**OBJECTIVE:** To analyze the 1800 SNPs in a population of women with Turner syndrome.

**ORGANIZATION**

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**Funding Source:** NHLBI SCCOR

**BACKGROUND AND RATIONALE**

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 are proposing to analyze the 1800 SNPs in a population of women with Turner syndrome, in which there is an estimated frequency of the constellation of aortic coarctation/BAV/aneurysm/dissection in up to 30% of the patients.

**DESIGN**

**Hypothesis:** Polymorphisms on autosomal chromosomes lead to a high risk for a spectrum of cardiovascular conditions in women with Turner syndrome, specifically bicuspid aortic valve, aortic coarctation, and thoracic aortic aneurysms and dissections.

**Inclusion criteria:** Women with Turner syndrome who have been assessed for cardiovascular disease (BAV, ascending aneurysms and dissection, and aortic coarctation) from the following cohorts

- GenTAC
- NIH phenotype collected by Carolyn Bondy
- SCCOR-TAAD cohort (women with Turner syndrome referred for aortic surgery)

**CONCLUSIONS**

**Results:** Our study is the first systematic comparison between the two methods and supports the utility of SNP array genotyping to address clinical and research questions in Turner syndrome.