

Genetic Science Spotlight

GECCO reported that alcohol consumption may modifies HIATL gene and increase CRC risk



A genome wide study (GWAS) found association between colorectal cancer (CRC) risk, alcohol consumption and variants in the 9q22.32/HIATL1. Through a logistic regression test using data from the Colon Cancer Family Registry (CCFR) and the Genetics and Epidemiology of Colorectal Cancer Consortium (GECCO), it is observed that alcohol consumption may be a modifying factor to the expression of HIATL gene and may influence colorectal cancer risk. However, the actual mechanism behind the effect of alcohol on HIATL gene remains unknown and warrant further studies. Non- or occasional alcohol drinkers are found to be at lower risk of CRC among individuals with rs9409565 CT genotype (OR, 0.82 [95% CI, 0.74–0.91]; P = 2.1×10–4) and TT genotypes (OR, 0.62 [95% CI, 0.51–0.75]; P = 1.3×10–6) but not associated among those with the CC genotype (p = 0.059) when compared to light and moderate alcohol drinkers. This might be able to better indicate the role of HIATL gene in respect to the environment changes in assessing risk of cancer.

https://www.ncbi.nlm.nih.gov/pubmed/27723779

You are welcome to contact us for more information!









©Copyright 2012-2016 Le GENE Limited | All Rights Reserved