Potential for earlier diagnosis of ovarian cancer

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(Medical Xpress) -- Australian scientists have identified biochemical changes that commonly occur in the DNA of women with ovarian cancer, which may help diagnose the cancer at an earlier stage in the future.

Using whole genome DNA profiling methods, Brian Gloss, Dr Philippa O'Brien and Professor Susan Clark from Sydney's Garvan Institute of Medical Research have identified a panel of 6 genes that are affected by an epigenetic process known as ' DNA methylation' in ovarian cancer.

The Garvan team collaborated with Professor Neville Hacker, Director Gynaecological Cancer Unit, Royal Hospital for Women Randwick, who provided tumour samples from ovarian cancer patients, as well as tissue samples from normal ovaries.

The findings are published in the journal *Cancer Letters*, now online.

Ovarian cancer is not easily diagnosed early, and people with advanced disease tend to die quickly.

Women diagnosed at a late stage – the majority – have a 30% 5-year survival rate. Women diagnosed at an early stage have a 90% 5-year survival rate.

Although ovarian cancer is a relatively rare disease, it is the leading cause of death due to gynaecological cancers, and the sixth leading cause

of cancer death in women. Around one in 70 women will develop the cancer, and around one in 100 women will die from it.

Ovarian cancers are usually diagnosed once the disease has spread past the pelvis and into other organs including the stomach, bowel and lungs. They are typically very hard to get rid of with surgery and they tend to become rapidly resistant to chemotherapeutics.

“This was one of first studies that used whole genome techniques to directly profile DNA methylation aberrations in ovarian cancer - with the aim of identifying diagnostic biomarkers,” said Brian Gloss, who focused on the project for his PhD.

“When we started in 2008, most other research groups were investigating single genes known to be methylated in other cancers. We decided to make use of new whole genome technologies – using DNA methylation profiling and gene expression profiling.”

“We wanted to see exactly which methylation changes led directly to aberrant gene silencing. In other words, which methylation changes have a functional role in ovarian cancer.”

“We did our discovery process in cell lines and then validated our findings in 27 cancers versus 12 normal ovarian tissue samples.”

“One of the key methylated genes we identified was a novel gene, which had not been identified as being misregulated in any cancer before.”

“When we then analysed a further 100 tumours, we found that the novel biomarker gene was methylated in 80% of them.”

“This paper represents the first half of our work. The next step will be to see how our panel of biomarker genes is methylated in a larger cohort of

ovarian tumours, and to identify the function of our novel gene."

"The most difficult aspect of ovarian cancer is that it is a molecularly heterogeneous disease, meaning that each tumour can be quite different from the next."

"We need to show, therefore, that our panel of biomarkers will be a sufficiently rigorous diagnostic tool, able to catch the requisite number of tumours.

More information: www.mendeley.com/research/inte … potential-novel-pan/

Provided by Garvan Institute of Medical Research