Science Program Review
February 08 - 10, 2017

CBEP
Cooperative Biological Engagement Program

Defense Threat Reduction Agency
United States of America

Department of Defense
Cooperative Threat Reduction Program

DEFENSE THREAT REDUCTION AGENCY
8725 JOHN J. KINGMAN ROAD, STOP 6201
FORT BELVOIR, VA 22060-6201

Dear Colleagues,

Welcome to the 9th Science Program Review of the U.S. Defense Threat Reduction Agency's Cooperative Biological Engagement Program (DTRA CBEP). The CBEP carries out its mission by collaborating with partner countries and the international community to minimize the threat of deliberate, accidental and natural infectious disease outbreaks through enhanced biosecurity, biosafety, and biosurveillance measures. Cooperative Biological Research (CBR) is an integral element of the threat reduction mission by supporting and informing operational biosurveillance, enhancing global health security, and establishing and fostering sustainable research partnerships. CBEP's achievements rely on successful collaboration with partner-country scientists, and we thank you for your dedication and cooperation in our shared efforts to better understand the biological threats that face our world today.

We have in attendance nearly 120 researchers from over 30 countries representing 70 CBR projects, and this three-day event will feature briefings by CBEP partner-country scientists and collaborators conducting CBEP-funded research. We look forward to engaging with researchers from around the globe and evaluating the spectrum of CBEP research activities, in order to strengthen the quality of projects supported by the program and ensure that current efforts meet research priorities and objectives.

A significant benefit of the CBEP Science Review is networking amongst fellow scientists. During the next few days, you will have the opportunity to meet with scientific and program colleagues from CBEP partner nations, the U.S. Department of Defense, other U.S. Government stakeholders, and international and U.S. program partners. With such a broad range of scientific expertise present, we hope that this environment will create new networks among subject matter experts and facilitate new partnerships within the scientific community.

Again, I want to thank you for your participation in this 2017 CBEP Science Program Review. I hope that you will enjoy your experience and find opportunities to expand your collaborative research network.

Sincerely,

Lance Brooks
Division Chief
Cooperative Biological Engagement
Program, J3CTB

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CBEP Mission

The Defense Threat Reduction Agency's Cooperative Biological Engagement Program is the Department of Defense's premier biological nonproliferation division protecting the United States and its allies from especially dangerous pathogens by collaborating with partner countries and the international community to minimize the threat of deliberate, accidental, and natural infectious disease outbreaks through enhanced biosafety, security, and surveillance measures.

The Defense Threat Reduction Agency's Cooperative Biological Engagement Program utilizes Science Diplomacy to promote scientific and technical collaborations among partner nations and the international community in [the disciplines of] biological safety, security and surveillance to build constructive and sustainable international partnerships that address threats posed to health security from deliberate, accidental, and natural infectious disease outbreaks.

General Information

- Posters may be displayed on the available poster boards in the Foyer area. An informal networking and poster session will be held following the “Doing Science in Difficult Places” session.
    - Posters displayed in the Foyer area must be removed by 1:00 PM on Friday, February 10, 2017. Posters that are not removed by this time will not be kept by DTRA.
- A designated Prayer Room is available next to the Registration area in the Dogwood Room. Please see attendants at the Registration desk for additional information.
- If temporary luggage storage is required, please see the hotel Front Desk.
- Meeting space is available during the event for collaborative discussions. Please see the Registration desk for more information.
- Please see the Registration Desk for any questions or concerns during the event.

Acknowledgments

The following individuals were instrumental in the development and implementation of this event.

CBEP Science Program Review Steering Committee

Dr. Carl Newman
Chief Scientist, Cooperative Biological Engagement Program (CBEP)

Dr. Martha Stokes
Southeast Asia Science Manager, CBEP

Dr. Mary Lancaster
Africa Science Manager, CBEP

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- Dr. Jarrad Marles
- Ms. Nicki Aleman
- Dr. Ayanna Flegler
- Dr. Dawn Defenbaugh
- Dr. Michael Patterson
- Dr. Elizabeth Waligora

Special Thank You to those who helped organize this event:

- Dr. Jeanne Fair
- Dr. Gavin Braunstein
- Mr. Andrew Kotila
- Dr. Mariam Lekveishvili
- Ms. Natalie Might
- Mr. Jeffrey Russin
- Mrs. Karla Somera
- Ms. Audrey Speer
- Ms. Danielle Wilbur

Science Program Review Panel

CBEP would like to acknowledge the following individuals for serving on the Review Panel for the 2017 CBEP Science Program Review. The Review Panel is comprised of experts with varied backgrounds in a broad range of scientific disciplines and expertise in public health security and program implementation. The Review Panel will provide CBEP with an external technical and programmatic evaluation of the CBEP-sponsored research portfolios to identify strengths and weaknesses in CBEP research engagements, along with recommendations for improving how the portfolios are designed and implemented.

Jessica Appler, PhD, is the Associate Director, Portfolio Development for the Biomedical Advanced Research and Development Authority (BARDA) Modeling and Visualization Hub within BARDA’s Division of Analytic Decision Support at the U.S. Department of Health and Human Services (HHS). She oversees the development of a portfolio focused on assessing the public health and medical consequences for chemical, biological, radiological, and nuclear (CBRN) incidents, emerging infectious diseases, and pandemic influenza events. Prior to joining HHS, she was at the Deputy Undersecretary of the Army for Test and Evaluation CBRN Defense Division, where her portfolio included oversight of CBRN test and evaluation programs, as well as the testing and standards development for the Transport Isolation Systems during the 2014-2015 West African Ebola crisis. Previously, she was a member of the Chemical and Biological Defense Division of Department of Homeland Security’s Science and Technology Directorate, where she provided subject matter expertise and strategic vision for existing and planned biosurveillance programs. She was part of the interagency team that identified critical needs and gaps across the government in biological detection and diagnostic technology for the National Biosurveillance Science & Technology Roadmap. Dr. Appler earned her Ph.D. in Neurobiology from Harvard University, and her B.S. in biochemistry from the University of Southern California.

Hillary H. Carter, PhD, is the Director for Countering Biological Threats on the National Security Council (NSC) staff. Dr. Carter's portfolio includes the Global Health Security Agenda, domestic and international biosecurity issues, implementation of the President's Strategy for Countering Biological Threats, biological threat reduction, and policies related to Dual Use Research of Concern. Dr. Carter is also an adjunct Professor at the George Washington University where she lectures on Global Health Diplomacy. Prior to joining NSC staff, Dr. Carter was the Senior Advisor for Biosecurity and a Team Chief in the Office of Cooperative Threat Reduction (CTR) at the U.S. Department of State. In this role, Dr. Carter led CTR's special project and management teams to develop policy and implement programs to combat global biological, chemical, and nuclear threats. Prior to this role, Dr. Carter served as the Acting Deputy Team Chief for the Biosecurity Engagement Program where she oversaw health security programs to reduce global biological risks. Dr. Carter received a Ph.D. in Cell and Developmental Biology from Vanderbilt University, where she studied intracellular transport during early development. Dr. Carter holds a B.S. in Neuroscience with a minor in Spanish from Vanderbilt University.

Marco De Nardi, DVM, has 15 years working experience in the field of animal health and epidemiology in both developed and less developed countries. He received a Degree in Veterinary Medicine (DVM) from Bologna University (IT) in 2002 and a MSc degree in Veterinary Epidemiology from the Royal Veterinary College and the London School of Hygiene and Tropical Medicine, UK in 2008. He is currently enrolled in the residency training (Population Medicine) of the European College of Veterinary Public Health. Following his DVM he practiced as a veterinary clinician in dairy farms in Italy. He then worked as a veterinary consultant and project coordinator for international organizations (non-governmental organizations and the Food and Agriculture Organization (FAO)) in East Africa from 2004 to 2007. In 2009-2013, he worked on research and capacity building programs at the "World Organization for Animal Health (OIE) and FAO Reference Laboratory for Avian Influenza" and the "FAO Reference Centre for Rabies" at Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) in Italy. In 2011, he coordinated the European Food Safety Authority (EFSA)-funded project "Flurisk," assessing the pandemic risk posed by animal influenza viruses.

In 2013 he joined the private veterinary consultancy company SAFOSO (www.safoso.com), where he is responsible for the development and implementation of consultancy, research projects and capacity building programs in the area of risk assessment, surveillance, veterinary epidemiology, animal health and food safety. As a SAFOSO consultant he worked in different projects in Europe, U.S., Ukraine, Armenia, Georgia, Kazakhstan, Mongolia and Vietnam.

Sam Howerton, **PhD**, is as a Senior Executive at the National Science Foundation. Hearing the call to service in 2001, he escaped the bounds of a traditional scientific career by seeking out organizations undergoing change. He oversaw the development of new drugs, negotiated new international agreements, and provided entrepreneurs training on transforming their ideas into business ventures.

With a healthy appetite for risk, Sam is known for his 'first unto the breach' leadership and willingness to try most any food.

Possessed of a strong imagination and an inquisitive mind, he earned a Ph.D. in Chemistry-Environmental Toxicology and completed Air War College. Sam's most important job is raising his sons to be good Southern gentlemen.

Paul Keim, **PhD**, is the executive director of The Pathogen and Microbiome Institute, which uses genomic tools for understanding infectious diseases and the microbiome. This is a joint institute between TGen and Northern Arizona University, where Dr. Keim holds the Cowden Endowed Chair in Microbiology. His work has employed genetic and genomic analyses for understanding bacterial pathogen population structure and evolution for more than 30 years. Linking populations to their ecology has also been a critical part of his program. His laboratory served as the evidence repository and genetic analysis lab for the Federal Bureau of Investigation during the 2001 anthrax-letter investigation. He has been a leader in the field of microbial forensics which uses evolutionary analysis to understand close relationships among pathogen isolates. This work was foundational for his pursuit in public health investigations and the development of novel clinical diagnostic tests. He is an elected fellow of both the American Association for the Advancement of Science and the American Academy for Microbiology. The National Institutes of Health appointed him to the National Science Advisory Board for Biosecurity in 2004 and served as its chairman for two years. He has published over 400 scientific research articles that have been cited over 20,000 times.

Jennifer Nuzzo, DrPh, SM, is a Senior Associate at the Johns Hopkins Center for Health Security (formerly the University of Pittsburgh Medical Center for Health Security), Visiting Faculty in the Department of Environmental Health and Engineering and Associate in the Department of Epidemiology at the Johns Hopkins Bloomberg School of Public Health. An epidemiologist by training, her work focuses on international and domestic biosurveillance, infectious disease diagnostics, and disease mitigation strategies. She also has worked on issues related to the Affordable Care Act, tuberculosis control, foodborne outbreaks, and water security. Dr. Nuzzo is an Associate Editor of the peer-reviewed journal *Health Security* (formerly *Biosecurity and Bioterrorism*).

In addition to her work at the Center, Dr. Nuzzo has advised national governments and nonprofit organizations. She has served as a consultant to the National Biosurveillance Advisory Subcommittee, as a member of the US Environmental Protection Agency's National Drinking Water Advisory Council (NDWAC), and as a member of the NDWAC's Water Security Working Group. She has also served as a project advisor for the American Water Works Association Research Foundation (now called the Water Research Foundation), a primary funding organization for drinking water research in the United States. She has also been consulted on pandemic planning efforts in the Republic of Indonesia and Taiwan.

Dr. Nuzzo received a Doctor of Public Health degree (DrPH) in epidemiology from the Johns Hopkins Bloomberg School of Public Health, an SM in environmental health from Harvard University, and a BS in environmental sciences from Rutgers University.

Martina Siwek, **PhD**, a native of the Czech Republic, obtained a Bachelor of Arts (BA) in Biological Science from Goucher College and a Doctorate of Philosophy in Molecular Microbiology and Immunology from the Johns Hopkins Bloomberg School of Public Health. She has extensive research experience in HIV vaccine research and human immunity and infectious diseases, especially viral pathogens. Dr. Siwek has worked in support of the Department of Defense since 2010. She started at the Joint Program Executive Office (JPEO) as the Technical Director for the Critical Reagents Program (CRP) and as a subject matter expert in infectious diseases and especially dangerous pathogens. Dr. Siwek eventually transitioned to serving as the Liaison Officer coordinating various inter- and intra-agency efforts and organizations, including the Armed Forces Health Surveillance Branch (AFHSB), the Centers for Disease Control and Prevention (CDC), the Defense Threat Reduction Agency (DTRA), and many others. She assumed her role as the Chief Scientist for the Global Emerging Infections Surveillance (GEIS) Section at the AFHSB in 2014. There she provides scientific guidance and oversight for emerging infectious disease surveillance projects conducted by or in conjunction with US military research laboratories in continental United States (CONUS) as well as outside of the continental United States (OCONUS) settings.

Wednesday, February 8, 2017		
Time	**Session**	**Notes**
1:30 PM - 2:00 PM	**CBEP EUCOM Overview**	Overview Briefs by DTRA/CBEP for Review Panel (Note: **Closed Session** for US Government Personnel and Review Panelists only)
2:00 PM - 2:30 PM	**CBEP AFRICOM Overview**	
2:30 PM - 3:00 PM	**CBEP CENTCOM Overview**	
3:00 PM - 3:30 PM	**CBEP PACOM Overview**	
3:30 PM - 4:00 PM	**Coffee Break**	Open to all Attendees
4:00 PM - 5:00 PM	**Session 1: Special Presentation** **“Doing Science in Difficult Places”**	Open to all Attendees
5:00 PM - 6:30 PM	**Poster Session & Networking Event**	Open to all Attendees

Thursday, February 9, 2017

Time	Speaker	Country	Project
8:30 AM - 8:50 AM	**Opening Remarks**		
8:50 AM - 10:10 AM	**Session 2: Chiroptera (Bats) - Important Reservoirs Hosts of Emerging Viruses**		
	Olival, Sidamonidze, & Al-Hmoud	Georgia & Jordan	(BAA) Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia
	Smith	Cambodia	(BAA) Investigating the Risk of Human Disease from Parasites of Small Mammals and Bats
	Kityo	Uganda	(Call) Arthropod-borne Viruses Associated with the Chiroptera of Uganda: Isolation and Characterization
	Mendenhall	India	(BAA) Bat Harvesting in India: Detection, Characterization and Mitigation of Emerging Infectious Disease Risk
	Ekiri	Tanzania	(BAA) Evaluating Zoonotic Viral Sharing Among Bats, Primates and People in High Risk Transmission Interface in Southern Tanzania.
10:10 AM-10:30 AM	**Coffee Break**		
10:30 AM-11:40 AM	**Session 3: Epidemiology & Biosurveillance - Group 1**		
	Chanturia	Georgia	GG-19: Epidemiology and Ecology of Human Tularemia in Georgia
	Jacobs	Azerbaijan	TAP-10: Ecological and Epidemiological Study of *Yersinia pestis* and *Francisella tularensis* in the Northern Part of Azerbaijan Regions of Gusar and Khachmaz
	Kilonzo	Tanzania	(BAA) One Health Approach to Brucellosis and Rift Valley Fever Surveillance in Tanzania
	Bhengsri	Thailand	(Call) Acute Febrile Illness Study Among Patients in Nakhon Phanom and Tak Province, Thailand
	Orynbayev	Kazakhstan	TAP-8: Especially Dangerous Pathogen Differential/Rule-Out Elimination Assays & Modeling (EDP-DREAM) of the Saiga Antelope Mortality

Thursday, February 9, 2017 (Continued)

Time	Speaker	Country	Project
11:40 AM-12:30 PM	**Session 4: Viral Pathogens of Security Concern**		
	Babuadze	Georgia	(Call) Assessing the Seroprevalence and Genetic Diversity of CCHFV and Hantaviruses in Georgia
	Eyangoh	Cameroon	Epidemiology of Emerging Viruses
	Karesh & Van Vuren	South Africa	(BAA) Understanding Rift Valley Fever in South Africa.
	Epstein	Malaysia	(BAA) Biosurveillance for Henipaviruses and Filoviruses at the Agricultural Animal-Human Interface in Malaysia
12:30 PM - 1:30 PM	**Lunch**		
1:30 PM - 2:20 PM	**Session 5: Community Outreach to Combat African Swine Fever**		
	De Nardi	Implementer	ASF Public Outreach Project Overview
	Niazyan	Armenia	TAP-A1: Community Outreach to Support Understanding of ASF Ecology and Epidemiology in Eastern Europe: Training and Implementation for Methods and Strategies for Control and Prevention
	Ninidze	Georgia	TAP-9: Community Outreach to Support Understanding of ASF Ecology and Epidemiology in Eastern Europe: Training and Implementation for Methods and Strategies for Control and Prevention
	Datsenko	Ukraine	TAP-4: Community Outreach to Support Understanding of African Swine Fever (ASF) Ecology and Epidemiology in Eastern Europe

Thursday, February 9, 2017 (Continued)			
Time	**Speaker**	**Country**	**Project**
2:20 PM - 3:20 PM	**Session 6: Transboundary Animal Diseases**		
	Dung	Vietnam	(Call) Foot-and-Mouth Disease Virus Surveillance and Ecology in Vietnam
	Okoth	Kenya	(BAA) Whole Genome Sequencing of African Swine Fever Virus in Kenya.
	Nevolko	Ukraine	TAP-6: Analysis of the Threat of Spread of African Swine Fever and Classical Swine Fever in Wild Boar Populations in Ukraine: Improving Diagnosis, Surveillance, and Prevention
	Mwiine	Uganda	UG-2: Research and Development of Countermeasures to Support the Control of FMDV in Uganda
	Filatov	Ukraine	(USDA ARS) African Swine Fever Threat Reduction Through Surveillance in Ukraine
3:20 PM - 3:40 PM	**Coffee Break**		
3:40 PM - 5:00 PM	**Session 7: Bacterial Pathogens of Security Concern - Group 1**		
	Motin & Shikhaliyeva	Georgia & Azerbaijan	(BAA) Molecular Epidemiology and Ecology of *Yersinia* spp. in the Transboundary Plague Endemic Territory in Georgia and Azerbaijan
	Sansyzbayev	Kazakhstan	KZ-31: Effect of *Rickettsia* spp. upon Fitness of *Yersinia pestis* in Fleas that Vector Plague in the Republic of Kazakhstan
	Tarasov	Ukraine	UP-2: Development of the Epidemiological Forecasting System for Zoonotic Diseases Employing GIS Technology
	Solomonia	Georgia	GG-23: Creation of Sustainable Immunodiagnostics
	Avetisyan	Armenia	AM-1: Medical/Biological Mapping of Tularemia Natural Foci and Epidemiology using GIS in Armenia
5:00 PM - 5:10 PM	**Break**		

Thursday, February 9, 2017 (Continued)

Time	Speaker	Country	Project
	Session 8: Avian Transmissible Diseases		
5:00 PM - 6:20 PM	Goraychuk	Ukraine	(USDA ARS) Genomic, Epidemiological, and Biological Characterization of Newcastle Disease Virus Isolates from Ukraine
	Ateya	Kenya	(Call) Newcastle Disease: Surveillance, Molecular Epidemiology, and Control of NDV in Kenya
	Strochkov	Kazakhstan	TAP-11: Molecular Characterization and Complete Genome Sequence of Newcastle Disease Virus Isolated in Kazakhstan
	Muzyka	Ukraine	UP-4: Risk Assessment of Selected Especially Dangerous Pathogens Potentially Carried By Migratory Birds Over Ukraine
	Kapur	India	(BAA) Detection and Molecular Epidemiologic Analysis of Especially Dangerous Pathogens in Backyard Poultry, Commercial Broilers and Waterfowl in India
6:20 PM - 6:30 PM	**Day 1 Wrap-up**		

Friday, February 10, 2017

Time	Speaker	Country	Project
8:30 AM - 8:40 AM	**Opening Remarks**		
8:40 AM - 10:20 AM	**Session 9: Bacterial Pathogens of Security Concern - Group 2**		
	Chanturia	Georgia	(BAA) Characterization of NCDC Strain Repository by Next Generation Sequencing (NGS)
	Shah	Pakistan	(BAA) High Resolution Chemical Characterization of *Yersinia pestis* Cells Within Soil Matrices: Implications for Understanding Natural Foci and Telluric Reservoirs of Plague
	Bitek	Kenya	(CDC IACRO) Estimating Incidence and Socio-economic Impact of Brucellosis in Humans and Animals in Kajiado County, Kenya
	Sidamonidze	Georgia	TAP-10: Molecular Epidemiology of *B. anthracis* and *Brucella* spp. in Turkey and Georgia
	Malania	Georgia	GG-27: Regional Study of the Ecology of Anthrax Foci in Georgia and Azerbaijan
	Ismayilova	Azerbaijan	AJ TAP-11: Regional Study of the Ecology of Anthrax Foci in Georgia and Azerbaijan
	Zimmerman	Lao PDR	Environmental Surveillance of *Bukholderia pseudomallei*, Pilot Study in Lao PDR
	Limmathurotsakul	Thailand	Melioidosis Regional Coordination Network
10:20 AM- 10:40 AM	**Coffee Break**		
10:40 AM - 12:00 PM	**Session 10: Emerging Infectious Diseases**		
	Reynolds	Georgia	(Call) Enhancing Capacity for Case Detection and Diagnosis of Febrile Zoonotic-related Cutaneous Lesions in Georgia
	Gulbani	Georgia	(BAA) Enhancing Capacity for Case Detection and Diagnosis of Febrile Zoonotic-related Cutaneous Lesions in Georgia
	Abubakar	Malaysia	(Call) Multi-Year Prospective Cohort Study to Evaluation the Risk Potential of MERS-CoV
	Orynbayev	Kazakhstan	KZ-33: Middle East Respiratory Syndrome Coronavirus (MERS-CoV): Surveillance for Distribution and Prevalence in Kazakhstan
	Buza	Tanzania	(BAA) Global Health, Emerging Infectious Diseases and Food Safety Implications of Bushmeat in Tanzania
	Sam	Malaysia	(BAA) Etiology of Severe Acute Respiratory Infections in Kuala Lumpur, Malaysia

Friday, February 10, 2017 (Continued)

Time	Speaker	Country	Project
12:00 PM - 1:00 PM	**Lunch**		
1:00 PM - 2:40 PM	**Session 11: Epidemiology & Biosurveillance - Group 2**		
	Ragan	Armenia	AM-4: One Health Surveillance for Brucellosis in Armenia
	Byarugaba	Uganda	(BAA) Acute Febrile Illness in Uganda.
	Mammadov	Azerbaijan	(Call) Infectious Etiologies of Acute Febrile Illness Among Members of the Azerbaijan Military
	Gulbani	Georgia	GG-20: Prevalence, Epidemiological Surveillance, and Laboratory Analysis of *Coxiella burnetii* in Georgia
	Sandybayev	Kazakhstan	KZ-32: Prevalence of *Brucella* Species and Bluetongue Virus Serotypes Among Domestic Livestock or Ruminants in Southern Kazakhstan
	Avetisyan	Armenia	TAP-H1: Identification of Etiology, Clinical Outcomes, Incidence, and Epidemiological Patterns of Hospitalized Febrile Patients in Armenia
	Burjanadze	Georgia	GG-21: Human Disease Epidemiology and Surveillance of Especially Dangerous Pathogens in Georgia
	Godbold	Armenia	AM-3: The Epidemiological Status of African Swine Fever in Domestic Swine Herds in the Tavush Marz Region, Republic of Armenia
2:40 PM - 2:50 PM	**Break**		
2:50 PM - 3:30 PM	**Session 12: Arthropods and Arboviruses**		
	Ismayilova	Azerbaijan	AJ TAP-13: Investigation of Mosquito and Tick-Borne Arboviruses in Southeastern Azerbaijan
	Sukhaishvili	Georgia	TAP-12: Analysis of Previously Identified *Rickettsia* Positive Georgian Ticks by Multi-locus Sequence Typing
	Khan	Pakistan	(BAA) The Role of Arboviruses as a Cause of Undifferentiated Febrile Illness in Sind, Pakistan
3:30 PM - 3:50 PM	**Closing Remarks**		

Presentation Summaries

February 8, 2017

Session 1

Doing Science in Difficult Places

PRESENTERS: Valerie DeThomas (CRDF)/ Jeffrey Skowera (CRDF)/ Robert Esler (CRDF)/ Matthew Bouton (Univ. of Michigan)/ Amir Abdulmawjood (Univ. of Veterinary Medicine Hannover – Germany)

Since 1995, CRDF Global has worked in over 40 countries using science to address priority issues in support of U.S. and foreign government agencies, foundations, and private sector organizations. Many of these countries may be considered difficult places to work due to past or ongoing war or other conflicts, political or economic instability, resource constraints, or significant differences in research capabilities, scientific norms and practices.

Application of tailored programming approaches, genuine commitment to understanding the environments in which partner country scientists operate, and flexibility form the foundation for effective science collaboration in difficult places. Ultimately, scientists are eager to engage and work together in search of solutions to the world’s problems.

In 2013-2016, CRDF Global’s work with scientists and researchers from Iraq and Afghanistan in support of CBEP included a research grant competition, science fellowships and network building and exposure programs. CRDF Global’s ability to meet program objectives required building trust and rapport with Iraqi and Afghan participants, regular communication, engagement of all necessary stakeholders, adaptability, flexibility, and creative solutions. The programs’ success is, in large part, attributed to participation of scientists in the U.S., Germany, Italy, India, Australia, Switzerland, Jordan and Malaysia, who hosted Iraqi and Afghan researchers at their labs for trainings, lab tours, exposure visits and fellowships.

Presentation Summaries

February 9, 2017

Session 2: Chiroptera (Bats) – Important Reservoir Hosts of Emerging Viruses

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

PRESENTERS: Kevin Olival/Ketevan Sidamonidze/Nisreen Al-Hmoud

COUNTRY: United States/Georgia/Jordan

Bats are natural reservoir hosts to several emerging viruses with pandemic potential, including Ebola, Marburg, Nipah, and SARS and MERS-coronaviruses, but current research on the distribution of bats, diversity of their viruses, and potential for zoonotic disease emergence in Western Asia is severely limited. To fill this gap and contribute to biological threat reduction, we propose a hypothesis-driven One Health research project focused on characterizing bat coronavirus diversity and the risk of bat-borne zoonotic disease emergence. This will include extensive non-lethal field sampling of bats, screening and characterization of viruses from bat specimens with two regional partner laboratories currently operating within the region, the Lugar Center in Georgia and RSS in Jordan, and modeling emerging disease risk by combining viral data with host, geographic, and ecological data. Data for risk modeling will be collated across a larger region than our field sampling will allow through the creation of a collaborative Western Asia Bat Research Network (WAB-Net) – including key researchers and public health representatives from >12 countries. Research activities will be strengthened via laboratory exchanges and annual data sharing and capacity building workshops. This integrated, multi-disciplinary approach presents a coordinated strategy to advance scientific knowledge around transboundary zoonotic disease emergence risk in Western Asia to inform early detection, diagnosis, and response to support the Global Health Security Agenda and CBEP goals.

Investigating the Risk of Human Disease from Parasites of Small Mammals and Bats

PRESENTER: Gavin Smith

COUNTRY: Cambodia

Emerging and re-emerging infectious diseases pose a significant public health challenge globally, with severe economic, social, and health consequences. It is estimated that the SARS outbreak alone cost over $50 billion dollars in lost global economic activity. The frequency of epidemics caused by newly emerging and re-emerging pathogens and the likelihood of rapid global spread have increased dramatically in recent decades, with Southeast Asia considered a hot spot for future emergence events. Small mammals and bats play an important role in the maintenance and transmission of select agents that infect humans such as *Brucella* species, coronaviruses, filoviruses, henipaviruses, hantaviruses/bunyaviruses, plague, rabies (lyssaviruses) and *Rickettsia* species. The global distribution of several species of small mammals and bats, in addition to the ever-increasing interface between humans and wildlife, ensures that cross-species transmission events will continue to occur, often with devastating effects. By proactively sampling animal populations in Cambodia to discern circulating parasitic genotypes and screening human sera for evidence of exposure, we can determine which parasites have human pathogenic potential. A standardized trapping regimen will allow us to understand which ecological and environmental variables are associated with host and parasite presence-absence, facilitating the creation of ecological niche maps and models to determine risk and inform future surveillance efforts across Southeast Asia.

Arthropod-Borne Viruses Associated with the Chiroptera of Uganda: Isolation and Characterization

PRESENTER: Robert Kityo

COUNTRY: Uganda

This project aimed to achieve a better understanding of bats, their ecology and their potential roles in virus ecology. This has been done through graduate training and research, training in field techniques of capture and processing of bats for virus detection and characterization, and a compilation of reference calls of micro-chiropteran bats for Uganda. Field biosurveillance training was held with participants from NADDEC, UVRI and Makerere University at Zika forest. A graduate student was recruited and completed an ecological study on bats in the Kaptum cave. We conducted bat surveys from around Uganda and have collected voucher calls from 28 microchiropteran bats from over 10 localities in Uganda.

From our graduate student's research, we now know there are 6 bat species (*Nycteris thebaica, Rhinolophus landeri, Rhinolophus hildebrandtii, Hipposideros caffer, Hipposideros ruber,* and *Myotis bocagei*) in Kaptum cave. Although they may mix up, these seem to have preferred roosting corners in the cave defined by slight differences in temperature and relative humidity.

Besides Kaptum Cave, we have documented the existence of many other caves around the country with bats. These caves are frequently visited by local people for various reasons. This could inevitably expose such members of the local communities to aerosols in the caves. Collectively, this project has advanced our knowledge of bat ecology in Uganda and enhanced collaborative research between US and Ugandan institutions which will promote cooperation during future biosurveillance and outbreak events.

Bat Harvesting in India: Detection, Characterization and Mitigation of Emerging Infectious Diseases Risk

PRESENTER: Ian Mendenhall

COUNTRY: India

Emerging infectious diseases pose a continual risk for humans, imparting major health and economic challenges. It is estimated that greater than 70% of these diseases originate in wildlife, which demonstrates the importance of understanding the diversity of parasites that circulate in animals. Bats are important reservoirs of several medically important viruses that have high case fatality rates, including rabies/lyssaviruses, the henipaviruses, SARS-like coronaviruses, and Ebola virus and the related filoviruses. India is one of the most biologically diverse countries in the world, however there are currently few reports of viruses detected in bats. Outbreaks will often begin from point source origins, as phylogenetic data from the recent Ebola outbreak in West Africa indicates. Therefore, studying specific interfaces where humans are exposed more frequently due to their proximity and heightened interactions with wildlife can provide critical information on exposure. Bat harvesting is a common practice across India, as concentrated efforts can yield high numbers of bats. This contact and processing of bushmeat is an opportune place for cross-species transmission to occur. By sampling the bat populations where harvesting occurs before, during and after the trapping, we can determine if bat harvests increase the shedding of viruses and what medically important viruses are circulating in these bat populations. This will allow us to generate risk models and understand which species may be natural virus reservoirs in India.

Evaluating Zoonotic Viral Sharing Among Bats, Primates, and People in a High-risk Transmission Interface in Southern Tanzania (VISHA Project)

PRESENTER: Abel Ekiri

COUNTRY: Tanzania

Through project partners, including Metabiota, University of California Davis, Sokoine University of Agriculture, and the Ifakara Health Institute, we are evaluating: 1) the risk of zoonotic virus transmission among bats, non-human primates (NHP), and people sharing a forest interface with high human-wildlife contact in Southern Tanzania; 2) the impact of bat and primate community composition on virus diversity; and 3) exposure to zoonotic viruses in high-risk human populations living at the forest interface. By investigating cross-species viral sharing at this high-risk interface, our team will increase the understanding of pathogen emergence risk and transmission between human and wildlife hosts, strengthen Tanzanian surveillance and diagnostic capacity for pathogens of pandemic and biosecurity concern, and identify key intervention points to reduce local viral spillover from wildlife into human populations. The VISHA project team is investigating the epidemiology of known and novel zoonotic viruses (including filoviruses) in bats, NHPs, and humans by: 1) characterizing forest field sites; 2) collecting bat and NHP specimens during wet and dry seasons; 3) collecting specimens from high-risk human groups near forest areas during wet and dry seasons; 4) testing wildlife and human specimens for potential zoonotic viral pathogens using virus family-level RT-PCR; 5) performing phylogenetic and other genomic analyses on all detected viruses; 6) identifying risk factors for human exposure to bat and NHP viral pathogens using spatial analyses and epidemiologic modeling; and 7) training Tanzanian scientists in surveillance, molecular diagnostics, genomic analyses, and field and laboratory biosecurity practices.

Epidemiology and Ecology of Tularemia in Georgia

PRESENTER: Gvantsa Chanturia

COUNTRY: Georgia

Our study investigated the epidemiology of human and animal tularemia in Georgia. The project included (1) the study of seroprevalence of tularemia among individuals living in geographic areas with tularemia, and healthy individuals; and (2) estimate risk factors for seropositive humans and animals. We also established active surveillance for human tularemia clinical cases with the goal of increasing the efficiency and tularemia diagnostic capability. Isolates from human cases (900 volunteers) for comparison to both current environmental and historical isolates (National Center for Disease Control and Public Health). From an environmental prevalence emphasis, we will establish active surveillance for *F. tularensis* in the environment, including a study of small rodents and associated vectors and identification of the sources of outbreaks among humans. Field sampling for active surveillance for *F. tularensis* in the environment included small rodents and associated vectors, linking with human cases and seroprevalence study among the population living in foci area. More than 60,000 vectors were collected and pooled into 6,000 collections. All strains were isolated, evaluated, and monitor patterns of antimicrobial resistance. A bacteriophage component of this project examined isolated *F. tularensis* strains by genomic sequencing, proteomics analysis (Ilia State University), and phage discovery (the Eliava Institute). Geographic information systems and genetic algorithm for rule-set production were used for pathogenic distribution. Ecological niche models were created for ectoparasite species and primary rodent vectors. Consistent differences were found by the expression of some proteins between the isolates. Real-Time PCR and Western immunoblotting further validated these differences.

Ecological and Epidemiological Study of *Yersinia pestis* and *Francisella tularensis* in the Northern Part of Azerbaijan Regions of Gusar and Khachmaz

PRESENTER: Jolanta Jacobs

COUNTRY: Azerbaijan

Robust surveillance of *Y. pestis* and *F. tularensis* was once carried out routinely, however since the collapse of the Soviet Union little funding has been allocated to such efforts, and thus almost no data are available on the current distribution of plague and tularemia foci and vectors in Azerbaijan.

TAP-10 project proposes to conduct surveillance of ectoparasite vectors of plague and tularemia in northern Azerbaijan, in an area with a historical presence of those diseases and located near known natural foci of plague and tularemia.

The project started in April 2015 and is being implemented by Khachmaz Anti-Plague Division (APD). Sample collection (arthropods: fleas and ticks) field activities were carried out over six months in spring, summer, and autumn of 2015. Sample collection was completed in total of 13 villages of Gusar and Khachmaz regions in September 2015. Collected ticks and fleas were sorted, counted, identified, pooled, homogenized and their nucleic acids were extracted. The extracted nucleic acid samples have been tested by PCR (Bio-Rad 96 instrument) for two targets for each of the pathogens. 8,216 ticks and 154 fleas have been counted, identified, and sorted. 1,269 tick pools and 55 flea pools have been created and homogenized and their DNA extracted. Primer and probe sets were optimized and testing is ongoing.

A One Health Approach to Brucellosis and Rift Valley Fever Surveillance in Tanzania

PRESENTER: Chris Kilonzo

COUNTRY: Tanzania

Our One Health team, including partners from Metabiota, the University of California, Davis, Sokoine University of Agriculture, and Ifakara Health Institute is utilizing a transdisciplinary approach to investigate the epidemiology and genomic diversity of the zoonotic pathogens Rift Valley fever virus (RVFV) and *Brucella* in south-central Tanzania. The primary objectives of the project are to evaluate the influence of risk factors such as animal contact and climatic conditions on increased RVFV and *Brucella* infection among livestock, wildlife, and humans, and to enhance in-country capacity for RVF and brucellosis surveillance, prevention, and control. To attain these goals, the team is engaged in: 1) characterization of sites with historical RVFV and *Brucella* activity in humans and animals that represent diverse climatic and animal density variables; 2) concurrent pathogen surveillance for acute and convalescent infections among humans, livestock, conspecific wildlife, and RVFV mosquito vectors to elucidate key disease transmission pathways, 3) identification of climatic conditions and temporal patterns that increase disease risk among vector and host species; 4) characterization of the RVFV and *Brucella* spp*.* diversity detected in mosquitos, animals, and humans; 5) identification of potential cryptic wildlife maintenance hosts using serologic evidence of prior infection, or in the case of RVFV by using blood-meal analysis of recently fed virus-infected mosquitoes, and 6) the development of integrated models to predict geographic areas of increased pathogen maintenance and transmission to identify locations for targeted intervention strategies and enhanced disease surveillance.

Acute Febrile Illness Study among Patients in Nakhon Phanom and Tak Province, Thailand

PRESENTER: Saithip Bhengsri

COUNTRY: Thailand

There are many causes of acute febrile illness (AFI) including various emerging infectious diseases in Southeast Asia and Thailand. Such diseases can be difficult to differentiate by clinical signs and symptoms, leading to misdiagnosis and possibly serious consequences for patient care. Therefore, laboratory testing is necessary to establish an accurate diagnosis. The objectives of this study are to: 1) describe the etiologies for patients hospitalized with AFI, 2) estimate incidence of specific pathogens and monitor trends over time, 3) evaluate the performance of rapid diagnostic tests (RDTs), and 4) assess laboratory diagnostic accuracy based on specimen types and testing methods for disease surveillance and outbreak identification. The study is being conducted in two Thai border provinces, Nakhon Phanom in the northwest and Tak in the east. The project is divided into 3 phases: pilot, surveillance and research phase. In the pilot phase, demographic data, clinical information and routine laboratory results will be collected from eligible patients. During the surveillance phase, patients hospitalized with undifferentiated fever will be tested for bacteremia and dengue. If dengue is not diagnosed, samples will be tested for chikungunya, *Leptospira*, *Rickettsia* species, *O. tsutsugamushi*, and Zika virus. During the research phase, new RDTs for *B. pseudomallei*, *O. tsutsugamushi*, Zika and chikungunya viruses will be evaluated. Additional testing will be performed on an expanded range of bacterial and viral pathogens. This project will provide an increased spectrum of pathogen detection, improve the timeliness of pathogen characterization, and assess promising new advanced diagnostic tests for surveillance and clinical management in the region.

Differential Diagnostics Performed by Eliminating Especially Dangerous Pathogens and Simulation (EDP-DREAM) in Cases of Saiga Antelope Mortality

PRESNTER: Mukhit Orynbayev

COUNTRY: Kazakhstan

Though several large die-offs in saiga antelope (*Saiga tatarica*) herds in Kazakhstan have been reported in the past decade, the intensity, and absolute threat to the species of the ongoing die-off in the Kostanay oblast of Kazakhstan is unprecedented. The loss of reproductive females and calves represents long-term impacts on herd recovery and may indicate an eminent threat to regional livestock health. Reports have suggested the saiga die-off may be related to pollution or plant toxins, yet it is unclear how such toxicity would result in 100% mortality of nursing calves. Such a rapid die-off could be explained by viral (or viral/bacterial) infection. Even though Foot and Mouth Disease Virus (FMDV) has been reported in saiga, relatively few viruses result in 100% mortality, particularly in calves. However, FMDV could potentially play a role in a multiple pathogen infection. This study will implement a differential diagnostic work flow to diagnose anthrax and other Especially Dangerous Pathogens (EDPs) that may be involved in the saiga die-off. The project will use high resolution GPS collar data from animals at-large during the die-off. The first field expedition began in September 2016, and experts from the lead KZ partner, the Research Institute for Biological Safety Problems (RIBSP), pursued saiga individuals of Ural population in West Kazakhstan and Atyrau Oblasts to take samples and fit them with collars. Fifty-four individuals were captured from the Ural population: fifty-two individuals in West Kazakhstan oblast, and two individuals in Atyrau Oblast. During the field expedition, the five available animal collars were placed on animals and found to provide a stable signal. All samples have been delivered to RIBSP and are being stored at the BSL-3 laboratory. Currently materials and reagents are bring procured. Dr. Jason Blackburn from University of Florida is the collaborator for the study.

Assessing the Seroprevalence and Genetic Diversity of CCHFV and Hantaviruses in Georgia

PRESENTER: Giorgi Babuadze

COUNTRY: Georgia

The proposed collaborative research project will assess the seroprevalence and genetic diversity of highly pathogenic bunyaviruses circulating in Georgia to include Crimean-Congo hemorrhagic fever virus (CCHFV) and hantaviruses causing hemorrhagic fever with renal syndrome (HFRS), such as Puumala (PUUV), Dobrava (DOBV), or Seoul (SEOV) viruses. Specific aims of the project are to: (1) Determine the prevalence and serological diversity of CCHFV and hantaviruses in patient populations using samples collected from previously funded CBEP projects, human samples (GG-21) and environmental samples (GG-19); (2) Establish multiplexed immunological and molecular diagnostic assays for detecting circulating strains of pathogenic bunyaviruses, and provide suitable training for sustainment of these assays and capabilities within Georgia; (3) Initiate active surveillance for CCHFV, and hantaviruses in the environment to include small rodents and ticks; (4) Identify and characterize the genetic diversity of CCHFV and hantaviruses detected in rodents and ticks; (5) Establish a DNA barcode reference library for local tick species, to facilitate future identification and incrimination of tick-borne disease in Georgia.

These studies will provide a baseline assessment of the potential for future outbreaks of CCHF and HFRS in this region. Rodent and tick samples will be tested by ELISA and RT-PCR for evidence of CCHFV or hantavirus infections. Selected samples will be sent to the USAMRIID for virus-specific neutralization tests in BSL-3 or BSL-4 containment laboratories.

Epidemiology of Emerging Viruses in Cameroon

PRESNTER: Sara Eyangoh

COUNTRY: Cameroon

The geographical and socio-cultural diversity of Cameroon makes it vulnerable to many emerging tropical viral infections like, Ebola, Zika, Dengue, Lassa, etc. While some studies have been done on the epidemiology of some of these viruses, these dispersed studies remain insufficient as a basis for the implementation of effective public health measures in this regard. Our objective was to assess the circulation of certain emerging viruses in the Cameroonian population in order to make recommendations to strengthen their surveillance and reinforce the rapid detection of any eventual epidemic.

In this respect, different samples were collected from 6 sites of Cameroon in different regions. These samples were serum/whole blood from 1500 blood donors, blood/oral swabs from 500 febrile patients susceptible of carrying a potential viral infection, and samples from bats to look for potential viral reservoirs. Collection of samples is complete, but analysis is ongoing at French Arbovirus National Reference Centre (Marseille, France). Preliminary data are available from blood donors. All donor blood samples were analyzed by ELISA. Positive samples underwent seroneutralisation analysis, RT-PCR (for DENV) and serotyping and phylogeny subsequently. Blood donor sample preliminary ELISA positive results were as follows: WNV(61.6%),TBE(39,9%), DENV(56,9% with 7.6% positive on RT-PCR, serotyping in progress), TOSV(7%), RIFTV(0%), ZIKV(10,4%).

Our definitive findings hope to build a framework upon which public health decisions can be made to increase preparedness for an eventual epidemic of an emerging viral infection and improve laboratory detection capabilities at the national level.

Understanding Rift Valley Fever in the Republic of South Africa

PRESENTERS: Billy Karesh & Petrus Van Vuren

COUNTRY: South Africa

Rift Valley fever virus (RVFV) is a vector-borne pathogen causing significant livestock, wildlife and human morbidity and mortality, and results in significant economic damages and food security concerns. RVFV has spread from Africa to the Arabian Peninsula, has the potential to spread to the Americas, and is considered a potential bioweapon. In South Africa, we have a multi-disciplinary team working to correlate environmental factors with vector succession and abundance, understand the role herd immunity may play in the occurrence of outbreaks and characterize the risk to people working in high-risk occupations. Initial analyses indicate that there are several vegetation and soil characteristics associated with locations of animal cases of RVF during the 2010-2011 outbreak. The baseline seroprevalence (representing herd immunity) in livestock have been established and experiments are running to understand how this may change. In people, the seroprevalence against RVFV is 0.1. Each year we hold national-level and local stakeholders’ meetings to disseminate the data to national and provincial departments of agriculture, health and wildlife, as well as to farmers and workers, animal production groups and the weather service. Through this collaborative, One Health approach the project has become more robust and has strong support locally. The resultant data represents a significant step toward improving prediction of outbreaks and understanding how RVFV might spread, what effect climate change may have on the virus, how vaccination strategies may affect the risk of an epizootic and the risk of translocation to naïve countries, such as the United States.

Biosurveillance for Henipaviruses and Filoviruses at the Agricultural Animal-Human Interface in Malaysia

PRESENTER: Jonathan Epstein

COUNTRY: Malaysia

The henipaviruses and filoviruses include Hendra virus (HeV) and Nipah virus (NiV), and several species of Ebola (EBOV) and Marburg virus (MARV), respectively, which are highly pathogenic viruses and select agents capable of causing public health emergencies of international concern. Bats are recognized as reservoirs for both henipa- and filoviruses, and zoonotic transmission of these viruses from bats to humans via domestic animals has occurred in Southeast Asia. The full diversity of henipa- and filoviruses in bats and their potential to infect livestock and people is unknown. This project will enhance early detection and surveillance capacity in Malaysia by: 1) transferring Luminex-based technology with validated reagents to detect IgG antibodies against henipa- and filoviruses to Government of Malaysia partner labs in wildlife, livestock and human health sectors; 2) training laboratory personnel to develop and utilize Luminex-based assays to identify exposure to henipa- and filoviruses; 3) conduct biological surveillance in wildlife (esp. bats), livestock and people around indigenous communities that hunt wildlife and on farms in Peninsular Malaysia, where there are high levels of contact among people and animals. Based on building local capacity for hypothesis driven research and improved use of technology, this project will help characterize the distribution and spillover potential from bats of henipa- and filoviruses in Peninsular Malaysia. Activities will be coordinated with and complimentary to the USAID Emerging Pandemic Threats: PREDICT program and surveillance data will be shared with the Govt. of Malaysia (GoM). The proposed project is closely aligned with the aims of the Cooperative Biological Engagement Program in that it will support biosurveillance and capability building, engages partner-country scientists, and promotes a One-Health approach to threat reduction.

Session 5: Community Outreach to Combat African Swine Fever

ASF Public Outreach Project Overview

PRESENTER: Marco De Nardi

The Defense Threat Reduction Agency (DTRA) sponsored a four-country regional public outreach project to combat African Swine Fever (ASF). The primary objective of the project was to develop a comprehensive and sustainable regional network of knowledge, expertise, and know-how for the control and prevention of ASF emerging events through a joint-effort based Threat Agent Detection and Response (TADR) Activity Project (TAP) that combines four countries (Armenia, Georgia, Kazakhstan, and Ukraine) in a common activity-based Science plan. To achieve this goal, delegates from each country worked with project implementers to identify gaps in knowledge, legislative framework, and outbreak preparedness. As a pathogen of high bioterrorism potential, veterinary health importance, and/or responsible for major economic instability, it is of critical importance that ASF-threatened and ASF-affected countries have appropriate infrastructure to accurately and rapidly identify and report ASF activity and types to international veterinary health agencies, as well as provide follow-up concerning the spread of the virus. This project sought to identify key human resources and veterinary health systems in order to initiate implementation of solutions to address recognized gaps, thereby enhancing the capacity by which to mitigate the risk of ASF. The project used a “train-the-trainer” approach to successfully reach over 10,000 farmers, veterinarians, pig traders, rangers, and hunters among others, teaching the signs and symptoms to identify ASF along with the proper reporting measures. This project was the first four-country public outreach project sponsored by DTRA and is considered a monumental success due to the large numbers reached. The project also improved collaboration among regional partners with the hopes of additional similar outreach efforts on other pathogens and diseases of public health importance in the years to come.

Community Outreach to Support Understanding of ASF Ecology and Epidemiology in Eastern Europe: Training and Implementation for Methods and Strategies for Control and Prevention

PRESENTER: Lyudmila Niazyan

COUNTRY: Armenia

African swine fever (ASF) is a highly contagious viral disease of swine populations that can have significant economic consequence. It was successfully eradicated from most of the Eurasian continent almost 30 years ago, but was re-introduced in Georgia in 2007. Since then ASF has spread widely affecting swine in Georgia, Azerbaijan, Armenia, Ukraine, and Russia.

The primary goal of this project was to develop a comprehensive and sustainable regional network of expertise for the control and prevention of ASF through a joint-effort-based project combining four countries: Armenia, Georgia, Kazakhstan, and Ukraine. The project aims to identify and then educate persons working in the pig production chain (e.g., pig keepers, butchers, community veterinarians) to recognize clinical and epidemiological patterns of ASF. The training will allow these workers to understand (1) common routes of exposure, (2) preventative measures, (3) how to recognize clinical signs, (4) the importance of reporting to veterinary authorities, and (5) how to respond to suspected ASF cases.

In Armenia, a Knowledge and Attitude survey was implemented through veterinary authorities to assess the knowledge of the chosen target groups in ASF. For the public outreach campaign ten inspectors and ten epidemiologists were selected to train target groups, but due to the short time just 301/603 veterinarians, 1000/2412 farmers and 100/2670 hunters have been trained to date (Map 1). An additional 1000 farmers were subsequently educated by community vets during their routine work after the public outreach campaign ended. Over the course of the project and its aftermath, 3000 booklets and 150 posters were distributed and 2401 total persons informed.

This project facilitated the development of a sustainable capacity to implement outreach campaigns for future disease outbreaks in the region. Countries receiving training were taught how to run an outreach campaign including how to identify the target audience, how to produce effective educational materials, and how to effectively distribute those materials.

Community Outreach to Support Understanding of ASF Ecology and Epidemiology in Eastern Europe: Training and Implementation for Methods and Strategies for Control and Prevention

PRESENTER: Lena Ninidze

COUNTRY: Georgia

In 2007, Georgia was affected by a nationwide outbreak of African swine fever (ASF), and outbreaks were simultaneously reported in three different locations across the country. Monitoring ASFV in Eastern European countries is a top priority for the U.S. Defense Threat Reduction Agency (DTRA). The primary objective of the project was to develop a comprehensive and sustainable regional network of expertise for the control and prevention of ASF events through a collaborative project that united four countries (Armenia, Georgia, Kazakhstan, and Ukraine). Gaps in knowledge, legislative framework, and outbreak preparedness in the partner countries were identified. Additionally, this project contributed to long-term sustainability by conducting outreach campaigns for future disease outbreaks. Georgian directors were taught to lead and implement outreach campaigns, including how to identify target audiences (e.g. local farmers, veterinarians, and members of the pork industry) and efficiently create and disseminate educational materials. Over 450 veterinarians and farmers were trained, and 20,000 educational materials were distributed. Pre and post ASF campaign tests were developed to track progress; post-test scores were 16% higher than pre-test scores, which indicates that the outreach program was successful. Regional and state veterinarians, along with government agencies will be responsible for measuring the long-term success of these programs through laboratory results, monthly disease reports, and veterinarian updates. The number of ASF outbreaks are an indicator of the long-term success of the outreach program.

Community Outreach to Support Understanding of African Swine Fever (ASF) Ecology and Epidemiology in Eastern Europe

PRESENTER: Roman Datsenko

COUNTRY: Armenia

In 2015, the State Scientific and Research Institute of Laboratory Diagnostics and Veterinary and Sanitary Expertise (SSRILDVSE) and Institute of Veterinary Medicine (IVM) of the National Academy of Agrarian Sciences took part in an ASF outreach activity implemented within the Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) in Ukraine. The project aimed at establishing a regional alliance between Armenia, Georgia, Kazakhstan, and Ukraine to exchange experience, raise awareness, and provide education on ASF. Specialists from SSRILDVSE and IVM were trained as trainers before implementing their own outreach program in Ukraine. During in-country workshops and 14 training sessions in 14 Oblasts of Ukraine, veterinarians from 307 rayons, 531 epizootologists of state regional veterinary administrations and 4482 veterinary doctors of district animal hospitals were educated in the country. Additionally, information materials (flyer and poster) were developed. They included information about the clinical and epidemiological patterns of ASF, common sources and routes of exposure, preventative measures, how to recognize symptoms, and how to respond to suspected ASF cases. 100,000 flyers were printed and distributed among farmers and populations, as well as 1,500 posters for veterinarians in 24 Oblasts. Due to these efforts, necessary information was brought to the attention of veterinary doctors at district animal hospitals who communicate directly with farmers and persons that work with swine. This project demonstrated an approach for conducting and applying a public outreach program in Ukraine that can be used to raise awareness and help mitigate future outbreaks of ASF and other diseases.

Foot-and-Mouth Disease Virus Surveillance and Ecology in Vietnam

PRESENTER: Do Huu Dung

COUNTRY: Vietnam

The purpose of this project is to improve understanding of the epidemiology of foot-and-mouth disease virus (FMDV) in the Vietnamese setting using state of the art tools for genetic characterization of the virus in this endemic context. The intended goal is to mitigate the impact of this disease on local agriculture and improve preparedness for potential disease incursions in the US homeland with awareness of emerging virus strains.

Foot-and-mouth disease (FMD) is a contagious viral disease of domestic and wild cloven-hoofed animals, most notably cattle, pigs, sheep, buffalo and goats. Despite recent successes in controlling the disease in Europe and some parts of South America, FMD remains one of the most important infectious diseases of livestock due to the potential impact of an outbreak on trade in animals and animal products.

The project is currently operating in the second year of the (expected) four year period of performance. Five of the seven defined project objectives are either completed or well-underway. Two objectives are still in the planning phase. Current and ongoing activities in the field consist of passive surveillance of all FMDV outbreaks reported to the Vietnam Department of Animal Health and active surveillance of healthy livestock in six provinces spanning northern, central and southern Vietnam.

This collaborative endeavor has already resulted in two published, peer-reviewed scientific papers and two more papers have been submitted for peer review. Specific accomplishments achieved within the project include 1) genetic characterization of over 160 novel strains of FMDV, 2) enhanced understanding of risk factors for FMDV infection, 3) unique analyses of movement of FMDV strains across regions of Vietnam, and 4) improved understanding of the role of asymptomatic carriers in FMD epidemiology in Vietnam.

Whole Genome Sequencing of African Swine Fever Virus in Kenya

PRESENTER: Edward Okoth

COUNTRY: Kenya

African swine fever (ASF) is a lethal disease of domestic pigs caused by a large DNA virus. In endemic areas ASF virus (ASFV) circulates in asymptomatic wild pigs and ticks and can remain stable in pork products for several months. ASF is endemic to Africa and was restricted only to that continent until 1957. Since then it has spread to Europe, Latin America and Asia. It is currently endemic in Russia and the Caucasus. There is a real risk of accidental or deliberate introduction of ASF to the United States of America (US), which would be devastating to the US $1.25 billion/year pig industry. There are at present no control measures other than test and slaughter. The objective of the proposed research is to determine the genome sequences of at least 60 ASFV isolates, selected so as to include as many as possible of the major genotypes for which genome sequences are currently lacking. These will be made available to veterinary and biosecurity authorities in the US and endemic countries through GenBank. This knowledge will enable more precise identification of the source of future ASF outbreaks, both within and outside Africa. It will also underpin development of future ASF control tools including diagnostic products and vaccines. The project will build ASFV research and surveillance capacity in Africa to support future disease control efforts.

Analysis of the Threat of Spread of African Swine Fever and Classical Swine Fever in Wild Boar Populations in Ukraine: Improving Diagnosis, Surveillance, and Prevention

PRESENTER: Oleg Nevolko

COUNTRY: Ukraine

Listed as high priority pathogens by the World Organization for Animal Health (OIE), African swine fever virus (ASFV) and classical swine fever virus (CSFV) cause epizootically and economically significant animal diseases. Since 2012, the number of reported ASF outbreaks in Ukraine has increased, with 148 confirmed ASF incidents registered in 18 Oblasts of Ukraine (households - 123; wild boar populations – 24; infected object - 1) including 91 in 2016 (84 in the households and 7 in wild boar population). In order to strengthen the accuracy and effectiveness of ASF/CSF diagnostics in the country and to provide Ukrainian scientists with the ability and infrastructure to quickly and accurately monitor ASF and CSF movement, DTRA supported TAP-6 project that commenced on 1 September 2016. The aims of this project are (1) to analyze the distribution of ASFV and CSFV among wild boar populations inhabiting regions of Ukraine, which border the Russian Federation, Belarus, and Poland, and (2) to evaluate the risk of transmission to domestic pigs in the country. In addition to ELISA and PCR, monitoring targeted wild boar populations in Ukraine for ASF and CSF will be accomplished by using genomic-based biosurveillance methods and trainings on real-time PCR, molecular analysis, phylogenetic analysis, and complex sequence data analysis. This will provide an improved scientific basis to optimize current interventions and develop new tools and strategies to reduce the risk of ASFV transmission to domestic pigs. These biosurveillance efforts will facilitate development of ASF and CSF control strategies, which will contribute to limiting the spread of both infectious agents.

Research and Development of Countermeasures to Support the Control of Foot and Mouth Disease Virus (FMDV) in Uganda

PRESENTER: Frank Mwiine

COUNTRY: Uganda

Foot and Mouth Disease (FMD) virus causes an acute and the most contagious vesicular disease of livestock. The causative agent is a virus of the *Aphthovirus* genus in the *Picornaviridae* family. This disease in endemic in Uganda. Here, we report on a cross-sectional surveillance study designed to monitor and isolate FMDV serotype(s) circulating in the country divided into four regions: Northern, Western, Central and Eastern. A total of 38 representative districts from all the regions of Uganda were selected where 10,321 cattle sera and 1,300 oral-pharyngeal fluid samples were collected. All sera were analysed by the presence of antibodies directed against the virus non-structural proteins (NSP) using commercially-available kits at Makerere University. In addition, all oral-pharyngeal fluid samples were tested by rRT-PCR and virus isolation (VI) tissue culture followed by virus capsid sequencing to determine the FMDV serotypes by ARS, USDA at Plum Island Animal Disease Center. From samples collected during 2014-2015, thirty two percent of the serum samples were positive towards NSP antibodies. FMDV serotype O was isolated from Northern and Eastern regions while serotype SAT 2 was isolated from Western region of Uganda during samples collected in 2014. However, FMDV serotype SAT 1 (from the same region) and O were isolated in oral-pharyngeal fluid samples collected in 2015. The phylogenetic analysis of the P1 sequences for the viruses isolated in relation to geographical distribution of FMDV serotypes isolated during 2014-2015 in Uganda will be discussed. This information is of great importance for the improvement of disease control strategies and for vaccine strain selection for Uganda in the future.

African Swine Fever Threat Reduction Through Surveillance in Ukraine: Surveillance of Potential Arthropod Vectors

PRESENTER: Sergiy Filatov

COUNTRY: Ukraine

African swine fever (ASF) is a high-consequence viral disease threatening the pig industry in Western Europe. In its native range, ASF virus (ASFV) is transmitted to pigs and maintained in Nature by soft ticks. Eastern European nations, including Ukraine, are considered to be endemic with ASF outbreaks occurring in pigs and wild boar. However, the factors underlying ASF westward expansion and reoccurrence on the affected territories remain to be fully understood.

Because certain soft tick species of the genus *Ornithodoros* can serve as biological vectors and reservoirs of ASFV, our research group focused on the development and implementation of vector surveillance in selected regions of Ukraine to establish methods that could be scaled up to the national level. The surveys conducted updated known soft tick distribution patterns. Field samples were identified morphologically as *Ornithodoros verrucosus*, and live specimens used to establish a laboratory colony of this suspected ASFV vector at the NSC IECVM. The *O. verrucosus* colony is a valuable resource to assess the risk of soft tick involvement in the epidemiology of ASF in Eastern Europe.

Ukrainian scientists developed research capacity in soft tick biology, collection methods, rearing and colonization techniques, and vector-host-pathogen interactions at USDA-ARS locations, and collaborating universities in Texas. Results of the project were presented at five scientific national and international conferences, summarized in a book published in Ukrainian and English, and two research papers published in international peer-reviewed journals.

Molecular Epidemiology and Ecology of *Yersinia* spp in the Transboundary Plague Endemic Territory in Georgia and Azerbaijan

PRESENTER: Vladimir Motin & Sheyda Shikhaliyeva

COUNTRY: United States, Georgia, and Azerbaijan

Plague has been known in Caucasus region for many centuries, with the reports in Georgia dated back to the XI century and in Azerbaijan to VII century. The absence of recent reports can be partially explained by reduced surveillance, but also by the possibility of existence of atypical strains of *Y. pestis*, which can be missed by the testing laboratory due to presence of non-culturable strains as well as an absence of some genetic loci which would render the use of common molecular markers ineffective. The investigations of natural foci of plague in both Georgia and Azerbaijan have resulted in numerous cases of isolation of *Yersinia* species other than *Y. pestis*. The exchange of genetic material between *Yersinia* strains can challenge the detection of the strains of *Y. pestis*. We hypothesize that: 1) diverse *Yersinia* species, including *Y. pestis* and *Y. pseudotuberculosis* coexist; 2) *Yersinia* diversification is driven by host ecology; 3) *Yersinia* diversification is driven by exchange of genes within rodent populations; and 4) novel genetic methodology can improve identification of *Yersinia* species. To test these hypotheses, we propose: 1) ecological surveys targeting rodent populations in the transboundary focus located in both Georgia and Azerbaijan; 2) development of culturing and PCR-based procedures for detection of multiple strains of *Yersinia*; 3) molecular screening of the collected rodent and ectoparasite samples; 4) comparative analysis of genomes of obtained strains of *Yersinia spp*; 5) spatial analysis of distribution of strains of *Yersinia spp.* This project will result in enhancement of the plague biosurveillance capacities in the endemic regions of Georgia and Azerbaijan. This will be the first comprehensive project investigating and modeling plague foci in the South Caucasian region, which will foster improvements in national and international public health, surveillance, and biodefense efforts. This project will not overlap with national surveillance efforts.

Effect of *Rickettsia* spp. upon Fitness of *Yersinia pestis* in Fleas that Vector Plague in the Republic of Kazakhstan

PRESENTER: Yerlan Sansyzbayev

COUNTRY: Kazakhstan

The goal of this study is to strengthen surveillance of important flea-borne human infectious diseases (plague and rickettsioses) in the context of vertebrate reservoirs, invertebrate vectors (e.g. ectoparasites), and infectious disease agents. Plague and certain rickettsiae are flea-borne diseases that share similar characteristics in disease symptoms, case definitions, and association with co-infections. These data will be very important to health authorities and government agencies in Kazakhstan and the US, where they will support important DTRA objectives including: enabling a partner country to detect/identify/report disease outbreak (naturally occurring or intentional) and providing a system that is sustainable by that partner country's budget and infrastructure. From a public health standpoint, it is important to know which vertebrate species are reservoirs for particular infectious agent(s) and if they are infested with ectoparasites. The Kazakh Science Center for Quarantine & Zoonotic Diseases (KSCQZD) is the lead institute in the implementation of the project, while the anti-plague stations will be involved in providing samples for research. This project will study the effect of flea-borne rickettsial infections upon the fitness of *Yersinia pestis* (causative agent of plague) within plague vector fleas obtained from small mammals in various environmental settings of Kazakhstan. Specifically, the study hypothesizes that in austere environments, rickettsiae and *Y. pestis* will compete for limited resources within the invertebrate host, allowing one species to out compete the other.

Development of the Epidemiological Forecasting System for Zoonotic Diseases Employing GIS Technology

PRESENTER: Oleksandr Tarasov

COUNTRY: Ukraine

The project was a multi-year study focused on surveillance, mapping, and modeling the spatio-temporal and ecological patterns of *Francisella tularensis* and *Bacillus anthracis* in Ukraine. Collaborative efforts of researchers from the institutes of the Ministry of Health of Ukraine and National Academy of Agrarian Sciences of Ukraine included:

- analyses of historical tularemia and anthrax data sets;
- active surveillance for *Francisella tularensis* in small mammals and ticks and validated integration of these collections with appropriate culture and PCR-based analyses at the laboratory;
- surveillance and environmental sampling for *Bacillus anthracis*, with the integration of appropriate PCR-based detection assays in the laboratory;
- serological (ELISA) tests of sera sampled from wild boars;
- forecast pathogen outbreak using advanced spatial analyses, analyses with Geographic Information Systems (GIS) and Remote Sensing (RS) approaches to define the geographic extent of the pathogens and landscape dynamics that effect those distributions.

Throughout the period of performance, databases related to the epidemiological situation of tularemia and anthrax in Ukraine and geospatial data were developed and analyzed and areas historically at risk were determined for each disease. Ukrainians obtained extensive training in a variety of GIS and spatial analytical techniques, as well as research support at the sites and at the University of Florida. GIS and laboratory capacity at UCDCM and IVM were established. The GIS sector at IVM is now capable of sustaining basic GIS data development. Much of the work from the UP-2 project has been or will be published in the peer-reviewed literature.

Creation of Sustainable Immunodiagnostics

PRESENTER: Revaz Solomonia

COUNTRY: Georgia

The primary goal of this project was to provide Georgian scientists with critical educational tools that will help detect biological threats using immunological assays developed within their own laboratories. This included training on developing and validating immunoassays for proteins and antibodies (monoclonal [mAbs] and polyclonal). The project also provided the tools necessary to develop novel diagnostic measures against new or re-emerging biological threats. Antigenic material from *Francisella tularensis* and *Brucella* species (both endemic in Georgia) were used for the development of antibodies and subsequently for immunoassay development and testing. Collaborators from the Naval Medical Research Center (NMRC), helped develop and validate antigen production, antibody production and purification, ELISA development, optimization, and validation. Polyclonal antibodies and mAbs were raised against *F. tularensis* and *Brucella* spp. whole cell extracts. Antibodies of interest were selected by affinity, and were purified; corresponding ELISA procedures were optimized and validated. In addition, the antibodies were characterized by Western immunoblotting. Antibodies protein targets were examined on polyacrylamide gels, in-gel digestion, and liquid chromatography-mass spectrometry. Using this approach, chaperone protein DnaK and GroEL/ES from *F. tularensis* were identified as a candidate targets of MAB 3.2 and MAB 8.2. As a result, this project yielded a comprehensive suite of protocols that can be used by Georgian scientists to develop assays and scale up production of reagents for commercial production and distribution.

Medical/Biological Mapping of Tularemia Natural Foci Cases, Reservoirs, and Vectors Using GIS in Armenia

PRESENTER: Lilit Avetisyan

COUNTRY: Armenia

Background: Past studies have reported over 95% of Armenia is endemic for tularemia. The development of a Geographic Information System (GIS) database and mapping system will provide a tool for tularemia data management and introduce a sustainable technology for continued surveillance in Armenia.

Methods: A retrospective study using the archives of NCDCP centers across Armenia. For GIS data processing we used the ArcGIS 10.1. The extensions Spatial Analyst and Geostatistical Analyst from ArcView GIS were utilized to process data.

Results: In the period 1981-2012, tularemia epizootics were recorded in 27 of the 38 administrative regions of Armenia. These cases involved five species of rodents, one type of insectivore, ticks of the *Ixodidae* and *Gamasidae* genera, and three species of flea. The optimal habitat was characterized by middle mountain steppe landscape zone at 2,065 to 2,407 meters above sea level, receiving 600-800 mm yearly precipitation, and moderate climates with short cool summer and cold winters or dry warm summers with cold winters. A total of 266 human cases of tularemia were recorded in Armenia from 1996-2012. GIS mapping showed that 199 tularemia human cases were registered in the steppe vegetation zone, 224 cases- in a zone with moderate, relatively dry warm summers and cold winters (1400-2300m), 206 cases in a middle mountain steppe zone.

Discussion: The developed model showed an association ($p < 0.05$) between number of human cases and the number of epizootic sites, number of isolates, and percent of samples with positive cultures. The analysis conducted using GIS methodology delineated the risk zones with a high probability of tularemia occurrence. Identification of high-risk areas will serve public health officials in focusing surveillance efforts.

Genomic, Epidemiological, and Biological Characterization of Newcastle Disease Virus Isolates from Ukraine

PRESENTER: Iryna Goraychuk

COUNTRY: Ukraine

The genetic diversity of Newcastle Disease virus (NDV) in Ukraine was studied for the first time. Newcastle disease (ND) is caused by the virulent forms of this virus that affects a wide range of wild and domestic bird species. At least 15 genotypes cause periodic large-scale outbreaks with extensive morbidity and mortality in avian species worldwide.

We conducted passive surveillance in poultry and active surveillance in wild birds in the Southern-Eastern territories of Ukraine and bordering regions with Russia. These studies characterized viral distribution and identification of predominant circulating strains from 1967 to 2016, including the characterization of repository viruses. Genotype identification and pathotype of NDV were determined by direct sequencing of the complete F-gene and full genome using next-generation sequencing. Based on the sequence of the fusion protein cleavage site a more precise pathotyping in eggs and chickens was conducted using isolates that represent the most typical isolates of each of the geno-groups.

Migratory birds in Ukraine are part of east-to-west and north-to-south migration routes. The phylogenetic study allowed to determine the relationship of Ukrainian isolates with other viruses from Eastern Europe, Asia and Africa and a better understanding the transcontinental movement of NDV.

In addition, training programs on standard operation procedures for BSL3 laboratories, biosecurity and biosafety practices were implemented for Ukrainian scientists. Results from this collaboration were presented at three conferences and summarized in six publications in an international journal.

Newcastle Disease: Surveillance, Molecular Epidemiology, and Control of NDV in Kenya

PRESENTER: Leonard Ateya

COUNTRY: Kenya

Although Newcastle disease (ND) is a notifiable disease in Kenya, the disease is under-reported. Current ND control measures include vaccinations after hatching and outbreaks. Currently, there is no active surveillance for ND. Project objectives are to: (1) improve ND surveillance, detection, and diagnosis and reporting of pandemics and (re-) emerging pathogens; (2) facilitate & improve collaborative research amongst Kenyan institutions employing modern methods; and (3) characterize NDV strains, assess ND socio-economic impacts and identify risk factors contributing to NDV spread in Kenya. The project hypothesis is that virulent NDV reservoirs are asymptomatically maintained in wild birds and pet avian species that reside in the proximity of domestic poultry. Samples will be collected in four agro-ecological zones: (1) Zone II (tropical highlands) with poultry markets and where poultry is culturally significant; (2) Zone III (Kenyan food basket with crop-livestock farming system); (3) Zone IV (part of seasonal wild bird migratory and poultry trade routes); and (4) Zone V (free-range small-scale poultry farming). Sampling will be mainly on case-based and passive and active response surveillance. Positive samples identified by antigen detection, hemagglutination of allantoic fluids, or RT-PCR will be used to characterize and define viral strains circulating in Kenya. Ten-year (2005-2015) historical data on ND incidence and outbreaks have been analyzed and used to validate the project's sampling sites. Some of the sites have been visited and samples collected. Four MSc students, the key players in transfer of acquired technologies, have been recruited.

Molecular Characterization and Complete Genome Sequence of Newcastle Disease Virus Isolated in Kazakhstan

PRESENTER: Vitalyi Strochkov

COUNTRY: Kazakhstan

Newcastle disease virus (NDV) is a highly contagious viral infection of birds, characterized by pneumonia, encephalitis, multi-site hemorrhages and destruction of internal organs. It is considered one of the two most devastating diseases in poultry and wild birds, similar to avian influenza. Since Kazakhstan is on the main pathways of transcontinental migratory routes of many wild birds, genomic analysis of circulating NDV strains in Kazakhstan can potentially provide insights to its genetic evolution and add insight to pathogenic characteristics. Only limited studies on the genetic variability of NDV strains in Kazakhstan have been conducted. The project aims to perform full genome sequencing of five (5) isolates, conduct phylogenic analysis, and develop correlation between genotypic features and pathogenicity of five isolates from chicken flocks of previous outbreak during a one-year period. The team will retrieve full genome sequence of representative isolates from open source genomic sequence repository (GenBank), design primer sets for sequencing, and conduct sequencing using the ABI 3130xl platform at the Research Institute for Biological Safety Problems (RIBSP). Bioinformatic analysis will be performed to determine phylogenetic placement of these isolates among those in Genbank, and analyze the likelihood of introduction to and spread from Kazakhstan. The sequence data will be deposited to the National Center for Biotechnology Information (NCBI) database.

Risk Assessment of Selected Especially Dangerous Pathogens Potentially Carried By Migratory Birds over Ukraine

PRESENTER: Denys Muzyka

COUNTRY: Ukraine

Highly pathogenic avian influenza (HPAI) and Newcastle disease viruses (NDV) cause serious diseases in domestic and wild birds, and also pose additional risk due to the potential for spillover into human populations. Monitoring of orthomyxoviruses and paramyxoviruses conducted by NSC IECVM in 2010-2015 within the USDA/ARS projects revealed 168 avian influenza virus (AIV) and ND viruses, 23 antigenic combinations, and new serotypes (APMV-13). The extreme variability of AIV can lead to new genetic variants of the virus with pandemic potential that could damage people. The geographical position, natural conditions, large amount of birds and several transcontinental migration routes contribute to the re-emergence of those pathogens that was confirmed by outbreaks of HPAIV H5N1 and NDV in 2005-2008 and HPAIV H5N8 in poultry in 2016-2017. Commencing on December 1, 2016 the project aims to survey areas of Ukraine for AIV and NDV that may be harbored by wild birds associated with major northern and southern migratory flyways in the country. The project will assess the ecologic, epizootic, and epidemiologic risk of disease transmission. Bird observations, viral detection data, and Geographic Information System will be used to analyze and predict the anthropogenic impact on viral prevalence and type. The project will support local capacity building through enhancement of diagnostic capability, data management and analysis, and reporting. The project supports a One Health approach through linkage of researchers from the Institutes of the Ministry of Health, National Academy of Agrarian Sciences, and State Service for Food Safety and Consumer Protection of Ukraine.

Detection and Molecular Epidemiologic Analysis of Especially Dangerous Pathogens in Backyard Poultry, Commercial Broilers and Waterfowl in India

PRESENTER: Vivek Kapur

COUNTRY: India

Emerging and re-emerging respiratory diseases in poultry, especially velogenic viscerotropic Newcastle disease (vvNDV) and highly pathogenic avian influenza (HPAI), present a major threat to animal and public health worldwide, particularly in rapidly developing nations such as India. The core viral pathogens of human and animal concern involved in Respiratory Disease Complex of poultry have not been studied. To fill this knowledge gap, we propose to test three hypotheses. **Hypothesis 1.** The respiratory tract viromes from commercial and backyard flocks (herein referred to as domestic poultry) and waterfowl in Haryana, Odisha and Kerala are a potential source of especially dangerous pathogens (EDPs); **Hypothesis 2.** Molecular genotyping approaches will identify host- and region-specific fingerprint profiles of select agents including vvNDV and HPAI; **Hypothesis 3.** Next generation sequencing will help identify nucleic acid signatures of novel / emerging viruses in domestic poultry and waterfowl. The overall goal of this project is to discover novel viruses and enable the development of genomics-based strain-typing capability of EDPs and emerging viral pathogens from avian sources in academic research settings in India. Molecular epidemiologic analysis and comparative metagenomics investigation of respiratory viromes of domestic poultry and migratory birds, using a comprehensive and statistically robust stratified random sampling approach, will provide a strong foundation for the development of evidence-based approaches for implementing sustainable measures to control EDP. This investigation will also help generate data and tools, build sustainable capabilities, and enhance domestic and international academic partnerships critical to characterizing the zoonotic pathogens associated with domestic poultry and waterfowl in India.

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Characterization of NCDC Strain Repository by Next Generation Sequencing

PRESENTER: Gvantsa Chanturia

COUNTRY: Georgia

The three year project was launched in March 2016. It is a collaborative effort of the Los Alamos National Laboratory (LANL), NM, USA and National Center for Disease Control and Public Health of Georgia (NCDC), Tbilisi, Georgia. LANL has been working alongside the Georgia National Center for Disease Control and Public Health (NCDC) Genome Center Facility at the R. G. Lugar Center for Public Heath Research in developing Next Generation Sequencing (NGS) and analytic capabilities. The proposed project leverages the technical capabilities at both institutes to complete sequencing and characterization of the especially dangerous pathogens stored in the freezer archive at the NCDC. Up to 100 isolates of *Yersinia pestis, Bacillus anthracis, Brucella spp*., and *Francisella tularensis* from the NCDC pathogens collections will be selected for draft sequencing on the Illumina MiSeq. The draft genomes will be comparatively analyzed against strains from worldwide databases, SNPs will be discovered and subjected to phylogenetic analysis.

During the past year, ten *Brucella spp*. and twelve *F. tularensis* were have been sequenced. *F. tularensis* strains were processed for genome assembly and phylogenetic analysis on CLC-Bio, EDGE and PHAME software. Two draft genome announcement manuscripts have been drafted. A two week training for one bioinformatician from the NCDC team was held at LANL in November 2016. The sequencing of the rest of the samples is in process at NCDC. Ten isolates will be chosen to forward to LANL for PacBio sequencing. NCDC staff, as well as students involved in the project, will exercise their sequencing and bioinformatics skills on the samples and data from this project. Additional skills will be acquired through advanced training on data generated by this project. Completion of this research project will provide novel genomic characterization of the NCDC's extensive pathogen archive, cement the collaborative network between the NCDC and US collaborators, and ensure the NCDC's ability to utilize advanced sequencing technologies as independent researchers.

High Resolution Chemical Characterization of *Yersinia pestis* Cells within Soil Matrices: Implications for Understanding Natural Foci and Telluric Reservoirs of Plague

PRESENTER: Muhammad Reza Shah

COUNTRY: Pakistan

The persistence of *Yersinia pestis* in soil matrices suggests a novel, yet completely uncharacterized, environmental reservoir for plague organisms. This has critical implications for understanding natural plague foci,non-traditional transmission routes between hostsand its changing risks for humans, and finally, the detection of *Y. pestis* in environmental samples.To address this challenge, we have constructed a multidisciplinary project to examine the chemical and physical response of *Y. pestis* cells after exposure to soil habitats. The project includes high-resolution, single cell analytics to characterize the metabolism, surface chemistry, and structural changes in individual *Y. pestis* cells within this unique growth environment. Results from this work will increase basic understanding of pathogen ecology and the molecular mechanisms by which*Y. pestis* functions in environmental reservoirs outside of traditional transmission vectors.

This project is a collaboration between Virginia Commonwealth University (Richmond, VA, USA) and the HEJ Research Institute of Chemistry at the University of Karachi (Karachi, Pakistan). VCU is leading culturing efforts and surface characterization of *Y. pestis* cells using a range of high resolution microscopy and mass spectrometry techniques and the University of Karachi is developing novel techniques for chemical analysis of cell surfaces and in situ assays with nanoparticle-based probes. Training in Biosafety practices and microbiological characterization will facilitate collaborative pathogen research and build new capabilities at the University of Karachi that will complement its existing analytical strengths and create a new center in Pakistan capable of identifying unknown bacterial samples and conducting basic research on endemic pathogens.

Estimating Incidence and Socio-economic Impact of Brucellosis in Humans and Animals in Kajiado County, Kenya

PRESENTER: Austine Bitek

COUNTRY: Kenya

Brucellosis is a common bacterial zoonotic infection, but there is limited data on burden of the disease in Kenya for humans and animals. To generate data to inform prevention and control strategies, we conducted a longitudinal study to determine incidence of brucellosis in humans and animals and estimate its socio-economic impact at the household level among a pastoralist community in Kajiado.

All households and their livestock in four sub-locations in Kajiado County were enrolled for follow-up for 12 months from 2015 to 2016. A subset of their livestock were recruited in to the study after screening for *Brucella* using RBPT, and sera was collected every four months and tested for *Brucella* IgG antibodies using ELISA. Incidence in humans was calculated from the number who were determined to be acutely ill with brucellosis from among those who presented at study health facilities, while incidence in livestock was the number of livestock that sero-converted for brucella antibodies between two sampling points. To calculate economic losses, direct losses in livestock were calculated using parameters derived from the incidence study and literature, and the results were analyzed in an analytical economic model.

801 households with a total of 4,729 humans and their 5,746 livestock were recruited in the study. Of the household members enrolled, 52% (n=2475) were males. The mean household (HH) size was 6 persons (range 1 – 19). Average HH income over a 3 months period was $ 820 (range $100 - $ 16,000). Overall incidence rate of brucellosis in livestock on ELISA sero-positivity between the first and the second visit was 0.0076 (8/1,000) cases per animal; 3 months at-risk equivalent to 0.0304 (30 animals per 1,000 animal-year at risk). Total direct losses due to brucellosis in livestock was estimated to be KES 6.6 Million (USD 66,000). The losses due to abortion accounted for 54% of the total losses in livestock. Estimated out of pocket expenditures incurred by HHs was $12.2 per human case (range $2 -$100). This study reports a high burden of brucellosis in humans in a pastoral community in Kajiado with substantial economic losses arising from brucella infection in livestock at the household level.

Lugar Center Regional Integration: Kafkas University Partnering for Molecular Epidemiology *of Bacillus anthracis* and *Brucella* species in Turkey

PRESENTER: Ketevan Sidamonidze

COUNTRY: Georgia

It is vital that effective collaborative links are built between the National Center for Disease Control and Public Health (NCDC), Richard G. Lugar Center for Public Health and institutions in neighboring countries to tackle shared common bacterial threats. Kafkas University's veterinary school, located in the northeastern Turkish city of Kars, serves a primarily agricultural region adjacent to the Georgian/Turkish border; diseases including anthrax and brucellosis, are endemic in these regions. Molecular typing tools were outdated at Kafkas. A study using the high-resolution molecular tools available at NCDC Lugar Center on common bacterial strains (*Bacillus anthracis* and *Brucella* spp.) on both sides of the border was developed. To achieve this aim, a team at the Lugar Center supported by WRAIR provided training to researchers from Kafkas University in the use of the state-of-the-art capabilities available at the Center. The project consisted of three main technical elements: bacterial DNA extraction; molecular analysis of *B. anthracis*; and molecular analysis of *Brucella* spp. Overall, 60 bacterial isolates including *B. anthracis* (n=30) and *Brucella* spp. (n=30) from Turkey were analyzed at the Lugar Center using multiple locus variable number tandem repeat analysis (MLVA) and single nucleotide polymorphisms SNP. MLVA and SNP typing results show genetic homogeneity of Georgian and Turkish *B. anthracis* strains, which may be caused by migration of the pathogens across the Georgia-Turkey border over time. This study also resulted in successful capacity-building efforts for pathogen typing for the Turkish researchers from Kafkas University.

Regional Study of the Ecology of Anthrax Foci in Georgia and Azerbaijan

PRESENTER: Lile Malania

COUNTRY: Azerbaijan

Anthrax is a livestock-borne zoonotic disease that is endemic in the South Caucasus region. It is hypothesized that both human and environmental factors affect the migration of *Bacillus anthracis* strains across borders and throughout regions. This study evaluates the following: (1) identify regional foci and spatial risk factors of anthrax to improve surveillance and documentation of the disease; (2) assess the genetic relationships of environmental *B. anthracis* isolates to better understand the organism's ability to persist in the environment and to allow for improved epidemiologic "trace-back" of human and livestock infections; and 3) collaborate on regional issues related to the control and management of a re-emerging infectious disease by sharing local/regional predictions of risk and molecular profiles of the pathogen. Collaborators from both Georgia and Azerbaijan have collected and tested soil samples for the presence of *B anthracis.* Positive samples were molecularly characterized and were examined using multilocus variable number tandem repeat analysis (MLVA), as well as global and regional single nucleotide polymorphisms (SNPs), including a well-established Georgian SNP typing panel. Spatial genetic pattern analysis and risk factor mapping were conducted using geographic information system. In turn, this regional collaboration will provide the potential for the cooperative development of strategies for the control and trans-boundary management of this disease.

Regional Study of the Ecology of Anthrax Foci in Georgia and Azerbaijan

PRESENTER: Rita Ismayilova

COUNTRY: Azerbaijan

Anthrax is a livestock-borne zoonotic disease that is endemic in the South Caucasus region. Not much is known about the regional epidemiology of this pathogen nor the transboundary factors related to its persistence. The aim of this collaborative (Azerbaijan and Georgia) effort was to ascertain both human and environmental factors that may affect migration of *Bacillus anthracis* strains across borders and through regions. There are seven Azerbaijan rayons (Gazakh, Agstafa, Tovuz, Samukh, Gakh, Zagatala, and Balakan) bordering Georgia with recurring cases of both human and animal anthrax; from those, 30 villages were selected for sample collection. Samples were to be collected from known animal burial sites and areas of previous contamination, as evidenced by livestock outbreaks or human case records. Organisms isolated from the collected soil samples were to be characterized by biochemical methods (Gram stain, motility, Trypticase Soya Broth) and then by gamma phage. The nucleic acids extracted from presumptive positive samples were to be tested by PCR using Amplisense kits on BioRad.

A total of 804 soil samples have been collected from five rayons Nov 2015 - Sept 2016. From the 768 processed, over 200 samples exhibited colony morphology suggestive of *B. anthracis*; 10 were deemed positive by gamma phage. DNA extractions from 60 presumptives (by biochemistry and gamma phage) have been sent to Georgia Lugar Center for genotyping in April 2016 and were negative for *B. anthracis*. The samples should be retested by Tetracore PCR kit.

Environmental Surveillance of *Burkholderia pseudomallei,* Pilot Study in Lao PDR

PRESENTER: Rosalie Zimmerman

COUNTRY: Lao PDR

The environmental bacterium *Burkholderia pseudomallei* (*Bp)* is the causative agent of melioidosis and a Tier 1 Select Agent. *Bp* is endemic in tropical soils and has been found in surface waters. To investigate the distribution of this pathogen in Lao PDR, its occurrence in rivers, and associated environmental factors, we studied 23 rivers (including the Mekong) in the South, Center and North of the country, applying culture-based methods and a specific quantitative real-time PCR assay to water filters and streambed sediments. Geochemical measurements included turbidity, a proxy for suspended sediment load which was measured on-site using a turbidity meter and confirmed in the laboratory by dry weight measurements. *Bp* was present in 9% of the rivers in the dry season. In contrast, we found *Bp* in the water of 57% of the rivers in the rainy season, 35% of them with associated *Bp*-positive sediments. Turbidity correlated positively with *Bp* presence (p=0.01). All *Bp* positive rivers were situated in the South and Center of the country. Our preliminary results provide evidence for a heterogeneous spatial and temporal distribution of *Bp* in Lao PDR. The seasonal dynamics and predominant occurrence of *Bp* in particle-rich water and the lower yield in sediments suggest that *Bp* is washed out with eroded soil during periods of heavy rainfall and transported by rivers. These findings will contribute to improved *Bp* risk modelling and health management strategies. Further laboratory and statistical analyses, including additional geochemical factors, and land-cover data analyses using geographic information systems, are in progress.

Melioidosis Research Coordination Network

PRESENTER: Direk Limmathurotsakul

COUNTRY: Thailand

Melioidosis is caused by *Burkholderia pseudomallei,* a Tier 1 select agent and an environmental bacterium commonly found in tropical countries. It is estimated that 89,000 deaths were caused by melioidosis per year worldwide. However, melioidosis remains under-reported due to its diverse clinical manifestation, incapacity of bacterial isolation and identification in low-resource settings, and limitation of national notifiable diseases surveillance systems in low and middle-income countries (LMICs). The unawareness of the disease becomes problematic for policy makers, clinicians and researchers in many LMICs because melioidosis is not perceived as a threat.

To solve the problems, the Melioidosis Research Coordination Network (RCN) was developed. The RCN aims (1) to make data of total number of culture-confirmed melioidosis cases and deaths worldwide openly available for policy makers, clinicians, funders and researchers worldwide, and (2) to support connections and communications among those stakeholders.

The RCN working group will call for information from clinicians and researchers at any hospitals or institutions worldwide for the total number of culture-confirmed melioidosis cases and deaths they observed yearly from 2012 to 2016. We will curate and make those data openly available on www.melioidosis.info. The system will be quite similar to PROMED but better curation and better supports from funders and melioidosis research community. The RCN will make the information of data contributors clearly available so that funders and other researchers know where they can fund melioidosis research and find collaborators, respectively. The RCN will also make information about potential support from contributors available, including bacterial identification and biosafety support.

Enhancing Capacity for Case Detection and Diagnosis of Febrile Zoonotic-related Cutaneous Lesions in Georgia

PRESENTER: Mary Reynolds

COUNTRY: Georgia

In the summer of 2013 an outbreak of febrile rash illness in herders in the Akhmeta region of Georgia was linked to a novel *Orthopoxvirus* (OPXV). The unique genetic profile of this emerging zoonotic disease made it difficult to identify using the existing molecular assays for OPXV species. Two other OPXV isolates have been identified in Georgia. One was found in 1986 in a rodent in the southeastern part of the country; the other was recently identified by the National Center for Disease Control and Public Health of Georgia (NCDC) and the Centers for Disease Control and Prevention (CDC) Poxvirus laboratory in a retrospective analysis of a suspected anthrax case that occurred in 2010. Activities undertaken by CDC Headquarters in conjunction with the CDC South Caucasus Office are part of a collaborative effort comprising three complementary proposals. The goal of these combined efforts is to: 1) identify the geographic distribution and natural hosts of the known virus, 2) determine if any other such viruses occur in this region, 3) investigate the impact of OPXV infection on dairy production and to at-risk individuals, and 4) increase in-country capacity to detect, identify, and respond to future outbreaks. Activities are approached through a One Health framework, promoting timely, actionable communication among in-country counterparts representing the animal and human health sectors.

Enhancing Capacity for Case Detection and Diagnosis of Febrile Zoonotic-related Cutaneous Lesions in Georgia

PRESENTER: Ana Gulbani

COUNTRY: Georgia

The discovery of a new *Orthopoxvirus* demonstrates the need for poxvirus detection and diagnosis capacity in Georgia (country). Human illness caused by this virus has implications for differential diagnosis of cutaneous lesion-producing zoonotic infections, principally anthrax. Simultaneously, animal infection may impact agricultural productivity and food safety. Therefore, accurate detection and case diagnosis is important for both humans and domestic animals. In collaboration with the CDC Atlanta, we are working to enhance capacity to detect, diagnose and report *Orthopoxvirus* infections. Health-care workers will be trained to recognize zoonotic-related cutaneous lesions to detect human cases; NCDC personnel will be trained to collect clinical specimens from patients with such lesions and from the rodents; NFA and regional veterinarians will be trained to recognize lesions associated with orthopoxviruses among domestic and wild animals as well as field collection of pertinent animal specimens. Emphasis will be placed on field and laboratory biosafety. Additionally, CDC Atlanta Poxvirus Team members will provide training for animal (LMA) and human sample (NCDC) processing with rapid qPCR-based diagnostic tests and serologic assays for case diagnosis. Retrospective case diagnosis is needed as testing by rapid qPCR on anthrax-negative samples has already identified an orthopox positive sample, thus warranting further investigation on stored samples. New assays will be developed and assessed for detecting any new orthopoxvirus variants in humans, rodents, domestic and wild animals found in Georgia. Activities will result in improved capacity for efficient identification of emerging orthopoxviruses, as well as biosurveillance capacity for orthopoxviruses in human and animal populations.

Multi-Year Prospective Cohort Study to Evaluate the Risk Potential of MERS-CoV

PRESENTER: Sazaly Abubakar

COUNTRY: Malaysia

Since its first appearance in 2012, the Middle East respiratory syndrome coronavirus (MERS-CoV) has emerged as a serious public health threat of global concern. As of December 2016, the World Health Organization has been notified of 1,879 laboratory confirmed cases and the case fatality rate is estimated at 35%. Beyond its high fatality rate, significant concern lies in the potential for MERS-CoV to spread beyond the Middle East, as was recently witnessed in the South Korea. In collaboration with the Ministry of Health Malaysia (MoHM) and the Malaysia Hajj Pilgrims Fund Board (MHPFB), a multi-year cohort of pilgrims departing for Hajj from Malaysia has been established to assess the risk that MERS-CoV infection poses to travellers to the Middle East. Pre- and post-pilgrimage blood specimens were collected for serologic analysis to estimate MERS-CoV exposure rates, while survey data will be used to stratify the risk of exposure by factors such as age, gender, geographic regions visited during the pilgrimage. For the 2016 Hajj cohort, a total of 568 participants were enrolled and 367 (65%) submitted to post-pilgrimage blood draws and data collection upon their return from the Hajj. To date, paired blood samples (pre- and post- pilgrimage) from 318 participants have been analyzed by ELISA for the presence of IgG antibodies to MERS-CoV. Preliminary findings suggest at least three individuals showed increases in MERS-CoV specific IgG titers post-Hajj. Confirmatory microneutralization assay is ongoing and planning has started for the 2017 Hajj cohort studies.

Middle East Respiratory Syndrome Coronavirus (MERS-CoV): Surveillance for Distribution and Prevalence in Kazakhstan

PRESENTER: Mukhit Orynbayev

COUNTRY: Kazakhstan

Middle East Respiratory Syndrome (MERS) is a viral respiratory illness caused by a recently identified zoonotic coronavirus, MERS-CoV, which is transmitted from camels to humans. The southern border regions of Kazakhstan contain more than 150,000 camels, which creates the potential for endemic circulation of the virus. Bats have also been associated with presence of the MERS-CoV, and there are 24 species of bats which may carry related coronaviruses. Due to camel trade with MERS-CoV endemic areas, the project hypothesizes that MERS-CoV is likely present in the Kazakhstani camel population. One of the objectives is to determine the sero-prevalence and epidemiology of MERS-CoV in adult and juvenile camels in seven regions of Kazakhstan to verify the prediction that camel populations in Kazakhstan have been exposed to and generated antibodies against MERS-CoV. Also, the MERS-CoV genetic diversity in camels across Kazakhstan will be determined as will the identity of coronaviruses in Kazakh bats. The project has been approved by DTRA and kick-off was held on 14 October 2016. The lead institute for the study, KZ's Research Institute for Biological Safety Problems (RIBSP), has submitted paperwork requesting permit from Ministry of Agriculture for sample collection for the study. RIBSP also reported that they have a small group of pre-existing samples from camels and bats in storage that may be of use to the project. RIBSP is currently seeking to identify the location of camel farms that have interaction with camels from the Middle East. Drs. Ian Mendenhall and Gavin Smith from Duke-NUS Medical School are collaborators for the study. Currently materials and reagents are being procured.

Global Health, Emerging Infectious Diseases, and Food Safety Implications of Bushmeat Consumption In Tanzania

PRESENTER: Joram Buza

COUNTRY: Tanzania

“Bushmeat”, the meat and organs derived from wildlife species, is a major source of protein in many parts of Africa, and is often hunted illegally and transported to markets in unsanitary conditions, thereby representing an important conduit for the transmission of zoonotic pathogens. Despite considerable evidence that select agents, including *Bacillus anthracis*, *Brucella* and *Coxiella,* are frequently found in animals harvested for consumption in Tanzania, their distribution in bushmeat and the related human health risks are not known. To fill this critical knowledge gap, we have initiated a program to map the distribution of especially dangerous pathogens in bushmeat from three major ecosystems in Tanzania (Serengeti, Ruaha-Rungwa, Selous-Mikumi) during wet and dry seasons to capture spatial and seasonal variation in pathogen prevalence.

Preliminary PCR based-analyses of more than 500 fresh and dried bushmeat samples collected from 25 villages in the Western Serengeti revealed nucleic acid signatures of *Bacillus anthracis* and *Brucella* species in bushmeat. Further, host species identification with PCR sequencing of the *cytochrome B* gene suggests initial misclassification by bushmeat traders in a significant fraction (~ 40%) of the samples. Together with 16S rDNA based microbiome profiling, our preliminary investigations reveal the presence of major zoonotic pathogens, in bushmeat in Tanzania, and provide an opportunity to discover novel emerging pathogens. In the long-term, our research is positioned to provide a rational basis for defining and mitigating the public health risk associated with the harvesting, trade, and consumption of bushmeat in Tanzania.

Etiology of Severe Acute Respiratory Infections in Kuala Lumpur, Malaysia

PRESENTER: Jamal I-Ching Sam

COUNTRY: Malaysia

The epidemiology of severe acute respiratory infections (SARI) in adults in Asia is relatively understudied, but of critical global importance. This is because of the potential emergence from this region of rare/new pathogens posing a pandemic threat or a danger as potential weapons of mass destruction. Malaysia, situated in Southeast Asia, a known hotspot for emerging diseases, has had previous imported human cases of SARS-CoV, MERS-CoV, and H7N9, and H5N1 in birds. Melioidosis, caused by *Burkholderia pseudomallei*, is also endemic in Malaysia. Kuala Lumpur, the capital, is a major travel hub for immigrants and tourists. We hypothesize that potential biological threats do cause SARI in Malaysia, but that these remain largely undiagnosed due to lack of awareness and laboratory diagnostic capacity. Therefore, we propose to study the etiology of SARI in adults admitted to a teaching hospital in Kuala Lumpur over 3 years. We will establish a comprehensive panel of molecular assays to detect respiratory viruses and bacterial select agents, supplementing existing diagnostics for bacteria and mycology. This will enable our centre to detect sporadic cases and outbreaks of respiratory agents which are potential global threats. We propose a workshop for biosafety practices in diagnostic microbiology laboratories, and a practical workshop to teach these newly established assays to other laboratories in the country, thereby enhancing national capacity to safely diagnose these agents, and contribute to threat reduction. In addition, a number of samples testing negative to known viral agents will be analysed by next-generation sequencing for potential viral pathogen discovery.

One Health Surveillance for Brucellosis in Armenia

PRESENTER: Valerie Ragan

COUNTRY: Armenia

Brucellosis is a highly infectious zoonotic disease caused by bacteria of the genus *Brucella*. It is reported to be the most common zoonotic disease worldwide. The disease causes abortion, infertility and reduction in milk production in animals and a serious, recurring febrile condition in man which may become chronic and may affect any organ of the body. Successful treatment of the chronic form is very difficult. No effective treatment for brucellosis in animals has been described. The incidence of brucellosis in humans in unknown, but is suspected to be between 10 and 25 times larger than indicated by the number of cases reported to public health agencies.

Prevalence of brucellosis in humans and animals in Armenia and neighboring countries is known to be significant. However, due to the fact that comprehensive surveillance for the disease is lacking in both the human and animal populations, and the lack of shared data between human and animal health authorities, little can be said with certainty about how widespread the disease is in either population.

A “One Health Surveillance for Brucellosis in Armenia” project has just been initiated whose objective is to strengthen coordination and collaboration between the Ministry of Health and the Ministry of Agriculture during epidemiological and outbreak investigations of brucellosis, and increase the understanding of the disease burden in Armenia. A project outcome will be a draft document outlining a comprehensive surveillance and control system for brucellosis in Armenia.

Acute Febrile Illness in Uganda

PRESENTER: Denis Byarugaba

COUNTRY: Uganda

Acute febrile illness (AFI) causes significant morbidity and mortality in the tropical countries including Uganda. While part of it is caused by malaria and other common treatable infections, a significant part is caused by unknown agents. VHFs have particularly occurred recently with more frequency in Uganda and the region. This study is undertaking systematic investigations to determine the occurrence of the select agents and other previously unknown highly pathogenic pathogens with potential for causing pandemic threats. The work leverages upon existing field and laboratory research capabilities within Makerere University Walter Reed Project (MUWRP) in the country. The project does sampling from already existing sentinel surveillance sites. We collect and test at least 26 samples from AFI patients per month from at least five geographically diverse hospital sentinel sites (Gulu, Mulago, Jinja, Bwera and Bombo Hospitals). In addition, disease vector distribution and mapping is being undertaken through vector collection and identification and climate data analysis for ecological niche modeling and risk assessment. The study is expected to generate data that contributes to create in-country capabilities for more robust systems for early detection and prediction of outbreaks and rapid response and to define risk factors and vector distributions important for long-term surveillance, early detection and rapid response, and intervention strategies in contribution to global biological threat reduction.

Infectious Etiologies of Acute Febrile Illness in the Azerbaijan Military

PRESENTER: Surkhay Mammadov

COUNTRY: Azerbaijan

Mortality rate attributable to infectious and parasitic diseases in Azerbaijan is 16.4 deaths per 100,000 population. After the collapse of Soviet Union, healthcare and public health deterioration created severe gaps in accessibility and allowed for emergence/re-emergence of infectious diseases. Epidemiological information about infectious syndromes in Azerbaijan is very limited, compounded by the lack of appropriate diagnostic assays and febrile illness knowledge, precipitating unconfirmed clinical diagnoses for most febrile illnesses. Infectious etiologies of acute febrile illness (AFI) among Azerbaijan military members have not been studied, thus causative etiologies are unknown. In the proposed study serum samples from patients with undifferentiated febrile syndrome will be tested for *Brucella* spp., Dengue, WNV, *F. tularensis*, rickettsia, Q fever, hantaviruses, CCHF and TBE using standard ELISA assays. Positive or indeterminate ELISA results will be confirmed using PCR or IFA. All laboratory analyses will be done at the Epidemiological Monitoring Station of the Ministry of Defense in Baku City. Most etiologies to be targeted are considered potential biological weapon agents. Identification of these along with incidence and probable transmission pathway will significantly increase preparedness of the Azerbaijan military medical system, develop sustainable biological agent detection capabilities, and contribute health surveillance data for Ministry of Defense (MoD) force health protection policy. This study will significantly improve laboratory skills for diagnosis to improve clinical management of AFI. In addition, findings will improve the capability to differentiate between infections with similar nonspecific clinical syndromes that are not currently diagnosed or are presumably underreported among military personnel in Azerbaijan.

Prevalence, Epidemiological Surveillance, and Laboratory Analysis of *Coxiella burnetii* in Georgia

PRESENTER: Ana Gulbani

COUNTRY: Georgia

Q fever is a zoonotic bacterial disease resulting from infection by the bacteria *Coxiella burnetii*. The goal of this study is to (1) investigate the seroprevalence of *C. burnetii* among exposed cattle and small ruminants across Georgia, (2) establish active surveillance and detection of cases of Q fever across Georgia, (3) collect isolates from veterinary cases, (4) implement and evaluate new diagnostic methods, and (5) study *C. burnetii* using GIS and DNA sequencing and genotyping. Samples were collected from nine regions by the National Food Agency (NFA) of the Ministry of Agriculture (MoA): 16,343 blood, 15,269 serum, 3,970 milk, and 5,156 swab samples were collected from these animals. Samples were tested by immunofluorescent assay (IFA), polymerase chain reaction (PCR), and bacteriology to detect *C. burnetii*. For IFA, 8,688 samples were tested: 218 were Phase I positive and 42 Phase I susceptive samples; and for Phase II 40 samples were positive, and 34 susceptive. In total, 1,311 samples were tested on ELISA: 1,218 were negatives, 76 positives, and 17 susceptive. We have tested 10,310 PCR samples and seven were positive. Bacteriological tests were performed on serologically positive/ susceptive samples, and PCR positive samples (n=340). Currently, we have isolated two cultures (confirmed by PCR). Due to the amount of sample processing, the project has been extended, and research is going.

Prevalence of *Brucella* Species and Bluetongue Virus Serotypes among Domestic Livestock or Ruminants in Southern Kazakhstan

PRESENTER: Nurlan Sandybayev

COUNTRY: Kazakhstan

Brucellosis and Bluetongue (BT) are high consequence infectious diseases that affect domestic animals in Kazakhstan and worldwide. *Brucella* spp. and an array of Bluetongue virus (BTV) serotypes are considered endemic in Southern Kazakhstan where the largest concentration of cattle, sheep and goat herds in the country are located. Southern Kazakhstan is thought to be at high risk for these two diseases. The project will determine the prevalence of circulating *Brucella* spp. and BTV serotypes over a period of two years in domestic cattle, sheep and goat holdings in Southern Kazakhstan. A disease survey is the first step to link distribution of brucellosis and bluetongue with potential risk factors. The project has been approved by DTRA and kick-off was held on 14 October 2016. The lead KZ partner, the Research Institute for Biological Safety Problems (RIBSP), has submitted paperwork requesting permit from Ministry of Agriculture for sample collection for the study. RIBSP has reported the BSL-3 laboratory has been validated and BSL-3 staff and KZ-32 participants received BSL-3 facility training. RIBSP has developed 13 SOPs focused on sample collection and transport which are currently being reviewed by the collaborators. RIBSP is working closely with collaborators and CBEP’s BTRIC (CH2M) to prioritize items for procurement of laboratory supplies. Dr. Risatti (University of Connecticut), Drs. Elzer and Hagius (Louisiana State University Agricultural Center) are collaborators for the study.

Identification of Etiology, Clinical Outcomes, Incidence, and Epidemiological Patterns of Hospitalized Febrile Patients in Armenia

PRESENTER: Lilit Avetisyan

COUNTRY: Armenia

Background: Hospitalized patients with fever represent a diagnostic challenge for physicians. Scant information is available on identification of etiology, clinical outcomes, and epidemiological patterns of hospitalized patients with fever in “Nork” Infectious Clinical Hospital. The goal of this study was to describe the most common causes, with a focus on zoonotic and arboviral infections.

Methods: Medical records of hospitalized patients with fever were retrospectively reviewed in 2014. Data were abstracted from medical charts of adults (≥ 18 years) with a fever (≥ 38°C), who were hospitalized (for ≥ 24 hours) in 2010–2012.

Results: Of the 600 patients whose charts were analyzed, 76% were from Yerevan and 51% were male; the mean age was 35.5 (± 16) years. Livestock exposure was recorded in 5% of charts. Consumption of undercooked meat and unpasteurized dairy products were reported in 11% and 8% of charts, respectively. The most common signs or symptoms reported were fatigue (97%), diarrhea (56%), nausea/vomiting (54%), shaking (52%), and abdominal pain (46%). The mean duration of hospitalization was 5.5 days. The most common physical examination findings reported were: pallor (64%), abdominal tenderness (52%), pharyngeal injection (43%), and lymphadenopathy (35%). Twenty-four percent of patients received antibiotics prior to hospital admission. Intestinal infections of known (30%) and unknown (21%) etiology were the most frequently reported final medical diagnoses, followed by diseases of the respiratory system (11%), infectious mononucleosis (9.5%), chickenpox (8.3%), brucellosis (8.3%), viral hepatitis (3.2%), and erysipelas (1.5%).

Conclusions: Half of the patients were diagnosed with enteric infections, nearly half of these had no clear etiologic agent. Brucellosis was the most frequently reported zoonotic disease. Solitary cases of anthrax, leptospirosis, FUO, imported malaria, rickettsiosis, and rat-bite fever were also reported. Further prospective studies are required to identify risk factors associated with febrile illnesses, as well as to estimate the burden of selected arthropod-borne and zoonotic infections.

Human Disease Epidemiology and Surveillance of Especially Dangerous Pathogens in Georgia

PRESENTER: Irma Burjanadze

COUNTRY: Georgia

Especially Dangerous Pathogens (EDPs), or select agents, represent a major concern for global public health. These highly pathogenic agents have the potential to be weaponized. Our project was designed to expand on the successes of the Cooperative Biological Engagement Program Collaborative Biological Research and TADR surveillance efforts, and examine the human disease incidence and prevalence of pathogens of public health and biodefense in Georgia. This project has three aims: (1) to study the epidemiology and clinical manifestations of selected pathogens among patients with undifferentiated fever and hemorrhagic fever/septic shock; (2) study the seroprevalence of selected pathogens in humans in Georgia; and (3) implement and evaluate diagnostic methods for selected pathogens and monitor patterns of antimicrobial resistance in identified bacterial infections. Laboratory surveillance for acute undifferentiated febrile illness (AUFI) was established in three major Georgian hospitals by the National Center for Disease Control and Public Health in collaboration with the U.S. Navy Medical Research Unit-3 and USAMRIID. Pathogens that are studied in the seroprevalence protocol include *Bacillus anthracis*, *Brucella* species, Crimean-Congo hemorrhagic fever virus, *Coxiella burnetii*, *Francisella tularensis*, Hantavirus, *Rickettsia* species, and tick-borne encephalitis virus. Furthermore, several other pathogens were tested to develop a comprehensive differential diagnostic algorithm and antibody prevalence of similar diseases. In patients treated at participating hospitals with an undifferentiated febrile illness were tested and involved in the developing process for a comprehensive diagnostic algorithm. Currently, 98.9% of seroprevalence tests and 69.4% of febrile studies are completed. These are preliminary results of screening trial; confirmatory testing continues.

The Epidemiological Status of African Swine Fever in Domestic Swine Herds in the Tavush Marz Region, Republic of Armenia

PRESENTER: Gene Godbold

COUNTRY: Armenia

The factors associated with the spread and persistence of African Swine Fever (ASF) in the Caucasus Region remain to be fully identified. It is assumed that large naïve domestic, free-ranging, and wild pig populations are critical to disease transmission and maintenance. Nonetheless, nine years since its epidemic introduction in the region in 2007, the virus that causes ASF is still circulating suggesting that an endemic cycle is established where contact between free ranging domestic pigs, wild pigs, and probably native *Ornithodoros* ticks serve as reservoirs. Thus, research is required to gather information on the epidemiological status of ASF in the Caucasus Region focusing on understanding modes of ASFV spread and persistence in the area

An active surveillance program was established in Armenia to determine the epidemiological status of ASF focusing on an area at high risk, Tavush marz. This region was the first to report the presence of ASF in Armenia in 2007 and 2010-2011. It is the main terrestrial point of entry for traffic into Armenia and it shares a border with Georgia where the disease was introduced. Most pigs in Tavush are kept in backyard operations and allowed to free-forage, providing contact with wild pigs and ticks.

A total of 1,506 pigs were sampled from small-scale farms clustered in 30 communities across the marz. Samples were taken from the sera, complete blood, and nasal swabs tested by ELISA, IPA, and qPCR. Fifty nine ticks were collected, but the *Ornithodoros* was not found among them. All samples were negative for ASFV and ASFV antibodies suggesting that AFSV is not circulating in the sampled population.

Since sporadic ASFV outbreaks in domestic pigs have continued to occur in the Caucasus, the capacity for long-term environmental survival should be investigated. Further research is required on the epidemiological status of ASF in ticks and swine populations deemed at high risk for ASF.

Investigation of Mosquito and Tick-Borne Arboviruses in Southeastern Azerbaijan

PRESENTER: Rita Ismayilova

COUNTRY: Azerbaijan

Twelve different arboviruses were identified between 1967 and 1980 in humans and animals in Azerbaijan. Despite the known presence of arboviruses, very little vector-borne pathogen research has been conducted within Azerbaijan since then. TAP-13 project is designed to identify selected arboviruses and their arthropod vectors in southeastern Azerbaijan (Lankaran, Masalli and Gizil-Aghaj State Reserve). The aim of the project was to facilitate the development of effective strategies for the biosurveillance, control, and mitigation of four arboviral pathogens (CCHF, TBE, Sindbis and WNV) and their arthropod vectors.

The project was initiated in August 2016 and is being implemented at Lankaran Anti-Plague Division (APD) with mentorship of the Republican Anti-Plague Station (RAPS). The UK Public Health collaborators provided two PCR trainings in Lankaran APD (November and April, 2016). Arthropods were collected from three regions in October 2015, April and May, 2016 using cloth dragging and livestock collection of ticks, as well as mosquito collection using CDC-light and BG-sentinel traps. Coordinates were recorded via GPS.

Out of 1,777 collected ticks, 1,606 ticks have been counted, identified, and sorted. 590 tick pools have been prepared; 46 pools have been homogenized, extracted, and tested for TBE, Tamdy and West Nile viruses, and all were negative. Out of 5,217 collected mosquitoes, 1,152 have been counted, identified, and sorted. 96 pools have been prepared. 37 mosquito pools were tested for West Nile and Sindbis viruses, and all were negative.

The project was temporarily halted, but will resume February 2017.

Analysis of Previously Identified *Rickettsia* Positive Georgian Ticks by Multi-locus Sequence Typing

PRESENTER: Roena Sukhiashvili

COUNTRY: Georgia

Preliminary studies have shown the presence of three spotted fever group *rickettsiae* (SFGR) species among ticks in Georgia: *R. aeschlimanii, R. raoultii*, and *R. slovaca*. The identity and prevalence of other *Rickettsia* species in ticks have not been determined. The overall goal of this project was to improve the surveillance of tick-borne pathogens in Georgia in the context of rickettsial diseases. This project used the Rickettsia-positive tick samples collected in Georgia from GG TAP-4 project. All tick samples were previously entered into a database, and pertinent sample information and GPS location data were recorded. The tick DNA preparations from the tick samples were tested using multi-locus sequence typing (MLST) to identify which Rickettsia species were present. Tick samples were not collected from the field; only tick DNA preparations already tested for Rickettsia were utilized. Overall, nine species were found among 12 different tick species from five different genera: *Ixodes, Hyalomma, Haemaphysalis, Dermacentor,* and *Rhipicephalus*. Geographical distribution maps of *Rickettsia* –infected ticks that were developed in eight regions eastern and western Georgia showed that the most common *Rickettsia* species were: *R. raoultii*, *R. slovaca*-also, *R. aeschlimannii*, and *R. monacensis*. For the first time the SFGR species *R. massiliae, R. monacensis*, *R. conorii* subsp. *conorii*, *R. hoogstraalii, R. helvetica* and *Ca. R. barbariae* were detected in ticks from Georgia. High prevalence and wide distribution of *Rickettsia* species among ticks make rickettsiosis a potential public health problem in Georgia.

The Role of Arboviruses as a Cause of Undifferentiated Febrile Illness in Sindh, Pakistan

PRESENTER: Erum Khan

COUNTRY: Pakistan

The objective of this study was to develop training in arboviral diagnostics and surveillance, to determine the burden of mosquito-borne viruses that can be used as biological agents of warfare. The Pakistani collaborators then trained other public health practitioners in Pakistan to expand arboviral diagnostics and surveillance capabilities. We recorded the presence of several co-circulating arboviruses in Pakistan. Our data show that a significant percentage of patients presenting with undifferentiated fever are afflicted with at least one arbovirus with 14.2% of patients infected with dengue or West Nile virus, 3% with chikungunya virus, and 10.7% with Japanese encephalitis virus. Diagnostic techniques developed through this project helped in the early diagnosis of Chikungunya during the Nov-Dec 2016 outbreak in Karachi. We published one paper disseminating preliminary project data and are currently drafting several more papers for publication in the coming year. Additionally, based on data from this project, a team member was awarded a 12-month Fellowship in One-Health by the National Academy of Science for 2016-2017.

During the next reporting period, we will complete validation via PRNT for all samples. In light of the global outbreak of Zika virus, we will screen our samples for Zika virus. We will present data at several conferences this year.

Event Logistics and Local Information

Venue Information

2017 Science Program Review Meeting Site

Hilton Alexandria Mark Center
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Alexandria, Virginia 22311
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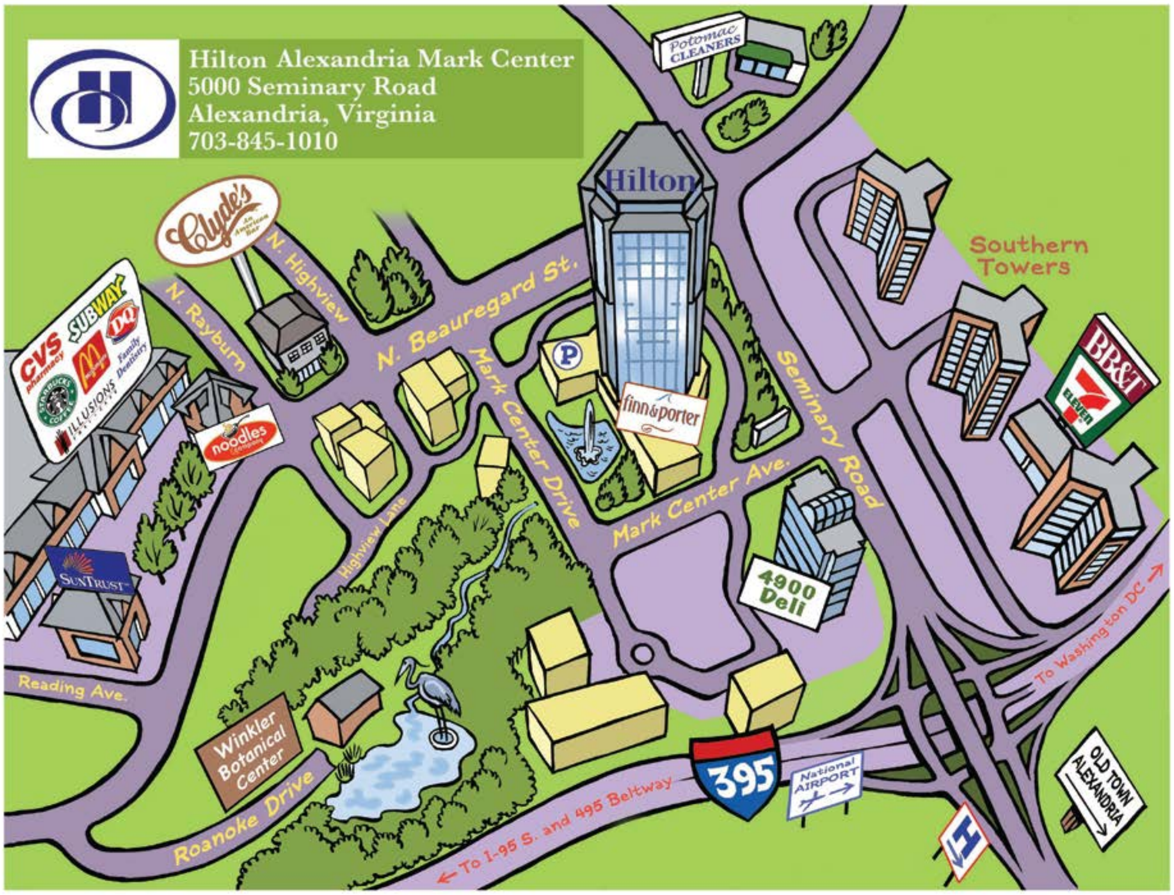
Local Information



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Lao PDR	Environmental Surveillance of *Burkholderia pseudomallei*, Pilot Study in Lao PDR	Zimmerman	Session 9: Bacterial Pathogens of Security Concern - Group 2	Friday 8:40 AM	53
Malaysia	Biosurveillance for Henipaviruses and Filoviruses at the Agricultural Animal-Human Interface in Malaysia (BAA)	Epstein	Session 4: Viral Pathogens of Security Concern	Thursday 11:40 AM	27
Malaysia	Multi-Year Prospective Cohort Study to Evaluation the Risk Potential of MERS-CoV (Call)	Abubakar	Session 10: Emerging Infectious Diseases	Friday 10:40 AM	57
Malaysia	Etiology of Severe Acute Respiratory Infections in Kuala Lumpur, Malaysia (BAA)	Sams	Session 10: Emerging Infectious Diseases	Friday 10:40 AM	60

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Pakistan	High Resolution Chemical Characterization of *Yersinia pestis* Cells within Soil Matrices: Implications for Understanding Natural Foci and Telluric Reservoirs of Plague (BAA)	Shah	Session 9: Bacterial Pathogens of Security Concern - Group 2	Friday 8:40 AM	48
Pakistan	The Role of Arboviruses as a Cause of Undifferentiated Febrile Illness in Sind, Pakistan (BAA)	Khan	Session 12: Arthropods and Arboviruses	Friday 2:50 PM	71
South Africa	Understanding Rift Valley Fever in the Republic of South Africa (BAA)	Karesh & Van Vuren	Session 4: Viral Pathogens of Security Concern	Thursday 11:40 AM	26
Tanzania	Evaluating Zoonotic Viral Sharing Among Bats, Primates and People in High Risk Transmission Interface in Southern Tanzania (BAA)	Ekiri	Session 2: Chiroptera (Bats) - Important Reservoirs Hosts of Emerging Viruses	Thursday 8:50 AM	18
Tanzania	A One Health Approach to Brucellosis and Rift Valley Fever Surveillance in Tanzania (BAA)	Kilonzo	Session 3: Epidemiology & Biosurveillance - Group 1	Thursday 10:30 AM	21
Tanzania	Global Health, Emerging Infectious Diseases and Food Safety Implications of Bushmeat in Tanzania (BAA)	Buza	Session 10: Emerging Infectious Diseases	Friday 10:40 AM	59
Thailand	Acute Febrile Illness Study Among Patients in Nakhon Phanom and Tak Province, Thailand (Call)	Bhengsri	Session 3: Epidemiology & Biosurveillance - Group 1	Thursday 10:30 AM	22
Thailand	Melioidosis Research Coordination Network	Limmathurot-sakul	Session 9: Bacterial Pathogens of Security Concern - Group 2	Friday 8:40 AM	54
Uganda	Arthropod-borne Viruses Associated with the Chiroptera of Uganda: Isolation and Characterization (Call)	Kityo	Session 2: Chiroptera (Bats) - Important Reservoirs Hosts of Emerging Viruses	Thursday 8:50 AM	16
Uganda	UG-2: Research and Development of Countermeasures to Support the Control of FMDV in Uganda	Mwiine	Session 6: Transboundary Animal Diseases	Thursday 2:20 PM	35
Uganda	Acute Febrile Illness in Uganda (BAA)	Byarugaba	Session 11: Epidemiology & Biosurveillance - Group 2	Friday 1:00 PM	62

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Ukraine	TAP-4: Community Outreach to Support Understanding of African Swine Fever (ASF) Ecology and Epidemiology in Eastern Europe (EE)	Datsenko	Session 5: Community Outreach to Combat African Swine Fever	Thursday 1:30 PM	31
Ukraine	TAP-6: Analysis of the Threat of Spread of African Swine Fever and Classical Swine Fever in Wild Boar Populations in Ukraine: Improving Diagnosis, Surveillance, and Prevention	Nevolko	Session 6: Transboundary Animal Diseases	Thursday 2:20 PM	34
Ukraine	African Swine Fever Threat Reduction Through Surveillance in Ukraine (USDA ARS)	Filatov	Session 6: Transboundary Animal Diseases	Thursday 2:20 PM	36
Ukraine	UP-2: Development of the Epidemiological Forecasting System for Zoonotic Diseases Employing GIS Technology	Tarasov	Session 7: Bacterial Pathogens of Security Concern - Group 1	Thursday 3:40 PM	39
Ukraine	Genomic, Epidemiological, and Biological Characterization of Newcastle Disease Virus Isolates from Ukraine (USDA ARS)	Goraychuk	Session 8: Avian Transmissible Diseases	Thursday 5:00 PM	42
Ukraine	UP-4: Risk Assessment of Selected Especially Dangerous Pathogens Potentially Carried By Migratory Birds Over Ukraine	Muzyka	Session 8: Avian Transmissible Diseases	Thursday 5:00 PM	45
Vietnam	Foot-and-Mouth Disease Virus Surveillance and Ecology in Vietnam (Call)	Dung	Session 6: Transboundary Animal Diseases	Thursday 2:20 PM	32