Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk.

Abstract:
The mechanisms underlying the association between diabetes and coronary artery disease (CAD) risk are unclear. We aimed to assess this association by studying genetic variants that have been shown to associate with type 2 diabetes (T2DM). If the association between diabetes and CAD is causal, we expected to observe an association of these variants with CAD as well. We studied all genetic variants currently known to be associated with T2DM at a genome-wide significant level ($p_0 < 0.05$), more than expected by chance ($p = 5.0 \times 10^{-5}$). Considering all 44 SNPs, the average CAD risk observed per individual T2DM risk allele was 1.0076 (95% confidence interval (CI), 0.9973-1.0180). Such average risk increase was significantly lower than the increase expected based on i) the published effects of the SNPs on T2DM risk and ii) the effect of T2DM on CAD risk as observed in the Framingham Heart Study, which suggested a risk of 1.067 per allele ($p = 7.2 \times 10^{-10}$) vs. the
observed effect). Studying two risk scores based on risk alleles of the diabetes SNPs, one score using individual level data in 9856 subjects, and the second score on average effects of reported beta-coefficients from the entire CARDIoGRAM data-set, we again observed a significant - yet smaller than expected - association with CAD. Our data indicate that an association between type 2 diabetes related SNPs and CAD exists. However, the effects on CAD risk appear to be by far lower than what would be expected based on the effects of risk alleles on T2DM and the effect of T2DM on CAD in the epidemiological setting.