

**CREID Network
2022 Pilot Program Awardees**

Principal Investigator	Ohnmar Aung, MA <i>Nature Conservation Society Myanmar</i>
Title	Investigation of ecological drivers of sarbecovirus spillover in Myanmar and Nepal
Pathogen Focus	Coronaviruses
Country	Nepal, Myanmar
Collaborating CREID Research Center	EpiCenter
Abstract	<p>More effort is needed to identify and characterize SARS-CoV-related viruses that circulate at wildlife human interfaces, particularly among communities in close proximity to bats, to not only inform on the origin of SARS-CoV-2 but to characterize the human communities that are most likely to be at the point of emergence of the next novel zoonotic coronavirus.</p> <p>Myanmar is a highly understudied hotspot for coronavirus diversity in wildlife and Ms. Aung's team has identified exposure to SARS-CoV-2-related viruses in humans in close contact with bats in this region. This project will further characterize specific sarbecovirus exposures and compare findings with similar ecosystems in Nepal. It will also build capacity for the CREID Network by including Myanmar, a critical ecosystem for understanding the emergence of SARS-CoV-related viruses and strengthening regional capacity through building Myanmar-Nepal collaborations, including providing advanced training for Pilot Program investigators at Duke-NUS, Singapore, and University of California at Davis (UC Davis).</p> <p>Ms. Aung is a Senior One Health Scientist at Nature Conservation Society Myanmar and will collaborate with and be mentored by members of the EpiCenter leadership team, including Drs. Tierra Smiley Evans (Co-PI) and Christine Kreuder Johnson (PI) with UC Davis.</p> <p>Ms. Aung's project will advance our understanding of the risk of zoonotic coronavirus spillover in Myanmar and Nepal by (1) investigating immune reactivity to a range of SARS-related viruses in human cohorts with frequent interaction with bats; (2) conducting epidemiological risk factor analyses to understand behaviors and interactions facilitating spillover; and (3) evaluating sarbecovirus exposure in bats sampled concurrently with human cohorts.</p> <p>This study will integrate molecular, serological, and behavioral epidemiological approaches to investigate zoonotic coronavirus spillover which are urgently needed to understand the frequency with which spillover into at-risk human populations is occurring and activities which could be targeted as mitigation points for communities at highest risk for future coronavirus emergence. The study will strengthen Myanmar and regional capacity for SARS-CoV-2-related investigation which will lead to improved disease surveillance and risk mitigation.</p>

Principal Investigator	Stephanie Seifert, PhD, <i>Washington State University</i> Isaac Ngere, PhD, <i>Washington State University – Kenya</i>
Title	Surveillance for known and novel viruses with zoonotic potential at the interface between humans and livestock in Kenya
Pathogen Focus	MERS-CoV
Country	Kenya, US
Collaborating CREID Research Center	CREID-ECA
Abstract	<p>Zoonotic viruses have a profound impact on human health, a fact that is underscored by the ongoing COVID-19 pandemic. Targeted surveillance for known or suspected viral pathogens can miss emerging or novel pathogens at critical human-animal interfaces, delaying the public health response. The diversity of viruses poses technical challenges that hinder low-cost and sensitive surveillance for emerging and novel viruses.</p> <p>For this CREID Pilot Program study, co-PIs Seifert and Ngere will deploy a novel assay for the detection of RNA viruses representing 20 viral families and more than 600 virus species to study viral diversity at the human-animal interface in Kenya. This assay targets conserved viral genomic regions and will recover sequence data from novel viruses with up to 20% sequence divergence in the RNA-dependent RNA polymerase gene of viruses represented in the library, making this an excellent tool for detecting both known and novel viruses.</p> <p>Drs. Seifert and Ngere will use the novel assay to conduct a value-added study complementing ongoing field surveillance for Middle East Respiratory Syndrome Coronavirus in camels and camel handlers in northern Kenya. Building upon an existing study framework, Drs. Seifert and Ngere propose to expand sampling efforts to include samples collected from camels held for slaughter, camel tissues following slaughter, and abattoir workers. Together, these data will assist in characterizing viral diversity at a critical interface for zoonotic transmission of a respiratory virus in Kenya.</p> <p>Dr. Seifert is an Assistant Professor and Dr. Ngere is a Medical Epidemiologist both in the in the Paul G. Allen School of Global Health at WSU. They will be mentored by Dr. Njenga Kariuki, PI of CREID-ECA and faculty member for the WSU Global Health Kenya Program.</p>

Principal Investigator	Laura Dickson, PhD, University of Texas Medical Branch Alioune Gaye, PhD, Institut Pasteur de Dakar
Title	Characterization of the mosquito microbiome and its role in arbovirus emergence and maintenance in Senegal
Pathogen Focus	Arboviruses
Country	Senegal
Collaborating CREID Research Center	WAC-EID
Abstract	<p>Arthropod borne viruses (arboviruses) such as chikungunya (CHIKV), yellow fever (YFV), dengue (DENV), and Zika viruses (ZIKV) pose a major public health threat across the tropics and have the potential for emergence or re-emergence from sylvatic environments into human transmission cycles. In Senegal, arboviruses are maintained in enzootic transmission cycles involving arboreal species of <i>Aedes</i> and non-human primates and in epidemic or endemic transmission cycles involving <i>Aedes aegypti</i> and humans in urban or semi-urban environments. Outbreaks occur sporadically with viral amplification occurring late in the rainy season. The mosquito microbiome influences its interactions with pathogens and is highly dynamic and subject to environmental change.</p> <p>2022 Pilot Program Awardees Drs. Dickson and Gaye, who are collaborating with the WAC-EID Research Center, will examine whether changes in the mosquito microbiome (both bacteria and viruses) can help explain the absence or low / undetectable level of the arboviruses' circulation at the beginning of the rainy season, or the amplification of arboviruses late in the rainy season.</p> <p>The team will test this hypothesis in an enzootic transmission system using the bridge vector, <i>Aedes furcifer</i>, and in an endemic/epidemic transmission system using <i>Aedes aegypti</i>. They will begin by establishing a baseline characterization of the microbiome of relevant <i>Aedes</i> species at different timepoints in the rainy season. This information will inform the isolation of both bacterial and viral members of the microbiome from field collections to functionally evaluate their role in arbovirus susceptibility.</p> <p>This project will establish a framework to study the role that seasonal changes in microbial symbionts play in the emergence, amplification, and outbreak of arboviruses in Senegal.</p> <p>Dr. Gaye is a Research Assistant at Institut Pasteur de Dakar (IPD) and has worked with the IPD Medical Entomology Unit since 2011. Dr. Dickson is an Assistant Professor at University of Texas Medical Branch at Galveston (UTMB) and has more than 14 years of experience in medical entomology research. Drs. Gaye and Dickson will be mentored by Dr. Scott Weaver, PI of WAC-EID and Dr. Mawlouth Diallo, head of Medical Zoology at IPD.</p>

Principal Investigator	Jurre Siegers, PhD and Vireak Heang, MS Institute Pasteur of Cambodia
Title	In the air tonight: Metagenomic pathogen discovery as tools in pathogen surveillance
Pathogen Focus	Pathogen Surveillance
Country	Cambodia
Collaborating CREID Research Center	EID-SEARCH
Abstract	<p>The ability to quickly assess risk of emerging infectious diseases at points of high exposure or contact is paramount for early warning systems and preventative actions. In addition, maintenance of surveillance systems in individual animals is costly and time consuming and prevents widespread coverage. One way to address this issue is to incorporate environmental sampling into surveillance programs to cast a wider net at high-risk interfaces and on a longitudinal basis.</p> <p>To this end, Dr. Siegers and Mr. Heang, who are both with the Institut Pasteur of Cambodia (IPC) have been exploring new ways to assess how environmental sampling at high-risk human-animal interfaces, including live animal markets, slaughterhouses, and domestic/wild animal interfaces can improve sampling efforts. Currently, these samples collected as part of previously funded active surveillance have only been tested for specific pathogens of interest by conventional or real-time PCR, limiting their utility. The ability to use these samples for expanded surveillance and targeted metagenomic discovery would not only increase surveillance capacity, but also contribute to our understanding of new or emerging pathogens at these high-risk interfaces.</p> <p>Dr. Siegers is a postdoctoral scientist in the Virology Unit and Mr. Heang is a research engineer with the Sequencing Mini-Platform at IPC. Both researchers will be mentored by Erik Karlsson, PhD, Deputy Head of the Virology Unit at IPC and Cadhla Firth, PhD, Senior Research Scientist with EcoHealth Alliance/EID-SEARCH.</p> <p>In the proposed project, the research team will: (1) utilize existing environmental samples from previously funded longitudinal pathogen surveillance to build targeted, enriched viral metagenomic sequencing and bioinformatics capacities and capabilities; (2) assess the suitability of using targeted, enriched metagenomics in an early warning system for endemic and emerging infectious diseases at high-risk interfaces in Cambodia; and, (3) potentially discover new, emerging, or zoonotic pathogens of concern in high-risk interfaces in Cambodia. Overall, the results from this study will contribute to improving surveillance systems through rapid and broad pathogen detection, reduced cost, lowered occupational risk, and diminished animal and environmental impact.</p>

Principal Investigator	Najia Ghanchi, PhD Aga Khan University
Title	Vector surveillance in context of urban transmission and spread of Crimean-Congo hemorrhagic fever virus (CCHFV)
Pathogen Focus	Crimean-Congo hemorrhagic fever virus (CCHFV)
Country	Pakistan
Collaborating CREID Research Center	UWARN
Abstract	<p>Crimean Congo Hemorrhagic Fever Virus (CCHFV) is a tick-borne hemorrhagic fever virus causing severe disease in humans. CCHFV is spreads through infected tick bites, animal handling, and human-to-human transmission. CCHFV epidemiology in Pakistan varies in rural areas vs. urban settings where prevalence is low. However, an increased number of cases are observed in urban areas post Eid al-Adha, a religious festival related to animal sacrifice. 2022 Pilot Program Awardee Dr. Najia Ghanchi hypothesizes that an increase animal influx during Eid al-Adha leads to urban transmission of CCHFV by maintaining a CCHFV reservoir in ticks. UWARN is the collaborating CREID Research Center for this project.</p> <p>Dr. Ghanchi is an Associate Professor of Pathology and Laboratory Medicine at Aga Khan University (AKU) in Pakistan and will be mentored by Dr. Peter Rabinowitz, Professor, Global Health, Environmental and Occupational Health Science, and Family Medicine at the University of Washington and Dr. Erum Khan, Professor, Clinical Microbiology and Molecular virology, Pathology and Laboratory Medicine at AKU.</p> <p>To determine the risk of CCHFV spillover in urban centers, Dr. Ghanchi will collect ticks from multiple cattle farms and markets to investigate tick infestations of cattle and CCHFV PCR-positive ticks. She will also utilize next-generation sequencing (NGS) to understand the genomic structure of CCHFV and phylogenetic analysis. Through this research project, Dr. Ghanchi aims to establish whether cattle movement from CCHFV-endemic regions of the country contributes to maintenance of a CCHFV reservoir in ticks infesting cattle leading to CCHFV spillover in urban environments. This CREID-funded research study will establish preliminary data points for expansion of this study to humans and animals and to conduct countrywide studies to inform policy decisions in the future. This model can also be applied to understand endemic and emerging pathogens.</p>