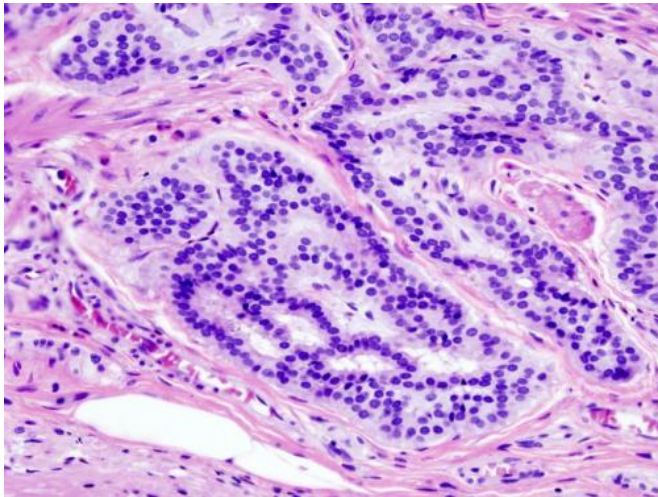


Study identifies novel genetic factors for colorectal cancer risk

11 January 2019, by Tom Wilemon



Cancer — Histopathologic image of colonic carcinoid.
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A large-scale study conducted among East Asians and led by Vanderbilt researchers has identified multiple, previously unknown genetic risk factors for colorectal cancer.

Wei Zheng, MD, Ph.D., Anne Potter Wilson Professor of Medicine, said the research published recently in *Gastroenterology* is the second largest discovery of novel genetic risk variants for [colorectal cancer](#) in a single study published to date. Zheng, the study's senior author, and colleagues identified 13 previously unknown variants after conducting a meta-analysis of studies from the Asia Colorectal Cancer Consortium that encompassed samples from more than 70,000 colorectal [cancer](#) patients and controls.

The researchers performed [genome-wide association studies](#) (GWAS) to search for genetic regions that may harbor genes affecting colorectal cancer. Carrying a risk variant in these genes does not mean that someone is destined to develop the

disease, but some genes do pose greater risks than others. For example, the study identified two relatively uncommon risk variants in the EFCAB2 and DENND5B genes that are associated with a much higher risk of developing colorectal cancer than the other 11 identified in the study.

Scientists began using GWAS about a decade ago to search for genetic characteristics associated with diseases. Most of the GWAS have been conducted among people of European descent, and the Vanderbilt research team has formed a consortia to widen the scope and compare findings. Zheng and colleagues in their study also found that most of the risk variants previously identified among people of European descent were also associated with colorectal cancer in people of East Asian descent. Additionally, they did a cross analysis of the 13 novel risk factors they discovered in East Asians, comparing those variants with data on people of European descent, and found that six were shared between the two population groups.

"Genetic structures are different from one population to another—not greatly different—but there are some differences," Zheng said. "That's why we need to do studies in non-European descendants to really understand the genetic basis for colorectal cancer."

The GWAS studies identify potential targets for new drug therapies and allow scientists to build genetic models to identify people at greater risk for colorectal cancer so they can take preventive measures. Globally, colorectal cancer is the third most common cancer.

More information: Yingchang Lu et al. Large-scale Genome-wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer, *Gastroenterology* (2018). DOI: [10.1053/j.gastro.2018.11.066](https://doi.org/10.1053/j.gastro.2018.11.066)

Provided by Vanderbilt University

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