



GEN42- Identification of Functional Variants for Sporadic TAAD

OBJECTIVE: To identify FGVs at 15q21.1 locus that are associated with an increased risk of developing STAAD.

ORGANIZATION

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Investigator:

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Funding Source: NIH

Samples:

- Genetic Material

Data:

- Demographic data

BACKGROUND AND RATIONALE

We recently conducted a three stage single nucleotide polymorphism (SNP) based genome-wide association study (GWAS) by using three sets of samples from patients of European American (EA) and identified SNPs at one locus, 15q21.1, associated with STAAD. Associations of SNPs at the 15q21.1 locus with different presentation of STAAD have also been investigated and the most significant association observed was with type A dissection. This locus encompasses FBN1 and it is the only gene at this locus. Mutations in FBN1 cause Marfan syndrome (MFS) and individuals with MFS have TAAD. It is unlikely that the associations demonstrated in this study are caused by a synthetic association due to multiple rare variants because these rare variants would have to fall on the same haplotype in all three stages of the association study.

CONCLUSIONS

Results:

- Results pending

DESIGN

Hypothesis

- Common genomic functional variants (FGVs) may alter a small proportion of FBN1 mRNA sequence, or sequence/expression level of non-coding RNAs at this locus, which results in an increased risk of developing STAAD

Inclusion criteria:

- Study participants of European American or African American with sporadic thoracic aortic dissections

Exclusion criteria:

- Age <31 years; aortic aneurysm associated with infection, aortitis, trauma, isolated pseudoaneurysm, or being known to have TAAD with a syndromic cause (such as MFS) or to have a first-degree relative with TAAD.