

Concise Descriptive Title:

Determining the Role of Human Genetics on the Outcome of Ebola Virus Infection

Samples Requested:

Cohort: Ebola-positive samples

Sample volume: 200 μ l

Background

The purpose of this study is to determine whether host genetic factors play a role in the outcome of Ebola virus infection. Two published studies in mice have identified a small, limited number of genes that may play a role in Ebola virus pathogenesis (1, 2). However, in humans, nothing is known about gene variants that could influence the outcome of Ebola virus infection. Since there are no genome-wide association studies associated with Ebola virus infection in humans, Ebola-positive samples are an extremely valuable resource to complete such a study.

During the Ebola outbreak, the research team collected samples from 11 survivors and 9 non-survivors and performed a limited analysis on this small number of samples and found a potential correlation between variants in three human genes and the outcome of infection (survivors vs. non-survivors; unpublished). However, given the small numbers of samples used in the analysis, this study failed to reach significance (p value = 10^{-8}). Therefore, we are requesting an additional 250 samples from Ebola-positive cases.

The group has received the most recent human subjects approval by the Office of the Sierra Leone Ethics and Scientific Review Committee in August 2016 and at their institutional ethics committee in December 2016.

Database Variables

In addition to the samples, we request the following metadata associated with the samples if available:

- Laboratory of origin
- Laboratory ID number
- Date tested
- Gender
- Patient Age
- Viral Load

Resources Required and Available

The lead investigator has sufficient discretionary funds to support this project. Additional funds will be applied for through parent or administrative supplemental grants.

