Unique Protocol ID: UOL 0676

Official Title:

A Study to Evaluate the Feasibility of Screening Relatives of Patients Affected by Non-Syndromic Thoracic Aortic Diseases: The ReST Study

Statistical Analysis Plan

Date:

25/07/18

STATISTICS

Description of Statistical Methods

As this is a feasibility study, the analyses of the data collected will be mainly descriptive, and any statistical comparisons made will be exploratory. Continuous data will be summarized as mean (standard deviation) or median (interquartile range), if data will be skewed, and categorical data will be expressed as number and/or percentage. We will calculate the summary scores for SF36, GAD-7 and PHQ-9, as well as the score of each domain assessed by these instruments. The change in the scores (3-month follow-up minus the baseline) will be computed and as a measure to evaluate the psychological impact of the screening. We will use mixed logistic regression model to explore the genotype-phenotype relationship in the family-based data and identify candidate genetic variants associated with NS-TADs. Exploratory comparison of the outcomes (e.g. aortic diameter, distensibility and pulse wave velocity) between mutation carriers and non-carriers may be conducted. Where appropriate, we will take into account of the family structure in the statistical analyses.

Number of Trial Participants

Recruitment will be primarily targeted at 16 probands (index patients) affected by NSTAD, of which n=8 affected by sporadic forms and n=8 from familial forms. The first degree relatives and second degree relatives of these probands will be identified and invited to participate in the study. In our pilot study, based on the data available in a recent systematic review and the fact that we will enrol first degree relatives as well as second degree relatives, we have calculated that an average of 6 to 8 relatives for proband will be recruited, giving a total number of 128 participants to be approached ("enrollable"), and 90 to be effectively screened.

The Level of Statistical Significance

For the genome-wide association analysis, we will use 10% false discovery rate to identify variants associated with NS-TADs. For other analyses a potential signal for statistical significance is assumed if $p < 0.05$. No multiplicity adjustment is planned due to the exploratory nature of the study.