Scientists find genetic marker associated with ovarian cancer risk

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A new genetic marker associated with ovarian cancer risk was recently discovered by an international research group, led by scientists from the Cancer Research Genetic Epidemiology Unit in the United Kingdom. Drs. Marc Goodman, Galina Lurie, Michael Carney, and Keith Terada of the University of Hawai'i at Mānoa's Cancer Research Center of Hawai'i participated in the validation of the discovered genetic marker as a part of the Ovarian Cancer Association Consortium, a worldwide forum of scientists performing ovarian cancer research.

"The discovery represents not only a triumph of team science, but also a fulfillment of the vision of the Ovarian Cancer Research Fund and its donors," says Dr. Andrew Berchuck at Duke University, chair of the consortium.

Over the last six years, the consortium has been supported by generous donations from the family and friends of Kathryn Sladek Smith in the New York area. The results of this work appeared in the July 2, 2009 issue of *Nature Genetics*.

Ovarian cancer is the eighth most common cancer and the fifth leading cause of cancer death among women in the United States. The five-year relative survival rates are currently 93 percent for localized disease, 71 percent for regional disease, and 31 percent for distant disease. However, only 25 percent of women with ovarian carcinoma are diagnosed at a localized stage mostly because symptoms are vague and a reliable screening method for early detection has not been established.

Ovarian cancer is already known to be linked to the variations in the breast cancer genes, BRCA1 and BRCA2. But these variations are rare, and alone they account for less than five percent of all cases of ovarian cancer. It is likely that the remaining risk is due to a combination of several unidentified genes that individually carry a low to moderate risk of the disease.

The study used a genome-wide association design in which the frequencies of hundreds of thousands of genetic variations across the genome are compared between large numbers of cases and unaffected controls. Overall more than 20,000 women participated in this study.

In the first stage, more than 620,000 genetic variations were analyzed in the whole genome of 1,817 women with ovarian cancer and compared to 2,353 women without the disease. Through the Ovarian Cancer Association Consortium, the most promising markers were subsequently investigated among an additional 7,922 women with ovarian cancer and 10,577 women without disease.

The new marker was found on chromosome 9, close to the BNC2 (basonuclin 2) gene that encodes a protein which plays a role in regulation of DNA transcription and is highly expressed in reproductive tissues. This marker is present among 32% of women and contributes an estimated 0.7% to ovarian cancer risk.The association of this marker with risk was stronger for serous carcinoma, the most common (and most lethal) ovarian cancer subtype.

Source: University of Hawaii at Manoa