High Impact Paper of the Month
March 2015

Genetic variation in alcohol metabolizing enzymes among Inuit and its relation to drinking patterns.

Paper commentary

A study to compare genetic variation in alcohol metabolism genes of the Greenland Inuit with published data from Denmark and Han Chinese populations. Researchers led by the National Institute of Public Health, Denmark used LGC’s genomic services to extract and genotype DNA from the Greenland Inuit for this fascinating look into the genetics of alcohol metabolism and drinking patterns in this indigenous population.

Highlights of the paper

- Research led by the National Institute of Public Health, Denmark
- Largest study of SNPs related to alcohol metabolism among the Inuit.
- 4162 Inuit participants genotyped across 7 SNPs which are all demonstrated to have an association with alcohol metabolism or drinking patterns.
- LGC’s sbeadexTM technology was used to extract DNA from buffy coats obtained from whole EDTA blood samples.
- All genotyping was performed using KASP genotyping assays.

Commentary

Alcohol problems have been a major public health problem among the Inuit since the 1950s. There is a demonstrated link between variation in alcohol metabolism genes and drinking behaviour; this study sought to determine the role of genetics in drinking behaviour in this indigenous population which has an increased incidence of undesired alcohol consumption.

All 7 of the SNPs selected for analysis are located within the two isoenzymes responsible for alcohol metabolism – alcohol dehydrogenase (ADH) and acetaldehyde dehydrogenase (ALDH) – or their regulatory regions. Despite the Asian heritage of the Inuit, the protective Asian genotype pattern including an inactive ALDH2 enzyme was not present among the Inuit in Greenland. However, the study clearly shows that the prevalence of other alcohol related SNPs may be important and appear to shape drinking patterns among the Inuit of Greenland.

Other articles you may be interested in

Genetic variants in or near ADH1B and ADH1C affect susceptibility to alcohol dependence in a British and Irish population.

Certain single nucleotide polymorphisms (SNPs) in genes encoding alcohol dehydrogenase (ADH) enzymes confer a significant protective effect against alcohol dependence syndrome (ADS) in East Asian populations. Recently, attention has focused on the role of these SNPs in determining ADS risk in European populations. To further elucidate these associations, SNPs of interest in ADH1B, ADH1C and the ADH1B/1C intergenic region were genotyped in a British and Irish population (ADS cases n = 1076; controls n = 1027) to assess their relative contribution to ADS risk. The rare ADH1B rs1229984 mutation provides significant protection against ADS in this British and Irish population; other variants in the ADH gene cluster also alter ADS risk, although the strong linkage disequilibrium between SNPs at this location precluded clear identification of the variant(s) driving the associations.