MedicalXpress

Novel gene drives development of different types of ovarian cancer

March 27 2013

Researchers at Mayo Clinic Cancer Center have identified a novel gene that can contribute to a woman's susceptibility for developing ovarian cancer. Researchers identified the gene, called HNF1B, through large-scale analysis of more than 16,000 women with ovarian cancer and more than 26,000 healthy women. Results of the study are published in the current issue of the journal *Nature Communications*.

The study is one of 13 papers to be published simultaneously in five journals by the Collaborative Oncological Gene-environment Study (COGS), an international research collaboration involving investigators from Europe, Asia, Australia and North America, including Mayo Clinic. This landmark series of papers provides genotyping results from more than 250,000 individuals that look at DNA sequences involved in three hormone-related cancers: ovarian, breast and prostate.

"Through the combined efforts of this consortium, and all the data sharing, we are much closer to understanding the inherited factors in these diseases," says Mayo Clinic investigator Ellen Goode, Ph.D., senior author of the HNF1B paper, and co-author of three additional papers among the 13, focusing on ovarian and breast cancer development. Ovarian cancer is the most common cause of death from gynecological cancers in the U.S.

In their study, Dr. Goode and her collaborators showed that variations in the HNF1B gene are overrepresented in one type of epithelial ovarian cancer and underrepresented in another type. They also found that

variation in DNA methylation, a process that moderates the expression of genes such as HNF1B, correlates with different ovarian cancer subtypes. This finding suggests that the activation and inhibition of gene expression by DNA methylation can be as important a factor in cancer as genetic mutations.

"The distinct methylation patterns suggest a molecular mechanism by which changes in this gene lead to increased cancer risk," says Dr. Goode. "This has potential clinical implications for improving our understanding of how the disease begins, for better identification of ovarian cancer subtypes and for developing novel treatment approaches."

Provided by Mayo Clinic