Alpha-1 Carrier Genomics Study

Statistical Analysis Plan (from study protocol)

Date of Document: 4/1/2016

NCT02810327

STATISTICAL ANALYSIS

1. **Primary Aim: The number of likely significant gene mutations between COPD and matched control groups will be compared using a paired T-test**

The variety of mutations in non-coding and coding regions of the *SERPINA1* gene will be large. Therefore, Biocerna will define if they believe mutations are likely to be in functional regions of the gene, independent of knowing if the patient has COPD or is a matched control. The number of likely significant gene mutations between COPD and matched control groups will be compared using a paired T-test.

2. **The nature of mutations identified will be correlated with COPD severity.**

Descriptive analysis at the genomic level will follow to link all areas of genomic variation with severity of COPD. Functional gene expression and likely pathogenicity as determined in Biocerna interpretation will be related to established COPD phenotypes using linear models.

3. **The portion of individuals who return a DNA1 test kit with sufficient blood sample for testing will be quantified for assessment of home testing feasibility.**

Sample Size

There is not a power analysis associated with this pilot study.
The goal is to analyze 50 matched pairs, or 100 total samples. This study will enroll up to 150 individuals in order to have at least 100 samples returned to the lab for testing, as there are some people who consent but never return their test kit. Enrolling up to 150 allows better chances of finding 50 matched pairs. All samples that are received by the lab will be analyzed. If we end up with uneven numbers in the COPD+ and COPD- arms, more than 100 samples analyzed, or have participants without a match, we will account for this in the statistical analysis and reporting.