**OBJECTIVE:** Common polymorphic variants predispose individuals to thoracic aortic disease and genome wide association studies provide a method to robustly identify these polymorphic variants.

**ORGANIZATION**

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**BACKGROUND AND RATIONALE**

Previously, a genome wide association study was completed on 800 Caucasian patients with sporadic thoracic aortic aneurysms and dissections (TAAD; cohort from the Specialized Center of Clinically Oriented Research (SCCOR) in TAAD) using the Illumina 377 SNP array. Multiple control populations have been used to identify SNPs associated with disease, including the 1958 British birth cohort, the NINDS control cohort, and the lung cancer control cohort. Our results represent associations confirmed when the cases are compared with at least two control cohorts or all three cohorts.

We have identified 4 loci containing a SNP or multiple SNPs in a linkage disequilibrium (LD) block that are associated with thoracic aortic disease with p values less the 10^-8_. When the SCCOR cohort is subdivided based on presence or absence of bicuspid aortic valve (BAV), the significance of association of these loci with aortic disease remain in both subgroups. We have also identified SNPs and imputed SNPs associated with aortic disease at a p value less than 10^-6_ (1800 SNPs).

**CONCLUSIONS**

*Results:* Identification of novel associations of polymorphic variants at the 15q21.1 locus, encompassing FBN1, with sporadic TAAD.