Womb cancer genome scan reveals prostate cancer link

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The first genome scan for womb cancer has revealed a genetic region that is associated with a reduced risk of the disease. The same region, called HNF1B, has been linked previously to lower prostate cancer risk in men.

The study, funded by the Wellcome Trust, the National Health and Medical Research Council in Australia, and Cancer Research UK, is the first to find a common genetic factor for these two different cancer types.

The findings offer a tantalising hint that there may be shared mechanisms of disease that have not been recognised previously.

Women with the protective 'version' of the gene are on average 15-18 per cent less likely to develop womb cancer, and men with the same version are 21 per cent less likely to develop prostate cancer. However, the same gene has also been linked to a 10-14 per cent greater risk of developing type 2 diabetes.

Lead author Professor Douglas Easton, director of Cancer Research UK's Genetic Epidemiology Unit at the University of Cambridge, said: "This study is the first to highlight a potential link between womb cancer in women and prostate cancer in men, providing new insight into the underlying genes and mechanisms that lead to the development of both diseases.

"Understanding how these influence a person's risk of developing cancer is a crucial step in being able to identify high-risk groups who may benefit from closer monitoring or measures to reduce their risk of developing the disease."

In the hunt for genes linked to womb cancer, the researchers began by scanning the genomes of 1265 womb cancer patents and comparing them to the genomes of 5190 women who did not have the disease.

This allowed them to pinpoint a total of 47 different points in the genetic code with one-letter alterations - known as single nucleotide polymorphisms (SNPs) - where genes linked to womb cancer were most likely to be found.

They then narrowed down their search by looking specifically at these regions in a further 3957 patients with womb cancer and 6886 without the disease.

This left just three SNPs that were shown to be significantly linked to a decreased risk of womb cancer, all of which overlapped with the gene HNF1B on chromosome 17.

Dr Lesley Walker, director of cancer information at Cancer Research UK, said: "This is only the second common genetic region to have been linked to the development of womb cancer.

"With faster, cheaper genome technologies now becoming available, we are on the cusp of being able to carry out powerful genome studies involving much larger groups of people. This will allow scientists to pinpoint subtler associations, helping to build a more complete picture of how genes influence a person's risk of developing womb cancer. Ultimately this will pave the way for more targeted approaches to treating and diagnosing the disease."

The study is published online today in the journal '*Nature Genetics*'.

More information: Spurdle AB et al. Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nat Genet 2011 [epub ahead of print]

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