Models answer key questions to predict and prevent pandemics

1. Where will the next pandemic originate?
2. What’s causing the rise in pandemics?
3. Which wildlife species harbors the most potentially pandemic viruses?
4. How can we prevent pandemics, and can we afford it?
<table>
<thead>
<tr>
<th>Variable</th>
<th>Relative Influence (%)</th>
<th>Std. Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>population</td>
<td>27.99</td>
<td>2.99</td>
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<td>mammal diversity</td>
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<td>change: pop</td>
<td>13.54</td>
<td>1.54</td>
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<tr>
<td>change: pasture</td>
<td>11.71</td>
<td>1.30</td>
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<tr>
<td>urban extent</td>
<td>9.77</td>
<td>1.62</td>
</tr>
</tbody>
</table>

**y-axis:** relative probability of an EID event in a grid cell with this characteristic

**x-axis:** min. to max. values of each driver (except ‘Pasture Change’)

The plots show effect relative to human pop. distribution, factoring out reporting bias

Model: 2 levels of interaction between drivers
Which species will the next pandemic spillover from?

PREDICT/NIAID work discovered >500 bat-CoVs in China

RdRp partial gene sequence. Size of circle proportional to the number of samples with identical viral sequences.

α – CoVs Clade 2b (SARSr-CoVs)

405 β – CoVs (SADSr), 361 from China
Bat-CoV risk is regional, not restricted to China

Distribution of bats harboring SARSr-CoVs

Distribution of *Rhinolophus affinis*
Bat coronavirus risk is regional, not restricted to China

▲ = Site in SW Yunnan where we conducted surveillance
Evidence of community exposure to bat CoVs (0.45% - 2.9% seropositive)

Across Southeast Asia: 1 - 7 million people likely exposed every year across the region
Bat coronaviruses are a “clear and present danger”

“Out of >20 PREDICT publications on bat CoV research in China and SE Asia”

“Our study provides the first serological evidence of likely human infection by bat SARSr-CoVs or, potentially, related viruses.” (Wang et al., 2018)

“Cell entry studies demonstrated that three newly identified SARSr-CoVs with different S protein sequences are all able to use human ACE2 as the receptor, further exhibiting the close relationship between strains in this cave and SARS-CoV. This work provides new insights into the origin and evolution of SARS-CoV and highlights the necessity of preparedness for future emergence of SARS-like diseases.” (Hu et al., 2017)

“We report the isolation and characterization of a novel bat coronavirus which is much closer to the SARS-CoV...this virus can use ACE2 as a receptor and infect animal and human cell lines. Our results provide further evidence of the bat origin of the SARS-CoV and highlight the likelihood of future bat coronavirus emergence in humans.” (Yang et al., 2015)

“We demonstrate that bats harbour a significantly higher proportion of zoonotic viruses than all other mammalian orders.” (Olival et al., 2017)

“Our study provides the first serological evidence of likely human infection by bat SARSr-CoVs or, potentially, related viruses.” (Wang et al., 2018)
Costs and Return on Investments for Disease Emergence

1. Key model assumptions: Reduction in the cost of zoonotic outbreaks from GVP grows from 1% in 2020 to 10% in 2035 and remains at 10% through 2050; global GDP starts at $73.4T and increases 2.4% annually (World Bank 2015 analyses); Annual number of EID events starts at 2.6 and increases 1.2% annually (Jones et al. 2008; Pike et al. 2014)

~$23.5T in average cumulative damages over 30 years from EIDs

~60% due to reduction in outbreak severity

~40% due to reduction in number of outbreaks
PREDICT
Surveillance
where it matters
Coordinated Disease Surveillance Workforce
Coordinated Disease Surveillance Workforce
PREDICT 2009-2019

PREDICT 2 only
Animals tested n = 67,679
Humans tested n = 16,499
One Health Surveillance

Partnership between wildlife, livestock, and human health experts

Concurrent triangulated design
One Health Surveillance

Credit: WCS & PREDICT/Viet Nam
## PREDICT FINDINGS in 14 Africa and 12 Asia countries (2009-2019)

<table>
<thead>
<tr>
<th>Category</th>
<th>Coronaviruses</th>
<th>Paramyxoviruses</th>
<th>Influenzaviruses</th>
<th>Flavivirus</th>
<th>Overall Total*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>% positive</td>
<td>n positive</td>
<td>% positive</td>
<td>n positive</td>
<td>n positive</td>
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<tr>
<td>bats</td>
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<td>3,070</td>
<td>0.78%</td>
<td>500</td>
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<td>rodents &amp; shrews</td>
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<td>0.37%</td>
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<td>camels</td>
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<td>0.00%</td>
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<td>0.00%</td>
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<td>0.10%</td>
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<tr>
<td>pangolins</td>
<td>0.00%</td>
<td>0</td>
<td>0.00%</td>
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<td>0.28%</td>
<td>4</td>
<td>0.42%</td>
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<td>cattle/buffalo</td>
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<td>0.00%</td>
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<td>goats/sheep</td>
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<td>0</td>
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<td>poultry/other fowl</td>
<td>10.43%</td>
<td>258</td>
<td>1.46%</td>
<td>36</td>
<td>1.94%</td>
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<td>swine</td>
<td>12.42%</td>
<td>99</td>
<td>0.88%</td>
<td>7</td>
<td>3.01%</td>
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<tr>
<td><strong>Total</strong></td>
<td><strong>4,483</strong></td>
<td><strong>705</strong></td>
<td><strong>333</strong></td>
<td><strong>10</strong></td>
<td><strong>7,379</strong></td>
</tr>
</tbody>
</table>

* varied by test type

based on number of samples tested
Direct and indirect contact with wildlife resulting in disease spillover

Bunyaviridae, Flaviviridae, Togaviridae, Arenaviridae, Rhabdoviridae, Poxviridae, Filoviridae, Paramyxoviridae, Retroviridae, Orthomyxoviridae, Picornaviridae, Reoviridae, Bornaviridae, Coronaviridae, Hepeviridae, Herpesviridae
Bats, primates, rodents and shrews more likely than other species to shed viruses among species targeted in PREDICT 1 and 2

Detections in specimen type highlight important animal-human interfaces for disease transmission
  - DNA viruses most commonly shed orally
  - RNA viruses most commonly shed in urine and feces

Where have we been most likely to find viruses with zoonotic potential in wild animals?
**Bats, primates, rodents, shrews, and birds** more likely than other species to shed RNA viruses in urine and feces

**Wildlife-human interfaces** with **more frequent** detection of RNA viruses (in order of magnitude of association, compared to situations where contact with animals is not likely)

- in transit along value chain
- caves
- for sale in large markets
- for sale in small markets
- for sale in medium markets
- wildlife sanctuary/confiscation, extractive industry, crop production

**Wildlife-human interfaces** with **less frequent** detection of RNA viruses

- wildlife restaurants, wildlife destined for consumption, wildlife in management settings, hunted wildlife, wildlife raiding crops, wild animal farms, private sale of wildlife
Where have we been most likely to find coronaviruses with zoonotic potential in wild animals?

- Bats, birds, rodents and shrews more likely than other species to shed coronaviruses in urine and feces
- Wildlife-human interfaces with more frequent detection of coronaviruses (in order of magnitude of association):
  - in transit along value chain
  - for sale in large, medium, and small markets

Where have we been most likely to find paramyxoviruses with zoonotic potential in wild animals?

- No strong species predilections, paramyxoviruses were more likely to be shed in urine
- Wildlife-human interfaces with more frequent detection of paramyxoviruses (in order of magnitude of association):
  - wild animal farms
  - guano farms
Virus Host Plasticity

Zoonotic Viruses
Reported through 2011

- 65% of zoonotic viruses in 3 or more taxonomic orders
- 45% of zoonotic viruses in 5 or more taxonomic orders
- High-risk interfaces with increased host plasticity
  - Situations that facilitate close contact between diverse hosts of wild animals, such as wildlife sold at markets, kept in sanctuaries

Viruses with Zoonotic Potential Detected by PREDICT 2009-2019
Human coronaviruses

Coronaviruses detected in people during PREDICT surveillance (2014-2019)
Human coronaviruses

Coronaviruses detected in people during PREDICT surveillance (2009-2019)
Emerging Threats Surveillance

Number of Viruses Detected

Number of animals tested

Taxa
- bats
- non-human primates
- rodents/shrews
Emerging Threats Surveillance

Detectable because of illness

Detectable because shedding at time of sampling

Subclinical Disease

Exposure

Cases

Time
Wildlife contact associated with human exposure to ebolaviruses

Secondary wild animal spillover hosts remain important sources of human exposure to Ebola virus and Sudan virus, two causes of hemorrhagic fever.

We enrolled 331 febrile patients presenting to two healthcare facilities near the Bwindi Impenetrable Forest, Uganda, a hotspot for primate diversity in East/Central Africa. Specimens were tested using PCR and Western blot for Ebola virus (EBOV), Sudan virus (SUDV), Bundibugyo virus (BDBV) and Marburg virus and questionnaires were used to collect information on interactions with wildlife. We did not detect active infection in patients by PCR but found evidence for past exposure to ebolaviruses in this population.
PREDICT Serology
in collaboration with USAMRIID

8 Countries in Africa

3 Countries in Asia

8 Virus Groups
- Crimean-Congo Hemorrhagic Fever Virus-like
- Rift Valley Fever Virus-like
- Lassa Fever Virus-like
- Hantaviruses
- Alphaviruses
- Flaviviruses
- Filoviruses similar to Ebolaviruses
- Filoviruses similar to Marburgvirus
IgM Seroprevalence

Alphaviruses

Crimean-Congo Hemorrhagic Fever Virus-like

Flaviviruses

Rift Valley Fever Virus-like
**Improved Awareness for Zoonotic Diseases = Pandemic Preparedness**

**Zoonotic Disease Preparedness**

Moved the paradigm towards prevention
Brought attention to events precipitating outbreaks
One Health in action

First detection of zoonotic disease outbreaks
Virus Detection and Discovery

- Overview of PREDICT strategy
- Summary of virus findings
- Highlights from priority virus families
Virus Detection and Discovery

- Overview of PREDICT strategy
- Summary of virus findings
- Highlights from priority virus families
Casting a Wide Net

1. **Sample**  
   wildlife, livestock, humans

2. **Detect**  
   consensus PCR - corona, filo, paramyxovirus, influenza (other)

3. **Characterize**  
   full-genome sequencing

4. **Assess risk**  
   experimental (specific viruses); eco-epidemiological (broad)
Virus Detection and Discovery

- Overview of PREDICT strategy
- Summary of virus findings
- Highlights from priority virus families
<table>
<thead>
<tr>
<th>Viral Family</th>
<th>Number of known viruses found in P1</th>
<th>Number of novel viruses found in P1</th>
<th>Number of additional known viruses found in P2</th>
<th>Number of additional novel viruses found in P2</th>
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</tbody>
</table>
Priority Virus Families

309

70

5

Human 16, Domestic species 14
Virus Detection and Discovery

- Overview of PREDICT strategy
- Summary of virus findings
- Highlights from priority virus families
Coronaviruses
## Coronavirus Results

<table>
<thead>
<tr>
<th>Taxa</th>
<th># tested</th>
<th># Pos</th>
<th># Neg</th>
<th>% Pos</th>
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<tbody>
<tr>
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<td>32928</td>
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<tr>
<td>Rodents and Shrews</td>
<td>17844</td>
<td>814</td>
<td>17030</td>
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<tr>
<td>Non-human Primates</td>
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<td>9523</td>
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<td>Humans</td>
<td>16101</td>
<td>71</td>
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<td><strong>Total</strong></td>
<td><strong>79329</strong></td>
<td><strong>3818</strong></td>
<td><strong>75511</strong></td>
<td></td>
</tr>
</tbody>
</table>

*based on number of individuals*
Species Richness
High : 36
Low : 1
= Sub-clade: 2c (MERS group)
Species Richness

High : 25
Low : 1

= Sub-clade: 2b (SARS group)
There are >3738 coronaviruses in bats

Average # CoV per species = 2.67
(limiting to species ≥110 individuals)

Extrapolate to all 1400 bat spp = 3738
MERS-CoV is a recombinant

Recombination is an evolutionary driver of host-switching
Coronaviruses – summary of major findings

- Bats are a major reservoir of CoVs
- Biogeography of CoVs is predictable based on host species
- Spike recombination is an important driver of host switching
Filoviruses
Bombali Virus (BOMV) is a new ebolavirus found in bats.

Bats were roosting in ceilings, providing an interface for potential transmission.
Marburg Virus in Sierra Leone

Rousettus aegyptiacus

Freetown
Kasewe Cave $n = 186$
Njala University

Kakoya Cave $n = 131$
University of Makeni

Koema Cave $n = 111$
Tailu Village $n = 7$

Koema Cave

Marburg Virus in Sierra Leone
M. nimbae

Gueckedou – origin of 2013-2016 outbreak
Location of EBOV-positive M. nimbae bat
Filoviruses – summary of major findings

• Discovery of a novel ebolavirus in Sierra Leone
• Expansion of known range for Marburg virus
• Detection of Ebola virus in *M.nimbae* bat in Liberia
Paramyxoviruses
Henipavirus

Jeilongvirus

Uncharacterized

Narmovirus

Salem virus

Morbillivirus

Myotis riparius; Brazil

Phyllostomus hastatus; Brazil

Morbiliviruses

JQ411014 feline morbillivirus

KC802221 phocine distemper virus

AF014953 canine distemper virus

PMV-11-PDF-3137 Myotis riparius; Brazil

PBZ-1381-1382 Phyllostomus hastatus; Brazil

AJ608288 dolphin morbillivirus

AJ849636 peste-des-petits-ruminants virus

X98291 rinderpest virus

A8016162 measles virus

AB195968 Sendai virus

0.4
Paramyxoviruses – summary of major findings

• Expansion of known diversity (e.g., entirely new genera)
• Discovery of multiple bat morbilliviruses
• First rescue of any bat paramyxovirus directly from sequence
Laboratory Capacity and COVID-19 Response

PREDICT improved testing capacity in 67 labs in 36 countries

Built a network of linkages between laboratories, countries and government ministries

Laboratories have additional tools and the ability to detect newly emerging viruses when assays or sequences do not yet exist

Importance of these skills was underscored following the emergence of SARS CoV-2 in China

Teams in Southeast Asia able to call on the PREDICT network to share experience using PREDICT assays to detect the new virus
Coordinated Surveillance for Influenza and Viruses with Pandemic Potential – LISN (Longitudinal Influenza Surveillance Network) in Viet Nam

Amanda Fine, Wildlife Conservation Society

Mapping of human, livestock, and wildlife surveillance planned at 1st multi-sector LISN ‘One Health’ coordination workshop in Hanoi
Coordinated ‘One Health’ Surveillance for Influenza and Other Viruses with Pandemic Potential (‘‘LISN’’)

The Vision:

1. Alignment of the surveillance localities, sampling time and laboratory testing algorithm.
2. Monitor and characterize influenza viruses and other viruses with pandemic potential.
3. Regular information sharing, situation analysis, and risk assessment.
4. Coordination of PREDICT-2, FAO/DAH influenza surveillance in poultry and swine, WHO and US CDC SARI and ILI surveillance with GDPM/MoH.
# Enhanced Existing Surveillance Systems in Viet Nam for Early Detection of Pandemic Threats

## Coordinated Surveillance "LISN" added
- More capacity, more data sharing, more analysis, more knowledge for informed decision making
Coordinated Surveillance and Testing for Influenza and Potential Pandemic Pathogens

- Quarterly coordination meeting between PPMC and Sub-DAH to review progress and trouble shoot.
- Six monthly meeting to review virological and epidemiological data.
- Annual meeting to review risk assessment results and identify potential intervention.

Results shared across the sectors for interpretation, risk assessment, and action from provincial to national level.
Coordinated ‘One Health’ Surveillance Results: The Wildlife Farm Interface

Dong Nai Province, Viet Nam

PREDICT Behavioral Risk Surveillance Research Reveals a Complex Wildlife Trade Chain

A masked palm civet on a wildlife farm in Viet Nam
### Community Surveillance

<table>
<thead>
<tr>
<th>Virus</th>
<th>No. of specimens</th>
</tr>
</thead>
<tbody>
<tr>
<td>Influenzas</td>
<td></td>
</tr>
<tr>
<td>Influenza A</td>
<td>1</td>
</tr>
<tr>
<td>Influenza B</td>
<td>1</td>
</tr>
<tr>
<td>Paramyxoviruses</td>
<td></td>
</tr>
<tr>
<td>Strain of Human Parainfluenzavirus 3</td>
<td>1</td>
</tr>
</tbody>
</table>

### Hospital Surveillance

<table>
<thead>
<tr>
<th>Virus</th>
<th>No. of specimens</th>
</tr>
</thead>
<tbody>
<tr>
<td>Flaviviruses</td>
<td></td>
</tr>
<tr>
<td>Dengue virus serotype 1</td>
<td>5</td>
</tr>
<tr>
<td>Dengue virus serotype 2</td>
<td>15</td>
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<tr>
<td>Influenzas</td>
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<tr>
<td>Influenza A</td>
<td>11</td>
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<tr>
<td>Paramyxoviruses</td>
<td></td>
</tr>
<tr>
<td>Measles virus</td>
<td>2</td>
</tr>
<tr>
<td>strain of Mumps virus</td>
<td>1</td>
</tr>
<tr>
<td>Swine Farm Surveillance</td>
<td>Virus</td>
</tr>
<tr>
<td>--------------------------</td>
<td>------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Coronaviruses</td>
<td>Strain of Alphacoronavirus 1 (Transmissible gastroenteritis virus)</td>
</tr>
<tr>
<td></td>
<td>Strain of Betacoronavirus 1 (Porcine hemagglutinating encephalomyelitis virus)</td>
</tr>
<tr>
<td>Paramyxoviruses</td>
<td>Strain of Porcine Parainfluenzavirus 1</td>
</tr>
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</table>
# Wildlife – Concurrent Surveillance
Results at the Wildlife Farm Interface

### Table: Wildlife – Concurrent Surveillance Results

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus</th>
<th>No. of specimens</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hoary Bamboo Rat</td>
<td>Strain of Longquan Aa mouse coronavirus</td>
<td>1</td>
</tr>
<tr>
<td>Hoary Bamboo Rat</td>
<td>Strain of Murine coronavirus</td>
<td>21</td>
</tr>
<tr>
<td>Malayan Porcupine</td>
<td>Strain of Murine coronavirus</td>
<td>6</td>
</tr>
<tr>
<td>Black Giant Squirrel</td>
<td>Strain of Murine coronavirus</td>
<td>1</td>
</tr>
</tbody>
</table>
Detection of Corona Viruses along the rodent trade chain in the Mekong Delta

Detection rates of coronaviruses

Field rat value chain interface

- trade: 18.2%, n=154
- large market: 32.8%, n=274
- restaurant: 51.3%, n=119
Viral Detection in the Bat Guano Farming Interface in the Mekong Delta

- Strain of bat corona virus 512/2005
- Two novel corona viruses
  - PREDICT_CoV-17
  - PREDICT_CoV-35
- Four novel paramyxo viruses
  - PREDICT_PMV-13
  - PREDICT_PMV-63
  - PREDICT_PMV-66
  - PREDICT_PMV-67
- Four novel Rhabdoviruses
  - PREDICT_RbdV-21
  - PREDICT_RbdV-24
  - PREDICT_PbdV-27
  - PREDICT_RbdV-28
Vietnam urgently plans to respond to SARS-CoV-2 in animals

The Department of Animal Health (MARD) is urgently working to develop a plan to cope with the risk of SARS-CoV-2 virus causing Covid-19 infection in animals.

Vietnam to ban wildlife trade following conservationists' demand

By Sen  March 9, 2020 | 09:17 am GMT+7
Behavioral Risk & Community Engagement

Moving from evidence to interventions
Beginning to dive deep into behavioral risk…

>20,000 EIDITH questionnaires for a broad, standardized view of behavioral risk…

>2,000 Qualitative interviews & focus groups for insight into hidden risks of behaviors:
  • Which interfaces are most risky?
  • Which behaviors are most likely to result in a spillover event?

Behavioral data, combined with PREDICT surveillance and virus data allows for contextualized risk analyses

Qualitative data looks more deeply at the dynamic, underlying behaviors and activities that drive zoonotic disease transmission

Cultural norms
Socio-economic drivers
Beliefs about animals
Animal care practices
Risk perceptions

Working towards roadmaps of potential intervention strategies
Identify behavioral and cultural practices promoting transmission of zoonotic viruses

- Qualitative data on perceptions of risk and illness: Interviews and Focus Groups
- Quantitative data using streamlined behavioral risk surveys: EIDITH
- Analyze data to identify behavioral risk and to inform intervention strategies
PREDICT Behavioral Risk Investigations
<table>
<thead>
<tr>
<th>Country</th>
<th>Bat Guano Farming &amp; Harvesting</th>
<th>Hunted Bats in the Value Chain</th>
<th>Bat-related Shared Food Resources</th>
<th>Bat-Community Interfaces</th>
<th>Bat-related Ecotourism</th>
<th>Market Value Chains</th>
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</thead>
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</tbody>
</table>

**Key**
- Blue square = Qualitative and Quantitative
- Purple square = Quantitative only
Examples of how qualitative findings were leveraged for behavior change intervention messaging

<table>
<thead>
<tr>
<th>Targeted Behavior Change</th>
<th>Findings from PREDICT Behavioral Risk Work</th>
<th>Country</th>
</tr>
</thead>
</table>
| Reduce **killing** of bats                     | • Respondents from Luoding and Shantou expressed little concern about bats entering households, stating that bats are useful because they eat mosquitoes  
  • While having bats nearby could lead to increased contact, the concept can be converted into positive messaging reinforcing why it is good to avoid killing them, in conjunction with recommended procedures for safe handling [resource: EIDITH protocols] | China   |
| Reduce **contact** with bat secretions, organs, or body fluids of living or dead bats | • Bat excrement has been used as fertilizer  
  • Raising awareness about excrement as a means for disease spread can reduce risk | DRC     |
| Reduce **eating** of bats and thereby contact with secretions | • Several respondents believe eating bats cures night sweats and nocturia  
  • Interventions can focus on enhancing knowledge to inform change in attitudes and practices regarding eating bats; they can be tailored to local beliefs revealed during interviews and discussed in conjunction with alternative therapies that are available locally  
  • Many no longer eat bats because they follow the practices of their ancestors, who stopped eating bats (Inongo Nkoye custom)  
  • Emphasizing following the practices of ancestors could be a means of preventing the consumption of bats | China   |
| Increase **help seeking** behavior from a certified medical professional when scratched, bitten, or cut while butchering | • When bitten by bats, professional medical treatment may not be sought  
  • Interventions could raise awareness that for more serious injuries (such as bites, scratches or if cut while butchering), certified medical professionals have medical treatments that traditional healers may not have access to; public health workers can also work more collaboratively with traditional healers | Indonesia |
Behavioral Risk Communication Tools

Living Safely with Bats

For the community members of coexistence:

Be aware of your surroundings and any unusual activity in the area.

For the caregivers of livestock:

Keep livestock away from bat roosts and ensure they are protected from bat droppings.

For all community members:

Avoid contact with bat bites or scratches.

KUJINGA NA MAAMBUKIZI KUTOKA KWA PANYA

For all community members:

Avoid contact with bat bites or scratches.

Comment se protéger contre les accidents au Cameroun

For those who live in rural areas:

Be aware of your surroundings and any unusual activity in the area.

For those who work with livestock:

Keep livestock away from bat roosts and ensure they are protected from bat droppings.

For everyone:

Avoid contact with bat bites or scratches.

ZUIA MAAMBUKIZI KUTOKA KWA NGEDERE

For all community members:

Avoid contact with bat bites or scratches.

Usalufisha ngedere/nyuzi.

Use nekumusa cha kubala kuchapunguzwa na kuhusira na kupa wako/nyuzi.

Usalufisha ne kula ngedere/nyuzi.

Ariko kumusa ngedere/nyuzi ika kuondoa uwegoza wa kuchapata huwa na kuchokera.

Hitadi cha kubala chombo chenyewe mfano.
TO DATE, THE NUMBER OF LANGUAGES INTO WHICH “LIVING SAFELY WITH BATS” HAS BEEN TRANSLATED

DRC

In 8 bushmeat markets in Kinshasa and in Inongo DRC, the PREDICT team conducted concurrent animal/human behavioral surveillance; while samples were taken from hunted wild animals, the behavioral team conducted interviews with the population living in contact with these animals, asking about animal exposure and behavioral risk factors and socio-economic drivers of subsistence hunting.

Based upon qualitative insights about the geographic origin of bushmeat coming into Kinshasa markets, we traced the animal value chain back to Mbandaka, the reported source of much non-human primate meat. Mbandaka is an Ebola outbreak site, so we used our interview data to generate hypotheses about Ebola exposure through bushmeat butchering, and did further sampling and serology of primates and bushmeat vendors to test this hypothesis.
Our Legacy: PREDICT’s Impact

Strengthening the Health Security Workforce
PROOF OF CONCEPT

DEVELOPED the One Health Workforce by training more than 6,800 people in over 30 countries.

OPERATIONALIZED One Health surveillance and sampled over 164K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.

DETECTED over 1,100 unique viruses, including zoonotic diseases of public health concern such as Bombali ebolavirus, Zaire ebolavirus, Marburg virus, and MERS- and SARS-like coronaviruses.

STRENGTHENED laboratory systems and zoonotic disease detection capabilities in over 60 labs around the world.
STRENGTHENING EMERGING THREATS SYSTEMS

Built capacity in both human and animal labs critical for strengthening national lab systems. Training of technicians occurred in university or partner labs.

Senior Lab Scientist Brett Smith from UC Davis trains the PREDICT lab team in Tanzania on detection of viruses of pandemic potential.

Predict labs around the world have been called to action during the COVID-19 response for early identification of cases and ongoing technical assistance.
ON THE JOB TRAINING FOR FIELD, LAB, DATA TEAMS

In the field, PREDICT activities were implemented in collaboration with government health professionals (District Medical & Veterinary Officers, Livestock Field Officers, clinicians, and nurses) at the subnational levels.

The Predict-trained workforce is one of the best response resources available for COVID-19 and the next Disease X emergence. Our teams are helping improve capabilities where they are needed most.
PREDICT Training Guides

15 Publicly Available Training Modules for the One Health Workforce

- Biosafety and Emergency Preparedness
- One Health Surveillance & Field Sampling Guides
- Behavioral Risk & Qualitative Research Guides
Demographics of Individuals Trained in PREDICT 2009-2019, n (%)  

<table>
<thead>
<tr>
<th>Trainee Home Country</th>
<th>Individuals n (%)</th>
<th>PREDICT-1</th>
<th>PREDICT-2</th>
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</thead>
<tbody>
<tr>
<td>Africa</td>
<td></td>
<td>1975 (46)</td>
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</tr>
<tr>
<td>Asia</td>
<td></td>
<td>1387 (32)</td>
<td></td>
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<tr>
<td>Middle East</td>
<td></td>
<td>43 (1)</td>
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<tr>
<td>North America</td>
<td></td>
<td>97 (2)</td>
<td></td>
</tr>
<tr>
<td>Latin America</td>
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<td>-</td>
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<tr>
<td>Unknown</td>
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<td>36 (1)</td>
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</table>

<table>
<thead>
<tr>
<th>Gender</th>
<th>Individuals n (%)</th>
<th>PREDICT-1</th>
<th>PREDICT-2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
<td></td>
<td>2481 (57)</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td></td>
<td>1858 (43)</td>
<td></td>
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<tr>
<td>Unknown</td>
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<td>1 (~0)</td>
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</table>

<table>
<thead>
<tr>
<th>PREDICT affiliation</th>
<th>Individuals n (%)</th>
<th>PREDICT-1</th>
<th>PREDICT-2</th>
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</thead>
<tbody>
<tr>
<td>Student</td>
<td></td>
<td>716 (16)</td>
<td></td>
</tr>
<tr>
<td>Staff</td>
<td></td>
<td>1125 (26)</td>
<td></td>
</tr>
<tr>
<td>Other-Community</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>members, government</td>
<td></td>
<td>2148 (49)</td>
<td></td>
</tr>
<tr>
<td>officials, etc.</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Total PREDICT Trainees</td>
<td></td>
<td>2500 (100)</td>
<td>4340 (100)</td>
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PREDICT’s Workforce are the World’s Leading Experts on Disease X
The Future of Pandemic Preparedness
Readiness for responding to Disease \( X = \text{COVID-19 (THIS TIME)} \)
The Future of Pandemic Preparedness
Readiness for responding to Disease X = COVID-19 (THIS TIME)

Proof of Concept

• Feasibility assessment for finding viruses ahead of outbreaks
  • Determined emerging threats can be identified before spillover
  • Developed financial projections for forecasting

• Identified & trained a cadre of qualified professionals

• Protocols in place for detection in high-value geographic & species targets

• 60 laboratories in 30 of world’s most vulnerable regions enabled

• Begun to catalogue the high-risk viruses & the metadata on transmission risk for mitigation, including for SARS-related CoVs

• Identified high-risk behaviors for surveillance & mitigation targeting

• Demonstrated the importance of multi-sectoral, One Health collaborations in emerging infectious disease control and prevention
SPILLOVER
VIRAL RISK RANKING

Developed by infectious disease scientists, SpillOver: Viral Risk Ranking is an interactive and adaptive platform for use by policy professionals, scientists and the general public to compare and explore the relative impacts of virus, host and environmental factors to evaluate the risk of zoonotic virus transmission.
PREDICT-wide tools for community outreach & systems strengthening: “Living Safely with Bats” book
PREDICT-wide tools for community outreach &
systems strengthening: “Living Safely with Bats” book
Impact of Continuing Work & Identifying Targets for Spillover Prevention

Reducing Risk of & Preventing Impacts from Disease X

DISEASE X: MYSTERY ILLNESS COULD KILL MILLIONS
Impact of Continuing Work & Identifying Targets for Spillover Prevention

Reducing Risk of & Preventing Impacts from Disease X

• Better characterization of viral risks & **INSPIRING CALM** by providing data on:
  
  - Geography
  - Hosts
  - Risk interfaces

  *Ability to identify and control the transmission of viruses from animals to people at the source at the earliest possible stages of spillover*

• Lowered risk for and impacts from future outbreaks

• Enable prevention measures, public health campaigns, differential diagnoses by clinicians & possibly even early development of prophylactics and treatments when warranted
Assisting Governments with Outbreaks

Successes and Impact
Specific guidelines for PREDICT Involvement

Key Questions:

– Known etiology/cause?
– Credible threat to human health?
– Infectious cause?
– Multi-species involvement (host-jumping)?
– Evidence of animal origin?
PREDICT’s Workforce in Action: Outbreak Assistance

More than 46 events in 15 countries

- Liberia
  - Logistics
  - Human GI outbreak

- Cameroon
  - Gorilla, bat mortality
  - Technical assistance
  - Lab testing

- Mongolia
  - Avian influenza
  - Bird sampling
  - Lab testing support

- DRC
  - Suspect VHFs/Ebola (human)
  - Avian influenza
  - Lab testing

- Sierra Leone
  - Monkeypox (human)
  - Rodent sampling – Lassa fever

- Ghana
  - Suspect Lassa fever
  - Rodent sampling

- Nepal
  - Aflatoxin
  - Avian influenza
  - Bird sampling
  - Lab testing support

- Thailand
  - COVID-19
  - Bat die-off
  - (Rescued cave hikers testing)*
  - Lab testing support

- Cambodia
  - COVID-19
  - Lab testing support

- Nepal
  - Lassa fever
  - Rodent sampling

- Kenya, Tanzania, Uganda, Rwanda
  - Tanzania – COVID-19
  - Avian influenza
  - Yellow fever
  - Technical information
  - Partner communications
  - Info only reports (RVF- Uganda)

- Bangladesh
  - Bird and Bat mortality - sampling
  - Avian influenza
  - Human Encephalitis
  - Lab testing

- Thailand
  - COVID-19
  - Lab testing support
PREDICT Workforce Outbreak Assistance

Capacity gains:
- Technical information to government (Training modules)
  - safe sampling, specimen collection/transport, cold chain
- PPE or other equipment
  - N95, gloves, Tyvek suits, faceshields, cryotubes, boxes, cold chain (LN2), freezer packs
- Laboratory Testing Protocols
- Assist communication and coordination
  - MoH, MoAg, MoW, MoF, NGOs, WHO, FAO, MSF, etc…

Democratic Republic of Congo 2014
Ebola virus - Zaire
Nine suspected cases of Human Viral Hemorrhagic Fever and 2 deaths in the Bas-Uele Province was reported, and the laboratory at INRB confirmed Ebola virus (EBOV) in a subset of five patient specimens. PREDICT participated in GoDRC taskforce meetings and was requested by the INRB Director to utilize PREDICT protocol testing for secondary confirmation of EBOV. PREDICT continued to participate in National task force meetings and provide technical assistance until the cessation of the outbreak.
• Technical information to governments (training modules)
  • Safe sampling, specimen collection/transport, cold chain
• PPE & other equipment
  • N95, gloves, Tyvek suits, faceshields, cryotubes, boxes, cold chain (LN2), freezer packs
• Laboratory testing protocols
• Assisting communication and coordination
  • MoH, MoAg, MoW, MoF, NGOs, WHO, FAO, MSF, etc…

Nepal, Thailand, Cambodia, Tanzania 2020 COVID-19 Pandemic
PREDICT testing platforms and outbreak response network used for initial rule-in/rule-out testing in several countries. Systematic investment and technical capacity building resulted in rapid first detections of COVID-19 cases.
The Power of PREDICT is the PEOPLE

• Throughout the PREDICT network of 30 countries teams have been supported to:
  • Understand what is needed for successful outbreak investigations
  • Understand the biosafety and biosecurity needs
  • Understand the critical importance of timelines, cold-chain, and rapid-action!
  • Constitute an important frontline in each country to support zoonotic disease investigations
Policy and Partnerships for Health Security

Evidence-based advocacy to prevent pandemics at the national and global scale
Sharing Best Practices from Countries
High Cost of Epidemics

Putting costs in tangible, local terms to inform budgeting for zoonotic disease prevention and control
One Health Economics

Multisectoral data collection to inform cost-effective disease prevention and control options
Multisectoral Risk Reduction Guidance

Over 12,400 downloads from World Bank websites
Making One Health Operational
# Prevention Policies & Practices

## ONE HEALTH

**Operational Framework for Strengthening Human, Animal, and Environmental Public Health Systems at their Interface**

## Prevention Policies & Practices

<table>
<thead>
<tr>
<th>DOMAIN</th>
<th>STAGE</th>
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<tbody>
<tr>
<td><strong>PREVENT</strong></td>
<td><strong>DETECT</strong></td>
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<tr>
<td>Access to information for risk assessment and mitigation: List of pathogens in country; list of known disease hosts and reservoirs in country; prioritization of exposure in country (e.g., antibodies to pathogens, risk forecasting e.g., weather data for climate-sensitive diseases)</td>
<td>Chain of command for information reporting and verification</td>
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<td>Contacts established between ministries</td>
<td>Regional risk profile</td>
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<td>Population-specific and sensitive messaging (e.g., gender or cultural)</td>
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<td>National, regional, or international access to laboratory diagnostics (known and novel)</td>
<td>National access to laboratory diagnostics (known pathogens and toxigens); confirmatory analysis at reference laboratory, if needed</td>
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<td>Sentinel surveillance in animals (wild or domestic) or vectors and investigation</td>
<td>Disease prioritization</td>
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<td>Hazard identification and other relevant stages of risk analysis</td>
<td>Detection at point of entry</td>
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<td>Risk mitigation (e.g., at points of entry)</td>
<td>Identification of vulnerable populations</td>
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<tr>
<td>Identification of vulnerable populations (heightened risk and/or severity)</td>
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<td>Identification of vulnerable populations</td>
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## References

[World Bank Group](https://www.worldbank.org)
Moving from Pandemic Response toward Risk Reduction
Technical Expertise: In Emergencies and in Peacetime
Intergovernmental Policy Change

More reliable, efficient movement of emergency diagnostic specimens from wildlife for investigation of animal and public health disease threats

Adoption of One Health approaches for integrated health and biodiversity risk assessments, sentinel surveillance, and cost-effective prevention strategies
Identifying Health Security Gaps

Are One Health-relevant policies in place for health security?
• Do countries consider infectious disease risk in land use planning?
• Do they have a cross-ministerial effort to address zoonotic diseases?
• Do they share surveillance data across veterinary, wildlife, and public health professionals?

73% of countries reported gaps, mainly:
• Poor coordination (e.g. planning, response)
• Poor data integration from wildlife and/or environment sector
• Wildlife disease surveillance not operational
• Workforce shortages
PREDICT

Ministries of Health, Agriculture & Environment and Implementing University and NGO Partners in 35 Countries