Integrating Tiered Orthogonal Strategies into a Global Immune System for BioSurveillance

OakRidge National Labs Biosurveillance Conference
August 27, 2012, Washington DC

David L Hirschberg, PhD
Assistant Professor of Clinical Pathology
Chief Technology Officer

Columbia University Medical Center

Center for Infection and Immunity
the path forward
...the only sensible defense against biologic warfare, whatever its immediate nature, is the cultivation of science, its orientation towards basic research that will be broadly applicable, and an orderly growth of well-rounded institutions where such developments are possible and are encouraged.

- Gilbert Dalldorf; New York State Department of Health, 1949
Deaths related to West Nile virus reach 22 across Texas

FORT WORTH, Texas - The deaths of two more North Texans have been blamed on the West Nile virus.

Tarrant County officials Monday reported the deaths of a Fort Worth man and a North Richland Hills woman, both of whom were in their 80s and had underlying medical conditions.

That brings to four the number of dead in Tarrant County, to 16 the number of West Nile-related fatalities in the Dallas-Fort Worth area, and to 22 the number of dead in Texas.

Tarrant County officials are performing ground spraying to kill mosquitoes that carry the virus, while Dallas County is performing aerial spraying. Dallas County has reported 10 West Nile deaths.

© 2012 The Associated Press. All rights reserved. This material may not be published, broadcast, rewritten or redistributed.

Cambodia mystery illness kills 61 kids

(AP) PHNOM PENH, Cambodia - Health officials in Cambodia are searching for the cause of a mystery disease that has killed more than 60 children over the past three months, the World Health Organization said Thursday.

The "undiagnosed syndrome" has killed 61 of the 62 children admitted to hospitals since April, but there's no indication that it is spreading from person to person, said WHO spokeswoman Aphaluck Bhatiasevi.

She said health workers are trying to determine whether the cases were all the same disease or a collection of various illnesses.

The children were less than 10 years old and first fell ill with a high fever, followed by neurological symptoms and severe respiratory problems that quickly progressed. The cases have been reported in hospitals in 14 provinces, with most occurring in southern Cambodia.

The statement quoted Health Minister Man Bung Heng as saying identification of the cause may take some time. It said neighboring countries have been alerted.

© 2012 The Associated Press. All Rights Reserved. This material may not be published, broadcast, rewritten, or redistributed.
Current gaps in the Federal Government’s strategy

- Incomplete & fractured biosurveillance efforts have led to delayed outbreak recognition & prolonged response times.

- Current infrastructure is unfocused & inadequate to respond to emerging & re-emerging public health threats.

- Incomplete understanding of innate & adaptive immunity and host/pathogen interactions is a barrier to broad-based solutions.

- Existing strategies do not take advantage of modern science base & its full potential.

Result: Vulnerability to bioterrorism & emerging health threats
Solutions and Objectives

- Establish global awareness, surveillance & collaborations in regions considered highest risk for emerging diseases.
- Create a sustainable, comprehensive global biosurveillance program through development of outbreak response infrastructure & protocols.
- Develop pipelines for biomarker discovery & host/pathogen interactions that can be harnessed quickly to develop diagnostic assays, vaccines & therapeutics.
- Use cutting-edge, advanced technologies to rapidly develop global solutions.
Deliverables

- Rapid, global outbreak detection, characterization & diagnostics
- Predictive global risk models for emerging & re-emerging disease hotspots
- Community access to global sample & sequence repository
- Training program for domestic & international collaborators & government agencies in disease diagnostics, bioinformatics & hotspot modeling
- Rapid development & implementation of immunotherapies, vaccines & small molecule therapeutics
It is ten years since the alarm bells first began to ring about 'the bushmeat crisis', as the booming trade in the meat of wild animals quickly became known. In this decade, we have seen bushmeat rise from a fringe concern of a few NGOs to being firmly on the international agenda, of equal concern to both conservation and development agencies.

The problems raised by the commercial bushmeat trade – whether its activities are legal or illegal – are complex, and any solutions proffered must reflect this. Bushmeat cuts across concerns about endangered species and biodiversity loss, poverty alleviation, food security, livelihoods and the sustainable utilisation of natural resources.

The problems it raises are widespread and cannot be approached in isolation from other global environmental challenges, such as climate change, desertification, declining marine fish stocks and emerging diseases in an increasingly crowded world.

Prevailing scientific opinion is that we are entering a period of mass extinction, for which the human species is almost entirely accountable. The geographic nuclei of these extinctions are areas where human populations and pressure from hunting and agriculture are most intense (Ceballos & Ehrlich, 2002). Human use of biodiversity is natural, but the scale of that use has risen exponentially in the past century.
Assembling Global Health

- Discovery Diagnostics
- Surveillance
- Host Discovery
- Outbreak Response
Influenza Research Activities Emerging Infections Department NAMRU-6

Population ~29 million
~1.3 million km$^2$ total land coverage
2,414 km of coastline
Climate – tropical in east to dry desert in west
– temperate to frigid in Andes
Terrain – Coastal plains – Highlands in the center – Eastern lowland jungle of the Amazon Basin –

Tuesday, August 28, 12
Handshake Phase

- Central research/clinical lab identified
- 200 samples selected and sent to Columbia
- Samples processed through our staged strategy (MassTag, GreeneChip and sequencing)
- Phase 1 training at Columbia (personnel and more samples)
- MassTag platform and other technologies installed at remote site
- Phase II training- Columbia personnel travel to remote site and run samples on site
- Survey of site and satellite research stations
- Site personnel begin to run process samples on MassTag independently
- Samples sent to CII for confirmation
- Remote site can independently run several hundred samples a month
- End handshake phase
Iterative Phase

- Columbia preps samples that are negative by MassTag and arrays and send out to a trusted sequencing lab

- Data is shared with bioinformatic and interface collaborators in conjunction with remote site to develop streamlined analysis pipelines that will enable remote interactions

- MassTag probes are developed to identify new pathogens. MassTag panels are updated along with GreenChip array

- Assays are validated and transferred to remote site
CII begins assessing technologies that would have applications in remote lab and satellite labs

- robotics
- lateral flow pathogen detection assays
- advanced \textit{in situ} hybridization assay for pathogen diagnosis
- sample prep methodology
- sequencing platforms

Informatics and sequencing laboratories begin to directly interact with the remote lab

- Samples sent directly for sequencing
- Direct access and training on sequencing pipeline
- trouble shooting and advanced analysis for complex samples
- optimized informatics and analysis
Collaborative Phase

- Assistance for technical issues
- Outbreaks
- Technology fit assessment
NAMRU-6 Program Overview

Animal Studies

- Live Birds Market Surveillance
- Wild Birds Surveillance
- Swine Surveillance (community & slaughterhouses)

Human Studies

- Live Birds Market (KAP)
- Occupational Exposure to Zoonotic Flu
- Intra-household Transmission
- Prospective Cohorts, Burden of Disease, Economic Costs & Seasonability (Flu Cohorts)
- Economic Cost of SARI

Human Animal Interface Studies
Demographics & Geography of Peru

- Population ~29 million
- Area ~1.3 million km$^2$ total land coverage
- 2414 Km of coastline
- Climate
  - tropical in east to dry desert in west
  - temperate to frigid in Andes
- Terrain
  - Coastal Plains
  - Highlands in center
  - Eastern lowland jungle of the Amazon Basin
Disease Pyramids

Sources to estimate disease prevalence and burden

- Deaths
- Hospitalizations
- Medically attended ILI
- Non-medically attended ILI
- Mild / asymptomatic

Local health authority data

Household survey

Serosurvey

Prospective Population-based Cohort
Methods

Multi-site, population-based prospective cohort - active ILI surveillance (3 years)

Location
- 4 sites (375 households per site)
- Randomly selected households - using a census list
- At least 60% of household members required for participation
- All households are georeferenced

Population
- 6000 individuals (~1800/site)
- all ages
Peru Influenza ILI Surveillance Cohorts

- Prospective Population Based Cohort:
  - Objective: To better define epidemiology of influenza virus & other respiratory viruses
- Methods
  - Four geographically distinct regions of Peru
    - Tumbles
    - Lima
    - Cuzco
    - Madre de Dios
  - Active surveillance (3d w household visit) for ILIs
  - Oropharyngeal swabs for qPCR & serum for Luminex testing
  - Follow up of ILI cases for 2 weeks
## Other Etiologies by Luminex Antibody Serology

### ILI samples (N=201)

<table>
<thead>
<tr>
<th>Virus</th>
<th>Count</th>
<th>Co-occurrence</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adenovirus</td>
<td>4</td>
<td>Influenza B, Bocavirus</td>
<td></td>
</tr>
<tr>
<td>Bocavirus</td>
<td>1</td>
<td>Para 1</td>
<td></td>
</tr>
<tr>
<td>Corona 229E</td>
<td>1</td>
<td>Para 2</td>
<td></td>
</tr>
<tr>
<td>Corona HKU1</td>
<td>8</td>
<td>Para 3</td>
<td></td>
</tr>
<tr>
<td>Corona NL63</td>
<td>2</td>
<td>Para 3, Adenovirus</td>
<td></td>
</tr>
<tr>
<td>Enterovirus/Rhinovirus</td>
<td>59</td>
<td>Para 3, Bocavirus</td>
<td></td>
</tr>
<tr>
<td>Enterovirus/Rhinovirus, Adenovirus</td>
<td>2</td>
<td>Para 3, Enterovirus/Rhinovirus</td>
<td></td>
</tr>
<tr>
<td>Enterovirus/Rhinovirus, hMPV</td>
<td>1</td>
<td>Para 4</td>
<td></td>
</tr>
<tr>
<td>hMPV</td>
<td>10</td>
<td>RSV</td>
<td></td>
</tr>
<tr>
<td>Influenza A (H3)</td>
<td>6</td>
<td>RSV, Para 2, Enterovirus/rhinovirus</td>
<td></td>
</tr>
<tr>
<td>Influenza A Matrix</td>
<td>8</td>
<td>RSV, Para 4, Enterovirus/rhinovirus</td>
<td></td>
</tr>
<tr>
<td>Influenza B</td>
<td>7</td>
<td>No result</td>
<td></td>
</tr>
</tbody>
</table>
## Other Etiologies by Cell Culture

### ILI samples (N=1254)

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Frequency</th>
<th>Co-Infections</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>ADENOVIRUS</strong></td>
<td>32</td>
<td>FLU A-PARAFLU 2</td>
</tr>
<tr>
<td><strong>COXSACKIE B</strong></td>
<td>7</td>
<td>FLU A-PARAFLU 3</td>
</tr>
<tr>
<td><strong>ECHOVIRUS</strong></td>
<td>1</td>
<td>FLU B</td>
</tr>
<tr>
<td><strong>ENTEROVIRUS</strong></td>
<td>13</td>
<td>FLU B - HSV</td>
</tr>
<tr>
<td><strong>ENTEROVIRUS-PARAFLU 3</strong></td>
<td>1</td>
<td>FLU B-ADENOVIRUS</td>
</tr>
<tr>
<td><strong>FLU A</strong></td>
<td>394</td>
<td>HMPV</td>
</tr>
<tr>
<td><strong>FLU A - COXSACKIE B</strong></td>
<td>1</td>
<td>HSV</td>
</tr>
<tr>
<td><strong>FLU A - PARAFLU 3</strong></td>
<td>1</td>
<td>HSV-ADENOVIRUS</td>
</tr>
<tr>
<td><strong>FLU A-ADENOVIRUS</strong></td>
<td>8</td>
<td>HSV-ENTEROVIRUS</td>
</tr>
<tr>
<td><strong>FLU A-COXSACKIE B</strong></td>
<td>2</td>
<td>PARA FLU 1</td>
</tr>
<tr>
<td><strong>FLU A-ENTEROVIRUS</strong></td>
<td>3</td>
<td>PARA FLU 2</td>
</tr>
<tr>
<td><strong>FLU A-HMPV</strong></td>
<td>1</td>
<td>PARA FLU 3</td>
</tr>
<tr>
<td><strong>FLU A-HSV</strong></td>
<td>6</td>
<td>MUESTRA CONTAMINADA</td>
</tr>
<tr>
<td><strong>FLU A-HSV</strong></td>
<td>696</td>
<td>NO AISLAMIENTO</td>
</tr>
</tbody>
</table>
Puerto Maldonado

- Southern Amazon 55 km west of Bolivia
- Temperature 24-38°C
- >1000 mm of rainfall/year
- City of Puerto Maldonado has a population of 92,000 people
- The study site involves a small peri-urban community
- Poultry and small mammals are raised for consumption
- Interoceanic highway is being constructed through the center of the town
- New study site
Interoceanic Highway Will Bring Change to the Region
Multiplexed Approaches
A Staged Strategy for Pathogen Discovery

MassTag PCR Panels
- Respiratory disease
- Hemorrhagic fevers
- Meningoencephalitides
- Poxviruses
- $15/assay, 96 samples in 6 hours

GreeneChips
- Viral
- Pan-pathogen
- Respiratory
- $75/assay, 8 samples in 15 hrs

Shotgun Sequencing
- $5,000/assay – 3 days

Quantitative Real-Time PCR

Consensus PCR Cloning & Sequencing

Serology (IgM, increase in IgG titer)
Pathology (agent distribution)
Challenge experiments (reproduce disease)
MassTag Pathogen Detection

1. PCR amplification with conjugated primers
   120 minutes

   ![PCR amplification diagram]

2. PCR purification on filter plate
   30 minutes

   ![PCR purification diagram]

3. Elution into 96-well loading plate
   for mass spectrometer analysis

   ![Elution diagram]

4. Automated sample injection, photocleavage & detection
   1 minute/sample

   ![Automated sample injection diagram]

5. Identification of pathogen by signal analysis

   ![Identification diagram]
Detection of 58 Different Mass Tags by APCl-MS

Counts (relative)

m/z

350 400 450 500 550 600 650 700

0 20 40 60 80 100
30-Plex Assay of Patient Samples

- FLUA V H1N1
- CoV-SARS
- HPIV 3
- RSV B
- HPIV 1
- EV

Tuesday, August 28, 12
Co-Infection in Clinical Samples

- HPIV-3 / EV co-infection
  - Previously identified by multiplex PCR
  - Confirmed in duplicates

- HMPV / EV co-infection
  - Previously diagnosed as EV; not tested for HMPV
  - Confirmed by single-plex for both
Mass Tag Panels

- **West African fever panel**
  - Lassa fever virus
  - Chikungunya virus
  - Yellow fever virus
  - LCMV
  - O’nyong’nyong virus
  - Dengue fever virus
  - Bacillus anthracis
  - Yersinia pestis
  - Plasmodium spp
  - Rickettsia spp
  - Borrelia spp relapsing fever
  - Leptospira interrogans
  - Neisseria meningitides
  - Francisella tularensis

- **Hemorrhagic fever panel**
  - Lassa IV virus
  - Seoul virus
  - Yellow fever virus
  - Rift Valley fever virus
  - Crimean Congo Hemorrhagic fever virus
  - Ebola Zaire
  - Marburg virus
  - Chikungunya virus
  - Hantaan virus
  - Dobrava virus
  - Kyasanur forest virus
## MassTag PCR Panels

<table>
<thead>
<tr>
<th>Meningitis/Encephalitis</th>
<th>DNA agents</th>
<th>Respiratory Disease</th>
<th>DNA agents</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>RNA agents</strong></td>
<td><strong>DNA agents</strong></td>
<td><strong>RNA agents</strong></td>
<td><strong>DNA agents</strong></td>
</tr>
<tr>
<td>Eastern Equine Encephalitis virus</td>
<td>Adenovirus</td>
<td>Influenza A</td>
<td>Adenovirus</td>
</tr>
<tr>
<td>Nipah/Hendra virus</td>
<td>Cytomegalovirus</td>
<td>Influenza B</td>
<td>Chlamydia pneumoniae</td>
</tr>
<tr>
<td>Japanese Encephalitis virus</td>
<td>Epstein Barr virus</td>
<td>RSV</td>
<td>Legionella pneumophila</td>
</tr>
<tr>
<td>Powassan virus</td>
<td>Varicella Zoster virus</td>
<td>HPV1</td>
<td>Mycoplasma pneumoniae</td>
</tr>
<tr>
<td>Lymphocytic Choriomeningitis virus</td>
<td>Herpes Simplex virus 1</td>
<td>HPV2</td>
<td>Neisseria meningitidis</td>
</tr>
<tr>
<td>St. Louis Encephalitis virus</td>
<td>Herpes Simplex virus 2</td>
<td>HPV3</td>
<td>Haemophilus influenzae</td>
</tr>
<tr>
<td>Enterovirus</td>
<td>HHV6</td>
<td>HPIV4</td>
<td>Streptococcus pneumoniae</td>
</tr>
<tr>
<td>Rabies virus</td>
<td>Haemophilus influenzae</td>
<td>MPV</td>
<td>Mycobacteria tuberculosis</td>
</tr>
<tr>
<td>Influenza A virus</td>
<td>Neisseria meningitidis</td>
<td>CMV</td>
<td>Moraxella catarrhalis</td>
</tr>
<tr>
<td><strong>RNA agents</strong></td>
<td><strong>DNA agents</strong></td>
<td><strong>RNA agents</strong></td>
<td><strong>DNA agents</strong></td>
</tr>
<tr>
<td>Eastern Equine Encephalitis virus</td>
<td>Adenovirus</td>
<td>Influenza A</td>
<td>Adenovirus</td>
</tr>
<tr>
<td>Nipah/Hendra virus</td>
<td>Cytomegalovirus</td>
<td>Influenza B</td>
<td>Chlamydia pneumoniae</td>
</tr>
<tr>
<td>Japanese Encephalitis virus</td>
<td>Epstein Barr virus</td>
<td>RSV</td>
<td>Legionella pneumophila</td>
</tr>
<tr>
<td>Powassan virus</td>
<td>Varicella Zoster virus</td>
<td>HPV1</td>
<td>Mycoplasma pneumoniae</td>
</tr>
<tr>
<td>Lymphocytic Choriomeningitis virus</td>
<td>Herpes Simplex virus 1</td>
<td>HPV2</td>
<td>Neisseria meningitidis</td>
</tr>
<tr>
<td>St. Louis Encephalitis virus</td>
<td>Herpes Simplex virus 2</td>
<td>HPV3</td>
<td>Haemophilus influenzae</td>
</tr>
<tr>
<td>Enterovirus</td>
<td>HHV6</td>
<td>HPIV4</td>
<td>Streptococcus pneumoniae</td>
</tr>
<tr>
<td>Rabies virus</td>
<td>Haemophilus influenzae</td>
<td>MPV</td>
<td>Mycobacteria tuberculosis</td>
</tr>
<tr>
<td>Influenza A virus</td>
<td>Neisseria meningitidis</td>
<td>CMV</td>
<td>Moraxella catarrhalis</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>West African Fever</th>
<th>Hemorrhagic Fever</th>
<th>Tick-borne</th>
<th>Biothreat</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lassa fever virus</td>
<td>Lassa virus</td>
<td>Babesia spp</td>
<td>Bacillus anthracis</td>
</tr>
<tr>
<td>Chikungunya virus</td>
<td>Seoul virus</td>
<td>Coxiella burnetti</td>
<td>Francisella tularensis</td>
</tr>
<tr>
<td>Yellow fever virus</td>
<td>Yellow fever virus</td>
<td>Ehrlichia spp</td>
<td>Yersinia pestis</td>
</tr>
<tr>
<td>LCMV</td>
<td>Rift Valley fever virus</td>
<td>Francisella tularensis</td>
<td>Burkholderia mallei</td>
</tr>
<tr>
<td>Onyong nyong virus</td>
<td>CCHF virus</td>
<td>Rickettsia spp</td>
<td>Burkholderia pseudomallei</td>
</tr>
<tr>
<td>Dengue virus</td>
<td>Ebola Zaire</td>
<td>Brucella spp</td>
<td>Brucella spp</td>
</tr>
<tr>
<td>Bacillus anthracis</td>
<td>Marburg virus</td>
<td>Rickettsia prowazekii</td>
<td>Rickettsia prowazekii</td>
</tr>
<tr>
<td>Yersinia pestis</td>
<td>Hantaan virus</td>
<td>Francisella tularensis</td>
<td>Clostridium botulinum</td>
</tr>
<tr>
<td>Plasmodium spp</td>
<td>Dobrava virus</td>
<td>Coxiella burnetti</td>
<td>Cloxiella burnetti</td>
</tr>
<tr>
<td>Rickettsia spp</td>
<td>Kyasanur forest virus</td>
<td>Orthopox virus</td>
<td>Orthopox virus</td>
</tr>
<tr>
<td>Trypanosoma brucei</td>
<td></td>
<td>Ebola virus</td>
<td>Ebola virus</td>
</tr>
<tr>
<td>Borrelia spp relapsing fever</td>
<td></td>
<td>Marburg virus</td>
<td>Marburg virus</td>
</tr>
<tr>
<td>Leptospira interrogans</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Neisseria meningitidis</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Salmonella spp</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Bacterial Enteric</th>
<th>Viral/Parasitic Enteric</th>
</tr>
</thead>
<tbody>
<tr>
<td>Listeria monocytogenes</td>
<td>Astrovirus</td>
</tr>
<tr>
<td>Clostridium perfringens</td>
<td>Rotavirus-A,B,C</td>
</tr>
<tr>
<td>Clostridium difficile</td>
<td>Norovirus-GI</td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>Norovirus-GII</td>
</tr>
<tr>
<td>Campylobacter coli</td>
<td>Sapovirus GI/II</td>
</tr>
<tr>
<td>Salmonella</td>
<td>Adenovirus F</td>
</tr>
<tr>
<td>Salmonella typhi/paratyphi</td>
<td>Giardia lamblia</td>
</tr>
<tr>
<td>Vibrio</td>
<td>Cryptosporidium</td>
</tr>
<tr>
<td>Vibrio vulnificus</td>
<td>Entamoeba histolytica</td>
</tr>
<tr>
<td>Yersinia enterocolitica</td>
<td></td>
</tr>
<tr>
<td>Yersinia pseudotuberculosis</td>
<td></td>
</tr>
<tr>
<td>Escherichia coli</td>
<td></td>
</tr>
</tbody>
</table>
Oropharyngeal swabs from 162 individuals in Cuzco & Puerto Madonado with ILI symptoms tested

Cases
- 38 rhinovirus
- 11 influenza A viruses (7 H1N1) and 4 (H3N2)
- 11 parainfluenza viruses (3 HPV-1, 1 HPV-2, 5 HPV-3, 2 HPV-4)
- 9 non-rhino enteroviruses (2 subsequently have been shown to be novel)
- 7 metapneumoviruses
- 6 influenza B viruses
- 6 respiratory syncytial viruses
- 3 Chlamydophila pneumoniae and 2 Legionella pneumophila
- 14 adenovirus (10 HAdV-A, 2 HAdV-B, 2 HAdV-C, 1 HAdV-D & 2 HAdV-F)

Many of the infections were co-infections (virus-virus or virus-bacteria)
Etiologic agents were identified in 85 (52%) of the 162 patients with ILI including 75% of the cases where no diagnosis was previously known from monoplex assays
Small outbreak of ILI due to enterovirus identified that was not identifiable with existing monoplex assays

Latest results indicate that the majority of cases in July and August is largely HEV

Unresolved and some FUO serum were prepared for Illumina and Sequenced at ECBC
New York City Department of Health

Distribution of Influenza and Enterovirus/Rhinovirus

Samples Positive by Agent

- FLUA
- EV/RV

MAY JUN JUL AUG SEP OCT NOV DEC JAN FEB MAR APR
Influenza Surveillance
Collaboration with the Federal Government

- Act as consultant to the Federal Government through regular meetings
- Liaise with existing government agencies to streamline implementation of comprehensive biosurveillance program nationally & globally
- Participate in governmental committees in order to shape the country’s outbreak response strategies
We live in a world that is increasingly interconnected, making us more susceptible to harmful pathogens. Now, more than ever, we need a unified public health strategy.

Our international group of investigators has been instrumental in several outbreak response efforts, including the anthrax crisis, the SARS epidemic, West Nile and LuJo virus and Nipah virus encephalitis.

By working in collaboration with the Federal Government, we can promote public health on a global scale, ensuring more efficient prevention, detection and management of potential health threats.
Collaborators

- University of Houston
  - Yuriy Fofanov
  - Georgiy Golovko
  - Mark Rojas
  - Kamil Khanipov

- ECBC
  - C. Nicole Rosenzweig
  - Stacey Broomall
  - Mohamed Ait Ichou

- OptiMetrics
  - Greg Donarum
  - Alvin Liem

- NAMRU-6
  - Daniel Bausch
  - Matthew Kasper
  - Maria Silva Ibañezm
  - Mariana Leguia
  - Marita Silva
  - Giannia Lina
  - Andrew Bennett