

USAID EPT-2 PREDICT PROJECT COVID-19 EXTENSION SUMMARY

March - September 2020

Prepared by:
The PREDICT Consortium



PREDICT-2 COVID-19 Extension Summary

The **PREDICT Project** was initiated as part of USAID's Emerging Pandemic Threats Program in 2009 to strengthen global capacity for the detection and discovery of viruses with pandemic potential. Over the past decade, PREDICT teams around the world worked to identify and characterize emerging viruses. Our teams sampled over 160,000 animals and people in some of the world's most vulnerable hotspots for emerging viruses and performed more than 1.3 million tests for known and new viruses, including coronaviruses (PREDICT Consortium, 2020). Because of this foundation, the PREDICT project partners were crucial frontline responders and technical experts for emerging virus surveillance, detection, and response, especially in the early days of the COVID-19 pandemic.

In March 2020, PREDICT received an emergency supplement extension through September 2020 to assist our global network of collaborating laboratories in the initial detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), support national response plans to the emerging COVID-19 pandemic, and explore our specimen archives to further investigate SARS-related coronaviruses in animals.

Call to Action

Upon receiving the extension, select PREDICT Consortium partner awards in engaged countries were rapidly reactivated to:

1. Identify optimal SARS-CoV-2 testing procedures and support access to laboratory consumables and supplies necessary for testing
2. Support laboratory technicians and infectious disease experts called on to participate in local COVID-19 task forces
3. Implement risk communication and disease control strategies, such as community engagement and outreach, contact tracing, and surveillance
4. In collaboration with implementing partners and laboratories in the Asia region, test potential animal sources of SARS-related coronaviruses using prioritized archived specimens from wildlife species at highest risk of harboring SARS-related viruses

The re-activated PREDICT teams supported the training of expanded laboratory personnel, healthcare workers, and others on an array of topics including infection prevention and control, biosafety and biosecurity, PPE best practices, and COVID-19 diagnostic testing in compliance with established protocols (Table 1; Figure 1; Figure 2). PREDICT's legacy and leadership were clearly demonstrated by the work of our network in the earliest stages of the pandemic. As the virus emerged, PREDICT partners in Asia and Africa were among the first to deploy virus detection protocols before SARS-CoV-2 virus-specific assays were available. These laboratories were able to detect the new virus in some of the first patients that traveled outside China.

PREDICT leaders worked tirelessly to promote health security and support national prevention, detection, and response efforts for the pandemic.

Table 1. COVID-19 technical support to PREDICT host country governments (March -September 2020).

Support Provided	Africa	Asia
SARS-CoV-2 testing supplies	Cameroon, DRC, Côte d'Ivoire, Kenya, Rwanda, Tanzania, Uganda	Cambodia, Lao PDR, Myanmar, Nepal, Thailand
Salary support for SARS-CoV-2 testing	Cameroon, Ghana, Côte d'Ivoire, Rwanda, Tanzania	Cambodia, Lao PDR, Nepal, Thailand
Providing government with technical assistance	Guinea, Côte d'Ivoire, Liberia, Rwanda, Sierra Leone, Uganda, Tanzania	Lao PDR, Nepal
Training - Laboratory staff	Tanzania, Cameroon, Kenya	Nepal
Training - Healthcare workers	Senegal	Nepal
Training - Community members	Guinea, Senegal	–

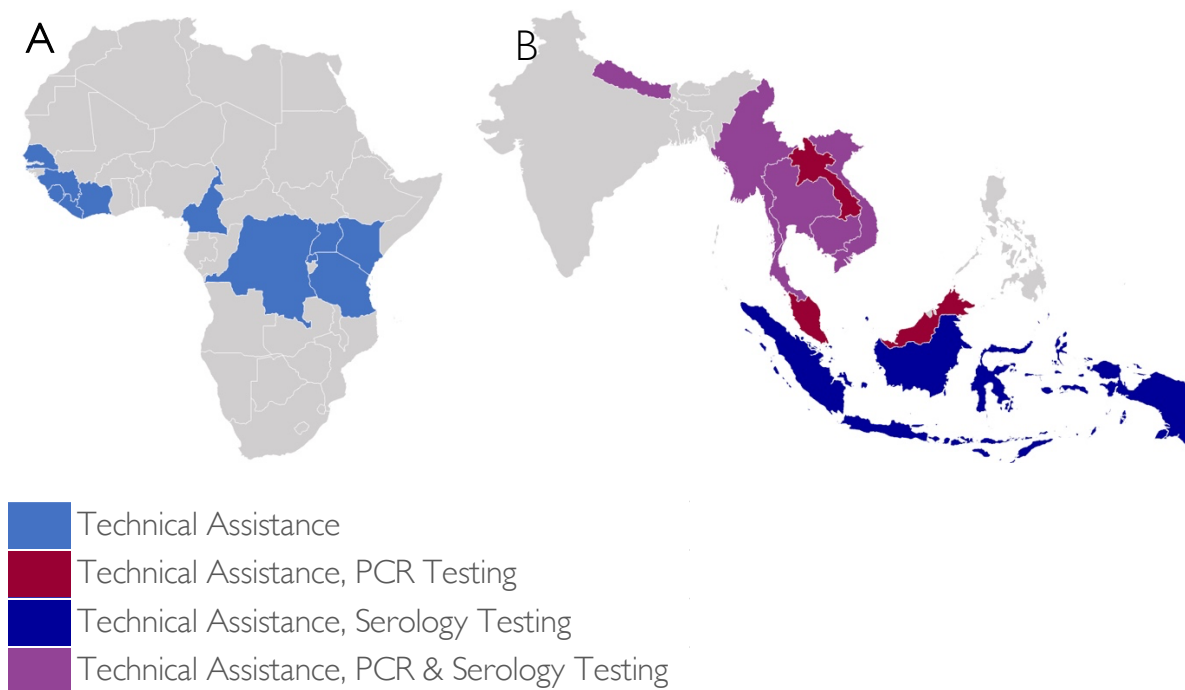


Figure 1. COVID-19 technical support and SARS-CoV-2 testing by country in (A) Africa and (B) Asia (March - September 2020).

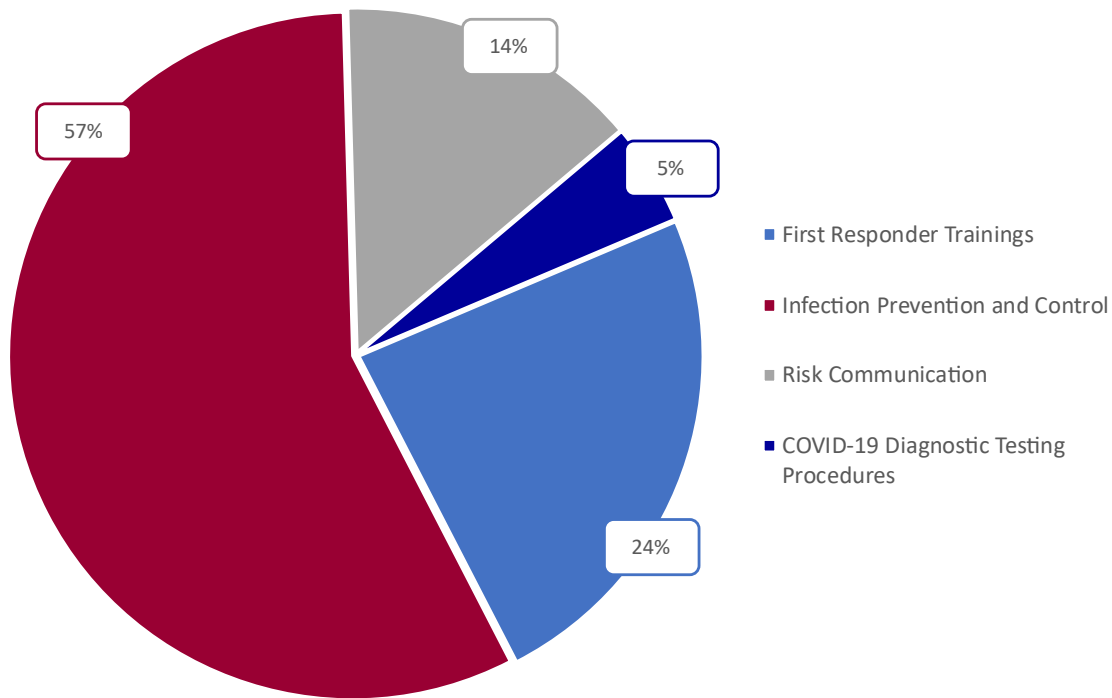


Figure 2. Training (including activities not supported by PREDICT-2 extension funds) by re-activated PREDICT partners in support of national COVID-19 response plans. Data summarized from the first monthly poll of PREDICT partners conducted in early June 2020.

PREDICT COVID TESTING OF ANIMALS PREVIOUSLY SAMPLED IN ASIA

Over the course of the PREDICT project, surveillance teams in Asia and Southeast Asia collected specimens and data on animals and humans, including bat species that we determined are especially likely to carry SARS-related coronaviruses. These specimens that were archived safely in local and regional laboratories working on the PREDICT project were of value to provide insight into potential animal hosts.

During the extension, PREDICT’s collaborating laboratories in the Asia region conducted SARS-CoV testing on archived specimens from priority wildlife species that likely represent the highest risk of harboring SARS-related coronaviruses at animal-human interfaces where people were in contact with high-risk species. We analyzed project data to identify animal species, value chains, and animal-human interfaces that would be most likely to inform on SARS-related coronavirus spillover and spread in the region.

With partner labs in seven countries (Cambodia, Lao PDR, Malaysia, Myanmar, Nepal, Thailand, and Viet Nam), we performed 7,997 tests on 4,510 archived specimens from 3,631 animals (bats, civets and other carnivores, pangolins, and non-human primates) using two consensus-based PCR assays for coronaviruses (PREDICT Consortium, 2020). Early testing efforts during SARS-CoV-2 emergence in the Southeast Asia region before WHO protocols or CDC tests

were available confirmed that one of these assays was sensitive for SARS-CoV-2 detection. In addition when available, we screened these specimens with the Berlin SARS-CoV-2 real-time PCR assays, considered the global standard for detection (WHO, 2020), as well as with US Centers for Disease Control and Prevention real-time assays.

Preliminary findings to date

We detected SARS-related coronaviruses in specimens from nine animals and non-SARS-related coronaviruses in specimens from 72 additional animals. Detailed results by country and taxa are shown below (Table 2; Table 3; Figure 3). In this period, the PREDICT Consortium detected SARS-related coronaviruses in two Shamel's Horseshoe Bats (*Rhinolophus shameli*) and seven Sunda pangolins (*Manis javanica*), expanding insight on species shown to host SARS-related coronaviruses. Previous insights from PREDICT and others have shown that insectivorous bats belonging to the Hipposideridae and Rhinolophidae families are known to have a close association with SARS-related coronaviruses (Anthony et al., 2017), and strains of SARS-related coronaviruses have been isolated from several *Rhinolophus* bat species including *R. affinis*, *R. ferrumequinum*, *R. macrotis*, *R. pearsoni*, *R. pusillus*, and *R. sinicus* (Lau et al., 2005; Li et al., 2005), Sunda pangolins (Liu et al., 2019; Lam et al., 2020; Xiao et al., 2020), and Himalayan palm civets (Guan et al., 2003). The SARS-related coronavirus (bat strain) we found is 97.2% similar to Bat coronavirus RaTG13 (GenBank Accession No. MN996532; the closest known relative to SARS-CoV-2 across the genome) and 95.8% similar to SARS-CoV-2 (GenBank Accession No. NC_045512).

Table 2. Summary of animals tested for SARS-related and other coronaviruses (March to September 2020) using samples collected between October 2009 and September 2019 in Asia.

	Specimens Tested	Animals Tested	No. of Animals with SARS-related Coronaviruses (Sarbecoviruses)	No. of Animals with Other Coronaviruses
Cambodia	485	282	2	12
Bats	450	264	2	12
Civets	32	17	0	0
Other Carnivores	3	1	0	0
Lao PDR	446	287	0	7
Bats	322	196	0	7
Civets	124	91	0	0
Malaysia	1,221	1,207	0	0
Bats	925	925	0	0
Civets	60	51	0	0
Pangolins	236	231	0	0
Myanmar	351	240	0	0
Bats	351	240	0	0
Nepal	438	337	0	0
Bats	254	153	0	0
Non-Human Primates	184	184	0	0
Thailand	334	194	0	7
Bats	310	182	0	7
Pangolins	24	12	0	0
Viet Nam	1,235	1,084	7	46
Bats	539	534	0	46
Civets	299	299	0	0
Pangolins	397	251	7	0
Total	4,510	3,631	9	72

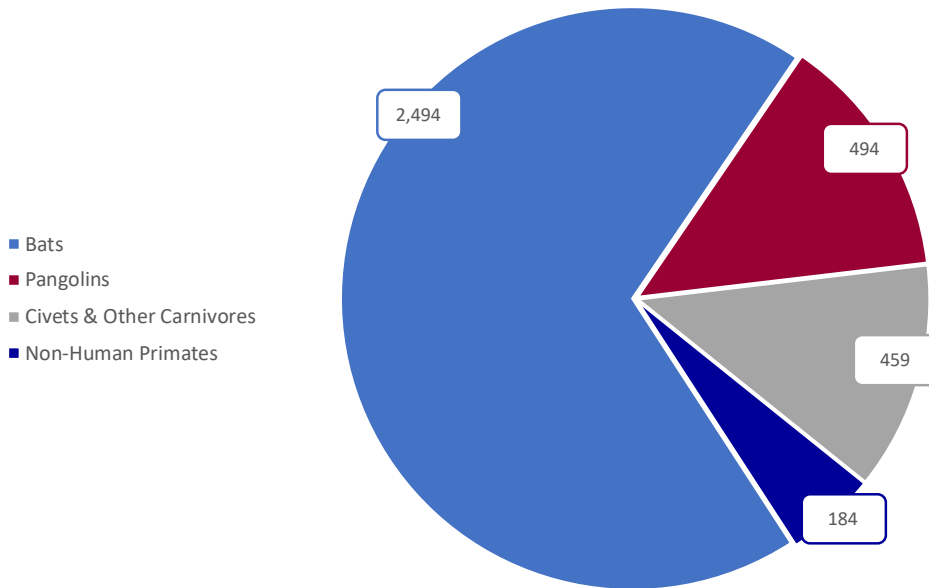


Figure 3. Animals tested by PCR for SARS-related and other coronaviruses by taxa.

Table 3. SARS-related coronaviruses (Sarbecoviruses) and other coronaviruses detected during the extension period (March to September 2020) in samples collected between October 2009 and September 2019 in Asia.

Virus	Species	Country	Number of Positive Animals
SARS-related betacoronavirus (Bat strain)*	Shamel's Horseshoe Bat	Cambodia	2
SARS-related betacoronavirus (Pangolin strain)*	Sunda Pangolin	Viet Nam	7
Alphacoronavirus I	Unidentified Vespertilionid Bat	Viet Nam	1
Bat coronavirus I	Croslet Horseshoe Bat, Malayan Horseshoe Bat	Thailand	3
Bat coronavirus 512/2005	Unidentified Vespertilionid Bat, Lesser Asian House Bat	Cambodia, Viet Nam	50
Bat coronavirus HKU2	Shamel's Horseshoe Bat	Thailand	1
Bat coronavirus HKU9	Dawn Bat, Unidentified Rousette Bat	Lao PDR	2
Bat coronavirus HKU10	Large Asian Roundleaf Bat	Thailand	3
PREDICT_CoV-35	Unidentified Vespertilionid Bat, Lesser Asian House Bat	Cambodia, Viet Nam	4
PREDICT_CoV-56	Greater Nectar Bat	Cambodia	1
PREDICT_CoV-89	Unidentified Rousette Bat	Lao PDR	4
PREDICT_CoV-118*	Shamel's Horseshoe Bat	Cambodia	2
PREDICT_CoV-119*	Thomas's Horseshoe Bat	Lao PDR	1

*Newly detected viruses by the PREDICT Consortium during the extension period (March-September 2020).

Conclusions and Future Directions

Given the diversity of coronaviruses increasingly recognized in wildlife, including the likelihood of undiscovered coronaviruses, further investigation of viruses closely related to SARS-CoV-2 is urgently needed. Through our work and that of colleagues working on animal coronaviruses, we know that coronaviruses are often able to spillover into new species and adapt to new hosts, characteristics common to pathogens that pose a threat to health security. For over 10 years, PREDICT teams around the world worked to identify and characterize coronaviruses, searching for them in hotspots like live animal markets, caves where bat guano is harvested, and communities that border wildlife habitats. We advanced the world's knowledge of coronaviruses, detecting 181 coronaviruses in animals and people (Table 5; PREDICT Consortium, 2020). Of these, 115 were coronaviruses previously unknown to science. As a result, the coronaviruses we detected have been used by other scientists to develop countermeasures, to test the potency of antiviral drugs, and to help in the rapid assessment of the only antiviral currently in use for COVID-19 patients.

As our world becomes more globalized, identifying and combating pandemic threats should be a global priority. Investments in preparedness allowed the PREDICT project to prepare laboratories and countries to be able to react and effectively respond to a coronavirus threat in real-time.

Table 5. Coronavirus surveillance effort throughout the PREDICT project (2009 – 2020).

Host Taxa	No. of Individuals Tested	No. of Positive Individuals	No. of Distinct Viruses Detected
Bats	38,553	3,050	151
Rodents/Shrews	18,090	817	18
Non-Human Primates	9,957	4	2
Humans	16,101	73	4
Domestic Species	3,931	321	9
Other Wildlife	2,050	32	5
Total	88,682	4,297	181*

**Numbers do not total as some viruses were found in more than one taxa*

References

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Guan, Yi, et al. "Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China." *Science* 302.5643 (2003): 276-278.

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USAID
FROM THE AMERICAN PEOPLE

PREDICT



REDUCING PANDEMIC RISK, PROMOTING GLOBAL HEALTH

PREDICT, a project of USAID's Emerging Pandemic Threats (EPT) program, was initiated in 2009 to strengthen global capacity for detection and discovery of zoonotic viruses with pandemic potential. Those include coronaviruses, the family to which SARS and MERS belong; paramyxoviruses, like Nipah virus; influenza viruses; and filoviruses, like the ebolavirus.

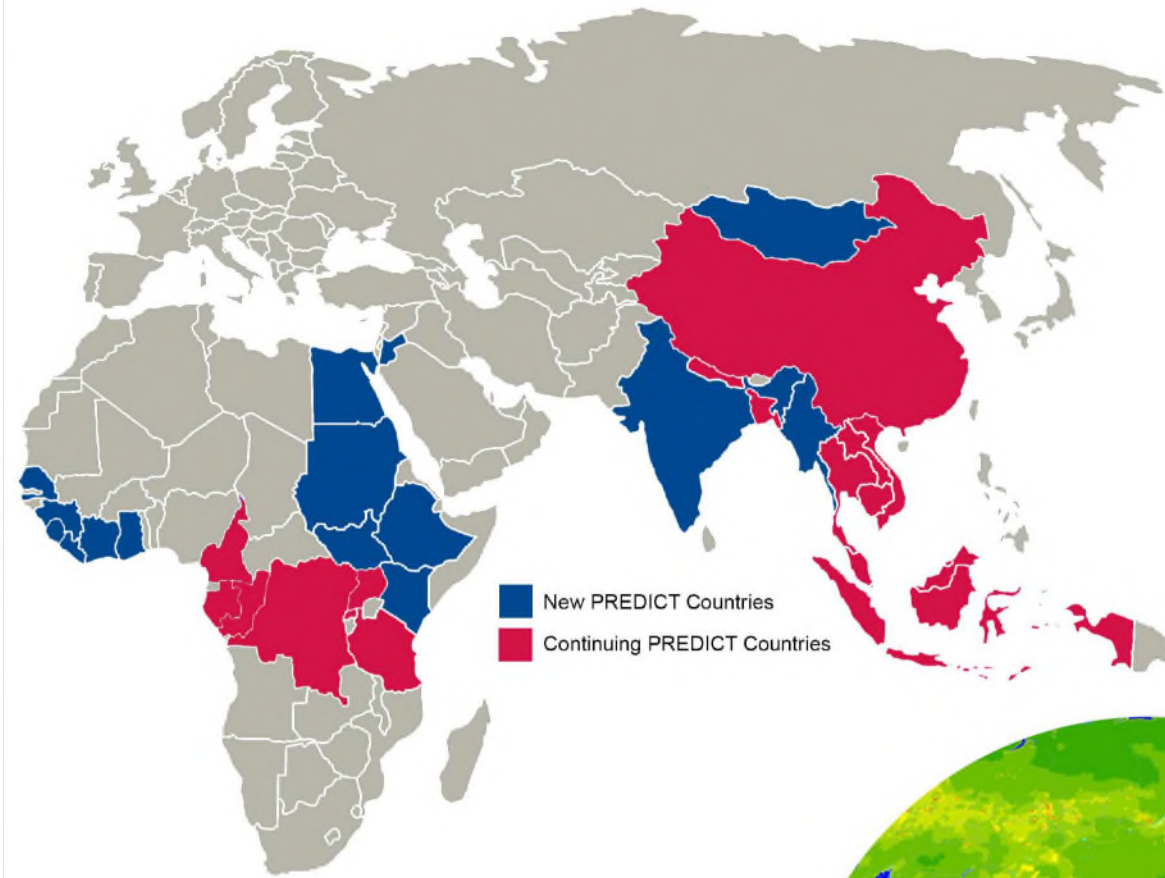
PREDICT has made significant contributions to strengthening global surveillance and laboratory diagnostic capabilities for new and known viruses.

Now working with partners in 31 countries, PREDICT is continuing to build platforms for disease surveillance and for identifying and monitoring pathogens that can be shared between animals and people. Using the One Health approach, the project is investigating the behaviors, practices, and ecological and biological factors driving disease emergence, transmission, and spread. Through these efforts, PREDICT will improve global disease recognition and begin to develop strategies and policy recommendations to minimize pandemic risk.

SURVEILLANCE

PREDICT's surveillance for emerging pathogens focuses on areas of the world at the highest risk for zoonotic disease emergence. The goal is to move countries away from a reactive post-outbreak response to a proactive approach in which pathogens of pandemic potential are discovered at their source before large-scale epidemics occur in people.

PREDICT's disease surveillance strategy is based on the inextricable link between animals, humans, and the environment. Rather than prescribing an across-the-board surveillance plan, PREDICT works in each focus country to cultivate targeted, measurable, adaptive, and responsive approaches that are integrated across health and environmental sectors.



CAPACITY STRENGTHENING

Preparing for emerging disease threats requires investments in infrastructure, institutions, and human resources across a broad array of health and social systems to operationalize One Health platforms. In collaboration with country governments and EPT partners, PREDICT is committed to developing the infrastructure and core skills and capabilities required by tomorrow's One Health workforce.

Through PREDICT, more than 2,500 people (and counting) have been trained in biosafety, field epidemiology and surveillance, laboratory diagnostics, social sciences and behavioral risk investigations, and modeling and analytics, creating an extensive network of global One Health professionals to support long-term zoonotic disease surveillance.

PATHOGEN DISCOVERY & DIAGNOSTICS

PREDICT's diagnostic success lies in the use of broadly reactive consensus (genus/family level) PCR supplemented with high throughput sequencing. These powerful tools produce specific, high-resolution data allowing for rapid detection of known and new potential pathogens. To date, PREDICT has developed and optimized detection protocols and capacities in laboratories in all of the countries in which we have engaged, ensuring regional capacity to detect pandemic threats.

The PREDICT approach is especially important for the diagnosis of mystery illnesses in medical hospitals and veterinary labs where testing options are often limited. By testing targeted samples based on the circumstances that promote disease transmission and the route of exposure, PREDICT can detect known and novel pathogens in tandem, rather than sequentially.

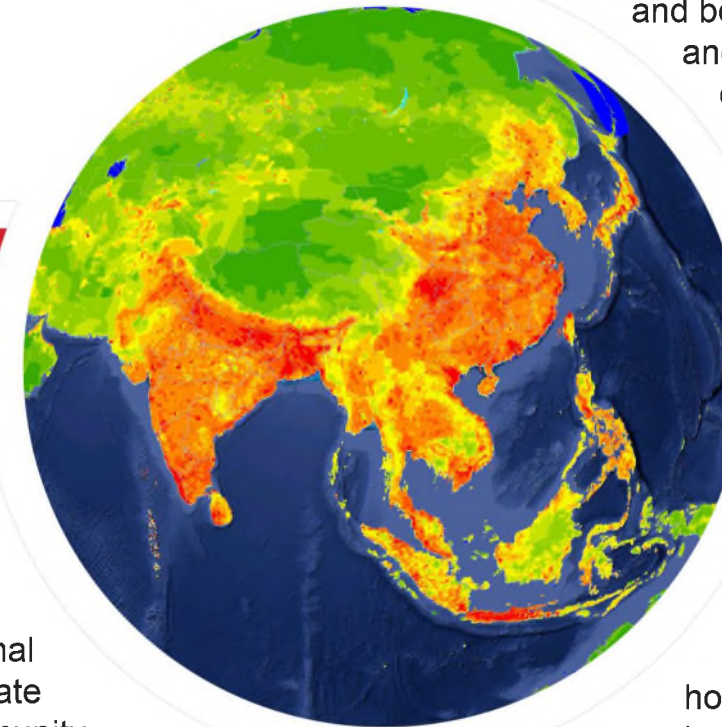


BEHAVIORAL RISK

PREDICT uses a multidisciplinary approach to identify groups of populations at highest risk of exposure to emerging pathogens, and the 'how' and the 'why' of risk.

Our teams assess community perceptions of animal exposure and disease risk and evaluate widely held assumptions of community practices (e.g., high risks from bushmeat hunting). PREDICT is identifying and monitoring the risk factors for zoonotic diseases with pandemic threat potential.

Our methods will lead to well-rounded understanding of disease spillover and transmission dynamics, essential to the design and evaluation of mitigating interventions, and to informing policy by identifying barriers to change and acceptable alternatives.



MODELING & ANALYTICS

PREDICT will use state-of-the-art modeling and analytic approaches to guide surveillance and help countries develop disease control and prevention strategies. PREDICT is producing next-generation, fine-scale hotspots maps, combining in-country data on land use, socioeconomic, and agricultural changes with surveys of human behavior, market value chains, and livestock production to identify where zoonoses will spillover, where they will amplify, and who is at risk.

By using data direct from PREDICT viral testing and conducting outbreak scenario modeling, PREDICT will provide information on which pathogens are most likely to become pandemic and which control and mitigation strategies can be most effective.

INFORMATION MANAGEMENT

PREDICT works closely with host governments and partners to interpret and share information through systems designed to protect and ensure data quality and accuracy. PREDICT data are managed in a purposefully-designed internal information management system, in which all data undergo a rigorous quality control process. Diagnostic test results are interpreted in light of all available scientific literature by PREDICT virologists.

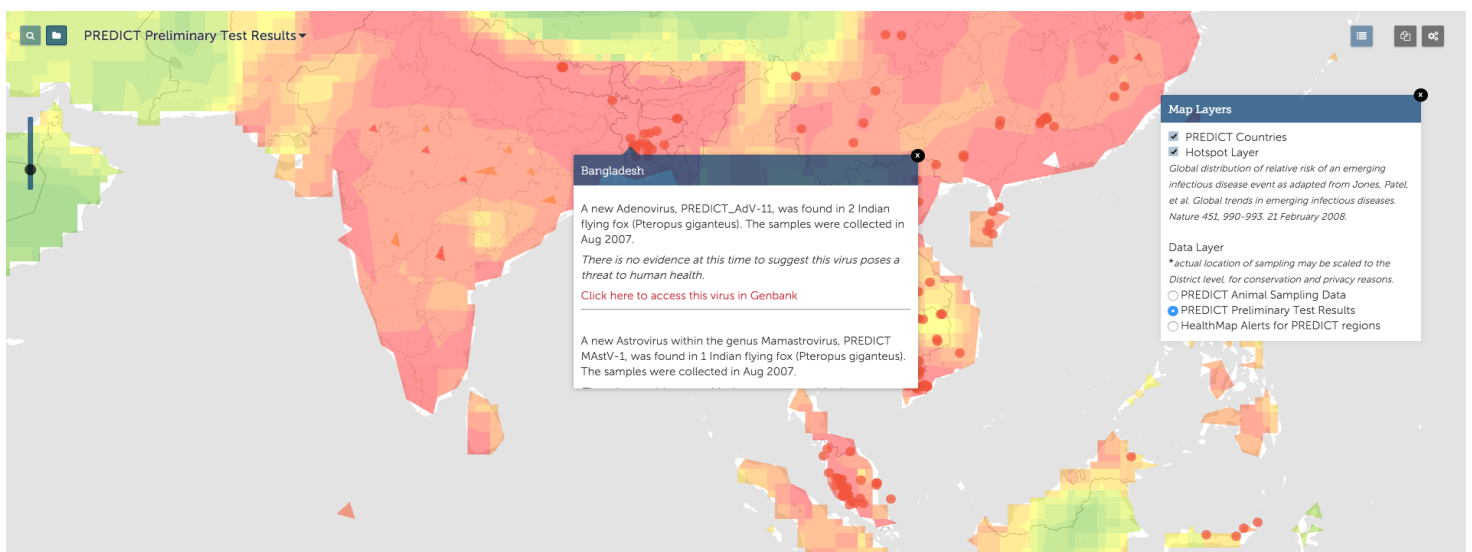
After interpretation, results are provided to host governments for examination, to inform policy, and for approval for public release through the PREDICT data site powered by HealthMap. This open access platform allows users to visualize PREDICT data along with disease events worldwide (<http://data.predict.global>).



ONE HEALTH PARTNERSHIPS

PREDICT at its core is built upon One Health partnerships. Cross-disciplinary collaborations are critical for gaining a more full understanding of the integral links between human, animal, and environmental health that can provide opportunities for prevention or early detection and control of disease threats. By working across sectors and including a diverse range of stakeholders and expertise, PREDICT helps operationalize efforts that promote public health, effective natural resource management, and development.

On a country basis and at a global level, PREDICT enables and supports implementation of One Health practices. Toward this goal, PREDICT has worked closely with a wide range of government ministries, scientific institutions, local organizations, and other stakeholders to further One Health initiatives. These have taken the form of inter-ministerial data sharing and interpretation, interdisciplinary capacity building and surveillance, and coordinated outbreak response activities. Building on these best practices, PREDICT is working with Emerging Pandemic Threats program partners to develop an evidence base to demonstrate the value of the One Health approach.



Western Asia Bat Research Network



Bat One Health Research Network (BOHRN) Biological Threat Characterization Discussion

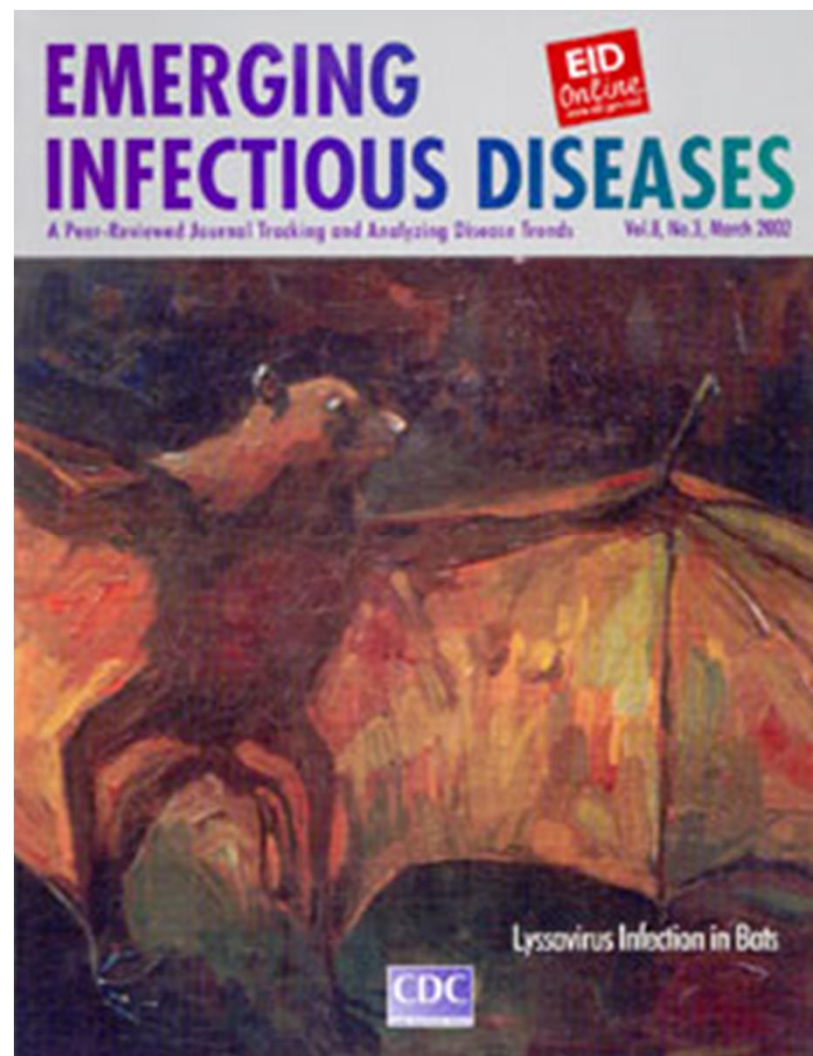
*Biosurveillance Network of the Silk Road
25 September 2018*

Western Asia Bat Research Network



Emerging Diseases from Bats

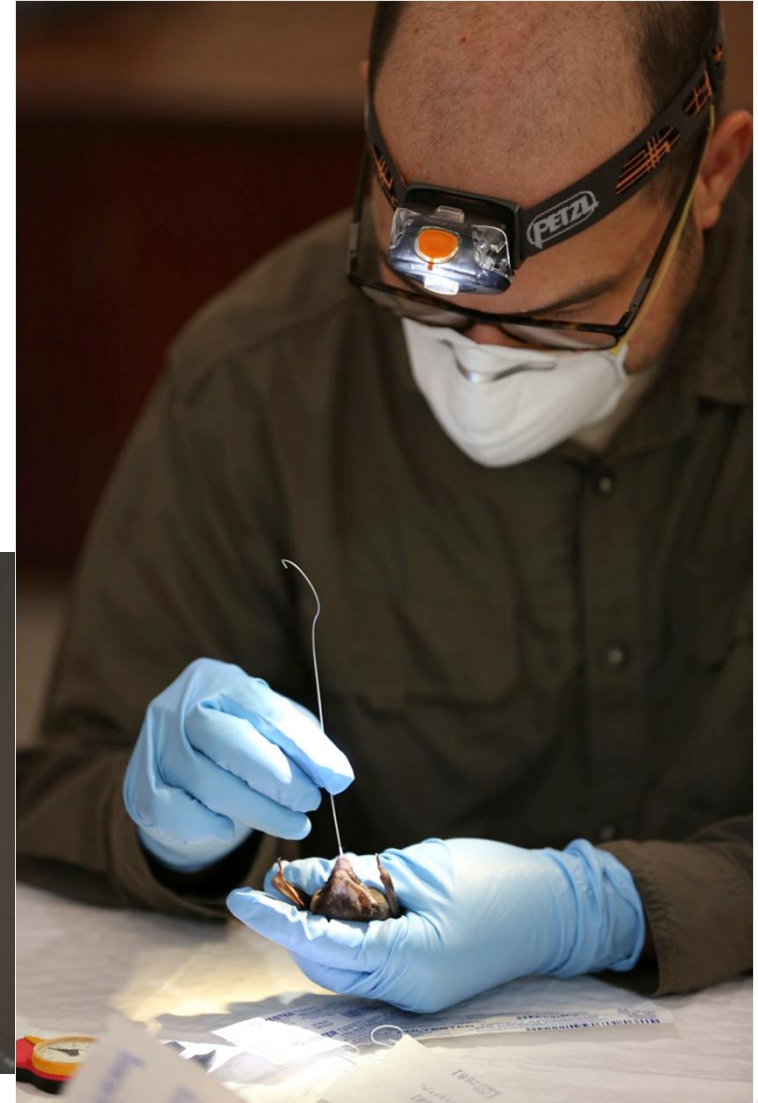
- Notable bat-borne viruses: Ebola, Marburg, Nipah, Hendra, SARS-CoV
- Bats harbor a greater proportion of zoonoses than other mammalian orders (Olival et al. 2017, *Nature*)



Importance of understanding potential routes transmission for human exposure



Blood,
saliva,
feces,
Urine.



Defining Western Asia



Origins of the Western Asia Bat Research Network (WAB-Net)

- EcoHealth Alliance's experience with other Research Coordination Networks (EcoHealthNet 2012- and SEABCRU 2007-)
- MERS-CoV surveillance in KSA (2012-13)
- Singapore bat training May 2014
- Early discussions with DTRA about supporting Western Asia/Middle East bat research and capacity building efforts (2015)
- Side meeting at Int'l Bat Research Conf (2016)
- Grant funded by DTRA-CBEP, project launched Sept 2017

DTRA WAB-Net Project Primary Objectives (2018-22)



- i. Characterize bat coronaviruses across Western Asia, and test hypotheses that:**
 - i. CoV diversity correlates with host species diversity in a given geographic area.
 - ii. Ecological and host species traits predict CoV diversity.
 - iii. Bats and their CoVs have co-evolved

- ii. Analyze and map bat pathogen spillover risk by including broader, regional ecological data**

- iii. Strengthen regional scientific capacity and collaboration through the Western Asia Bat Research Network (WAB-Net)**
 - i. Annual workshop; field training events associated w CoV study; research exchanges from field-to-lab

**Assessing priorities and gaps in bat research
from the Middle East/Western Asia**
International Bat Research Conference
Durban, South Africa, 3 August 2016



1st Annual Western Asia Bat Research Network (WAB-Net) Workshop, 17-19 Sept 2018

Tbilisi, Georgia



1st Annual WAB-Net Workshop

Participants by country

<u>Country</u>	<u># Attending</u>	<u># Invited</u>
Armenia	1	3
Azerbaijan	1	1
Georgia	8	8
Iran/Germany	1	1
Iraq	0*	4
Israel	0	1
Jordan	3	5
Kazakhstan	3	3
Lebanon	1	1
Oman	1	2
Pakistan	1*	7
Saudi Arabia	1*	2
Singapore	1	1
Turkey	3	5
United Kingdom	2	2
USA	12	16
TOTAL	37	62



* Some participants were unable to attend due to visa issues

WAB-Net Workshop Topic Areas

- One Health Model: Linking Bat EID Surveillance and Ecology
- WAB-Net and the Threat Reduction Network model and links to global health security
- Bat Diversity and Practical Taxonomy for Western Asia
- Bat Ecology and Understanding Viral Ecology



WAB-Net Workshop Topic Areas, continued

- Field methods for joint disease and ecology investigations
- Sample processing and testing methods
- Biosafety, Biosecurity & PPE ‘Olympics’
- Linking WAB-Net to BOHRN



WAB-Net Bat Coronavirus Surveillance and Field Training, Georgia, Sept 2018



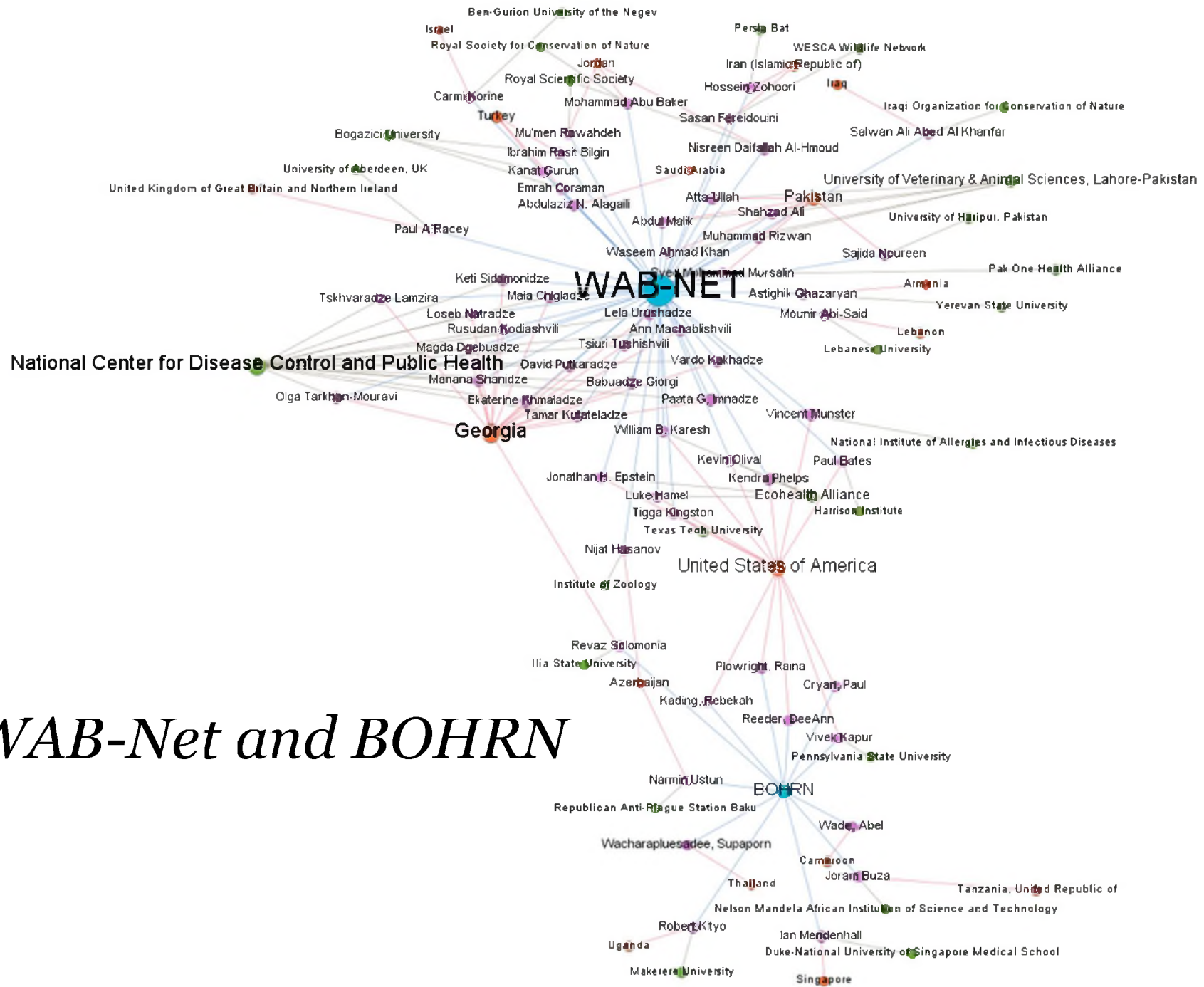
WAB-Net Coronavirus and Risk Characterization

- i. R. Lugar Center will serve as one of two regional laboratory hubs for the network.
 - i. Characterize and sequence diverse bat-CoVs
 - ii. Serve as training mentors for 2-3 week long field-to-lab fellows from other countries in the region
- ii. Data from viral sequences and greater ecological data on bat species and environment will be used to improve bat-human spillover risk models for threat reduction

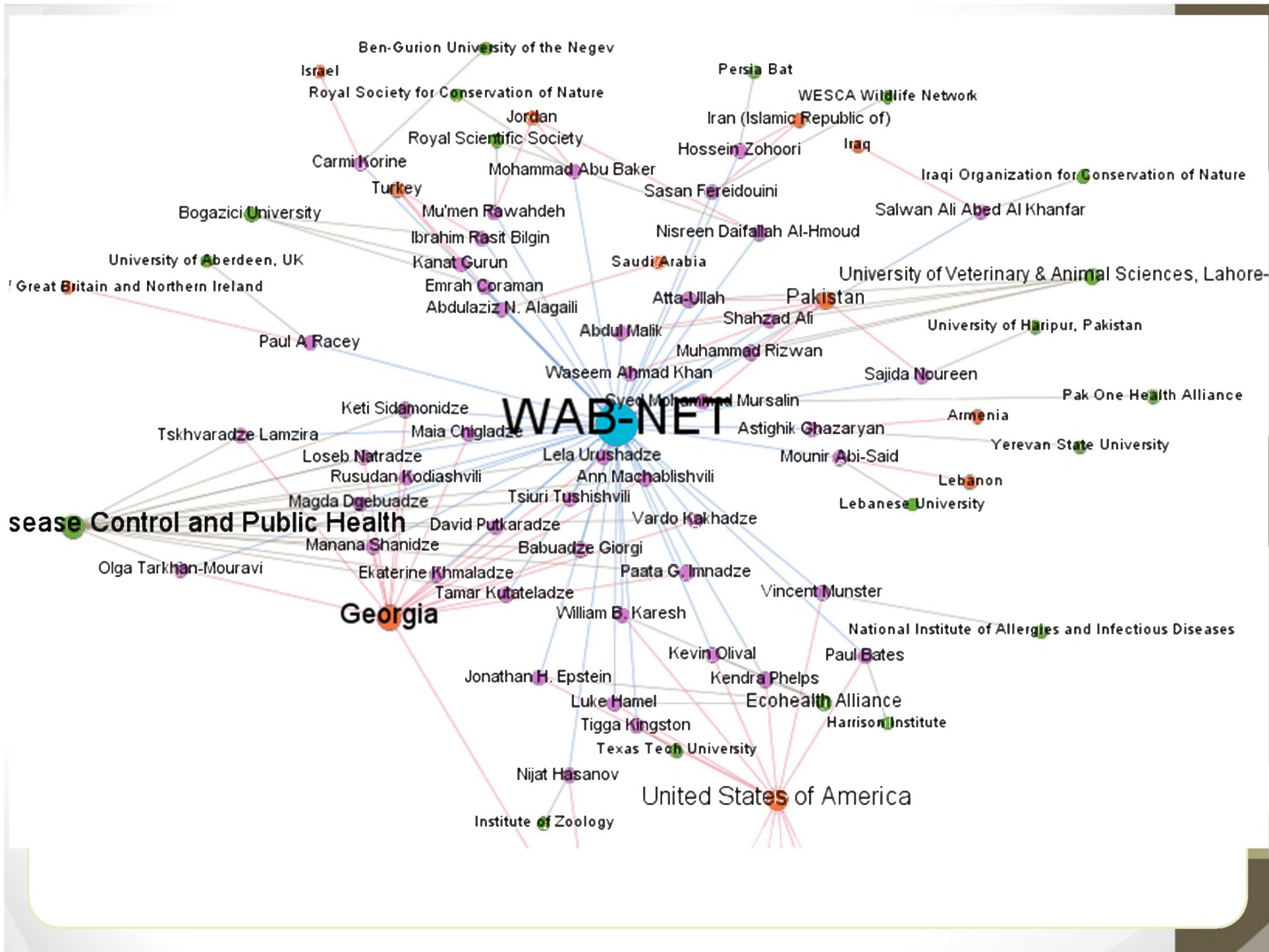
Sci-Net

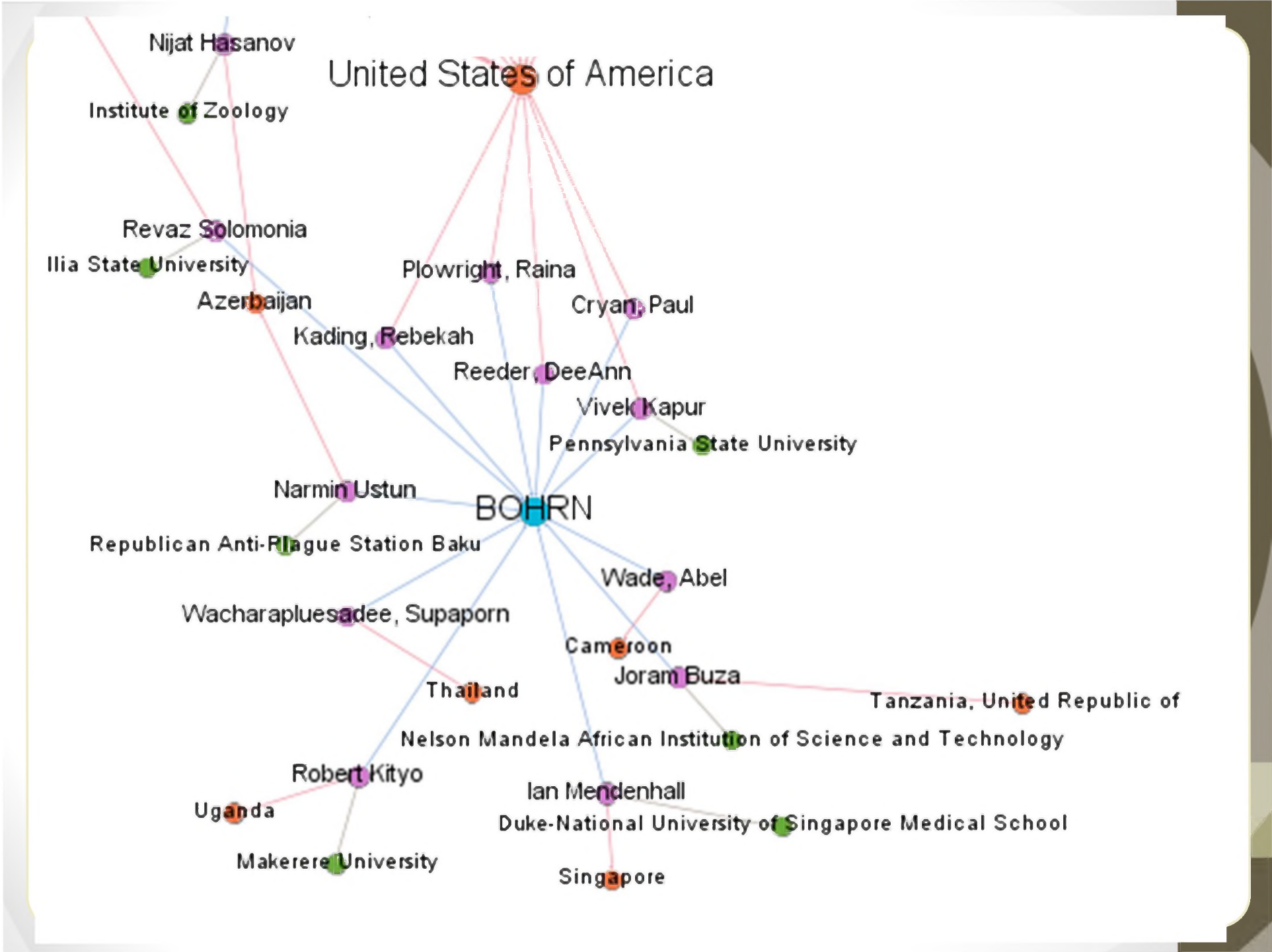
The Dynamics of
Threat Reduction Networks of
The Biological
Threat Reduction Program





WAB-Net and BOHRN





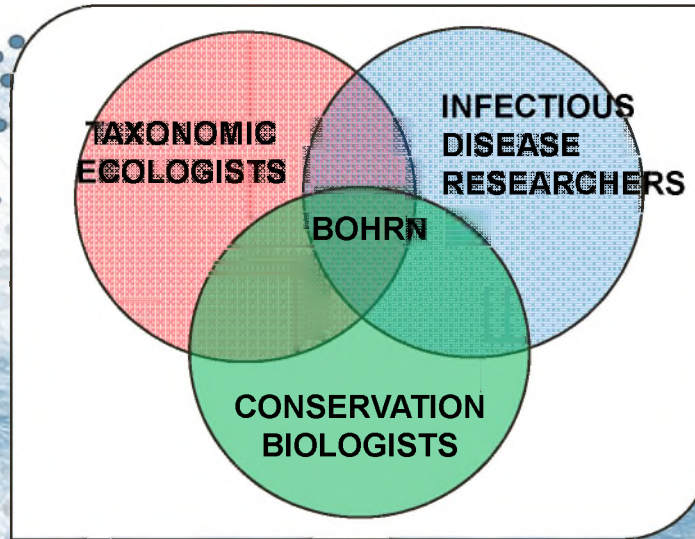
The background of the slide is a sunset sky with a bright sun partially obscured by clouds. Silhouettes of many bats are flying across the sky, some in the upper left and some in the lower right. A central white text box with a thin black border and a light green horizontal bar on each side contains the title text.

Bat One Health Research Network
(BOHRN) Biological Threat
Characterization Discussion

How BOHRN was born

- Directed to address the spillover threats
- Initiated and convened regional efforts into a global consortium of networks
- Starting in 2014, BTRP established threat reduction networks for high-risk, priority pathogen research
 - Biosurveillance and Transformative Science (BATS!) in Singapore
 - WAB-Net
 - BOHRN
 - Melioidosis in SEA
 - Rickettsias world-wide
 - African Swine Fever

Vision



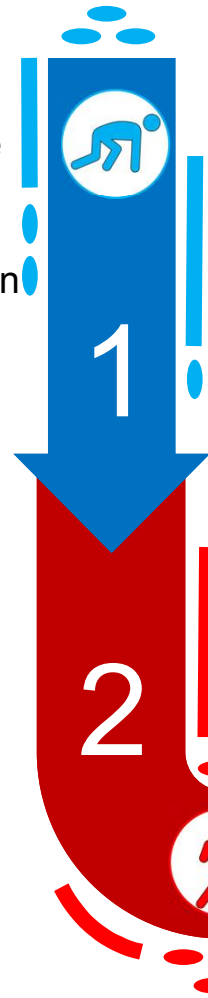
Convene a multidisciplinary consortium of disease researchers, conservationists, policy makers, and medical/veterinary practitioners into a network to characterize global threats of bat-borne pathogens and formalize community standards and conservation-conscious practices for One Health disease research.

BOHRN Steering Committee Participants

- EcoHealth Alliance
- Penn State University (U.S.)
- Royal Scientific Society (Jordan)
- Research Institute for Tropical Medicine (Philippines)
- U.S. Geological Survey (U.S.)
- Colorado State University (U.S.)
- Texas Tech University (U.S.)
- Makerere University (Uganda)
- NCDC (Georgia)
- Bucknell University (U.S.)
- WHO CC for Research and Training in Viral Zoonoses (Thailand)
- Duke NUS Medical School (Singapore)
- National Veterinary Laboratory (Cameroon)

BOHRN Strategy Map

Establish a bat-borne pathogen network that operates at the BTRP to support the BTRP mission



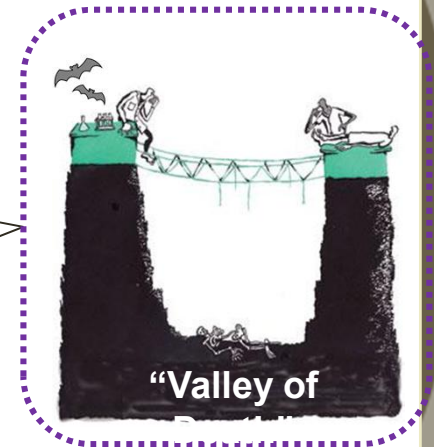
Collaborate with country partners and stakeholders to promote interdisciplinary science, and create synergies



Build leverage with other communities of funding and support, coordinate resources to achieve scale and impact



SUCCESS



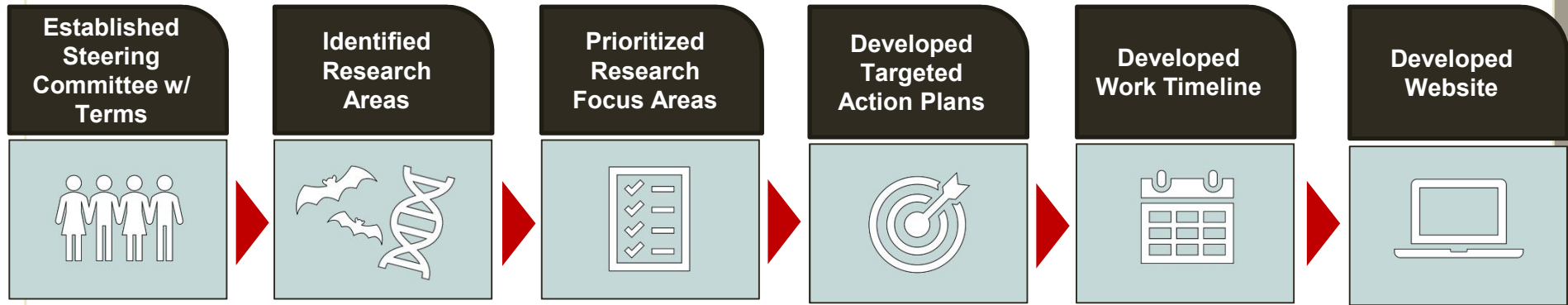
Transform scientific practice and policy from bat-borne disease research discovery



BOHRN Network Objectives

- Facilitate interdisciplinary collaboration to identify research goals and needs for bat-borne disease research and broader threat reduction
- Create a common action plan that yields collaborative and sustainable projects, which:
 - Better inform policy makers;
 - Better inform the scientific community regarding funding targets and gaps in areas of research and development;
 - Better define the threat of bat-associated pathogens to global health security
 - Improve national, regional, and global capacity to detect and respond to pathogens of security concern
- Enable better communication, coordination, and outreach at the research and conservation interface

BOHRN Progress



BOHRN Kick-off Meeting
 Fort Collins, CO – 29 June 2017
 2nd International Symposium on EID

BOHRN Steering Committee Strategy Meeting
 Bangkok, Thailand – 30 January 2018
 Prince Mahidol Award Ceremony

BOHRN Steering Committee Strategy Meeting
 Saskatoon, Canada – 20-21 June 2018
 International One Health Congress



GROUP 1

Group 1 is working on projects that study host / pathogen biological interactions



Bat physiology and immunology

Not enough is known about bat immune response to pathogens; perhaps bats' daily flight-induced increase of body temperature may explain why they are able to co-exist with pathogens without clinical signs.¹

Bat pathogen community biology

Very few studies have involved hypothesis testing regarding pathogen associations (e.g., co-infections, co-morbidities, and the bat microbiome).²

Distribution of pathogens amongst species

Bats belong to the second most species-rich order of mammal with more than 1100 species, but only a few species have been identified as natural or suspected reservoirs of pathogens of security concern.³

GROUP PRIORITIES:

- Identify new technologies that are species independent, which could provide insight into interactions between bats and viruses
- Address how pathogen ecology drives infection dynamics in bats
- Address the role of host-ecological dynamics in driving bat infection

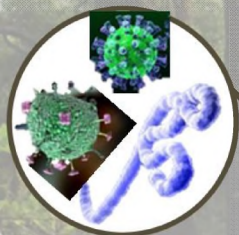
¹ <https://blogs.scientificamerican.com/guest-blog/why-don-t-bats-get-ebola/>
² [Zoonoses Public Health](#), 2013 Feb; 60(1): 2–21.
doi: [10.1111/zph.12000](https://doi.org/10.1111/zph.12000)
³ [Viruses](#), 2014 Dec; 6(12): 4880–4901.
Published online 2014 Dec 8. doi: [10.3390/v6124880](https://doi.org/10.3390/v6124880)

WORKING GROUP RESEARCH MENTORS:

Dr. Deeann Reeder, *Bucknell University* | Dr. Vivek Kapur, *Penn State University* | Dr. Joram Buza, *The Nelson Mandela Institute of Science and Technology*

GROUP 2

Group 2 is working on projects that study pathogen surveillance, diagnostic capacity, and epidemiology



Detection, diagnosis, and reporting of bat-associated pathogens

It is important to understand distribution of bats, diversity of their pathogens, and potential for zoonotic disease emergence.

Molecular epidemiology

Not enough is known about the genetic diversity of pathogens within bat species. Certain advanced molecular and diagnostic methods could be interlinked with flexible statistical methods and experimental studies.¹

GROUP PRIORITIES:

- Better understand viral shedding and transmission of pathogens in bats
- Better understand the epidemiological links between bats, pathogens, and other hosts
- Conduct field research: sampling, screening, and characterizing viruses of bats

Geographic and phylogenetic distribution of pathogens

An important question is what determines the range of pathogens found in bats and geographic variability of the community of pathogens within bat species.

¹ *Viruses*. 2014 Apr; 6(4): 1759–1788.
Published online 2014 Apr
17. doi: [10.3390/v3041759](https://doi.org/10.3390/v3041759)

WORKING GROUP RESEARCH MENTORS:

Dr. Abel Wade, *LANAVET* | Dr. Jon Epstein, *EcoHealth Alliance* | Dr. Catalino Demetria, *RITM* | Dr. Lela Urushadze, *NCDC Georgia* | Dr. Supaporn Wacharapluesadee, *Bangkok University* | Dr. Tamar Kutateladze, *NCDC Georgia*

GROUP 3

Group 3 is working on projects that research ecology (bat, domesticated animal, and wildlife interface)



Bat behavior, distribution, and movement

Relatively little information is available about bat behavior and ecology during migration, which is in part due to limitations of current technology to track small animals.

Anthropogenic disturbance and modification

Human impact on the environment (anthropogenic disturbances) such as livestock grazing, forest clearing, and the introduction of invasive species.

Domesticated animals and wildlife behavior, distribution, and movement impact on interaction with bats

The challenge of understanding the changing dynamics of domestic and wild animal populations, and how those changes impact bat populations and disease exposure.



GROUP PRIORITIES:

- Explore new and existing tracking technology commonly used for wild bird populations
- Understand full scope of changing landscapes, deforestation, encroachment, and other activities that create opportunities for disease interactions with bats
- Communicate a public health and conservation perspective; to prevent vilification of bats



WORKING GROUP RESEARCH MENTORS:

Dr. Paul Cryan, *USGS Fort Collins Science Center* | Dr. Tigga Kingston, *Texas Tech University* | Dr. Robert Kityo, *Makerere University*

GROUP 4

Group 3 is working on projects that research human – bat interactions, risk characterization

Hunting and commodity chain

Harvesting, consumption, and trade of bushmeat, guano, and pets are important causes of biodiversity loss and potential disease emergence; there is a need to understand the scale of hunting and the full scope of the global commodity chain as it relates to bat-associated pathogens.



Interactions in human dwellings

Better communication strategies are needed for areas where human-bat interactions are common, since they most frequently occur with sick or injured bats.



Ecotourism

Worldwide, bat roosts are becoming an increasingly popular attraction for ecotourists; educating these populations can encourage roost site protection, education, and awareness about bats.

GROUP PRIORITIES:

- Understand the full scope of human interactions with bats
- Characterize risk of human-bat interaction

WORKING GROUP RESEARCH MENTORS:

Dr. Kevin Olival, *EcoHealth Alliance* | Dr. Ian Mendenhall, *Duke / NUS*

BOHRN Next Steps

- 1st Annual BOHRN Meeting, 8-9 November 2018 in Vienna, Austria
 - Concurrent with International Meeting on Emerging Diseases and Surveillance
 - Objectives – (1) convene focus area groups for discussions on global priorities and potential projects, with additional participation from relevant experts; (2) identify available funding programs, their interests, and their funding timelines
- 2nd Biological Threat Characterization Discussion, TBD Feb/Mar 2019 in Muramagambo Forest, Uganda
- BOHRN Steering Committee Side-Meeting, TBD July 2019 in Phuket, Thailand
- 3rd Biological Threat Characterization Discussion, Feb / Mar 2020 in SEA

Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia

Dr. Kevin Olival¹ (PI), Dr. Nisreen Al-Hmoud², Dr. Ketevan Sidamonidze³
EcoHealth Alliance¹; Royal Scientific Society²; R. Lugar Center – NCDC³
USA¹; Jordan²; Georgia³



الجمعية العلمية الملكية
Royal Scientific Society



EcoHealth Alliance



Technical Description and Background

Technical Description

Characterize the diversity of bat-borne coronaviruses (CoVs) in Western Asia.

Combine host (bat), viral, and ecological data to better understand the risk factors to **reduce the risk threat of CoV emergence in the region.**

Promote multi-disciplinary scientific collaboration and training opportunities to improve preparedness for zoonotic virus emergence.

Current Understanding

- Bats are known to harbor zoonotic viral threats worldwide
- Coronaviruses of bat origin are of particular concern for human and livestock health (SARS, MERS, SADS)
- Virtually nothing is known about viruses in natural bat populations from Western Asia.
- More effort needed to strengthen zoonotic disease surveillance, risk assessment, and information sharing in the region

Threat Reduction Objectives

Threat Reduction Objectives

1. Enhance understanding of endemic coronaviruses to allow differentiation of natural vs. nefarious emergence events in the future
2. Support biosurveillance capacity building by enhancing partner capabilities to detect, diagnose, and report select agents
3. Engage partner country scientists in high-quality, hypothesis-driven research to elucidate the risk factors associated with bat-borne regional disease emergence
4. Employ responsible bio-risk management best practices to strengthen biosafety capacity in the region
5. Create and foster a regional network of researchers (WAB-Net), designed to increase communication and collaboration between bat biologists, virologists, and public health officials.

Key Partners and Regions of Study

Key Partners

- **Royal Scientific Society (RSS)** – *Jordan* – Regional laboratory for pathogen characterization; field data collection
- **R. Lugar Center, NCDC** – *Georgia* – Regional laboratory for leading pathogen characterization; field data collection
- **Boğaziçi University** – *Turkey* – ‘High-Engagement’ country partner, field data collection
- **University of Veterinary & Animal Sciences (UVAS)** – *Pakistan* – ‘High-Engagement’ country partner, field data collection
- **Yerevan University; Armenian Association of Mammologists** – *Armenia* – ‘Medium-Engagement’ country partner; field data

Regions

- **EUCOM** (Armenia, Azerbaijan, Georgia, Israel, Turkey)
- **CENTCOM** (Afghanistan, Bahrain, Iraq, Jordan, Kuwait, Lebanon, Oman, Pakistan, Qatar, Saudi Arabia, UAE)

Networks

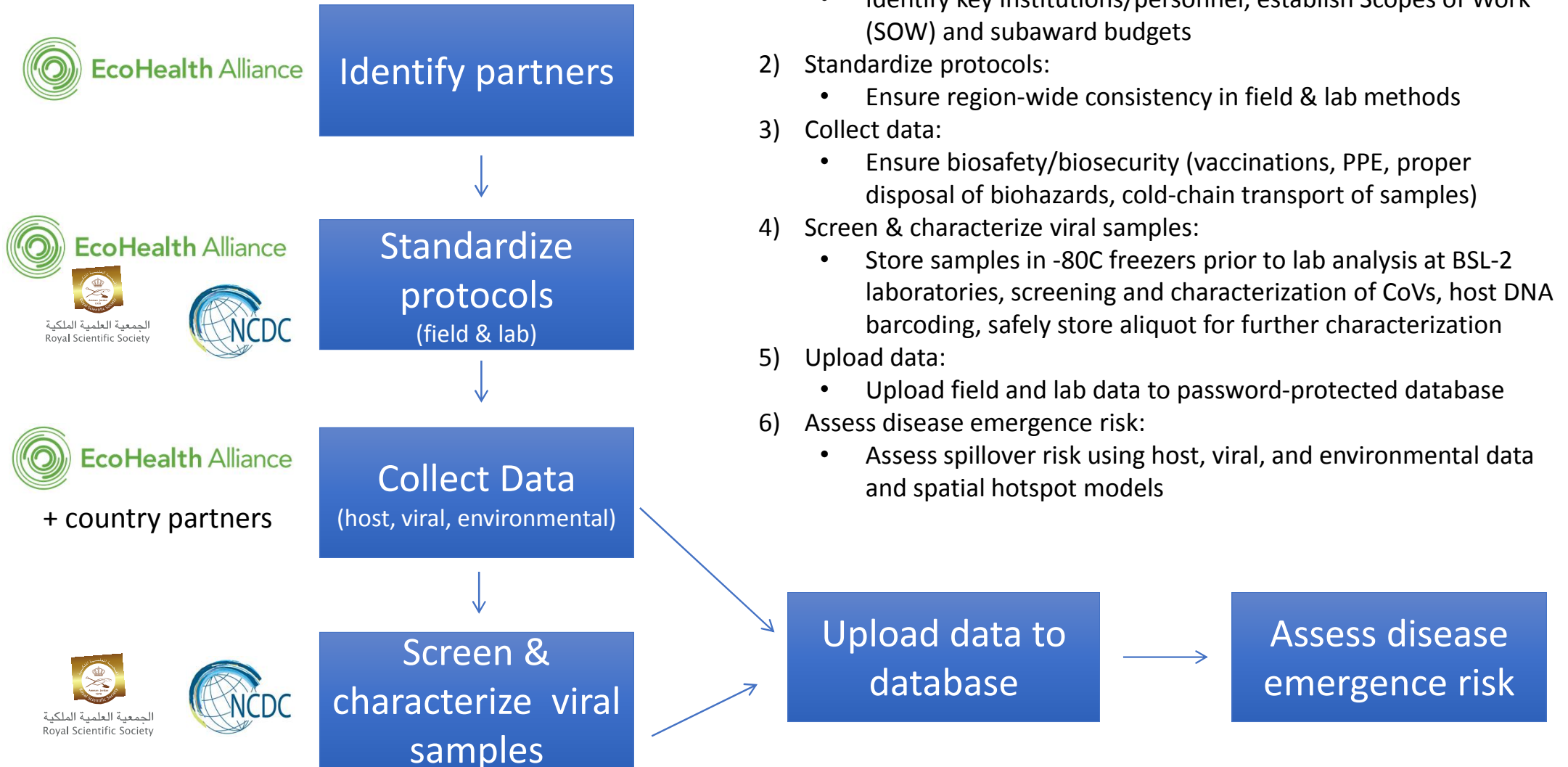
- **Western Asia Bat Research Network (WAB-Net)** Founding and strengthening this network as part of project
- **Bat One Health Research Network (BOHRN)** Co-hosted a joint workshop in Tbilisi, Georgia in September 2018
- **Southeast Asia Bat Conservation Research Unit (SEABCRU)** Active members – Drs. Kevin Olival and Kendra Phelps of EHA; and Dr. Tigga Kingston SEABCRU founder is member of WAB-Net SAB
- **EUROBATS** Dr. Paul Racey, is founding member and *on* WAB-Net SAB
- **PREDICT** – Informal partnership with USAID’s wildlife surveillance program; and comparison of CoV data, esp. w Jordan

Timeline and Major Milestones

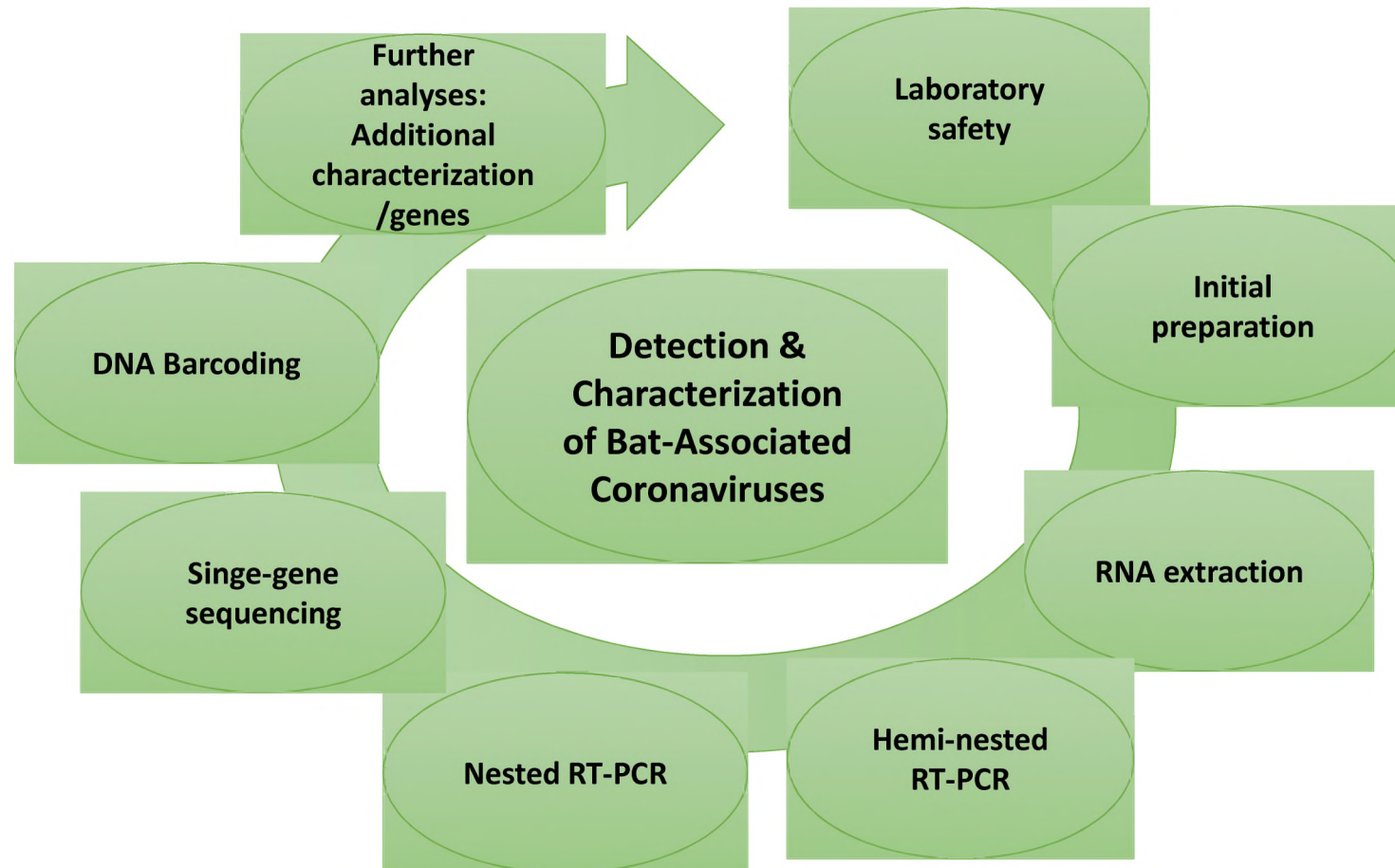
PERFORMANCE SCHEDULE.

Task	Year 1	Year 2	Year 3	OY 1	OY 2
Task 1: Establish robust scientific research platform to understand zoonotic disease risk in Western Asia					
1.1 Confirm and identify research partners and diagnostic laboratories					
1.2 Develop, pilot and implement core scientific competency assessment					
1.3 Host workshop and data-sharing meeting in a high-engagement partner country					
1.4 Refine hypotheses for CoV study					
1.5 Organize and implement field-to-lab research exchange program					
1.6 Develop and maintain website for project					
1.7 Develop and maintain information sharing database					
Task 2: Bat specimen and disease ecology field data collection					
2.1 Equip country partners with field supplies					
2.2 Conduct field-based specimen collection training in core countries					
2.3 Assist countries with study design and implementation plan for standardized surveys and implement bat study transects					
2.4 Collect bat specimens for CoV study and species distribution and taxonomic data					
2.5 Transport specimens to approved laboratories for storage					
Task 3: Regional bat Coronavirus characterization					
3.1 Equip country partners with laboratory supplies					
3.2 Conduct laboratory-based diagnostic training					
3.3 Store and update repository data for bat specimens					
3.4 Screen specimens for coronaviruses					
3.5 Confirm and sequence positive specimens					
Task 4: Compile and disseminate research results and reports to stakeholders					
4.1 Submit annual report, including sample repository data, to DTRA					
4.2 Analyze and disseminate study findings to local, regional, and global stakeholders					
4.3 Conduct presentations/meetings at times and places specified in the grant schedule, including DTRA Annual Technical Review					
4.4 Prepare/submit peer-reviewed manuscripts					
Task 5: Synthesize data and conduct analyses of bat pathogen spillover risk					
5.1 Clean and refine field and laboratory data from database for analyses					
5.2 Conduct viral phylogeny and co-phylogenetic analyses					
5.3 Conduct epidemiological analysis of CoV prevalence and diversity					
5.4 Refine ecological niche and species distribution analyses					
5.5 Develop and refine bat spillover risk assessment model					
5.6 Develop final technical report and policy brief from risk assessment					

Methods Overview



Laboratory Methods



Results

Quantitative Results

- **Identified key personnel,, partner organizations, and sampling sites in 7 countries in Western Asia**
- Georgia, Jordan, Pakistan, Turkey, Armenia, Azerbaijan, Oman



Results (cont.)

- **Trained over 25 regional scientists** in best practices of non-lethal bat capture, viral sampling, biosafety and cold-chain specimen transport and storage



Results (cont.)

- Collected and stored **2,700 clinical samples** from free-ranging bats
- **Over 450 individual bats (of 17 species)** in 4 WAB-Net partner countries: Turkey, Georgia, Jordan, Armenia

WAB-Net Partner Country	Turkey	Georgia	Jordan	Georgia	Armenia
Sampling Dates	21-25 Aug 2018	10-13 Sept 2018	4-7 Oct 2018	7-11 Jun 2019	12-16 Jun 2019
Species (no. sampled/site)	Cilingoz Cave	Ghliana Cave	Pella Cave	Letsurtsume Cave	Areni 1 Cave
<i>Barbastella capsica</i>	0	0	0	0	32
<i>Eptesicus serotinus</i>	0	0	0	0	20
<i>Hypsugo savii</i>	0	0	0	0	1
<i>Miniopterus schreibersii</i>	30	78	0	9	0
<i>Myotis capaccinii</i>	15	0	0	0	0
<i>Myotis blythii</i>	0	8	0	7	20
<i>Myotis davidii/aurascens</i>	0	0	0	1	0
<i>Myotis emarginatus</i>	0	0	0	11	1
<i>Myotis tschuliensis</i>	0	0	0	0	2
<i>Pipistrellus pipistrellus</i>	0	0	0	0	11
<i>Rhinolophus blasii</i>	17	1	0	0	0
<i>Rhinolophus euryale</i>	27	2	0	58	0
<i>Rhinolophus ferrumequinum</i>	1	1	0	3	3
<i>Rhinolophus hipposideros</i>	0	0	0	1	0
<i>Rhinopoma cystops</i>	0	0	2	0	0
<i>Rhinopoma microphyllum</i>	0	0	60	0	0
<i>Rousettus aegyptiacus</i>	0	0	28	0	0
Total Samples/Sites	90	90	90	90	90

Results (cont.)-Jordan

Year 1

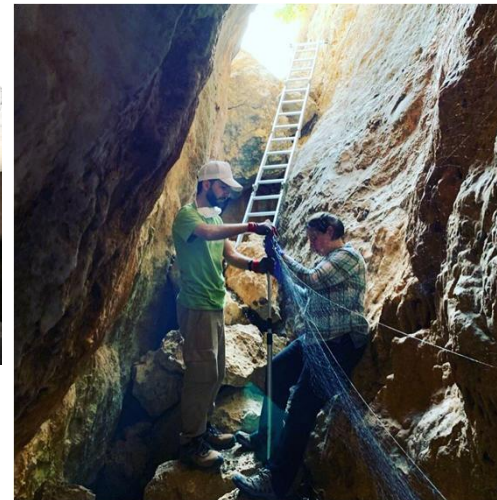
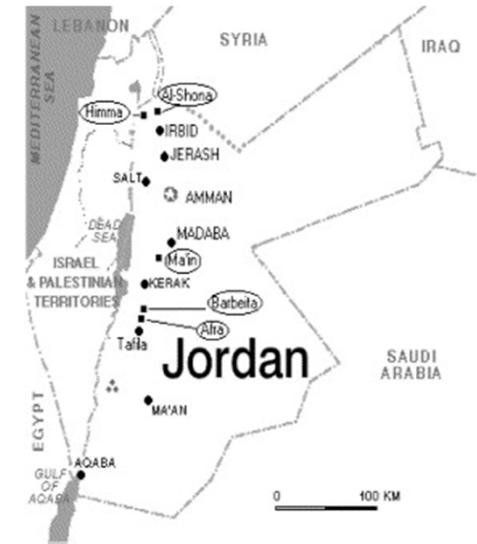
- One sampling trip (October 2018)
 - Pella Cave
- Bat species:
 - *Rhinopoma microphyllum*
 - *Rhinopoma cystopes*
 - *Rousettus aegyptiacus*



Results (cont.)-Jordan

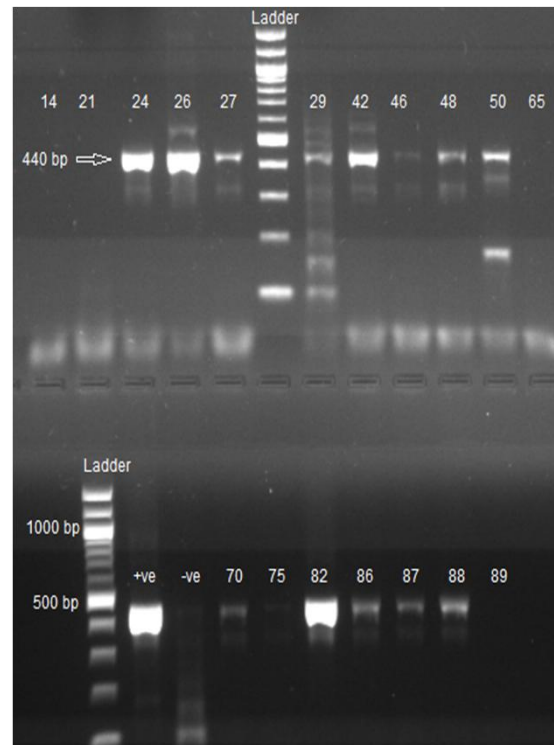
Year 2

- First sampling trip (July 2019)
 - Al-Himma cave (Irbid)
- Second sampling trip (August 2019)
 - Baoun Canyon (Ajloun)
- Bat species:
 - *Rhinolophus ferrumequinum*
 - *Rhinolophus euryale*
 - *Rhinopoma microphyllum*
 - *Rhinopoma cystopes*
 - *Rousettus aegyptiacus*

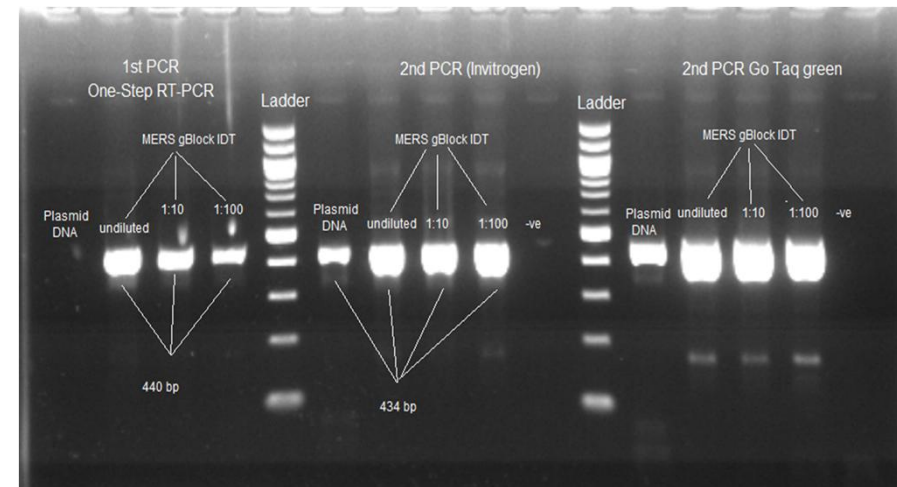


Results (cont.)-Jordan: *Lab Results for Year 1 Samples*

- A total of 90 fecal samples collected in TRIzol reagents were analyzed against Coronaviruses.
- More than 60 samples were *presumptive* positive by Pan Coronavirus PCR assay.
- Samples were sent for sequencing to confirm the results and identify the Coronavirus strains.



Lab Protocol and PCR Optimization



Results Year 1- Georgia

Year 1

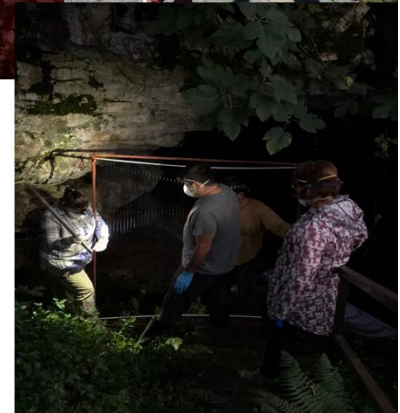
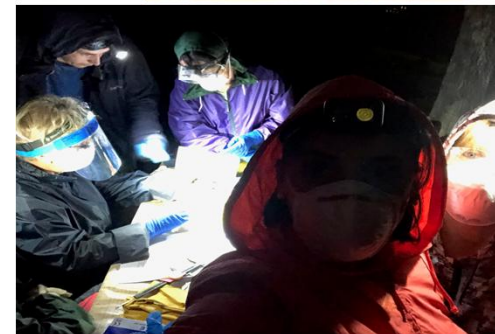
- First sampling training/trip
- Giana Cave
- Bat species:
 - *Miniopterus shreibersii*
 - *Myotis blythii*
 - *Rhinolophus euryale*
 - *Rhinolophus blasii*
 - *Rhinolophus Fenemaquinum*
 - *Hipposideros euryale*



Results Year 2- Georgia

Year 2

- First sampling trip (June 2019)
 - Letsurtsume cave
- Second sampling trip (August 2019)
- Tetri Senakebi
- Third sampling trip (September 2019)
 - Samertskhle klde
- Bat species:
 - *Myotis emarginatus*
 - *Rhinolophus euryale*
 - *Rhinolophus hipposideros*
 - *Rhinolophus ferrumequinum*
 - *Rousettus aegyptiacus*
 - *Miniopterus shreibersii*
 - *Myotis blythii*



Results - Georgia

- Totally 360 bat samples were collected in Georgia
 - ✓ 720 Fecal swab
 - ✓ 720 Oral swab
 - ✓ 360 Blood samples
 - ✓ 360 wing puch
- 90 Bat samples were reseived from Turkey
- 450 RNAs were extracted from fecal samples obtained in Georgia and Turkey

October LC will receive samples from Azerbaijan and later from Armenia.

Results (cont.)

- Held inaugural, capacity-building WAB-Net workshop from 17-20 September 2018 in Tbilisi, Georgia with 40 participants from 11 countries in Western Asia
- This workshop included a **Biological Threat Characterization Discussion (BTCD)** led by Mr. Lance Brooks and Dr. Marty Stokes of DTRA's Bat One Health Research Network (BOHRN)



Threat Reduction Impacts

Regional / Country Impact

- **Standardized field and lab protocols** to ensure region-wide consistency in bat surveillance and CoV sampling and screening methods
- **Strengthened One Health approaches to biosurveillance** and **improved biosecurity practices** among W. Asia partner nation scientists and at two regional laboratories

Biological Impacts

- **Will identify new strains** of Coronaviruses
- **Will characterize ecological risk factors** for bat-borne disease spillover and **develop recommendations for risk mitigation**

Non-Scientific Impacts

- Establishment of regional bat/biosurveillance research network (WAB-Net)
- Successful scientific information and data-sharing workshop in Tbilisi, Georgia (in collaboration with BOHRN), with 40 participants representing 11 different countries in Western Asia

Publications and Presentations

- Publication
 - Phelps et al., “Bat Research Networks and Viral Surveillance: Gaps and Opportunities in Western Asia”, *Viruses*, 2019
- Presentations
 - Keynote and research talk at 18th International Bat Research Conference
 - ...
- Poster
 - 4th International Southeast Asian Bat Conference (SEABCO), 2018
 - 48th Annual North American Symposium on Bat Research (NASBR), 2018
 - 18th International Bat Research Conference (IBRC), Thailand, 2019

Challenges

Challenges

- *Challenge:* Bat seasonality and scheduling simultaneous work across multiple countries in the region.
 - *Our solution:* Prioritized work in partner nations based on: a) bat activity and b) needs for training, and c) identifying joint training opportunities across borders (e.g. Iraq/Jordan; Georgia/Armenia).
- *Challenge:* Procuring permission for wildlife sampling and export; procuring vaccines and necessary materials and supplies for wildlife capture and sampling.
 - *Our solution:* Leveraged our experienced partners in the region, to jump ahead of potential issues and establish relationships with in-country officials re: our project, to ease any concerns and ensure that everyone involved is fully informed. Most supplies successfully procured in country, EHA obtains items that cannot be procured in-country. Export of some specimens to regional labs already achieved.

Next Steps

Next Steps

- Continue field surveillance in partner countries, to collect additional specimens and host, viral, and environmental data
- Screen for and characterize (sequence) CoVs in regional laboratories using standardized protocols
- Expand the geographic scope of sampling and further develop the biosurveillance capacity of scientific institutions across Western Asia
- Quantify the risk of regional disease emergence, by identifying correlates of CoV diversity and distribution, and characterizing interactions between humans and bats