Identification of human epidemic threats in sentinel hosts
One Health Interface

- Majority of emerging infectious diseases (EIDs) in people are of animal origin (zoonotic)
- 75% of emerging zoonoses have wildlife origins
- Human activities at the interface linked to EIDs (Nipah virus, SARS, Ebola)
- On the order of 3 new infectious diseases in people each year

Land Use Change & Human Population Growth

Livelihood Impacts & Economic Pressures

Increased Contact Between Humans, Livestock, & Wildlife

Health Risks to Humans, Livestock, & Wildlife

Enhanced Flow of Pathogens
Global travel & trade can turn local epidemics into pandemics
PREDICT

The Ministries of Health, Agriculture & Environment and Implementing University and NGO Partners in 35 Countries
Training a Disease Surveillance Workforce
Training a Disease Detection Workforce
One Health Testing Strategy

Priority Zoonotic Diseases with Pandemic Potential
Multi-valent testing platform
Standardized across wildlife, livestock, and people

- Filoviruses (Ebola, Marburg and new variants)
- Influenza viruses (Flu and new variants)
- Coronavirus (MERS, SARS, and new variants)
- Flaviviruses (YFV, Zika, and new variants)
- Paramyxoviruses (Nipah, Hendra, and new variants)
- Arena, Bunya, Rhabdo, Retro, . . . . .
MERS-like Virus Identified in Uganda

Bat sampled in Kisoro District, Southwest Uganda

Distribution of *Pipistrellus hesperidus*
Novel ebolavirus found in Sierra Leone

Positive sampling site

Sampling site

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Distribution of bats:
- Angolan free-tailed bat (*Mops condylurus*)
- Little Free-tailed Bat (*Chaerephon pumilus*)
Comparison to other Ebolaviruses

Full Genome

EBOV/1976/H.sapiens/DRC
EBOV/1995/H.sapiens/DRC
EBOV/2007/H.sapiens/DRC
EBOV/2014/H.sapiens/LBR
EBOV/2014/H.sapiens/GIN
EBOV/2015/H.sapiens/SLE
BDBV/2007/H.sapiens/UGA
TAHV/1994/H.sapiens/CIV
BOMV/2017/M.condylurus/SLE
BOMV/2017/C.pumilus/SLE
SUDV/2000/H.sapiens/UGA
RESTV/1989/M.fascicularis/USA
LLOV/2003/M.schneideri/ESP
MARV/1999/H.sapiens/DRC
MARV/2009/R.aegyptiacus/UGA

AIM 4

BOMV

Map of West Africa
TRAINED a One Health workforce (over 4,300 individuals) in over 30 countries

SAMPLED over 142,000 animals and people in the most vulnerable and at-risk areas for zoonotic disease emergence

STRENGTHENED over 60 laboratories for improved disease detection and national and global health security

DETECTED over 1,100 unique viruses in animals and humans, including a new ebolavirus as well as MERS- and SARS-like coronaviruses
Ranking Which Viruses Are Most “Risky”

VIRUS + HOST + ENVIRONMENT = RISK OF SPILLOVER

- Host species traits, Geographic range, Relatedness
- Virus-specific traits
- Viral infectivity / Virulence
- Transmission abilities

- Host plasticity
- Epidemiology
- Host ecosystem
- Land use change

USAID PREDICT

VIRAL RISK RANKING
Have a question? For online attendees, click on the Live Q&A tab, type your question into the pop-up box, and click "submit."
Developed by infectious disease scientists, SpillOver: Viral Risk Ranking explores and directly compares hundreds of virus, host and environmental risk factors to identify viruses with the highest risk of transmission from animals to humans.
Have a question? For online attendees, click on the Live Q&A tab, type your question into the pop-up box, and click "submit."
Found Something New?

Have you found a new virus? Or detected a known virus in a new host species or location? In a few simple steps see how your virus compares to others in the SpillOver database.

SpillOver is a crowd-sourcing platform intended to evolve alongside scientific advances. Contribute your ideas and thoughts for improvements on the discussion forum.

For more details on the science behind SpillOver, please see the associated publication by Grange, Mazet et al.
Discovery curves show the number of samples required

- PREDICT research has demonstrated that far fewer samples than previously expected are required to identify all the viruses in a given species
- These viral discovery curve studies provide a roadmap to sampling needs for GVP
Making the unknown known

111 viral families recognized to-date infecting all hosts around the globe

24 of these families likely contain zoonotic species

To-date a total of 385 viruses are known to have infected humans

~1.6 million viral species spanning the 24 viral families are estimated to be circulating in mammals and water fowl

Of these 500,000 - 800,000 viral species are likely to be of pandemic or epidemic potential
Towards a proactive paradigm for early disease detection and response

One Health approach to understanding the dynamics of zoonotic virus evolution, spillover from animals to people, amplification, and spread to inform prevention and control