

# Providing better data on the Ebola virus

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Researchers are exploring new and innovative methods to solve the complex mystery that is the Ebola virus.

"Quantifying the Epidemic Spread of Ebola Virus (EBOV) in Sierra Leone Using Phylodynamics," is featured in an upcoming issue of the journal *Virulence*. Authored by Samuel Alizon, Sébastien Lion, Carmen Lía Murall and Jessica Abbate, this article studies the use of phylodynamics to discover how the Ebola virus has spread throughout the West African country of Sierra-Leone.

Phylodynamics is the study of genetic variations in pathogens, and the effect of such variations on their transmissions.

"Phylodynamics is used to discover how viruses spread throughout a population," article co-author Samuel Alizon said. This can affect the virus' transmission rate or duration of the virus' infection.

"We managed to infer epidemiological parameters reflecting how fast the recent Ebola virus outbreak was initially growing in Sierra-Leone using only phylogenies inferred from the viral DNA sequences obtained from 78 infected patients," Alizon said.

The co-author goes on to mention that this method is especially important because the results are more impartial.

"Inference via virus sequences is less subject to biases than inference based on reported incidence data, particularly when public health

systems collecting those data are overwhelmed," Alizon said.

Studying the epidemic parameters early in the outbreak, the authors say, will play a pivotal role in eventually being able to control the virus, though there is still much work to be done in the field.

According to Alizon, "The community still awaits the publication of more sequences that will surely help to better understand the spread of the [virus](#)."

**More information:** "Quantifying the epidemic spread of Ebola virus (EBOV) in Sierra Leone using phylodynamics" [DOI: 10.4161/21505594.2014.976514](#)

Provided by Taylor & Francis

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