Background: Despite the decline in their incidence rates, the recurrent myocardial infarction (MI) events are associated with significant morbidity, short- and long- term mortality. Relative to our understanding of risk for first events, the aetiology of recurrent MI is poorly understood.
Methods: We used UK-Biobank, a large prospective cohort of 500,000 individuals, to investigate the genetic predisposition of recurrent MI. We performed a GWAS in 3386 UK-Biobank participants admitted to hospital due to MI at least twice within a period of 28 days - 1.5 years and 8567 controls with one unique hospital record with MI diagnosis or MI hospital admissions, which occurred outside the aforementioned period.
Results: In total, 215 variants representing 27 loci reached a suggestive significance level of 10^{-5}. Among these, 17 loci have been implicated in coronary artery disease (CAD) and other cardiovascular phenotypes (eg. *KCNN2*, *KLF4*, *CACNB2*, *ADIPOR2*, *KLF5*, *PKD1L3*), known CAD risk factors (blood pressure*, CACNB2*; lipid levels, *ABHD4*), cardiac remodelling (*MAP3K5*, *SEMA3A*), and abnormalities in platelets and coagulation (*GRM7*, *KALRN*, *P2RY1*).
Five of the identified genes (*CHD7*, *IST1*, *KIAA1958*, *MAP3K5*, *UBFD1*) were also found to be differentially expressed six months after a MI in 39 MI survivors (Greek Recurrent Myocardial Infarction Cohort) that had not experienced any recurrent event during that period (p-adj $\leq 10^{-5}$).
Conclusions: We identified 27 loci associated with increased risk of recurrent MI. We aim to identify independent datasets to replicate our findings, aiming to a greater understanding of recurrent MI determinants.
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