



# NEWS

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## **Novel gene-diet interaction may help explain association between eating red & processed meat and colorectal cancer risk**

A newly discovered potential gene-diet interaction for colorectal cancer was reported today (Thursday, Oct. 24) at the American Society of Human Genetics 2013 meeting in Boston. The interaction may shed light on the statistically significant increased risk of colorectal cancer that is associated with consumption of red and processed meat, the researchers said.

“If replicated, our findings have a relevant public health significance because diet is a modifiable risk factor for colorectal cancer,” said Jane Figueiredo, Ph.D., Assistant Professor of Preventive Medicine at the University of Southern California Keck School of Medicine, who presented the study this morning at the ASHG meeting.

“It is conceivable that selected individuals at higher risk of colorectal cancer based on genomic profiling could be targeted for screening, diet modification and other prevention strategies,” added Dr. Figueiredo, one of the scientists collaborating in the international NIH-funded Genetics and Epidemiology of Colorectal Cancer Consortium (GECCO).

The scientists also determined that the lower colorectal cancer risk associated with vegetable, fruit and fiber intake also was linked to genetic variants.

The possibility that genetic variants may modify an individual’s risk for disease based on diet has not been thoroughly investigated but represents an important new insight into disease development, said Ulrike Peters, Ph.D., M.P.H, who headed the study and is a Member of the Fred Hutchinson Cancer Research Center’s Public Health Sciences Division in Seattle.

The study is the first colorectal cancer investigation with the statistical power to identify gene-dietary interactions across the genome of a large population of individuals, said Li Hsu, Ph.D., Member of the Fred Hutchinson Cancer Research Center and the study’s lead biostatistician.

The study population totaled 9,287 patients with colorectal cancer and a control group of 9,117 individuals without cancer, all participants in 10 GECCO observational studies.

Scientists systematically searched 2.7 million variants to identify those that are associated with the consumption of red meat and processed meat as well as fruits and vegetables. The genetic sequences and information about the participants’ medical history and diet are in the GECCO database.

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A significant interaction between the genetic variant rs4143094 and processed meat consumption was detected. This variant is located on the same chromosome 10 region that includes *GATA3*, a transcription factor gene previously linked to several forms of cancer. The transcription factor encoded by this gene normally plays a role in the immune system.

On chromosome 8, a statistically significant diet-gene interaction was found in another variant, rs1269486. This variant was associated with reduced risk of colorectal cancer.

How specific foods affect the activities of genes has not been established. Drs. Peters and Figueiredo speculate that digestion of processed meat may promote an immunological or inflammatory response that may trigger tumor development. The *GATA3* transcription factor normally would help suppress the immunological or inflammatory response. However, if the *GATA3* gene region contains a mutation, it may encode a dysregulated transcription factor that impacts its ability to suppress the response.

In addition to uncovering a novel gene-diet interaction for colorectal cancer, the GECCO study may have important implications for understanding the underlying causes and biological pathways of cancer, said Dr. Peters.

“Our study highlights two genetic regions that are biologically interesting in cancer,” she said, referring to the variants located near *GATA3* and at 8q23.3.

“These genetic loci may have interesting biological significance given their location in the genome, and further functional analyses are required,” said Dr. Peters.

The GECCO multi-institutional research team continues to investigate gene-diet interactions through independent studies on a well-characterized large cohort of European colorectal cancer patients and a collaboration with the Colorectal Cancer Trans-disciplinary study (CORECT) consortium.

“GECCO aims to continue to discover additional colorectal cancer-related variants by investigating how genetic variants are modified by other environmental and lifestyle risk factors, including biomarkers as well as how they influence patient treatment response and survival,” Dr. Peters said.

Colorectal cancer is a multi-factorial disease attributed to lifestyle, environmental and genetic causes. Over 30 genetic susceptibility alleles for colorectal cancer have been pinpointed throughout the genome. They include rare variants that have a strong impact on risk and common variants that are low risk.

The scientists’ ASHG abstract is titled, “[Genome-wide analyses highlight gene interaction with processed meat and vegetable intake for colorectal cancer risk.](#)”

### **About ASHG**

The American Society of Human Genetics is the primary professional membership organization for nearly 8,000 human genetics specialists worldwide. The ASHG Annual Meeting is the world's largest gathering of human genetics professionals and a forum for renowned experts in the field. For more information about ASHG, visit: <http://www.ashg.org>.