

Colorectal cancer gene database helpful in furthering research

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The CRCgene database, which gathers all genetic association studies on colorectal cancer, allows for researchers to accurately interpret the risk factors of the disease and provides insight into the direction of further colorectal cancer research, according to a study published September 27 in the *Journal of the National Cancer Institute*.

Approximately 950,000 new cases of colorectal cancer are diagnosed each year. The risk of developing the disease also increases with age, and as life expectancy rises, the incidence continues to grow. These factors paired with rising [health care costs](#) have made both diagnosis and treatments for the disease costly. While diet and lifestyle may affect colorectal cancer incidence, so may [genetic factors](#), and it is important to determine which genetic factors are most heavily associated with colorectal [cancer incidence](#).

In order to determine the genetic factors associated with colorectal cancer, Julian Little, Ph.D., of the Department of Epidemiology and Community Medicine at the University of Ottawa and colleagues, gathered data from previously published guidelines for assessing cumulative evidence on genetic association studies, and performed meta-analyses on all the data, compiling all genetic association studies published in the field. The credibility of the studies was determined by the Venice criteria and the Bayesian False Discovery Probability (BFDP) test.

The researchers found 16 independent gene variants had the most highly

credible links to colorectal cancer, with 23 variants. "The number of common, low-penetrance variants that appear to be associated with colorectal cancer is very much less than anticipated, therefore decreasing the feasibility of combining variants as a profile in a prediction tool for stratifying screening modalities on primary prevention approaches," the authors write. Still, they feel that, "the analysis here provides a resource for mining available data and puts into context the sample sizes required for the identification of true associations."

Provided by Journal of the National Cancer Institute

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