Scientists tracing Ebola's mutations hope to answer questions about latest outbreak

The picture is not yet complete, but intriguing discoveries have been made. Virus mutations first detected in Sierra Leone were found later in Liberia and Mali, and scientists are examining whether this resulted from the chance movements of people across borders.

While some scientists think it is unlikely that the mutations made a difference in how the virus functioned, others are looking at whether this version of the virus had properties that made it more capable of causing infection.

Scientists look for viral mutations because of their potential influence on the effectiveness of diagnostics or treatments. Researchers have changed Ebola diagnostic tests and experimental treatments based on information about how the virus has evolved from previous outbreaks to the one in West Africa.

Tracking changes in the virus' genetic sequence is an objective endeavor, unlike interviewing people on the ground.

"We can tell you with a high likelihood that this sequence is derived from this other sequence," said Jeffrey R. Kugelman, the chief of the bioinformatics branch of the Center for Genomic Sciences at the Army Medical Research Institute of Infectious Diseases.

One of the most intriguing findings so far is that viral descendants of what is known as cluster two have been found in the blood samples of all Liberian Ebola patients whose viruses have been sequenced and made public, and in patients in Mali who had traveled from and lived in Guinea.

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis. Read full original post: Scientists trace Ebola's genetic path in Africa, weighing role of mutations