Predicting and preventing emerging infectious diseases in a changing world

A Project of USAID’s Emerging Threats Program
One Health Approach

- Veterinary Medicine
- Comparative Medicine
- Human Medicine
- Social Sciences
- Humanities
- Animals
- Biology
- Ecology
- Environment
- Engineering
- Earth Sciences
The Challenge

Pre-empt or combat, at their source, the first stage of emergence of zoonotic diseases that pose a significant threat to public & animal health (potentially pandemic infections)
Whose food needs to be safe?
Emerging Infectious Diseases

• Majority are of animal origin (zoonotic)

• 75% of emerging zoonoses have wildlife origins

• Human activities at the interface are linked to EIDs (Nipah virus, SARS, Ebola)

• Annual population growth among highest in buffers to protected areas near wildlife
One Health in Action

Source: Karesh et al. 2012. The Lancet & WHO
One Health in Action

Source: Karesh et al. 2012. The Lancet & WHO
Global Vulnerability - Zoonotic EIDs
Targeted, Risk-based Surveillance

- Primates
- Bats
- Rodents
- Birds
- Suids
- Carnivores
- Ungulates
Targeted, Risk-based Surveillance

**High Risk Interfaces**
Specific situations enabling contact between wild animal hosts and people

**Pathogen**
Zoonotic disease emergence in humans

**Host**

**Environment**

**Large-scale Ecological Drivers**
- Wildlife biodiversity
- Human population density
- Land use change
- Agricultural industry change
Bat Guano Farms

Vietnam, Cambodia & Thailand
MAJOR GLOBAL ACHIEVEMENTS
Safely Sampled More than 56,000 Animals
Developed & Operationalized Diagnostic Platform
Laboratory Capacity Building

- Trained 32 laboratories globally
- 27 screening for targeted viral families

Baseline Laboratory Capacity Prior to PREDICT
- 28
- 6

Laboratory Capacity at the end of PREDICT
- 27
- 5
- 2

- Laboratories screening for target viral families
- Laboratories receiving training and beginning to screen for target viral families
- Laboratories on track to screen for target viral families
Ran Over 400,000 Diagnostic Tests

- Ungulates
- Bats
- Carnivores
- Nonhuman Primates
- Rodents and Shrews
- Other Mammals

Proportion of Positive Test Results
Emerging Threats Program

Viral Detection Success

Overall 984 known and new viruses:

- 812 novel and 147 known in animals
- 3 novel and 31 known in human pilot studies

<table>
<thead>
<tr>
<th></th>
<th>Bats</th>
<th>Nonhuman Primates</th>
<th>Rodents and Shrews</th>
<th>Humans</th>
<th>Other taxa**</th>
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<td>Novel</td>
<td>431</td>
<td>234</td>
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<td>55</td>
<td>15</td>
<td>31</td>
<td>1</td>
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<tr>
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<td></td>
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Bats Are Natural Reservoirs of SARS-Like Coronaviruses


Severe acute respiratory syndrome (SARS) emerged in 2002 to 2003 in southern China. The origin of its etiological agent, the SARS coronavirus (SARS-CoV), remains elusive. Here we report that species of bats are a natural host of coronaviruses closely related to those responsible for the SARS outbreak. These viruses, termed SARS-like coronaviruses (SL-CoVs), display greater genetic variation than SARS-CoV isolated from humans or from civets. The human and civet isolates of SARS-CoV nestle phylogenetically within the spectrum of SL-CoVs, indicating that the virus responsible for the SARS outbreak was a member of this coronavirus group.

In this study, conducted from March to December of 2004, we sampled 408 bats representing nine species, six genera, and three families, from four locations in China (Guangdong, Guangxi, Hubei, and Tianjin) after trapping them in their native habitat (Table 1). Blood, fecal, and throat swabs were collected; serum samples and cDNA from fecal or throat samples were independently analyzed, double-blind, with different methods in Wuhan and Geelong (14).

Among six genera of bat species surveyed (Rhinolophus, Hipposideros, Miniopterus, and Myotis), three commensal, cavedwelling species from the genus Rhinolophus (horse-shoe bats) in the family Rhinolophidae demonstrated a high SARS-CoV antibody prevalence: 13 out of 46 bats (28%) in R. pumilio from Guangxi, 2 out of 6 bats (33%) in R. presilius from Guangxi; and 5 out

Li et al. (2005) Science; Ge et al. (2013) Nature
Novel beta CoV from bat guano

Thailand bat CoV

MERS-CoV, Saudi Arabia

Wacharapluesadee et al. (2013) EID
Outbreak Investigations
With Governments: Making Data Available to the Public
Scientific Strategy: Virus Risk

Expanded characterization of viruses with epidemic and unknown pandemic potential combined with risk assessment

Spillover risk
Pandemic risk
Targeted, Risk-based Training & Surveillance
Scientific Strategy: Ecological Risk

Identify large-scale trans-boundary ecological processes underlying human activities at high-risk interfaces

Characterize pathways for disease emergence
PREDICT

THE WORLD’S MOST COMPREHENSIVE ZOONOTIC DISEASE SURVEILLANCE & CAPACITY DEVELOPMENT PROGRAM

TRAINED 2,500 government personnel, physicians, veterinarians, resource managers, laboratory technicians, hunters, and students on biosafety, surveillance, lab techniques, and disease outbreak investigation.

SAMPLED 56,000+ nonhuman primates, bats, rodents, and other wild animals (including bushmeat samples) at human-wildlife interfaces with high-risk and opportunity for viral spillover from wildlife hosts to humans.

DEVELOPED & OPTIMIZED low-cost viral family level consensus PCR methods and synthetic controls for the detection and discovery of new viruses from the target viral families in 32 labs in 20 developing countries around the world.

DETECTED a total of 984 unique viruses in wild animals and humans: 815 novel viruses and 169 known viruses - the most comprehensive viral detection and discovery effort to date.

32 LABS

815 NOVEL

169 KNOWN
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
The Ministries of Health, Agriculture & Environment and Implementing University and NGO Partners in 31 Countries