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.