

BIOSAFETY BACKGROUNDER

How are the Ebola samples collected, handled, stored, and studied?

In Sierra Leone:

- Blood samples are taken from patients suspected of having an Ebola infection. Samples are collected in the Kenema government hospital by technicians and scientists as part of the diagnostics program that they have for Lassa and other infectious diseases.
- Blood samples are centrifuged. Serum is then removed and put into an inactivation buffer, which breaks down all the cell walls and proteins. No active viral proteins or live cells remain, so the virus is no longer able to replicate. Color and volume indicate that the inactivation buffer has been added.
- Before samples are shipped to Harvard, the outsides of the tubes are disinfected with bleach and the tubes are put into boxes with dry ice.
- The protocols for collection and inactivation were created in collaboration with the US Army Medical Research Institute for Infectious Diseases (USAMRIID).

At Harvard:

- When Harvard scientists receive the samples, they extract the nucleic acid from the sample and eliminate the DNA.
- RNA is put into tubes and into the freezer. Samples are stored at Harvard initially.
- Harvard submits a formal request through the Broad's Genomics Platform and receives a sample intake kit that is used to prepare and label samples for shipment and arrival at the Broad.
- Harvard sends RNA (viral nucleic material only) to Broad.

At Broad:

- Samples are brought into Broad labs and handled using appropriate protocols. (These are the same protocols Broad has used while studying Lassa fever for the last 3 years.)
- Broad lab technicians "gown up" (face shields, disposable gowns, two layers of gloves, etc.), in adherence to safety protocols.
- The RNA samples are converted into complementary DNA (cDNA), a procedure that stabilizes the genomic material and prevents the sample from deteriorating during handling.
- The cDNA samples can then be moved from more restrictive labs to the main labs (where standard lab gloves, lab coats, etc., are worn), and prepared for genome sequencing on high-end Illumina sequencers.
- Any remainders of the samples (one or two microliters) are kept in secure labs. When researchers dispose of them, chemicals are added to destroy any remaining RNA before leaving the lab, and then the samples are taken out as biohazardous waste and disposed of off-site.
- After the cDNA is sequenced, sequencing data from each sample is then filtered to remove any human genomic data, so that the sample can be analyzed and published anonymously to protect patient information.

Is there a threat of infection with Ebola in the Broad's BL2+ or BL1 labs?

- There is no identifiable risk of infection with Ebola in the Broad laboratories. When samples are brought to the Broad, they consist of purified RNA only without the viral protein machinery necessary

for infection, eliminating the hazard. By itself, viral RNA from Ebola and other hemorrhagic fever viruses is non-infectious.

Have these safety measures been used in Broad labs previously?

- Yes. Researchers at the Broad are using the same safety protocols that have been used for the past three years at the institute to study Lassa fever, a virus of similar danger level to Ebola.
