

Mining Zika for genetic data may reveal how virus evolves, spreads and how it can be stopped

Pardis Sabeti is a computational geneticist who works at the Broad Institute of MIT Harvard, where she pinpoints the genetic factors in genomes that allow diseases to take hold.

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One of our strengths is computational biology: taking genomes and trying to understand what's meaningful and what changes have been important.

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As new cases emerge we're sequencing [genomes] to understand where they might have come from and how they might relate to others. Also, there is an interesting case of individuals who are likely reservoirs for the virus. They have Ebola in their semen and in their breast milk...People will say: "Oh, they survived Ebola," but with both Lassa and Ebola the long-term effects on health are dramatic.

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The technologies we've been developing for Ebola work well for many viruses, but [Zika](#) is more challenging as it often occurs at very low concentrations in patient samples. For this reason, researchers have only been able to sequence a small number of samples over the past year, leaving many questions about the virus's evolution and diversity.

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion, and analysis. Read full, original post: [A cure for Zika may lie in mining viruses for genetic data](#)