GENETIC VARIANTS PREDICTING LEFT VENTRICULAR HYPERTROPHY IN A DIABETIC POPULATION

Poster Contributions
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Authors: Helen Parry, Louise Donnelly, Natalie Van Zuydam, Alex Doney, Douglas Elder, Andrew Morris, Allan D. Struthers, Colin Palmer, Chim Lang, University of Dundee, Dundee, United Kingdom

Background: Diabetes is an independent risk factor for left ventricular hypertrophy (LVH). Little research has addressed genetic aspects of LVH. We aimed to identify genetic variants predicting LVH in diabetic individuals.

Methods: We utilised databases managed by the University of Dundee within the Genetics of Diabetes Audit and Research in Tayside, Scotland project. Demographic, echocardiographic, prescribing, morbidity, mortality and genotyping data were accurately linked using a patient-specific identifier. Cases of LVH were identified using echocardiographic data. Genotyping data from LVH cases and non-LVH control subjects were analysed using PLINK and SNP TEST, investigating whether any single nucleotide polymorphisms (SNPs) associated with LVH in previous Genome Wide Association Studies were associated with LVH in our population. Meta-analysis assessed overall significance of these SNPs. Gene scoring based on published SNPs also predicted LVH.

Results: Two SNPs previously associated with LVH were significant in this study: rs17132261: OR 2.07 SE 0.31, p-value 0.02 and rs2292462: OR 1.21, SE 0.06 and p-value 1.90x10-3. Meta-analysis confirmed both rs17132261 and rs2292462 were associated with LVH (p=1.06*10-8 and p=5.86*10-10 respectively). Gene scoring based on published SNPs also predicted LVH in our study.

Conclusion: We created a resource to study genetics of LVH in diabetes and validated our LVH phenotype in replicating SNPs previously identified by previous GWAS investigating LVH.