



## GEN40 - Parental Analysis of Rare Copy Number Variants in GENTAC Patients with Early Onset Aortic Disease

**OBJECTIVE:** A subset of early onset, genetically triggered aneurysms, either associated with syndromic features or not, will result from insertions and deletions in the human genome. The identification of rare de novo CNVs in affected individuals will strengthen our hypothesis that these CNVs are causally related to TAAD.

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### ORGANIZATION

*Lead Investigator:* Siddharth Prakash, MD  
*Co-Investigators:* Diana Milewicz, MD  
*Funding Source:* GenTAC and NHLBI SCCOR

*Samples:*

- Genetic material from blood will be obtained from parents whom consent is obtained.

*Data:*

- None

### CONCLUSIONS

*Results:*

- *Results pending*

### BACKGROUND AND RATIONALE

Research project GEN03 recently completed a genome wide copy number variation (CNV) study of 96 GenTAC samples with early onset thoracic aortic aneurysms and dissections (TAAD). Analysis of the data has identified several large genetic copy number variants (CNVs) that are either present at increased frequency in the patients compared with 5000 controls or not present at all in the controls. Examination of de novo CNV status will provide data that the CNV is disease-causing and has the potential to identify a set of recurrent CNVs that are highly penetrant for thoracic aortic disease.

### DESIGN

*Hypothesis*

- A subset of early onset, genetically triggered aneurysms, either associated with syndromic features or not, will result from insertions and deletions in the human genome.

*Inclusion criteria:*

- Parents of 18 GenTAC subjects with potentially pathogenic rare CNVs of TAAD candidate genes will be enrolled
- Additional parental samples may be requested as ongoing research identifies more candidate genes and regions. The total number of parental samples requested will not exceed 60.

