EXTINGUISHING Outbreaks

by Dr. Alex Dornburg, *Research Curator of Ichthyology*

The year 2014 marked the worst outbreak of Ebola in human history. Within a few months, the world witnessed a battle to control its spread while death tolls climbed into the thousands. It seemed the virus was swiftly outpacing all efforts to control it. This unparalleled outbreak quickly spanned several countries in western Africa and prompted a massive international collaborative response among health organizations. The magnitude of effort devoted to controlling this disease was enormous. In addition to treating those already documented with Ebola, the initial estimates for undocumented cases ranged from the thousands to the Center for Disease Control's estimate of 1.4 million. This high uncertainty made it difficult for health officials to determine the appropriate amount of resources to send to each afflicted area. It was clear that rapid eradication of the virus was of the utmost importance, but just how do you begin to calculate the extent of an outbreak?

Determining how many people are infected with Ebola is a question deeply rooted in evolutionary biology. As a virus enters a new host, it begins to replicate. During replication the DNA of the virus can undergo slight changes, and new hosts will receive these genetically distinct copies during transmission. This pattern then repeats as viruses are transferred from person to person. In this way, the generational DNA changes in Ebola create a record of the virus's family tree as they are passed between patients, a record that is kept in the viruses found within host patients.

During the outbreak of 2014, Dr. Jeffrey Townsend of the Yale School of Public Health led a study demonstrating that, with the help of a reconstructed Ebola family tree, health officials could estimate the number of missing cases by measuring the rate of DNA changes between patients. (A disproportionately high number of genetic changes between two consecutively documented cases indicated the presence of missing cases.) Using this approach, the problematic gap between estimates of undocumented cases began to close, and calculating the extent of a viral outbreak became a reality.

I recently joined Dr. Townsend's team to help refine these missing case estimation techniques so health officials can more effectively combat future virulent outbreaks. This collaboration formed from an unlikely origin: Townsend and I originally worked together researching the ancient origins of fish biodiversity. These efforts led to the recent creation of software that enables researchers to extract information from DNA to better construct accurate evolutionary family trees (detailed in the journal *BMC Evolutionary Biology*). Just as it is useful for understanding the history of fish DNA, this software is also useful for studying infectious diseases. We hope to use the software to more precisely estimate the numbers of undocumented cases during outbreaks and to further develop tools to detect regional clusters of such cases.

Emerging infectious diseases are among the biggest modern-day threats to global human health. Using tools developed to understand the evolution of DNA might provide key information for health officials with time-sensitive needs and limited resources. Such information is pivotal in responding effectively to outbreak locations in dire need of fast, effective aid when combating emerging pathogens like Ebola, Zika or Marburg virus.

[ABOVE] Colorized scanning electron micrograph of filamentous Ebola virus particles (green) attached and budding from a chronically infected VERO E6 cell (orange) (25,000x magnification).