



### BACKGROUND READING

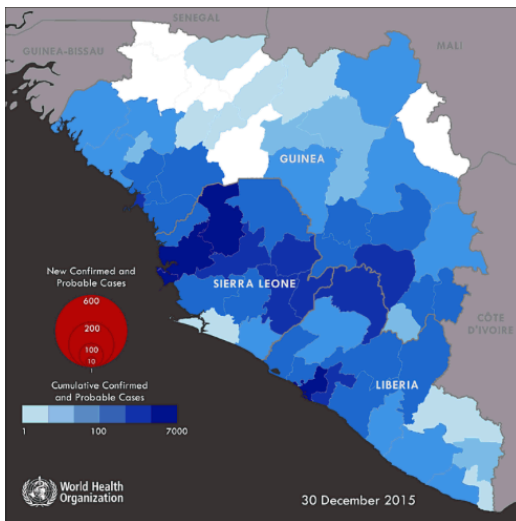
The Ebola virus is a zoonotic virus, which means that it can spread from animals to humans. Once a person is infected, the virus affects multiple organ systems in the body. Infected cells can attach themselves to blood vessels, causing uncontrollable internal bleeding in some patients, accompanied by high fever—a condition known as hemorrhagic fever. Other common symptoms include liver and kidney failure, vomiting, and diarrhea. On average, 50% of people that contract Ebola die from the disease, though fatality rates of past outbreaks have varied from 25% to 90%.

The first documented outbreak occurred in 1976 in the Democratic Republic of the Congo, in Central Africa, and infected about 300 people. Since then there have been several other outbreaks in Central Africa, but the largest on record began in Guinea, a country in West Africa, in December 2013. The virus spread to the neighboring

countries of Sierra Leone and Liberia. By April 2016, over 28,000 cases, and more than 11,000 deaths, were reported in West Africa.

The 2013–2016 outbreak was unprecedented in size and duration. This drastic increase in cases could be attributed to several possible factors. As this was the first known Ebola outbreak in West Africa, regional differences could be one factor. Central Africa is predominantly forested with limited access to roads, while West Africa has several large cities and better transportation infrastructure, making it easier for infected patients to travel between communities and across borders, spreading the disease.

During the 2013–2016 outbreak, the Kenema Government Hospital in Sierra Leone collaborated with scientists in Pardis Sabeti’s lab at the Broad Institute to use genetic analysis to screen suspected patients and accurately diagnose infection. They also wanted to determine how the virus was changing over time.



Map of Ebola cases in West Africa from January 2014 to December 2015.  
WHO

**Figure 1. Map showing the spread of the 2013–2016 West African Ebola outbreak.** Regions shaded darker had more cases. (Source: World Health Organization.)

### Tracking Virus Spread

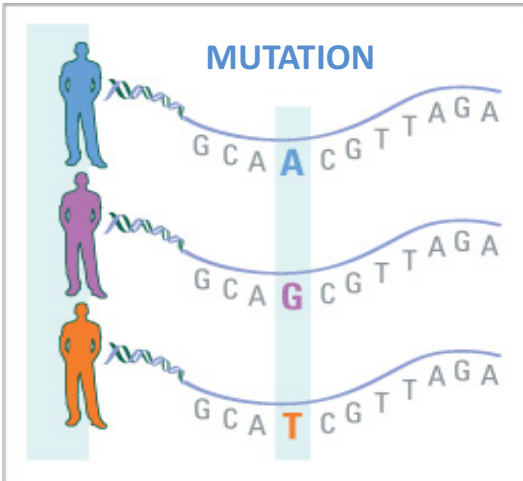
Ebola spreads by close contact with an infected patient’s bodily fluids, such as blood, saliva, urine, or sweat. In addition to contact tracing, in which outbreak responders try to identify those exposed to infected people, scientists can also track how Ebola spreads from person to person by using DNA sequencing. Each Ebola patient has the virus in his or her blood. The Ebola virus has a genome made of **RNA**, made up of a sequence of letters (G, C, A, and U). Over time, as the virus replicates, random changes to the sequence of letters occur, referred to as **mutations**. During infection, the virus replicates many times, creating many possible mutations. Many of these mutations will be detrimental to the virus and even result in defective viruses, others will be neutral, and a small number of mutations may confer some type of advantage. If the infected patient passes the virus on to a



second person, the second person may inherit the mutated virus, which will, over the duration of the infection, accumulate additional mutations. In this way, viruses transmitted from one person to another are related to one another and may accumulate differences over time.

Scientists isolate virus RNA from blood samples and then convert the RNA to DNA. Using DNA sequencing, they

then compare virus sequences isolated from individuals in different locations and at different times in an outbreak. By identifying differences in the viral genomes, scientists can reconstruct the history of how the virus spreads and mutates. Tracking mutations over time can also reveal whether the virus is becoming potentially more dangerous.



Within the first few weeks of the outbreak in Sierra Leone, scientists from Sabeti’s lab sequenced Ebola samples from 78 patients. They compared the data to a reference sequence from a patient in Guinea, where the Ebola outbreak began. In the activity, you will analyze a subset of the actual virus sequences collected by the Sabeti lab and compare your results to theirs.

**Figure 2. A mutation is a change in the nucleotide sequence.** These mutations show changes in a DNA sequence. The Ebola virus has a genome made of RNA, but it was converted to DNA for sequencing.