

Investigation of the effect of genetic polymorphisms on aortic growth in patients with abdominal aortic aneurysm (AAA)

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Introduction: Abdominal aortic aneurysm (AAA) is a disease with strong genetic background, based on evidence from epidemiological studies. At least four genome-wide association studies (GWAS) have identified genetic loci associated with AAA-presence and several single nucleotide polymorphisms (SNPs) have been identified through candidate-gene studies. However, there is limited evidence regarding the effect of genetics on AAA-growth.

Methods: We identified a population of 389 patients of common geographical origin (mean age: 69 ± 8 years, 88% males) with available AAA sizes over >1 year and matched them to a control group (age, sex, smoking-habit) of patients with no AAA. We subsequently analysed nine functional SNPs linked with aortic inflammation and proteolysis (identified through a systematic review of candidate-gene association studies) and 4 polymorphisms previously associated with AAA-presence in the AAA-GWASs available to date.

Results: The rs6511720 low-density lipoprotein receptor (LDLR) SNP and the rs1795061 SNP were associated with both AAA presence [odds ratio (OR): 1.7, $p=0.03$; OR: 1.9, $p<0.001$ - respectively] and change in annual aortic size (OR: 1.2, $p=0.02$; OR: 1.4, $p=0.01$ – respectively, analysis adjusted for age, sex, hypertension, hyperlipidaemia and smoking). Both SNPs had been associated with AAA-presence in previous GWASs. None of the other 11 SNPs analysed were associated with annual aortic growth in this population; even though the SNPs previously identified through GWASs and the rs3091244 C-reactive protein (CRP) SNP were associated with AAA presence independently.

Conclusions: Two SNPs were found to be associated with aortic growth in this population of patients with AAA, which represents a novel finding.