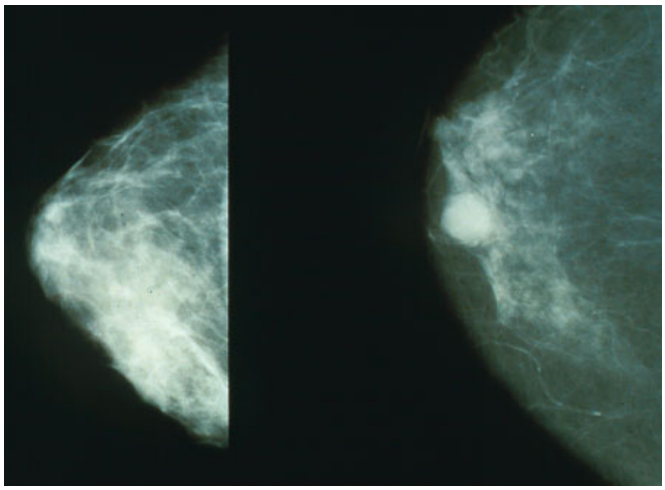
Fifteen new breast cancer genetic risk 'hot-spots' revealed

9 March 2015



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

Scientists have discovered another 15 genetic 'hot-spots' that can increase a woman's risk of developing breast cancer, according to research published today in *Nature Genetics*.

In a study funded by Cancer Research UK, scientists compared tiny variations in the genetic make-up of more than 120,000 women of European ancestry, with and without breast cancer , and identified 15 new variations - called single nucleotide polymorphisms (SNPs) - that are linked to a higher risk of the disease.

This new discovery means that a total of more than 90 SNPs associated with breast cancer have now been revealed through research.

On average, one in every eight women in the UK will develop breast cancer at some stage in their lives. The researchers estimate that about five per cent of women have enough genetic variations to double their risk of developing breast cancer - giving them a risk of approximately one in four. A much smaller group of women, around 0.7 per cent, have genetic variations that make them three times more likely to develop breast cancer, giving them a risk of around one in three. It's hoped that these genetic markers can be used to help identify high-risk women and could lead to improved cancer screening and prevention.

Study author Professor Doug Easton, professor of genetic epidemiology at the University of Cambridge, said: "Our study is another step towards untangling the breast cancer puzzle. As well as giving us more information about how and why a higher breast cancer risk can be inherited, the genetic markers we found can help us to target screening and cancer prevention measures at those women who need them the most.

"The next bit of solving the puzzle involves research to understand more about how genetic variations work to increase a woman's risk. And we're sure there are more of these variations still to be discovered."

The study was carried out by dozens of scientists across the world working together in the Breast Cancer Association Consortium, part of the Collaborative Oncological Gene-environment Study. Each of the genetic variations, identified through this study and other research, is known to raise a woman's risk of breast cancer by a small amount - but some people have lots of these variations which add up to a more significantly increased risk.

Breast cancer is the most common type of cancer in the UK, with almost 50,000 women diagnosed every year. Death rates are falling as we learn more about the disease and how to diagnose and treat it, and around 78 per cent of people now live for at least 10 years after diagnosis.

Nell Barrie, senior science communications manager at Cancer Research UK, said: "We're

gradually uncovering breast cancer's secrets at a genetic level and learning how best to tackle this disease which still claims far too many lives. This latest study adds more detail to our genetic map of breast cancer risk and could help to develop new ways to identify women most at risk so we can spot breast cancer earlier in the future."

More information: 'Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer' Kryiaki Michailidou et al. DOI: 10.1038/ng.3242

Provided by Cancer Research UK