UT Austin researchers inform development of Ebola vaccine trials

April 21 2015

An Ebola candidate vaccine is readied for frontline worker study in Sierra Leone. Credit: US Centers for Disease Control and Prevention (CDC)

As the current Ebola outbreak wanes, scientists have to make the most of every opportunity to prepare for future outbreaks. One such opportunity involves the identification of a safe and effective Ebola vaccine. Texas supercomputers have aided researchers in modelling which types of clinical trials will provide the best information. That's according to University of Texas at Austin researchers Steve Bellan and Lauren Meyers, who are studying Ebola vaccine trials with the U.S. Centers for Disease Control and Prevention (CDC).

Ebola vaccine trials are underway in Guinea and Liberia, two of the three hardest-hit countries in the ongoing epidemic, and the CDC just initiated a vaccine trial in Sierra Leone.

The researchers found that changing the vaccine study design from the approach used originally proposed by the CDC would lead to better information about the effectiveness of the vaccine. The CDC is, in fact, using the phased-rollout randomized controlled trial recommended in the paper. Ebola has declined at different rates throughout Sierra Leone, which could impact the findings of a vaccine study.

The scientists' results, published April 14 in *The Lancet Infectious Diseases*, show that the "stepped wedge" trial design originally planned would have been less likely to provide clear information than the phased-rollout randomized controlled trial that the CDC now plans to use. They also found that the stepped wedge design would not have provided any of the ethical advantages that originally motivated this design.

The University of Texas at Austin research team includes Professor Lauren Meyers, Postdoctoral Researcher Steve Bellan, and graduate student Spencer Fox, as well as experts from the CDC, University of Florida, Gainesville, McMaster University in Canada, Yale University, Monash University in Australia, and University of California, San Francisco.

From a computing standpoint, the researchers had to simulate and analyze data several thousand times for each scenario to see how effective a trial design was at detecting whether a vaccine did or did not work. "We considered 2,000 simulations for 300 scenarios, a total of 600,000 simulations, fitting 800 statistical models to each of these simulations. This means that we used the Lonestar4 supercomputer at the Texas Advanced Computing Center to fit 500 million models," says Bellan of the Center for Computational Biology and Bioinformatics at

UT Austin.

"If I hadn't had an HPC system like Lonestar, I would not have been able to complete this research because of the sheer amount of computing time that this took, and Lonestar's massive ability to parallelize and get things done quickly. Using my laptop would have taken years, and this is a timely project involving human health where you simply can't wait months or years to get the results," Bellan concluded.

Provided by University of Texas at Austin