

NINE BREAST CANCER GENES THAT LEAD TO AGGRESSIVE BREAST CANCERS



Genes predict what kind of breast cancer will develop.

A [study](#) co-led by the National University Health System and the Genome Institute of Singapore revealed that certain genes not only increase the chances of a woman developing breast cancer, but also predict whether the cancers developed are more aggressive. In 8,852 breast cancer patients of Asian descent, the study team members found that carriers of mutations leading to a loss-of-function in any of nine breast cancer genes examined were more commonly diagnosed with high-grade tumours and breast cancers of the luminal B and triple-negative subtypes.

One in 13 women in Singapore will develop breast cancer in their lifetime. Close to 2,000 women are diagnosed with the disease every year, and over 400 die from it. These figures will continue to increase with our existing risk factors, compounded by our ageing population.

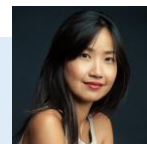
Early detection of breast cancers is known to save lives. Routine mammography screening (low-dose breast X-ray) is currently the most reliable tool for finding cancers at an early stage, when treatment is most successful. The knowledge of a person's risk of getting breast cancer can empower women to take charge of their breast health through regular checks and routine screening. This is especially crucial if they have breast cancer genes.

However, not all breast cancer genes are equal. The more well-known breast cancer genes are BRCA1 and BRCA2, made famous by celebrity Angelina Jolie's choice to remove both her breasts to reduce the likelihood of her developing the disease. As many as four out of five women carrying a harmful BRCA mutation will get breast cancer at some point in their lives. In addition, some breast cancers have "nicer" features which make them easier to treat, while others have characteristics that make them more deadly. The scientific community has shown that harmful mutations in several other genes (*ATM*, *CHEK2*, *PALB2*, *BARD1*, *RAD51C*, *RAD51D*, and *TP53*) are also highly predictive of which women in the population will develop breast cancer. The current study continues this line of research and pinpoints nine other breast cancer genes that not only increase the chances of a woman developing breast cancer, but also predict what type of breast cancer will develop.

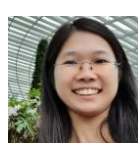
The breast cancer patients studied are recruited from the Singapore Breast Cancer Cohort study, which comprises six participating hospitals that collectively see over 70% of the breast cancer cases diagnosed in Singapore. Included in this study are also breast cancer patients recruited by collaborators from Malaysia and Korea.

The results from this study forms one of the components of building breast cancer profiles for individuals. Using established breast cancer risk calculators that take into account information from genes and self-reported questionnaires, the study team is leading a new BREast screening Tailored for HEr (BREATHE) study funded by the JurongHealth Fund. This pilot study identifies women at above average risk of developing the disease. Women predicted to be more likely to develop breast cancer are referred to specialists at study sites, and given breast health recommendations in addition to the prevailing screening guidelines. Overall, the BREATHE study will increase breast cancer awareness, education, and screening adherence.

"A person who is told that he or she has high blood pressure or high blood sugar is likely to make lifestyle changes to reduce the risk of developing stroke or diabetes. We hope to help women appreciate their individual level of breast cancer risk, so that women at high risk can consult breast specialists about interventions (i.e. what they can do to reduce their risks)."



Dr Li Jingmei, Group Leader of the Laboratory of Women's Health & Genetics, GIS



"Earlier detection of aggressive tumours at a lower stage may lead to less extensive treatment and potentially better quality of life."

Dr Ho Peh Joo, Research Associate at the Laboratory of Women's Health & Genetics, GIS