Six months into the worst Ebola epidemic in history, the world is losing the battle to contain it. - Dr. Joanne Liu, President, Doctors Without Borders

Largest Ebola outbreak, first outbreak in W. Africa
2,240 cases as of Aug 22, 2014

17,145 cases as of Dec 3, 2014
8 countries, 3 continents
We study recent human evolution

... largely shaped by infectious disease

Genomic signals of malaria's adaptations to drugs

Mostly neutral variants

Beneficial allele affects nearby variants

Genomic signals of human adaptations to Lassa virus

We developed tools to analyze genomes of highly diverse RNA viruses

Laboratory tools:
- Biosafety & viral inactivation
- Human RNA depletion
- RNA virus sequencing

Computational tools:
- Viral assembly & informatics
- Phylogenetics
- Intrahost variation
- Evolution and adaptation
We developed the capacity to study a BL4 pathogen in rural field settings (Nigeria & Sierra Leone)

Ebola: March 2014

Sierra Leone, March 2014: Pre-Outbreak Preparedness

Laboratory Supplies & PPE
Containment & Biosafety
Ebola PCR Diagnostics

May 25, 2014: First confirmed case of Ebola in Sierra Leone
Augustine Goba, Director MoHS-KGH Laboratory
Sierra Leone outbreak originates at the Guinea border

Contact tracing during the 1st week of the outbreak by the Sierra Leone Ministry of Health and Sanitation (MoHS)

1 month in: Harvard/Broad receives samples from ~70% of all Ebola patients in Sierra Leone

10 days from sample to Genbank

The first NGS data set for Ebola

Complete, reliable genomes

Largest, deepest dataset from an Ebola outbreak
But why are we sequencing Ebola genomes?

How can viral genomes inform public health?
- Where did this virus come from?
- How is it different from before?
- How is it changing?
- How is it spreading between people, towns, countries?
  - Can we track transmission?
  - Animal exposure risks?

Phylogenetics to trace viral origins

Initial entry of two viral lineages into Sierra Leone with no further entries

Can view viral evolution in near real-time
New mutations fall in temporal and spatial patterns

Intrahost variation elaborates transmission epidemiology

New mutation is rapid and random during the outbreak

The changing genome may affect diagnostics and therapeutics

An unbiased look at all bloodborne microbes

Predicting whether a patient is infected or will survive based on simple clinical tests

Correlates w/infection:
- Temperature

Correlates w/outcome:
- Kidney damage
- Liver damage
- Temperature
- Patient age
Frequently Asked Questions …

- Will it go airborne?
- Won’t it go away on its own?
- Is this just a W. African problem?
- What do we do?

Will it burn itself out?

Is the virus adapting?

Is it just a problem for Africa?

Long term solution?

“Our hope is that next time this happens, we will be able to perform deep sequencing right on African soil.”

—Prof. Christian Happi
Aug 28, 2014

Countries with recent transmission: USA, Mali, GIN/SLE/LIB

Countries with transmission in 2014: Spain, Nigeria, USA, Mali, GIN/SLE/LIB

Countries with patients in 2014: Germany, France, Sweden, Switzerland, Italy, UK, Senegal, Spain, Nigeria, USA, Mali, GIN/SLE/LIB
In memoriam…