

News Highlights

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New genetic risk factor identified in a large trans-ethnic genome-wide association study

By Chantal Jackson

HONOLULU, HI - In a large collaborative effort, University of Hawai'i Cancer Center's Dr. Loïc Le Marchand has highlighted a new association between colorectal cancer risk and a common genetic variant. Dr. Le Marchand is a professor in the Cancer Epidemiology Program at University of Hawai'i Cancer Center, as well as a clinical professor in Public Health at John A. Burns School of Medicine, University of Hawai'i at Manoa. His research focuses upon the interaction between genetic and lifestyle factors which contribute to increased cancer risk among ethnic/racial populations in Hawai'i and California. With a specific focus on colorectal, lung and breast cancer, the aim of his research is to better understand the causes of cancer and develop new means of prevention.

Colorectal cancer (CRC) is the second leading cause of cancer deaths and the third most common cancer in the United States. Although it has been established that genetics play an essential role in CRC susceptibility, genome-wide association studies (GWASs) have primarily been conducted within European-descent populations; furthermore, these studies have only identified 30 common risk variants, which is significantly fewer than for prostate or breast cancer.

Le Marchand notes, "We have seen varying risks of developing colorectal cancer associated with ethnicity. In particular, an increased risk of colorectal cancer has been observed among Japanese individuals who migrated to Hawai'i and their descendants; furthermore, in Japan since 1950, there has also been a notable increased risk in colorectal cancer development". Due to this, Le Marchand has conducted decade-long studies to explain this susceptibility associated with the incorporation of a Westernized lifestyle.

To better understand the genetic basis of non-familial colorectal cancer (CRC), Le Marchand and his team performed genome-wide association studies in 2,627 cases and 3,797 controls of Japanese ancestry, and in 1,894 cases and 4,703 controls of African ancestry. They observed an association between CRC risk and a common variant in the VTI1A gene in both populations. They, then, reproduced their findings in a large collaborative study of European descent populations.

This finding demonstrates the usefulness of multiethnic studies in identifying new genetic risk factors. "The next step is to demonstrate that genetic risk variants, considered together, are sufficiently predictive of risk to help in determining who should be screened by colonoscopy", says Dr. Le Marchand. The use of these genetic markers, along with more typical risk factor information, may facilitate in more

efficient screening. The study: "[Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A](#)," was published on August 8, 2014 in *Nature Communications*.