Epidemiological evidence suggests that patients with celiac disease are at increased risk for coronary artery disease (CAD). Genetic-epidemiological analyses identified many single nucleotide polymorphisms (SNPs) associated with celiac disease. If there is a causal relation between celiac disease and CAD, one might expect that risk alleles primarily associated with celiac disease also increase the risk of CAD. In this study we identified from literature 41 SNPs that have been previously described to be genome-wide associated with celiac disease ($p < 5 \times 10^{-08}$). These SNPs were evaluated for their association with CAD in the Coronary ARtery DIsease Genome-wide Replication and Meta-analysis (CARDioGRAM) dataset, a meta-analysis comprising genome-wide SNP association data from 22,233 CAD cases and 64,762 controls. 24 out of 41 (58.5 %) risk alleles for celiac disease displayed a positive association with CAD (CAD-OR range 1.001-1.081). The remaining risk alleles for celiac disease ($n = 16$) revealed CAD-ORs of $\leq 1.0$ (range 0.951-1.0). The proportion of CAD associated alleles was greater but did not differ significantly from the proportion of 50 % expected by chance ($p = 0.069$). One SNP (rs653178 at the SH2B3/ATXN2 locus) displayed study-wise statistically significant...
association with CAD with directionality consistent effects on celiac disease and CAD. However, the
effect of this locus is most likely driven by pleiotropic effects on multiple other diseases. In conclusion,
this genetically based approach provided no convincing evidence that SNPs associated with celiac
disease contribute to the risk of CAD. Hence, common non-genetic factors may play a more important
role explaining the coincidence of these two complex disease conditions.