

## Massive study closes in on cancers risk markers

May 15 2013



Cancer research has taken a huge leap forward with scientists now able to identify more than 80 genetic markers found to increase the risk of breast, ovarian and prostate cancer. The COGS international research initiative is believed to be the largest of its kind.

Although the results have been widely reported, the cross-border efforts behind this monumental initiative have not. Neither has the EU-funding of EUR 12 million, which has played a significant part in making this global effort a tremendous success. The main findings of the project COGS ('Collaborative Oncological Gene-Environment Study') have been published in a special issue on genetic risk factors for cancer in the prestigious scientific journal *Nature Genetics*.



The research was led by scientists at the Karolinska Institutet in Sweden, the University of Cambridge and the Institute of <u>Cancer Research</u> (ICR) in the UK, with support from more than 160 research groups worldwide. This international network brought together five global studies on 100 000 patients with breast, ovarian or <u>prostate cancer</u>. Another 100 000 healthy volunteers comprised a control group.

Scientists took DNA from all 200 000 subjects and compared those with cancer, and those without, to assess each individual's inherited risk.

Overall, the study found that <u>common genetic variation</u> links all these cancers. This can be described as a genetic 'spelling mistake', where an A, G, C or T in the <u>genetic code</u> has been replaced with another letter. The spelling mistake is called Single Nucleotide Polymorphism (SNP).

Each alteration was seen to raise the risk of ovarian, breast or prostate cancer by a small amount, although a small minority of men with several markers saw their risk of prostate cancer increase more than fourfold. Prostate cancer is the second most common cancer in men worldwide, contributing to 14 % of all new cancer cases. It is predicted that the number of cases will almost double to a figure of 1.7 million by 2030.

Results of the studies on women revealed that with certain spelling mistakes the risk of <u>breast cancer</u>, which affects 28 % of women in Europe, increased threefold. In addition, the test also identified those with a smaller than average risk of developing the cancers.

Breast cancer is usually diagnosed at a more advanced stage, but scientists believe this research could also help the one in 300 women who carry a faulty gene known as BRCA1 or BRCA2.

One of the study authors, Professor Doug Easton from the University of Cambridge who led several of the studies, said: 'We're on the verge of



being able to use our knowledge of these genetic variations to develop a test that could complement breast cancer screening and take us a step closer to having an effective prostate cancer screening programme.'

With this new information, researchers now have a clearer picture of the total number of genetic changes that can explain the risk of getting these cancers. The next step is to calculate the individual cancer risk, which will help to better understand how these cancers start and grow so that new treatments can be developed. It is possible this could lead to a DNA screening test within five years.

COGS coordinator Professor Per Hall from the Karolinska Institutet says: 'COGS is the largest genotyping project in the world targeting identification of genetic changes that influence the risk of common cancers. The collaborative efforts have been tremendous and the key to its success.'

Other financial contributors to the COGS project are the Märit and Hans Rausing Initiative against Breast Cancer, the Swedish Research Council, Cancer Research UK and the <u>Cancer</u> Risk Prediction Center (CRisP).

More information: COGS <u>www.cogseu.org</u> <u>www.nature.com/icogs/</u>

## Provided by CORDIS

Citation: Massive study closes in on cancers risk markers (2013, May 15) retrieved 28 April 2024 from <u>https://medicalxpress.com/news/2013-05-massive-cancers-markers.html</u>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is



provided for information purposes only.