BRCA1 or BRCA2 genes.

The results showed that the BOADICIA and IBIS models which have multigenerational family history data were more accurate in predicting breast cancer risk than the other models. This held true even for women without a family history of breast and without BRCA1 and BRCA2 mutations. The other two models BRCAPRO and BCRAT models did not perform as well overall and in women under 50 years of age. The BCRAT model was well-calibrated in women over 50 years who were not known to carry deleterious mutations in the BRCA1 and BRCA2 genes. Of the 15,732 eligible women, 4 percent were diagnosed with breast cancer during the median follow-up of 11-plus years.

"Our study, which was enriched based on family history, was large

enough to evaluate model performance across the full spectrum of absolute risk, including women with the highest risk of cancer in whom accurate prediction is especially important," said Dr. Terry, who is a Professor of Epidemiology at the Columbia Mailman School, and the Herbert Irving Comprehensive Cancer Center. "Independent validation is particularly important to understand the utility of these models across different settings."

Breast cancer risk models are used to help inform decisions about primary prevention and increasingly, in screening programs, including when women should have mammographies. There are several different models to assess breast cancer risk, and they vary in how they take into account family history and genetics.

"Mathematical models can help estimate a woman's future risk of breast cancer. There are several available, but it is uncertain which models are the most appropriate ones to use. These findings might help provide better guidance to women with their decision-making on breast cancer screening strategies," says Dr. Robert MacInnis, who is a Senior Research Fellow in the Cancer Epidemiology and Intelligence Division at the Cancer Council, Victoria Australia and co-led the analyses with Dr. Terry.

"Our findings suggest that all women would benefit from risk assessment that involves collection of detailed family histories, and that risk models would be improved by inclusion of family history information including ages at diagnoses and types of cancer," said Dr. Terry.

More information: *The Lancet Oncology* (2019). DOI: 10.1016/S1470-2045(18)30902-1 , www.thelancet.com/journals/lan … (18)30902-1/fulltext