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P2BR Process_Methods & Lessons Learned.docx

Hi everyone.
Please find attached our team's manuscript for your review. As we are aiming for the Monday deadline of the One Health Outlook, we'd appreciate your comments and edits by Friday.

Thanks so much and happy holidays!

Best,
Karen, David and Emily

Title:

- **Socializing One Health: An Innovative Strategy to Investigate Social and Behavioral Risks of Emerging Viral Threats**

Other title options…open to your votes! ☺

- A Mixed-Methods Approach to Behavioral Risk Investigations under a One Health Framework
- Perceptions of Behavioral Risk: Lessons Learned from a Global One Health Project

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And PREDICT Consortium

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Introduction

Globalization has radically catalyzed the everyday movements of people, animals, technology, goods, capital, and services worldwide. While this transformation has been broadly regarded as an economic boon, it has also increased the opportunities for diseases to spread geographically and potentially between species (Saker et al. 2004; Wolfe et al. 2005). Anthropogenic land use change, such as the building of roads or cities where once there were forests, creates a chain reaction of ecological, socio-economic, human behavioral, and regional fauna impacts that are believed to be linked to how infectious diseases emerge. Globally, urbanization has led to drastic growth in the density of human populations living in cities, increasing the potential for large infectious disease outbreaks (Neiderud 2015, Hassell et al. 2017). Per capita meat consumption has rapidly expanded over the last half century, driving the development of high-density livestock operations that provide opportunities for large-scale animal disease outbreaks (Ritchie & Roser 2017). Constant demand for cropland and grazing land, as well as aggressive resource extraction, has resulted in drastic environmental transformations, including habitat destruction, forest encroachment, and interspecies mixing (Ancrenaz, Dabek, and O'Neil, 2007). Zoonotic diseases – those with an animal host or reservoir – are responsible for some of the most impactful and devastating outbreaks in recent years. Seventy-five percent of emerging infectious diseases (EIDs) are zoonotic in origin, including Ebola, Influenza A strains H5N1 and H9N2, Hantaviruses, and human sleeping sickness (Morse et al. 2012; Taylor, Latham & Woolhouse, 2001). Trends in the transmission of pathogens across species, coupled with the knowledge that human, animal, and environmental health are inextricably linked, have been a driving force for the use of a One Health approach in recent emerging infectious disease research and surveillance efforts, which has proven valuable (Bidaisee & MacPherson, 2014).

The concept of One Health is a revitalization and expansion of the concept of One Medicine, developed in the 1970s by Calvin Schwabe to recognize the inextricable interconnection of humans and animals in the domains of nutrition, livelihood, and health (Zinsstag et al. 2011). In the 2000s, the concept of One Health was adopted to further broaden the concept of One Medicine to include ecosystem health – including the influence of climate, plants, and wildlife on global health (Zinsstag et al. 2011). International organizations, including FAO, OIE, WHO, and The World Bank, soon codified a One Health strategy to guide research and capacity-development efforts towards the prevention, detection, and response of infectious diseases (FAO et al. 2008). The One Health approach, encompassing "the integrative effort of multiple disciplines working locally, nationally, and globally to attain optimal health for people, animals, and the environment," (AVMA 2019) is increasingly recognized as a critical paradigm in addressing key global health challenges.

While the inclusion of the environment in One Health thinking has greatly increased our ability to tackle today's complex health problems (driven by climate, mobility, and land-use changes), a growing number of scholars argue that much of the resulting One Health work has perpetuated a false dichotomy between "natural" and "social" systems and prioritized the study of "natural" ecological systems over "social" systems (Rock et al. 2009; Zinsstag et al. 2011; Woldehanna & Zimicki 2015). These scholars point out that domesticated animals, plants, and wildlife, are as much a "part of the environment of humans" as they are a "part of the social systems of humans" (Zinsstag et al. 2011). It is not enough to track ever-shifting geographic territories of plant and animal species, they argue, we need to understand how these species' geographic territories, behaviors, and biologies are co-constituted by human social systems. Without a nuanced understanding of specific human activities, "how, where and when people interact with animals," they argue, it is impossible to understand the actual risk for zoonotic spillover events (Woldehanna & Zimicki 2015). To adequately understand human activity as an integrated part of both the physical and social environment, One Health teams should strive to include professionals from disciplines such as anthropology, economics, political science, psychology, and sociology (Rock et al. 2009).

The imperative to understand human activity in the context of zoonotic disease outbreaks was perhaps best exemplified during the 2014 West Africa Ebola epidemic, where dysfunctional health systems, denial of Ebola, and burial practices involving contact with the deceased exacerbated containment of the outbreak (Lo et al. 2017). Following recent EVD outbreaks in DRC, West Africa, and Uganda, the behavioral sciences – medical anthropology in particular – have been highlighted as having a critical contribution to understanding the social dynamics of zoonotic disease emergence and spread, as well as developing effective response interventions for disease control (Hewlett and Hewlett 2007; de Vries et al. 2016). In particular, the WHO's Ebola Strategy guidelines clearly articulate several critical contributions medical anthropology (and the behavioral sciences by extension) can have towards outbreak management (WHO 2014). First, such research contributes towards "better knowledge of disease transmission chains," identifying behavioral mechanisms that may be perpetuating spread, such as forms of wildlife contact, exposure to infected medical items, or burial practices. Second, the behavioral sciences can identify "psychologically, socially, and culturally diverse behaviors of local populations" and propose appropriate interventions. By understanding the culturally specific context and meaning of behaviors driving disease transmission, response efforts can react faster and design more culturally appropriate interventions that are acceptable to populations. In addition, contributions from social scientists can help to identify rumors, fears, and misinformation that may be amplifying risks for transmission. Finally, these contributions can help guide the development of "empathetic approaches" to outbreak response and disease control, striving to engage the participation of affected communities to develop sustainable interventions that benefit the largest number of people, as opposed to "coercive approaches" that are largely indifferent to the needs and opinions of specific individuals and communities.

A major global health security lesson learned from the West Africa Ebola epidemic was that "more work is needed at national and global levels to ensure that populations are empowered to protect themselves from diseases, and to ensure that the mass media have the knowledge and understanding to contribute to health protection and understanding of risks and their management." (Koser, 2015) One way to strengthen a population's ability to protect themselves is to better understand how certain behaviors put people at risk, and what changes we can make to mitigate that risk. For example, during the 2009 influenza H1N1 pandemic, work pattern adjustment, self-isolation of symptomatic individuals and advice to their caregivers, and cancellation of mass gatherings helped to mitigate the pandemic; these were all self-protective behavioral adjustments that were made based on shared public health information on risk behavior and disease spread (WHO, 2010). By improving our collective understanding of the dynamics of infectious disease transmission and how certain behaviors put individuals and populations at risk, we can

elucidate evidence-based ways to control disease transmission that can empower individuals to adopt preventive and protective behaviors. Additionally, being able to communicate to public health decision-makers how human interactions facilitate the emergence of wildlife pathogens in human populations, and advocating for behavioral change communication, education and prevention efforts, can improve compliance with and the effectiveness of medical interventions and public health efforts (Berger et al. 2019).

Since the 2014 West Africa Ebola epidemic, rigorous behavioral science and qualitative methods have been built into outbreak response: multiple social science implementers are actively engaged in the current Ebola outbreak in eastern Democratic Republic of the Congo (DRC), including Anthrologica, an applied anthropology research group which conducts formative and operational research in emergency settings; the GOARN-R Social Science Group; Réseau Anthropologie des Epidémies Emergentes/Projet SoNAR-GLOBAL; and Social Science in Humanitarian Action, which produces rapid briefs on key socio-cultural considerations (Bedford 2019). The use of these social scientific tools and participatory approaches helps ensure that intelligence and analytics guiding response efforts remains grounded, while providing valuable insights at the community, institutional, and policy-levels, enabling timely and strategic recommendations. The difficulty containing the ongoing Ebola outbreak in DRC, now the second largest Ebola outbreak in history, is in part due to the vulnerability of the affected area, a long history of armed regional conflict, and subsequent community resistance, skepticism, and lack of trust in government and international actors, including the outbreak response teams and Ebola treatment centers (Vinck et al. 2019). Within this context, applied social science research adds critical value to response teams, improving their understanding of the social dimensions of risk and helping identify solutions for more effectively engaging communities in outbreak response and control efforts (Abramowitz et al. 2015).

USAID's Emerging Pandemic Threats Program: Using Social Sciences to Understand Spillover Risk Before Emergence

While especially critical in outbreak scenarios, the contributions of the behavioral sciences are equally important prior to disease emergence, as they can improve our understanding of the risks associated with pathogen spillover and spread and inform strategies and interventions for risk reduction and mitigation. Quantitative modeling approaches have been used to extrapolate data to help understand pathogen-host dynamics and estimate outbreak frequency and severity, as seen in recent disease hotspot mapping (Allen et al. 2017) and current research exploring high-risk human-animal interfaces (Kreuder-Johnson et al. 2015). Qualitative human behavioral research can add further depth to our understanding of behavioral drivers of zoonotic disease spillover, amplification, and spread (Woldehanna & Zimicki 2015). Human behaviors are complex, dynamic, and highly contextual and are influenced by a myriad of socio-cultural factors that elude traditional disease modeling methods (Leach et al. 2013; Arthur et al. 2017). A multidisciplinary approach to exploring the social dimensions and human behaviors associated with disease transmission is fundamental to more holistically understanding the conditions and circumstances of humans, animals, and environments through which zoonotic diseases emerge and spread.

In an effort to strengthen global capacity to prevent, detect, and control infectious diseases in animals and people, the United States Agency for International Development's (USAID) Emerging Pandemic Threats (EPT) program funded several projects to develop regional, national, and local One Health capacities for early disease detection, rapid response and disease control, and risk reduction (Morse et al. 2012). From the outset, the EPT approach was inclusive of social science research methods designed to understand the contexts and behaviors of communities living and working at human-animal-environment interfaces considered high-risk for virus emergence, in order to shed light on the social dimensions of zoonotic disease transmission and identify potential intervention strategies for prevention and risk reduction. From 2009-2014, EPT's PREVENT project focused on formative research intended to identify risky behaviors,

attitudes, and practices, and to increase the prevalence of protective habits and preferences. Led by the Academy for Educational Development (later FHI360), PREVENT conducted behavioral research in the Congo Basin and Southeast Asia and worked to identify and characterize vulnerable populations, and the high-risk behaviors and practices for disease transmission from animals to humans. In addition, PREVENT worked to develop a strategic framework for risk reduction and suggestions for policy and structural changes for risk mitigation and disease prevention. At the same time, the USAID EPT PREDICT project developed a global consortium to strengthen capacity for surveillance and early detection of virus threats from wildlife and to identify high-risk areas and human-animal interfaces for virus spillover, amplification, and spread for targeted surveillance, monitoring, prevention and control efforts. Working with partners in over 20 countries, PREDICT teams collected samples for virus testing from more than 56,000 animals and detected thousands of unique viruses in what is considered the largest virus detection and discovery effort to date (PREDICT Consortium, 2015).

Building on this foundation, USAID's EPT program funded another 5-year investment to strengthen health system capabilities in low and middle income countries for improved zoonotic disease prevention, detection, and response. In 2014, a second phase of the PREDICT project was launched in Sub-saharan Africa, South and Southeast Asia, and East Asia as a multi-disciplinary effort with a revised One Health surveillance strategy reliant on the concurrent samping of animals and people in identified at-risk interfaces for virus emergence. This new scope included an expanded emphasis on understanding behavioral risks along with data collection, synthesis, and aggregation on biological and ecological risks at these interfaces. From the inception, PREDICT incorporated social science methods into the design of One Health surveillance plans and the data collection and capture tools used in the field by the project's multi-disciplinary teams. Using a mixed qualitative and quantitative methods approach, PREDICT teams conducted investigations and collected data that more comprehensively addressed the multiple dimensions of virus spillover risk and better enabled the development of informed risk reduction and intervention strategies. PREDICT's behavioral risk strategy was implemented in 27 countries from 2014-2019. Our strategy was adapted to the host country contexts and specific human-animal- environment interfaces, yet was standardized globally to enable cross-country, regional, and ultimately global comparisons.

Here we present a synthesis of our unique and innovative behavioral risk strategy. In addition, we share some preliminary insights and lessons learned for incorporating the social sciences into complex disease surveillance programs grounded in the One Health approach.

Building Behavioral Sciences into One Health Surveillance

By design, the PREDICT Consortium integrated global expertise from the conservation, veterinary medicine, public health, and social science communities to develop truly collaborative and multidisciplinary approaches for the early detection of virus threats and the development of disease control and prevention recommendations. In 2014, our team worked collaboratively to incorporate behavioral risk investigations using a mixed methods quantitative and qualitative data collection strategy into field activities targeting the sampling of wildlife, domestic animals, and people in areas identified as high-risk for virus spillover and spread. Data collection tools were collaboratively designed to address ecological risks for emergence (using a standardized observational tool) and behavioral risks (using a standardized questionnaire with option for additional in-depth ethnographic interviews and focus group discussions). Standard operating procedures and training materials were developed and shared to assure standardization of the strategy through the life of the project. Consortium leads provided guidance and plans for continued mentorship in all methods and techniques to support successful implementation. The strategy and tools, once approved by US and host country Institutional Review Boards and ethics committees, were put into action with partners across all project countries.

At the country level, personnel were identified by partners to lead the behavioral risk scope and teamed up with Consortium partners for training and mentorship. Because of differences in personnel background, the training and mentorship plan was structured to introduce the basics of social science methodology for rapid onboarding while also diving deep into the PREDICT strategy and behavioral risk tool kit using a combination of lecture, discussion, and hands-on experiential learning. Training covered techniques for successful community engagement and outreach, how to conduct interviews using the questionnaire, and ethnographic methods and techniques for leading effective qualitative interviews and focus group discussions. Trainings also covered data management, coding, and analysis, along with strategies for sharing project findings and communicating risk reduction strategies.

During implementation, trained behavioral risk personnel joined teams comprised of local professionals from diverse disciplines, and worked together in the field to engage at-risk communities and conduct behavioral investigations while animal and public health professionals led One Health surveillance and sampling efforts. Though team composition varied, members often included field veterinarians and ecologists/wildlife biologists for animal sampling; medical doctors, nurses, phlebotomists, or other public health paraprofessionals for human sample collection; and anthropologists, sociologists, community health workers, or other public health professionals for behavioral interviews. Field work and data collection were tightly coordinated across space and time, with community engagement, behavioral risk investigations, animal sampling, and human sampling often occurring simultaneously in targeted communities.

Figure 1. Global behavioral risk team composite

Bringing together a transdisciplinary team of scientists and practitioners was central to the human behavioral risk surveillance arm of PREDICT. Featured on the right are examples of disciplines represented by local team members who took part in the behavioral risk investigations, with female team members in italics.

Assessing Behavioral Risk and Operationalizing One Health Surveillance

From an epidemiological perspective, behavioral risk assessments often seek to quantify the influence of known risk factors on disease emergence and transmission dynamics. PREDICT's focus was broader, as we aimed to identify and assess a range of known and unknown socio-cultural behaviors that could be influential in zoonotic disease emergence, amplification, and transmission. This broad approach to behavioral characterization enabled us to identify and characterize a milieu of human activities that could be later studied to investigate the transmission dynamics of new and emerging viruses. For diseases whose etiology is known and characterized, such as zoonotic Influenza infection, this approach allowed us to determine behaviors that might be risk factors for certain groups (e.g., agricultural workers) and to understand the socio-cultural contexts necessary to develop effective risk mitigation strategies. For example, potential Influenza risks among agricultural workers include smoking in or around swine or poultry facilities and a lack of available personal protective equipment; mitigation strategies included heightened biosafety and biosecurity procedures, assuring use of personal protective equipment, frequent hand washing, and occupational health programs integrating monitoring and surveillance of high-risk groups with countermeasures such as influenza vaccines (Ramirez et al. 2006).

In implementation, our teams built partnerships and relationships at the national, subnational, and community levels. Before the roll-out of activities, our staff worked with a range of municipal and traditional stakeholders, including officials, leaders, and elders in the target communities, to help our One Health teams effectively engage with communities and to facilitate permissions and access for animal and human sampling efforts. Our teams also conducted site scoping visits, and in some cases formative behavioral risk research in collaboration with ministry partners, which helped determine One Health surveillance priorities and at-risk site selection. Through this multi-level stakeholder engagement process, our staff were able to build the relationships and teams necessary for gaining community buy-in, trust, and support for our unconventional surveillance strategy.

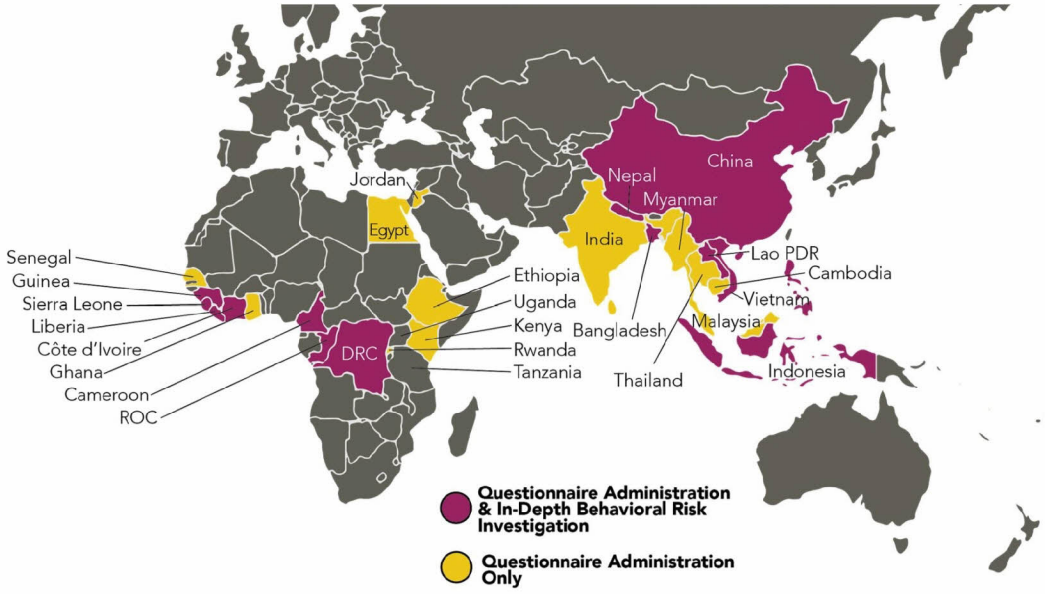
In each country, standard with serosurveillance studies (Miller and Hagan, 2017), a structured quantitative questionnaire was administered whenever a human sample was collected. This 57-question questionnaire contained questions on demographics, travel, hygiene, self-reported illness history, indirect and direct contact with domestic and wild animals, and knowledge, attitudes, and behaviors related to animals and animal meats and bi-products. In addition to the core questionnaire, 10 focused occupational modules were also available and were were administered based on a participant's reported occupation or livelihood strategy in the past year. The questionnaire was administered in the 24 project countries implementing PREDICT's human surveillance scope. A separate questionnaire, developed to address the unique context of the countries affected by the 2014 West Africa Ebola epidemic under PREDICT's Ebola Host Project (a targeted effort to identify host species for ebolaviruses) was administered in Guinea, Liberia, and Sierra Leone. Over the course of the project, over 19,000 individuals were enrolled and completed questionnaires in these 27 countries (Table 1).

TABLE 1. Global summary of behavioral data collection

Country	# Surveys Administered+	# Interviews Conducted
Bangladesh	1,106	102
Cambodia	1,803	Interviews not conducted
Cameroon	651	292
China	718	172
Côte d'Ivoire	434	199
DR Congo	906	264
Egypt	1,097	Interviews not conducted
Ethiopia	313	Interviews not conducted
Ghana	641	Interviews not conducted
Guinea	294*	Interviews not conducted
India	65	Interviews not conducted
Indonesia	896	125
Jordan	1,085	Interviews not conducted
Kenya	327	Interviews not conducted
Lao PDR	234	22
Liberia	147*	Interviews not conducted
Malaysia	1,400	Interviews not conducted
Mongolia	0	Interviews not conducted
Myanmar	708	Interviews not conducted
Nepal	2,048	109
Rep. of Congo	23	108
Rwanda	400	Interviews not conducted
Senegal	824	Interviews not conducted
Sierra Leone	588*	179
Tanzania	1,172	402
Thailand	678	Interviews not conducted
Uganda	428	66
Vietnam	1,230	77
Total # of individuals enrolled	**19,187**	**2,117**

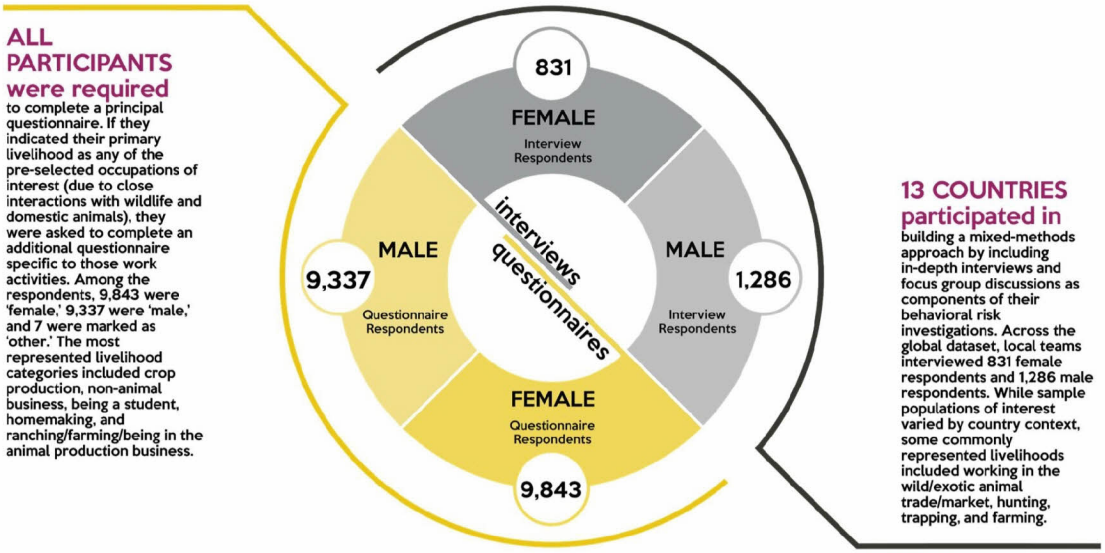
+ Surveys administered using PREDICT's standard questionnaire as part of the project's human surveillance and sampling scope.
** Surveys administered using a separate targeted questionnaire designed for countries affected by the 2014 West Africa Ebola epidemic.*

Figure 2. Where PREDICT investigated behavioral risk around the world



All countries implemented questionnaires for quantitative analysis, and many also conducted qualitative risk investigations.

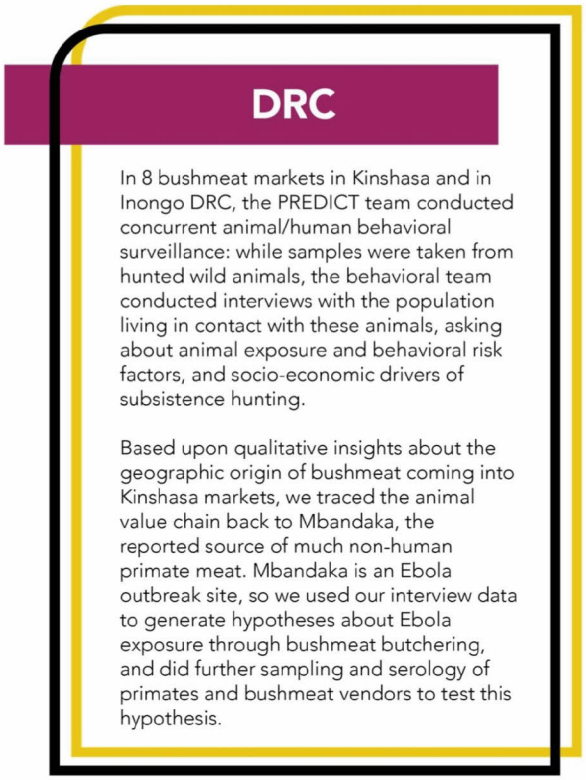
Figure 3. Implementation of questionnaires, ethnographic interviews, and focus groups



The summary above does not include questionnaire respondents from PREDICT's Ebola Host Project, conducted in Guinea, Liberia, and Sierra Leone.

As capacity, time, and funding allowed, each country team could also elect to incorporate PREDICT's qualitative research strategy into behavioral risk investigations. These qualitative methods were designed to compliment the standardized questionnaire, and 13 countries worked collaboratively to implement this mixed methods approach. Qualitative methods were implemented multiple times over the life of the project. First, to collect formative baseline data intended to inform the development and rollout of the standardized questionnaire; later to either continue exploratory work or follow up on preliminary baseline findings; and finally after evaluating preliminary data and insights, to refocus on the identification of intervention and risk reduction strategies. Each team targeted these efforts at locally relevant high-risk interfaces and contexts. In DR Congo and Cameroon, for example, investigations focused on wild animal 'bushmeat' markets and teams conducted ethnographic interviews to better understand the market dynamics and behavioral and exposure risks related to key taxa in the bushmeat value chain. In the 13 countries implementing this scope, more than 2,000 individuals were enrolled in ethnographic interviews and focus group discussions and all interviews were transcribed and translated (where necessary) for coding and analysis (Table 1).

Figure 4. DR Congo highlights: investigating risk in the bushmeat value chain



Insights from Implementing PREDICT's Behavioral Risk Strategy

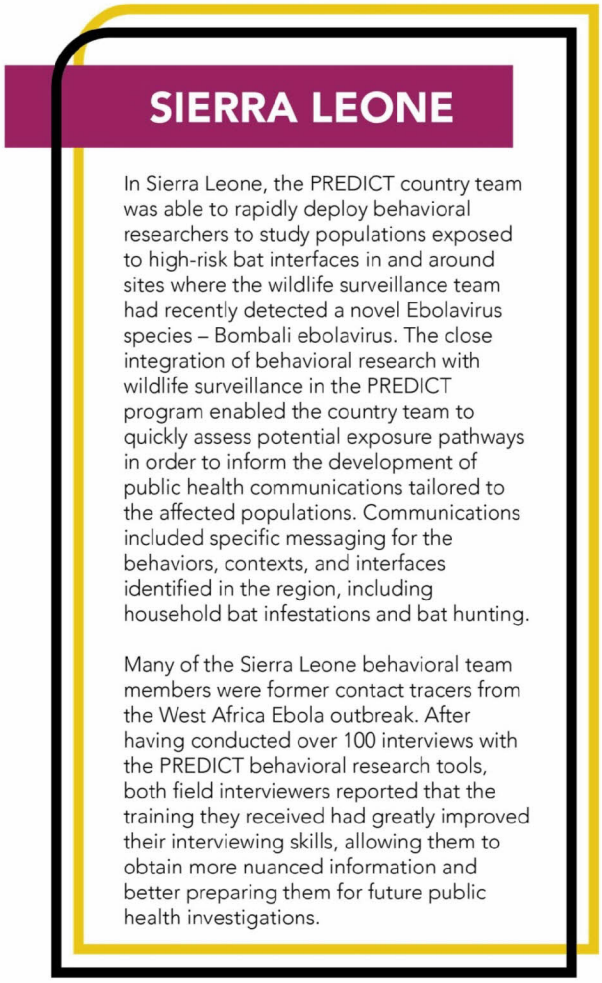
At this time, our collaborative teams are analyzing the vast quantity of data collected through this innovative One Health surveillance strategy, including the mixed methods behavioral risk data. Our scientists are working diligently to assess and characterize plausible exposure mechanisms and to identify potential strategies and recommendations for risk mitigation. As these analytics progress, we are excited to share some preliminary insights and lessons learned on our strategy and approach along with some highlights from a flagship intervention developed with input from across our One Health consortium and taken to scale in nearly all of PREDICT's partner countries.

In most countries, the teams charged with implementing the behavioral risk strategy were composed of both new and seasoned scientists from diverse professional backgrounds (Figure 1). Through standardized trainings aimed at strengthening skills and techniques needed in both the behavioral and biological scopes of PREDICT, we helped encourage a truly collaborative and multidisciplinary surveillance workforce that leveraged the experiences and skills of the broader team. Cross-training staff also enabled and facilitated the close integration and coordination of our behavioral risk strategy with One Health surveillance and sampling efforts and project scientists were able to investigate the attitudes, beliefs, behaviors, and broader social contexts of targeted at-risk populations.

This tight integration allowed our teams to conduct rapid assessments of community risks during early formative research, and eventually to develop truly multidisciplinary behavior change communication and risk reduction plans relevant to communities and stakeholders they engaged. Further, the inclusion of social scientists with animal surveillance teams strengthened zoonotic disease surveillance, as community knowledge and practices acquired through social science research helped inform the timing of wildlife sampling and identify additional locations for sampling and surveillance efforts. Our trained social science teams helped raise awareness about taboos or socio-cultural sensitivities that needed to be considered when developing and refining surveillance plans.

PREDICT's surveillance approach was designed to balance human health and conservation objectives with wildlife sampling targets. Animal species were live captured and released after sample collection. In communities where rodents are known to cause human illness, such as Lassa fever in the West Africa region, our teams needed to work closely with community members to explain the methods and context of this program, gain buy-in for sampling activities, and help identify effective strategies to minimize rodent contact and exposure. PREDICT sampling teams frequently refrained from engaging in animal sampling until sufficient time was spent with the community to gain their trust, often through dialogue on possible interventions and by providing and presenting specially tailored risk reduction recommendations.

Figure 5. Sierra Leone case study: assessing risks to inform public health communications



Lessons learned and recommendations for future One Health projects

Integrating the social sciences into PREDICT's One Health surveillance approach provided a range of secondary benefits beyond our primary goals. These included: building support, trust, and buy-in of populations hosting or involved in One Health initiatives; contributing sociological and anthropological insights on human activities to guide geographic targeting of surveillance initiatives; crafting "empathetic approaches" to behavioral interventions – either to mitigate outbreak risk or respond to outbreaks; and designing and implementing One Health interventions among at-risk populations.

Building trust and buy-in

In the spirit of community-based participatory research which integrates mutual education (between researchers and community experts) and social action in improving health, our PREDICT teams engaged national and subnational leadership and facilitated meetings with provincial/local authorities, allowing us to directly engage communities in project activities and the research process. In many cases, our country teams returned to communities every 3-6 months to sample and conduct interviews. Through these frequent interactions, teams gained trust with community members, an essential element which helped improve the richness and depth of interview data over time. In addition, towards the end of the project, between May and September 2019, our teams returned to these communities equipped with summaries and reports of available project findings along with risk reduction materials specially tailored to the unique human-animal-environment interfaces investigated by the surveillance teams. Returning the communities to share project findings is unfortunately extremely rare. We received reports from nearly all countries that community members were extremely grateful to hear about project findings along with our team's recommendations for improving health and conservation. Our teams strongly recommend that planning and budgeting for community engagement to share findings and recommendations at the end of a project is critical, ethical, and should be part of all project designs.

Social science insights on targeted surveillance

During formative research and the selection of surveillance sites, local subject matter experts or 'guides' provided entrée into what were often closed, tight-knit communities. Ethnographic interviews allowed for open-ended dialogue about target interfaces and the underlying dynamics and drivers of human activities that, from a public health/disease transmission perspective, could be considered 'risky', such as eating

bats, rodents, or non-human primates, or drinking raw blood. Some risk behaviors are considered taboo from one community to another, based on tribal, ethnic, or social beliefs, and these differences had to be explored, acknowledged, and respectfully addressed. One important approach was to enroll local interviewers, when possible, or local translators who spoke local dialects, who could clearly explain the purpose of the study and reasons for blood collection (a highly suspect procedure in many cultures), as well as the need to sample their animals (also a barrier for many, as animals, whether domestic or wild, are prized commodities and sampling was sometimes seen as damaging/tainting the meat or reducing its value). Early focus group discussions helped describe practices and beliefs about disease that warranted further exploration, and also catalyzed information exchange between our teams and local experts, which often informed sites for sampling. For example, discussions with bat hunters we learned about the location of bat roosts or caves for sampling, and in conversations with bushmeat vendors, we were directed to villages where they bought hunted meat and where we could move further upstream in the bushmeat value chain.

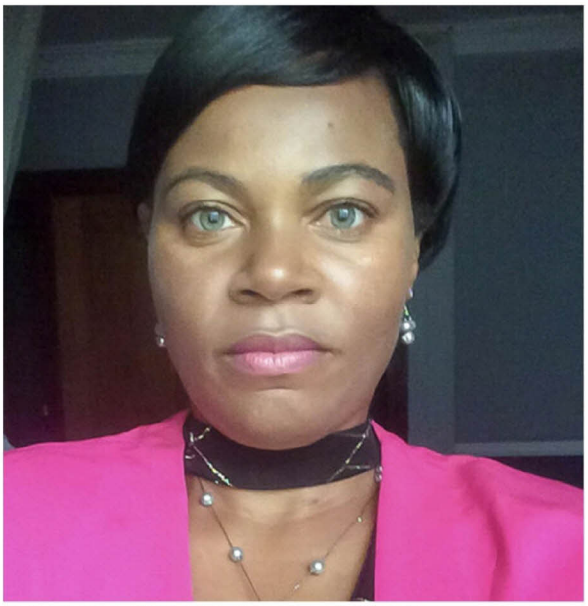
Figure 6. Profiles of PREDICT behavioral risk team members.

TINA KUSUMANINGRUM, PREDICT/Indonesia, Field Coordinator. *"There is no doubt that joining PREDICT is one of the best decisions in my researcher career. Learning how to design and implement a surveillance project, maintain networking and professional relationships with partners, and communicate the results back to the communities and decision makers—these were all exceptional experiences that will be very useful for my future career."*

MWOKOZI MWANZALILA, PREDICT/Tanzania, Behavioral Scientist & Community Engagement Liaison, Sokoine University of Agriculture. *"PREDICT Project has helped me to create more confidence when talking in front of people. In addition, I have gained new knowledge on zoonotic diseases."*

HILARION MOUKALA NDOLO, PREDICT/Republic of Congo, Behavioral Risk Survey Investigator. *"I was hired by PREDICT to perform ethnographic interviews, focus groups and questionnaires in the communities and bushmeat markets in Brazzaville. In these studies, we discovered there are those who don't understand the concept of*

protected animal species, nor that handling animal species presents multiple risks of contamination with zoonotic diseases agents. I want to find ways to better educate communities and raise awareness about wildlife conservation."



VICTORINE MAPTUE TOGEUM, PREDICT/Cameroon, Human Clinical & Behavioral Research Coordinator.

"The position I held in the PREDICT project has truly boosted my professional career. Indeed, the research carried out within the framework of this project enjoys great visibility and will be cited most often. This has helped increase my notoriety within the national and international scientific community. The Cameroonian government can turn the results of this research into concrete measures that build capacity in the health field."

Designing and implementing One Health interventions with at-risk populations

As PREDICT's laboratories detected and confirmed virus findings, including new discoveries of potentially dangerous pathogens, it became imperative to engage our host country government partners and community stakeholders to share these findings along with recommendations for continued surveillance and risk reduction. In Sierra Leone for example, PREDICT scientists discovered a new ebolavirus in bats, Bombali virus, which was the first time an ebolavirus had been detected in wildlife before causing human infection (Goldstein et al. 2018). The sampling sites for these bats were close to villages and human dwellings, as by design our surveillance sites were selected to explore risks between animal and human populations. A potentially deadly virus detected in an animal necessarily requires an empathetic and strategic human (public) health response. By using some of the contextual data about human exposure, collected through behavioral risk investigations, our team worked collaboratively with PREDICT Consortium ecology, bat biology, and virology experts to design and develop a rapid intervention strategy.

To identify the most culturally appropriate, feasible, and effective intervention resource format, our team developed a framework for assessing potential materials, channels of communications, respective audiences, and core messaging. A moderated picture book format, delivered by a trusted community leader, was selected as the best tool to put into the hands of our local team and in-country stakeholders.

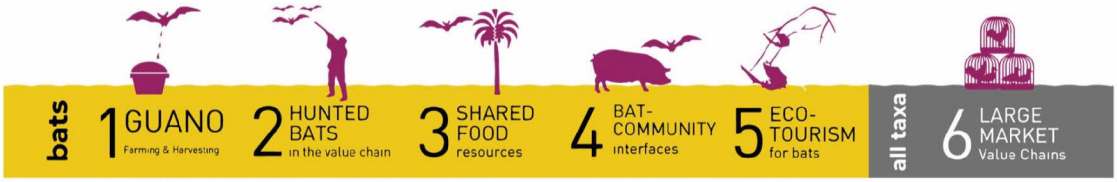
A communications plan was developed to ensure a well-coordinated effort and timely discussions with government and community stakeholders, following the release of the new Bombali virus finding. The resource, entitled *Living Safely with Bats (*PREDICT Consortium 2018*)*, leveraged the collective subject matter expertise of the consortium and featured illustrations from a team member trained in animal biology and visual arts ensuring accurate, consistent, and compelling visual representations. To refine and test the book format and key messages, focus groups held with project subject matter experts and feedback was solicited from project country teams. The book's content benefited from cultural vetting by 17 country teams (Bangladesh, Cambodia, Cameroon, Cote d'Ivoire, DR Congo, Ghana, Guinea, Indonesia, Lao PDR, Malaysia, Nepal, ROC, Senegal, Sierra Leone, Tanzania, Thailand, and Vietnam). Following vetting, the *Living Safely with Bats* resource was piloted in Sierra Leone and in Tanzania with feedback solicited to improve both the content and the process of delivery. A comprehensive review of the book was also conducted with the PREDICT team in Guinea.

Consortium experts, including our behavioral risk team embedded with our staff scientists in West Africa, helped train and support the implementation of the *Living Safely with Bats* resource during community outreach events in Sierra Leone, Guinea, and Liberia beginning in July and August 2018. Country teams utilized the resource in a variety of formats: official briefings with ministry partners, in-person presentations and community meetings, classroom sessions in local primary and secondary schools, and local radio broadcasts. In Guinea, radio broadcasts reached thousands of individuals across the entire Forest Region – the area where the 2014 West Africa Ebola epidemic originated, likely via a spillover event from a bat (Saez et al. 2015). This resource has been translated into 12 languages, including Amharic, Bahasa, Burmese, Dusun, English, French, Khmer, Kiswahili, Lao, Malay, Thai, and Vietnamese. The book was also adapted to share with the communities that PREDICT teams throughout Asia had engaged and worked with over time. Changes to content in this version included artistic modifications to incorporate locally salient fruits, foliage, and protective clothing items, in addition to content addressing Asia specific human-bat interfaces identified as particularly high-risk for virus spillover (date palm sap collection, bat guano farming and harvesting practices, and cave-related tourism).

Figure 7. Bat-related educational interventions

All versions of the Living Safely with Bats *resource provide talking points for moderators. These talking points cover themes such as bats as essential agents in the local ecosystem, basic ways to live safely with bats, disposal of dead bats, what to do when with them contact is unavoidable, and managing bats in and around the outside of the home.*

Figure 8. Bat-human interfaces investigated by PREDICT One Health surveillance teams.



Bat-related interfaces investigated by PREDICT's One Health surveillance team and explored in-depth through our human behavioral risk investigations included: guano farming and harvesting, hunted bats in the value chain, shared food resources with bats, bat-community interfaces, and ecotourism for bats. Large market value chains were a principal area of interest in relation to all wildlife taxa.

Sharing our findings for sustained One Health engagement

A major lesson learned towards the end of the project was managing expectations as project activities concluded. Due to our One Health surveillance design, PREDICT teams collected a vast quantity of data, an enormous and valuable archive of information that required a tremendous amount of data review for quality assurance prior to use. Taking inventory of this archive of hundreds of thousands of data points – generated from human and animal biological specimen data (including geolocation coordinates, other metadata, and virus level results) and data from behavioral questionnaires and qualitative interview transcripts – was a massive undertaking for consortium staff at both the global and country levels. Before it can be made available to the global community, this data needs to be prepared for analysis by our teams, a process requiring time, creativity, and technical skills in order to characterize the multiple dimensions of risk explored throughout the project.

PREDICT scientists around the world are currently cleaning and analyzing this data for development of manuscripts and summary reports, which is critical for sharing the fruit of this labor with the global health, conservation, and social science communities to advocate for continued investments in One Health programs that incorporate behavioral sciences. However, writing and publishing scientific manuscripts, which are valued especially by our rising scientists as part of our commitment to capacity strengthening, is a lengthy process due to the time needed for data curation, analytics, literature reviews, collaborative writing, consensus among authors, submission, and approval by journals. While continued engagement on publications was generally understood to extend beyond the end date of the project, this is not always practically feasible, especially for young scientists and the project's critical support staff: those individuals that often implemented the challenging field work, collected the samples and conducted the interviews, and worked on the bench to detect the actual viruses. Additionally, to help the careers of these rising national-level scientists, projects need to plan to sufficiently budget for publication costs and for participation in conferences and high profile international fora. Promotion and visibility through continued networking with the global and professional community, a secondary benefit that collaboration in a globally focused large-scale project such as PREDICT provided, helps gain important professional currency for rising scientists.

Conclusions

PREDICT was a watershed One Health endeavor for its systematic inclusion of human behavioral investigations in such a large, global zoonotic disease surveillance program. The project incorporated behavioral data into a transdisciplinary analytical framework, which integrated the behavioral data with viral, human biological, animal and environmental data. Through these ongoing analyses and subsequent publications, findings from our behavioral risk investigations will contribute to the evolving One Health evidence base and will provide a model of best practices and lessons learned for those looking to further

explore and understand the human drivers of zoonotic disease emergence and transmission. PREDICT successfully integrated behavioral risk investigations into country-level One Health surveillance efforts, enabling the collection of empirical and context-specific data on human activities related to disease emergence, amplification, and transmission, while also catalyzing an expanded scope of value-added activities: community outreach and trust building, sharing findings and results in an iterative feedback loop to help inform risk communications, and developing risk reduction and behavioral change communication strategies tailored to the unique contexts of affected communities.

To be successful, emerging infectious disease surveillance projects cannot focus on surveillance and detection of pathogens alone. Integrated mixed methods projects must include investigations of the specific human activities that are hypothesized to drive disease emergence, amplification, and transmission, in order to better substantiate behavioral disease drivers along with the social dimensions of infection and transmission dynamics. We encourage future programs to work with exposed communities in endemic areas on educational and capacity-building initiatives to improve community awareness of, and risk mitigation strategies for, those emerging and endemic pathogens. Involving at-risk communities in disease hotspot areas is critical, both for developing awareness of disease risk and encouraging community agency to define realistic strategies for disease mitigation for their particular community. PREDICT is a model for how to accomplish this, using mixed methods social science integration with animal and human surveillance while also focusing on effective community outcomes. During the last year of the project, as our country teams returned to participating villages and communities to share results, community members wanted and encouraged the team to share findings beyond just their local area, as they realized the value of the project's broader impact,and wanted to share this knowledge with other neighboring at-risk communities. They voiced appreciation of the value of One Health data and evidence, from the wildlife we captured and sampled and the viruses we detected, to the unique animal-human contexts identified as risks for infection Even though risk reduction or intervention strategies we identified might imply changes in behaviors that have been ongoing for generations, their interest and willingness to engage demonstrates the power of community buy-in for developing the foundation needed for adoption of prevention and sustained disease control efforts.

Perhaps the most positive outcome of PREDICT has been the integration of social science approaches, particularly training in participatory methods for engaging and developing long-term relationships with communities to work towards resiliency. Our global Consortium worked for over 10 years to strengthen the capacity for local scientists to safely, ethically, and humanely put One Health in action from identification of at-risk communities and sites for wildlife and human sampling activities, to collection and testing of those samples, and finally for sharing findings with our global, national, and local stakeholders. But bringing in the behavioral sciences allowed us to push toward fuller community integration and engagement. The One Health approach aims to break down barriers between silos in the scientific and health communities and importantly bridge divides between natural and social systems. PREDICT provides a model and framework for transforming theory into practice, for "socializing" One Health and taking it to scale.

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Appendix/Supplemental Materials

FOCUS GROUP GUIDE Version 2, May 1, 2015

The focus group discussion is initiated by naming all of the animals that can be found in the community. The goal of this exercise is to explore animal diversity.

The community mapping activity locates where the different kinds of animals can be found relative to the site of the focus group. It should be emphasized that this will not be an 'accurate' map. This exercise is designed to assess the distribution and overlap of animals. Prompts such as 'anywhere else?' should be used. The animal list will contain insects, reptiles and fish. Map only mammalian and avian species.

These two activities together should be limited to 10-15 minutes. The themes to be explored in the discussion are 1) contact and context, 2) illness in animals and humans, and 3) rules and restrictions. Events such as animal die-offs should be added to the map, if they are discussed.

1) Contact and context

- Which of these animals do you see the most often? The least? (Probe: where, why)
- What animals do you come into physical contact with? (Probe: where, why, how often)
- Which of these animals do you eat?
    - Where do you get them? How are they prepared? Which are for special occasions only?
- What are animals good for other than food? (probe: labor, medicinal, magic, pets, by-product uses)
- Which animals come into buildings or places where people are? Is water shared with animals?
- How are unwanted animals kept out? (probe: which animals, all methods used)
- Who takes care of the animals? (Probe: who, specific jobs, animal movements)

2) Illness in animals and humans

Animals

- What happens when animals get really sick? How are the animals cared for?
- Has this happened recently? Do people try to hide animal sickness?
- Is animal sickness reported to anyone? (probe for differences between wild and domestic animals)
- Have any animals been destroyed or killed by authorities? Describe.
- What happens to animals when they die? (probe: eaten, buried, left to rot, depends if wild or not)

Humans

- What is the most unusual or memorable sickness anyone has had? What happened?
- What are the causes of illness or sickness?
- Do you know anyone who has gotten sick from an animal? What happened?
- What do you know about animals that can give you infections or diseases?

3) Rules and restrictions

- Are there places in the community where you aren't allowed to go? Why not?
- Are there any rules about hunting or trapping animals? (Probe: cultural, legal)
- Are there any animals that you don't eat or that are avoided? Why?
- Are there official rules or laws about garbage disposal? Human waste? Animal waste?
- Is garbage a problem in this community? What's the problem?

Final question for all: If you could change one thing in your life, what would it be and how would you do it?

ETHNOGRAPHIC INTERVIEW GUIDE

Core Themes

1. Human movement
2. Socioeconomics
3. Biosecurity in human environments
4. Illness, medical care/treatment and death of humans
5. Human-animal contact

HUMAN MOVEMENT

GOAL: To understand living environment and 'home range' (e.g., how far people travel and why).

Home

Where do you live/what kind of dwelling? How many people are in the household? How many rooms? How many are children? Is everyone related? Sleeping arrangements?

How often do you move? Any seasonality of movements?—eg, for work, for food, for safety (e.g., against flood, drought, conflict)?

What are the things you do to protect your home (against predators, animals, outsiders, bad weather)?

Work

What kind of work or activities do you do? What do other household members do? Where do these activities happen?
How do you protect your activities and business interests? (e.g., grazing or crop land, business competition, hunting territory, animal stock)

Travel

How far do household members travel from home and why? (Follow up on animal related issues: shopping, selling/buying/trading, hunting, transport, etc)
How travel (by foot, bike, cart, truck, plane)? Is it ever for overnight? Where stay?
Why traveling? (work/migrant, family, religion, holidays, to sell/trade/buy animals)
Other family members in other areas of the country? Visit often?

Observed environment

Have there been any changes in the environment: new roads, more boats or ports, fields, buildings, population movement (in or out), land clearing or abandonment, new houses, other new buildings
Who is responsible for the changes? Are the changes good or bad?

SOCIOECONOMICS

GOAL: To understand a typical day and how money and social standing impact opportunity and risk.

Daily routine

Tell me about your daily routine (get description of work on a usual day, include purchasing and preparing food, timing of types of meals, responsibilities/duties related to animals, any changes by season)
How do people in the household contribute to earning money and getting food (and water)?
Where do the children play? Who takes care of the children when you are at work?

Animal responsibilities

Describe the animal related jobs and responsibilities for people at every age (i.e., young children, older children, young adults, adults, elderly).
What are the skills/knowledge needed before moving to the next stage of duties/responsibilities?
Are there differences in responsibilities between boys and girls, men and women, by ethnicity or class?

Education

How many children are currently in school? Until what age do your children go to school? (boys and girls?)
What is your level of education? Why did you stop?

Economics

Do you make more money than other people who do the same things as you? Why do you think that is?
Are there times of year when you make less money? What happens then?
Are there times when food is more expensive than others? Tell me about that (eg, different food availability, seasonal, festival related).
Do you think you and your household are better off than most people? Could you do things to make it better?

BIOSECURITY IN HUMAN ENVIRONMENTS

GOAL: To determine if any sanitation or hygiene factors could play a role in disease spillover

Water and food

Is there a central source of water? What is the source? (eg, pond, uncovered well, rainwater, taps, covered well)
Is there a water source you like better?
How far away is the water source? Do animals drink from the same source?
Do you do anything to your drinking water to clean it before you drink it?
How do you store your food? (e.g., open containers, covered, hanging, refrigerate)

Do you eat or drink things where you suspect animal contact? (e.g., teeth/scratch marks, feces or urine seen)
Do you regularly clean your food prep station/kitchen and tools? How?

Sanitation

Are there toilets, latrines or other designated areas for human waste? Are these cleaned and used regularly?
Are butchering and slaughtering areas separate? How often are they cleaned and how? Who does the cleaning?
Are there any official rules or laws about human waste and garbage disposal?
Are there any animal pest control laws? What do you do to control animal pests?

Hygiene

When are the best times to wash your hands? Do you use soap? How much does soap cost and where get it?
Do you wash your hands at home? at work?
How often and where do you and your household members bathe?

ILLNESS, MEDICAL CARE/TREATMENT, DEATH

GOAL: To identify any unusual disease experiences—signs, symptoms and sources

Household illness

Is anyone sick right now?
What do you do when someone in the household gets sick? Who takes care of that person?
The last time someone was seriously sick what happened (explore when, with what, how did they get sick, who told/consulted, anyone else get sick after, final outcome)?
Has anyone ever had an sickness that people don't usually get? What happened? Where did it come from?

Illness from animals

Do you know anyone who has gotten sick from an animal? What animal? What did they get? What happened?
Do you know any other diseases/illnesses people can get from animals? How does the animal give the illness to the person? How often does it happen?

Medical care/treatment

How sick would you have to feel to stay home and not do normal routine?
Where do you go when you are sick?
Do you prefer to use traditional medicine, western medicine or a combination?
How sick would you have to feel to go to doctor/clinic/hospital? What does that cost? (in time, lost wages/business, transport costs, etc) How far away?

Death

What is the tradition when someone dies? (Explore if reported to authorities, differ by age or gender, what happens to the body, does the community come together or is it private.)

HUMAN ANIMAL CONTACT

GOAL: To gain knowledge about interactions with animals, animal health and animal perceptions and knowledge.

Encourage but don't lead discussion about which animals. Allow respondent to name the animals. If no birds or bats are mentioned, follow up by asking specific questions about birds and bats.

Indirect contact

What kind of meat do people in your household eat? How do you get it/where does it come from? What is furthest away an animal comes from?
Is meat dead or alive when you get it? If dead(/prepared), how to tell if good/fresh?

If alive, how long are live animals kept before being sold or eaten? How do you get live animals home?
How is meat prepared (raw/undercooked)? Is meat prepared in the same place as other activities? (e.g., preparing vegetables, cleaning babies/changing diapers, where other food or drinking water is stored)
Do animals come in or near the dwelling? How do you know animals are there? Which animals?

Direct contact

Do you or someone in your household handle live animals? In what context? (e.g. ranching/animal husbandry, hunting, wet markets, work, around dwelling/other building, pets)
What are the animals that you keep/raise or sell? How many different kinds of animals? How many of each?
For how long do you have the animals?
Where do live animals come from? Where is the furthest away an animal comes from?
Who buys/trades for your live animals? Where do the animals go?
Have you been bitten, scratched or had bleeding after handling an animal? By a wild animal?
Where are live animals slaughtered? butchered? Do people buy or sell parts?
Do you travel with animals? Explore details of the process, specific routes and encounters (eg, with other animals, with animal transport supporting industries, such as holding areas, restaurants, hotels) along the way.
Explore for differences over time in animal handling, eg, seasonality, legal, religious, animal reproduction

Animal products/rituals

Other uses of animals—e.g., as pets, medicine, magic, fertilizer, for trading
Rules for children around wild animals as pets, playing with wild animals or dead animals

Animal health

How do you care for your animals: how are they fed, what do they eat, where do they eat/graze and sleep? Are they segregated or all together? Differences by season? day/night? Does anyone live or stay with the animals?
Is there a central area for animal waste? How often are animal cages, stalls, or penned areas cleaned? Who cleans them?
Do the animals get veterinary care? Vaccinations?
How do you know when an animal is sick? What's the first thing you do about a sick animal?
Have you seen an animal outbreak or die-off? What happened?

Perceptions and knowledge

What are the most unusual animals anyone can buy?—seasonal? Expensive? Who buys?
Are there any animals you avoid eating? Why? Ever heard of anyone eating/selling dead or infected animals?
Do people ever eat non-domesticated animals/wildlife? Where do they get them?
Who usually buys wildlife products? Have there been changes over time?
What do you do when you find a dead animal?
What laws about animals do you know? (eg, limiting/outlawing hunting, reporting and culling of sick animals)

Sent: Thu, 26 Dec 2019 10:54:53 -0800
Subject: Re: Predict Behavioral Draft for your review
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: David J Wolking <djwolking@ucdavis.edu>
Cc: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, "Olson, Sarah" [redacted], Karen Saylors [redacted] Emily Hagan <hagan@ecohealthalliance.org>
P2BR Process_Methods & Lessons Learned JM.docx

Hi,
My suggested edits are attached. Not sure who is vacationing & who is working. If working, Karen, I want to let you know that I think your (& David's) prose is eloquent and works very nicely. I had almost no comments on the first half of the paper. The second half, where we start adding in figures, is still very well-written but starts to get a little more sales-pitchy, reminiscent of content for a report or brochure, rather than written for a journal audience. So I have made more comments on that section for your consideration and a bit more substantive revision.
Text me if you want to clarify any of it.
Great work & I really appreciate the effort to get this great product out in the literature. I think USAID will love it, too.
Please make sure to get the acknowledgement stuff in there.
Under separate copy, I'll send the response to reviewers & galleys from Diego's paper in this journal for ease of reference.
Happy Holidays everyone,
Jonna

On Tue, Dec 24, 2019 at 8:00 AM David J Wolking <djwolking@ucdavis.edu> wrote:

> Thanks Karen!
> For those new to the conversation (mainly Chris and Peter), this is the article (an approach/perspectives piece) invited by the One Health Outlooks journal that Jonna and [redacted] are editing. The Dec. 30th deadline gets this into the review without journal fees, so we did our best to push this forward over the last 3 weeks and make the deadline. Huge thanks to Karen, Jason, Stephanie, and Emily for getting it there. We realize it's terrible timing for co-author review given the holidays...
>
> That said, it makes great Xmas reading ;-)
>
> David

On Tue, Dec 24, 2019 at 7:35 AM Karen Saylors [redacted] wrote:

> Hi everyone.
> Please find attached our team's manuscript for your review. As we are aiming for the Monday deadline of the One Health Outlook, we'd appreciate your comments and edits by Friday.
>
> Thanks so much and happy holidays!
>
> Best,
> Karen, David and Emily

Title:

- **Socializing One Health: An Innovative Strategy to Investigate Social and Behavioral Risks of Emerging Viral Threats**

Other title options…open to your votes! ☺

- A Mixed-Methods Approach to Behavioral Risk Investigations under a One Health Framework
- Perceptions of Behavioral Risk: Lessons Learned from a Global One Health Project

Authors:
Saylors, Karen; Wolking, David; Hagan, Emily; Martinez, Stephanie; Euren, Jason; Francisco, Leilani; Olson, Sarah; Miller, Maureen; Johnson, Christine Kreuder; Daszak, Peter;
PREDICT Consortium; and Mazet, Jonna

Target journal: Special One Health Outlook edition

Deadline: December 30, 2019

Introduction

Globalization has radically catalyzed the everyday movements of people, animals, technology, goods, capital, and services worldwide. While this transformation has been broadly regarded as an economic boon, it has also increased the opportunities for diseases to spread geographically and potentially between species (Saker et al. 2004; Wolfe et al. 2005). Anthropogenic land use change, such as the building of roads or cities where once there were forests, creates a chain reaction of ecological, socio-economic, human behavioral, and regional fauna impacts that are believed to be linked to how infectious diseases emerge. Globally, urbanization has led to drastic growth in the density of human populations living in cities, increasing the potential for large infectious disease outbreaks (Neiderud 2015, Hassell et al. 2017). Per capita meat consumption has rapidly expanded over the last half century, driving the development of high-density livestock operations that provide opportunities for large-scale animal disease outbreaks (Ritchie & Roser 2017). Constant demand for cropland and grazing land, as well as aggressive resource extraction, has resulted in drastic environmental transformations, including habitat destruction, forest encroachment, and interspecies mixing (Ancrenaz, Dabek, and O'Neil, 2007). Zoonotic diseases – those with an animal host or reservoir – are responsible for some of the most impactful and devastating outbreaks in recent years. Seventy-five percent of emerging infectious diseases (EIDs) are zoonotic in origin, including Ebola, Influenza A strains H5N1 and H9N2, Hantaviruses, and human sleeping sickness (Morse et al. 2012; Taylor, Latham & Woolhouse, 2001). Trends in the transmission of pathogens across species, coupled with the knowledge that human, animal, and environmental health are inextricably linked, have been a driving force for the use of a One Health approach in recent emerging infectious disease research and surveillance efforts, which has proven valuable (Bidaisee & MacPherson, 2014).

The concept of One Health is a revitalization and expansion of the concept of One Medicine, developed in the 1970s by Calvin Schwabe to recognize the inextricable interconnection of humans and animals in the domains of nutrition, livelihood, and health (Zinsstag et al. 2011). In the 2000s, the concept of One Health was adopted to further broaden the concept of One Medicine to include ecosystem health – including the influence of climate, plants, and wildlife on global health (Zinsstag et al. 2011). International organizations, including FAO, OIE, WHO, and The World Bank, soon codified a One Health strategy to guide research and capacity development efforts towards the prevention, detection, and response of infectious diseases (FAO et al. 2008). The One Health approach, encompassing "the integrative effort of multiple disciplines working locally, nationally, and globally to attain optimal health for people, animals, and the environment," (AVMA 2019) is increasingly recognized as a critical paradigm in addressing key global health challenges.

While the inclusion of the environment in One Health thinking has greatly increased our ability to tackle today's complex health problems (driven by climate, mobility, and land-use changes), a growing number of scholars argue that much of the resulting One Health work has perpetuated a false dichotomy between "natural" and "social" systems and prioritized the study of "natural" ecological systems over "social" systems (Rock et al. 2009; Zinsstag et al. 2011; Woldehanna & Zimicki 2015). These scholars point out that domesticated animals, plants, and wildlife, are as much a "part of the environment of humans" as they are a "part of the social systems of humans" (Zinsstag et al. 2011). It is not enough to track ever-shifting geographic territories of plant and animal species, they argue, we need to understand how these species' geographic territories, behaviors, and biologies are co-constituted by human social systems. Without a nuanced understanding of specific human activities, "how, where and when people interact with animals," they argue, it is impossible to understand the actual risk for zoonotic spillover events (Woldehanna & Zimicki 2015). To adequately understand human activity as an integrated part of both the physical and social environment, One Health teams should strive to include professionals from disciplines such as anthropology, economics, political science, psychology, and sociology (Rock et al. 2009).

The imperative to understand human activity in the context of zoonotic disease outbreaks was perhaps best exemplified during the 2014 West Africa Ebola epidemic, where dysfunctional health systems, denial of Ebola, and burial practices involving contact with the deceased exacerbated containment of the outbreak (Lo et al. 2017). Following recent EVD outbreaks in DRC, West Africa, and Uganda, the behavioral sciences – medical anthropology in particular – have been highlighted as having a critical contribution to understanding the social dynamics of zoonotic disease emergence and spread, as well as developing effective response interventions for disease control (Hewlett and Hewlett 2007; de Vries et al. 2016). In particular, the WHO's Ebola Strategy guidelines clearly articulate several critical contributions medical anthropology (and the behavioral sciences by extension) can have towards outbreak management (WHO 2014). First, such research contributes towards "better knowledge of disease transmission chains," identifying behavioral mechanisms that may be perpetuating spread, such as forms of wildlife contact, exposure to infected medical items, or burial practices. Second, the behavioral sciences can identify "psychologically, socially, and culturally diverse behaviors of local populations" and propose appropriate interventions. By understanding the culturally-specific context and meaning of behaviors driving disease transmission, response efforts can react faster and design more culturally appropriate interventions that are acceptable to populations. In addition, contributions from social scientists can help to identify rumors, fears, and misinformation that may be amplifying risks for transmission. Finally, these contributions can help guide the development of "empathetic approaches" to outbreak response and disease control, striving to engage the participation of affected communities to develop sustainable interventions that benefit the largest number of people, as opposed to "coercive approaches" that are largely indifferent to the needs and opinions of specific individuals and communities.

A major global health security lesson learned from the West Africa Ebola epidemic was that "more work is needed at national and global levels to ensure that populations are empowered to protect themselves from diseases, and to ensure that the mass media have the knowledge and understanding to contribute to health protection and understanding of risks and their management" (Koser, 2015). One way to strengthen a population's ability to protect themselves is to better understand how certain behaviors put people at risk, and what changes we can make to mitigate that risk. For example, during the 2009 influenza H1N1 pandemic, work pattern adjustment, self-isolation of symptomatic individuals and advice to their caregivers, and cancellation of mass gatherings helped to mitigate the pandemic; these were all self-protective behavioral adjustments that were made based on shared public health information on risk behavior and disease spread (WHO, 2010). By improving our collective understanding of the dynamics of infectious disease transmission and how certain behaviors put individuals and populations at risk, we can

elucidate evidence-based ways to control disease transmission that can empower individuals to adopt preventive and protective behaviors. Additionally, being able to communicate to public health decision-makers how human interactions facilitate the emergence of wildlife pathogens in human populations and advocating for behavioral change communication, education, and prevention efforts can improve compliance with and the effectiveness of medical interventions and public health efforts (Berger et al. 2019).

Since the 2014 West Africa Ebola epidemic, rigorous behavioral science and qualitative methods have been built into outbreak response: multiple social science implementers have been actively engaged in the 2018-2020 Ebola outbreak in eastern Democratic Republic of the Congo (DRC), including Anthrologica, an applied anthropology research group which conducts formative and operational research in emergency settings; the GOARN-R Social Science Group; Réseau Anthropologie des Epidémies Emergentes/Projet SoNAR-GLOBAL; and Social Science in Humanitarian Action, which produces rapid briefs on key socio-cultural considerations (Bedford 2019). The use of these social scientific tools and participatory approaches helps ensure that intelligence and analytics guiding response efforts remains grounded, while providing valuable insights at the community, institutional, and policy-levels, enabling timely and strategic recommendations. The difficulty containing the ongoing 2018-2020 Ebola outbreak in DRC, now the second largest Ebola outbreak in history, is in part due to the vulnerability of the affected area, a long history of armed regional conflict, and subsequent community resistance, skepticism, and lack of trust in government and international actors, including the outbreak response teams and Ebola treatment centers (Vinck et al. 2019). Within this context, applied social science research adds critical value to response teams, improving their understanding of the social dimensions of risk and helping identify solutions for more effectively engaging communities in outbreak response and control efforts (Abramowitz et al. 2015).

Using Social Sciences to Understand Spillover Risk Before Emergence

While especially critical in outbreak scenarios, the contributions of the behavioral sciences are equally important prior to disease emergence, as they can improve our understanding of the risks associated with pathogen spillover and spread and inform strategies and interventions for risk reduction and mitigation. Quantitative modeling approaches have been used to extrapolate data to help understand pathogen-host dynamics and estimate outbreak frequency and severity, as seen in recent disease hotspot mapping (Allen et al. 2017) and current research exploring high-risk human-animal interfaces (Kreuder-Johnson et al. 2015). Qualitative human behavioral research can add further depth to our understanding of behavioral drivers of zoonotic disease spillover, amplification, and spread (Woldehanna & Zimicki 2015). Human behaviors are complex, dynamic, and highly contextual and are influenced by a myriad of socio-cultural factors that elude traditional disease modeling methods (Leach et al. 2013; Arthur et al. 2017). A multidisciplinary approach to exploring the social dimensions and human behaviors associated with disease transmission is fundamental to more holistically understanding the conditions and circumstances of humans, animals, and environments through which zoonotic diseases emerge and spread.

In an effort to strengthen global capacity to prevent, detect, and control infectious diseases in animals and people, the United States Agency for International Development's (USAID) Emerging Pandemic Threats (EPT) program funded several projects to develop regional, national, and local One Health capacities for early disease detection, rapid response, disease control, and risk reduction (Morse et al. 2012). From the outset, the EPT approach was inclusive of social science research methods designed to understand the contexts and behaviors of communities living and working at human-animal-environment interfaces considered high-risk for virus emergence, in order to shed light on the social dimensions of zoonotic disease transmission and identify potential intervention strategies for prevention and risk reduction. From 2009-2014, EPT's PREVENT project focused on formative research intended to identify risky behaviors,

attitudes, and practices, and to increase the prevalence of protective habits and preferences. Led by the Academy for Educational Development (later FHI360), PREVENT conducted behavioral research in the Congo Basin and Southeast Asia and worked to identify and characterize vulnerable populations, and the high-risk behaviors and practices for disease transmission from animals to humans. In addition, PREVENT worked to develop a strategic framework for risk reduction and suggestions for policy and structural changes for risk mitigation and disease prevention. At the same time, the USAID EPT PREDICT project developed a global consortium to strengthen capacity for surveillance and early detection of virus threats from wildlife and to identify high-risk areas and human-animal interfaces for virus spillover, amplification, and spread for targeted surveillance, monitoring, prevention, and control efforts. Working with partners in over 20 countries, PREDICT teams collected samples for virus testing from more than 56,000 animals and detected thousands of unique viruses in what is considered the largest virus detection and discovery effort to date (PREDICT Consortium, 2015).

Building on this foundation, USAID's EPT program funded another 5-year investment to strengthen health system capabilities in low and middle income countries for improved zoonotic disease prevention, detection, and response. In 2014, a second phase of the PREDICT project was launched in Africa, South and Southeast Asia, and East Asia as a multi-disciplinary effort with a revised One Health surveillance strategy reliant on the concurrent sampling of animals and people in identified at-risk interfaces for virus emergence. This new scope included an expanded emphasis on understanding behavioral risks along with data collection, synthesis, and aggregation on biological and ecological risks at these interfaces. From the inception, PREDICT incorporated social science methods into the design of One Health surveillance plans and the data collection and capture tools used in the field by the project's multi-disciplinary teams. Using a mixed qualitative and quantitative methods approach, PREDICT teams conducted investigations and collected data that more comprehensively addressed the multiple dimensions of virus spillover risk and better enabled the development of informed risk reduction and intervention strategies. PREDICT's behavioral risk strategy was implemented in 27 countries from 2014-2019. Our strategy was adapted to the host country contexts and specific human-animal- environment interfaces, yet was standardized globally to enable cross-country, regional, and ultimately global comparisons.

Building Behavioral Sciences into One Health Surveillance

By design, the PREDICT Consortium integrated global expertise from the conservation, veterinary medicine, public health, and social science communities to develop truly collaborative and multidisciplinary approaches for the early detection of virus threats and the development of disease control and prevention recommendations. Data collection tools were collaboratively designed to address ecological risks for emergence (using a standardized observational tool) and behavioral risks (using a standardized questionnaire with option for additional in-depth ethnographic interviews and focus group discussions). Standard operating procedures and training materials were developed and shared to assure standardization of the strategy through the life of the project. The strategy and tools, once approved by US and host country Institutional Review Boards and ethics committees, were put into action with partners across all project countries.

At the country level, personnel were identified by partners to lead the behavioral risk scope and teamed up with Consortium partners for training and mentorship. Because of differences in personnel background, the training and mentorship plan was structured to introduce the basics of social science methodology for rapid onboarding while also diving deep into the PREDICT strategy and behavioral risk tool kit using a combination of lecture, discussion, and hands-on experiential learning. Training covered techniques for successful community engagement and outreach; how to conduct interviews using the questionnaire; ethnographic methods and techniques for leading effective qualitative interviews and focus

group discussions; data management, coding, and analysis; and strategies for sharing project findings and communicating risk reduction strategies.

During implementation, trained behavioral risk personnel joined teams comprised of local professionals from diverse disciplines and worked together in the field to engage at-risk communities and conduct behavioral investigations, while animal and public health professionals led One Health surveillance and sampling efforts. Though team composition varied, members often included field veterinarians and ecologists/wildlife biologists for animal sampling; medical doctors, nurses, phlebotomists, or other public health paraprofessionals for human sample collection; and anthropologists, sociologists, community health workers, or other public health professionals for behavioral interviews. Field work and data collection were tightly coordinated across space and time, with community engagement, behavioral risk investigations, animal sampling, and human sampling often occurring simultaneously in targeted communities.

Figure 1. Global behavioral risk team composite

Bringing together a transdisciplinary team of scientists and practitioners was central to the human behavioral risk surveillance arm of PREDICT. Featured on the right are examples of disciplines represented by local team members who took part in the behavioral risk investigations, with female team members in italics.

Assessing Behavioral Risk and Operationalizing One Health Surveillance

From an epidemiological perspective, behavioral risk assessments often seek to quantify the influence of known risk factors on disease emergence and transmission dynamics. PREDICT's focus also aimed to identify and assess a range of known and unknown socio-cultural behaviors that could be influential in zoonotic disease emergence, amplification, and transmission. This broad approach to behavioral characterization enabled us to identify and characterize a milieu of human activities that could be later studied to investigate the transmission dynamics of new and emerging viruses. For diseases for which etiologies are known and characterized, such as zoonotic Influenza infection, this approach allowed us to

determine behaviors that might be risk factors for certain groups (e.g., agricultural workers) and to better understand the socio-cultural contexts necessary to develop effective risk mitigation strategies. For example, previously identified potential Influenza risks among agricultural workers include smoking in or around swine or poultry facilities and a lack of available personal protective equipment; mitigation strategies included heightened biosafety and biosecurity procedures, assuring use of personal protective equipment, frequent hand washing, and occupational health programs integrating monitoring and surveillance of high-risk groups with countermeasures such as influenza vaccines (Ramirez et al. 2006).

In implementation, our teams built partnerships and relationships at the national, subnational, and community levels. Before the roll-out of activities, our staff worked with a range of municipal and traditional stakeholders, including officials, leaders, and elders in the target communities, to help our One Health teams effectively engage with communities and to facilitate permissions and access for animal and human sampling efforts. Our teams also conducted site scoping visits, and in some cases formative behavioral risk research in collaboration with ministry partners, which helped determine One Health surveillance priorities and at-risk site selection. Through this multi-level stakeholder engagement process, our staff were able to build the relationships and teams necessary for gaining community buy-in, trust, and support for our unconventional surveillance strategy.

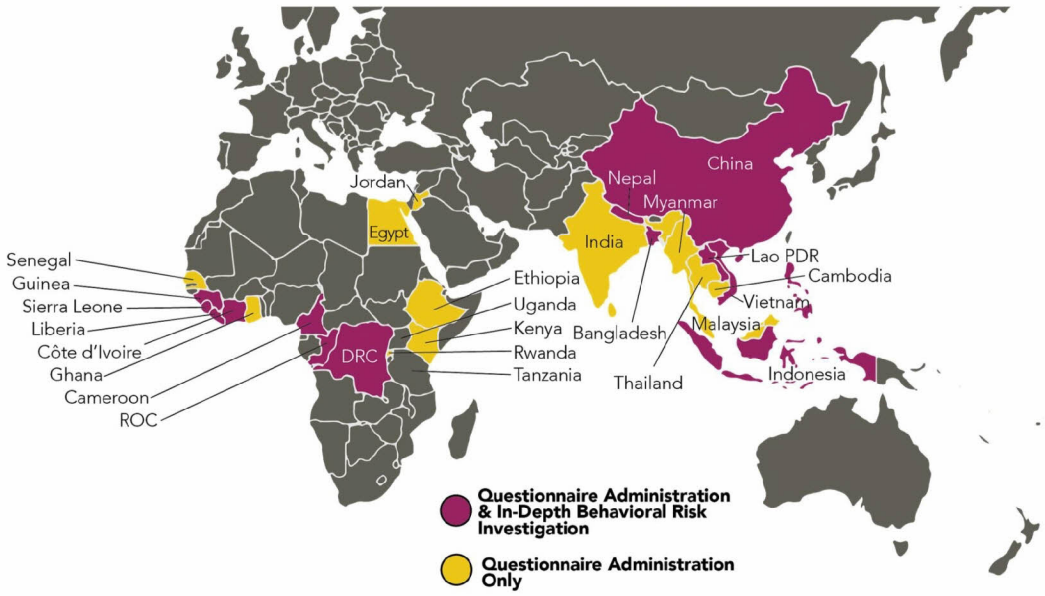
In each country, standard with serosurveillance studies (Miller and Hagan, 2017), a structured quantitative questionnaire was administered whenever a human sample was collected. This 57-question questionnaire contained questions on demographics, travel, hygiene, self-reported illness history, indirect and direct contact with domestic and wild animals, and knowledge, attitudes, and behaviors related to animals and animal meats and bi-products. In addition to the core questionnaire, 10 focused occupational modules were also available and were administered based on a participant's reported occupation or livelihood strategy in the past year. The questionnaire was administered in the 24 project countries implementing PREDICT's human surveillance scope. A separate questionnaire, developed to address the unique context of the countries affected by the 2014 West Africa Ebola epidemic under PREDICT's Ebola Host Project (a targeted effort to identify host species for ebolaviruses) was administered in Guinea, Liberia, and Sierra Leone. Over the course of the project, over 19,000 individuals were enrolled and completed questionnaires in these 27 countries (Table 1).

TABLE 1. Global summary of behavioral data collection

Country	# Surveys Administered+	# Interviews Conducted
Bangladesh	1,106	102
Cambodia	1,803	Interviews not conducted
Cameroon	651	292
China	718	172
Côte d'Ivoire	434	199
DR Congo	906	264
Egypt	1,097	Interviews not conducted
Ethiopia	313	Interviews not conducted
Ghana	641	Interviews not conducted
Guinea	294*	Interviews not conducted
India	65	Interviews not conducted
Indonesia	896	125
Jordan	1,085	Interviews not conducted
Kenya	327	Interviews not conducted
Lao PDR	234	22
Liberia	147*	Interviews not conducted
Malaysia	1,400	Interviews not conducted
Mongolia	0	Interviews not conducted
Myanmar	708	Interviews not conducted
Nepal	2,048	109
Rep. of Congo	23	108
Rwanda	400	Interviews not conducted
Senegal	824	Interviews not conducted
Sierra Leone	588*	179
Tanzania	1,172	402
Thailand	678	Interviews not conducted
Uganda	428	66
Vietnam	1,230	77
Total # of individuals enrolled	**19,187**	**2,117**

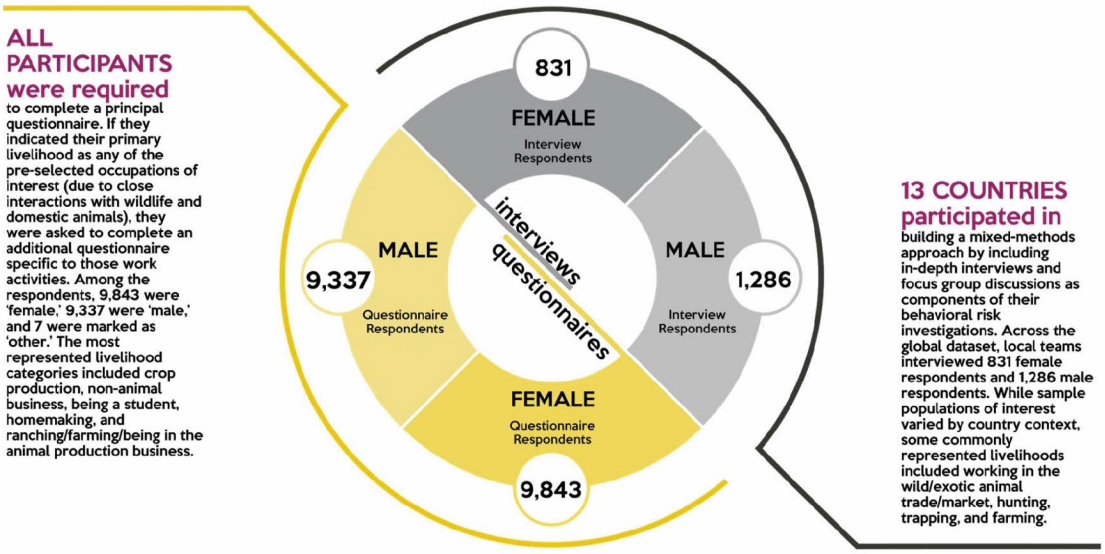
+ Surveys administered using PREDICT's standard questionnaire as part of the project's human surveillance and sampling scope.
** Surveys administered using a separate targeted questionnaire designed for countries affected by the 2014 West Africa Ebola epidemic.*

Figure 1. PREDICT behavioral risk investigations



All countries implemented questionnaires for quantitative analysis, and many also conducted qualitative risk investigations.

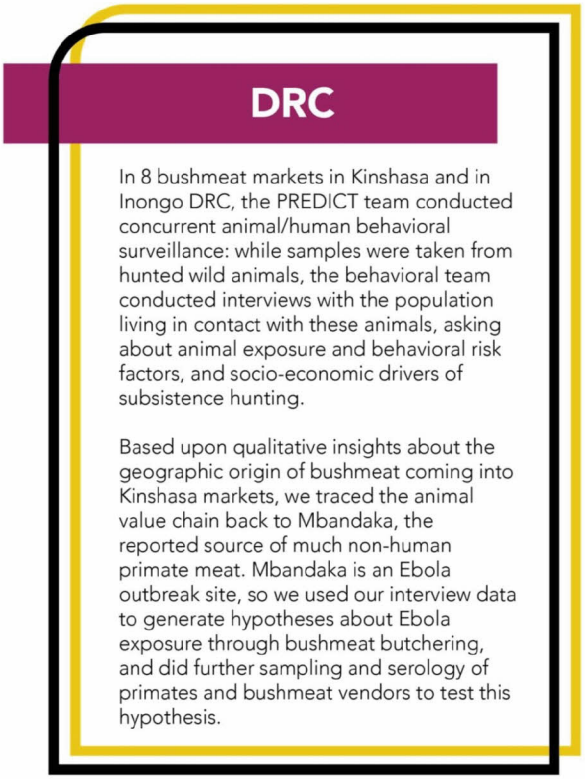
Figure 2. Implementation of questionnaires, ethnographic interviews, and focus groups



The summary above does not include questionnaire respondents from PREDICT's Ebola Host Project, conducted in Guinea, Liberia, and Sierra Leone.

As capacity, time, and funding allowed, each country team could also elect to incorporate PREDICT's qualitative research strategy into behavioral risk investigations. Qualitative methods were designed to compliment the standardized questionnaire, and 13 countries worked collaboratively to implement this mixed methods approach. These methods were first used to collect formative baseline data intended to inform the development and rollout of the standardized questionnaire; later they were employed to either continue exploratory work or follow up on preliminary baseline findings and finally, after evaluating preliminary data and insights, to refocus on the identification of intervention and risk reduction strategies. Each team targeted these efforts at locally relevant high-risk interfaces and contexts. In DR Congo and Cameroon, for example, investigations focused on wild animal 'bushmeat' markets and teams conducted ethnographic interviews to better understand the market dynamics and behavioral and exposure risks related to key taxa in the bushmeat value chain. In the 13 countries implementing this scope, more than 2,000 individuals were enrolled in ethnographic interviews and focus group discussions and all interviews were transcribed and translated (where necessary) for coding and analysis (Table 1).

Figure 4. Illustrative DR Congo highlights: investigating risk in the bushmeat value chain



Insights from Implementing PREDICT's Behavioral Risk Strategy

At this time, our collaborative teams are analyzing the vast quantity of data collected through this innovative One Health surveillance strategy, including the mixed methods behavioral risk data. Our scientists are working diligently to assess and characterize plausible exposure mechanisms and to identify potential strategies and recommendations for risk mitigation. As these analytics progress, we are excited to share some preliminary insights and lessons learned on our strategy and approach along with some highlights from a flagship intervention developed with input from across our One Health consortium and taken to scale in nearly all of PREDICT's partner countries.

In most countries, the teams charged with implementing the behavioral risk strategy were composed of both new and seasoned scientists from diverse professional backgrounds. Through standardized trainings aimed at strengthening skills and techniques needed in both the behavioral and biological scopes of PREDICT, we helped encourage a truly collaborative and multidisciplinary surveillance workforce that leveraged the experiences and skills of the broader team. Cross-training staff also enabled and facilitated the close integration and coordination of our behavioral risk strategy with One Health surveillance and sampling efforts and project scientists were able to investigate the attitudes, beliefs, behaviors, and broader social contexts of targeted at-risk populations. This tight integration allowed our teams to conduct rapid assessments of community risks during early formative research, and

eventually to develop truly multidisciplinary behavior change communication and risk reduction plans relevant to communities and stakeholders they engaged. Further, the inclusion of social scientists with animal surveillance teams strengthened zoonotic disease surveillance, as community knowledge and practices acquired through social science research helped inform the timing of wildlife sampling and identify additional locations for sampling and surveillance efforts. Our trained social science teams helped raise awareness about taboos or socio-cultural sensitivities that needed to be considered when developing and refining surveillance plans.

PREDICT's surveillance approach was designed to balance human health and conservation objectives with wildlife sampling targets. Animal species were live captured and released after sample collection. In communities where rodents are known to cause human illness, such as Lassa fever in the West Africa region, our teams needed to work closely with community members to explain the methods and context of this program, gain buy-in for sampling activities, and help identify effective strategies to minimize rodent contact and exposure. PREDICT sampling teams frequently refrained from engaging in animal sampling until sufficient time was spent with the community to gain their trust, often through dialogue on possible interventions and by providing and presenting specially tailored risk reduction recommendations.

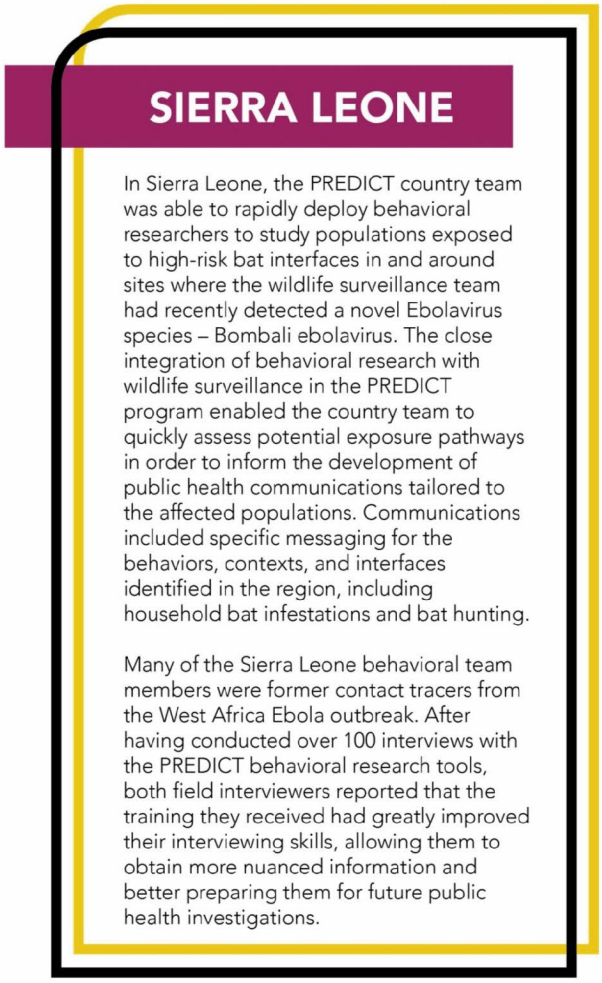
Lessons learned and recommendations for future One Health projects

Integrating the social sciences into PREDICT's One Health surveillance approach provided a range of secondary benefits beyond our primary goals. These included: building support, trust, and buy-in of populations hosting or involved in One Health initiatives; contributing sociological and anthropological insights on human activities to guide geographic targeting of surveillance initiatives; crafting "empathetic approaches" to behavioral interventions – either to mitigate outbreak risk or respond to outbreaks; and designing and implementing One Health interventions among at-risk populations.

Building trust and buy-in

In the spirit of community-based participatory research which integrates mutual education (between researchers and community experts) and social action in improving health, our PREDICT teams engaged national and subnational leadership and facilitated meetings with provincial/local authorities, allowing us to directly engage communities in project activities and the research process. In many cases, our country teams returned to communities every 3-6 months to sample and conduct interviews. Through these frequent interactions, teams gained trust with community members, an essential element which helped improve the richness and depth of interview data over time. In addition, towards the end of the project, between May and September 2019, our teams returned to these communities equipped with summaries and reports of available project findings along with risk reduction materials specially tailored to the unique human-animal-environment interfaces investigated by the surveillance teams. Returning the communities to share project findings is unfortunately extremely rare. We received reports from nearly all countries that community members were extremely grateful to hear about project findings along with our team's recommendations for improving health and conservation. Our teams strongly recommend that planning and budgeting for community engagement to share findings and recommendations at the end of a project is critical, ethical, and should be part of all project designs.

Figure 5. Sierra Leone case study: assessing risks to inform public health communications



Social science insights on targeted surveillance

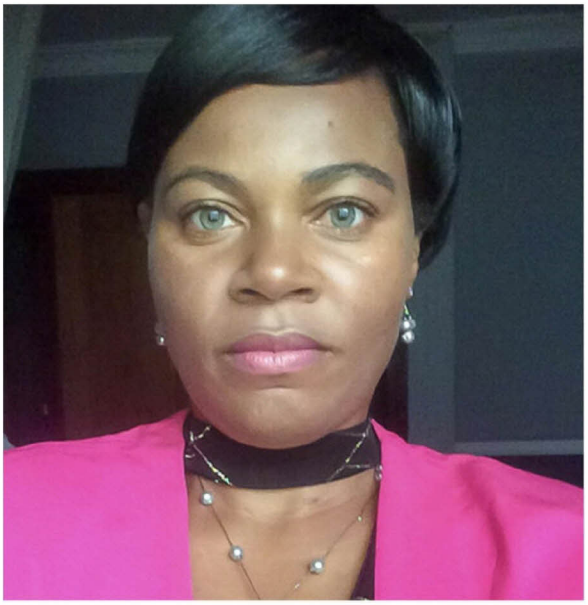
During formative research and the selection of surveillance sites, local subject matter experts or 'guides' provided entrée into what were often closed, tight-knit communities. Ethnographic interviews allowed for open-ended dialogue about target interfaces and the underlying dynamics and drivers of human activities that, from a public health/disease transmission perspective, could be considered 'risky', such as eating bats, rodents, or non-human primates, or drinking raw blood. Some risk behaviors are considered taboo from one community to another, based on tribal, ethnic, or social beliefs, and these differences had to be explored, acknowledged, and respectfully addressed. One important approach was to enroll local interviewers, when possible, or local translators who spoke local dialects, who could clearly explain the purpose of the study and reasons for blood collection (a highly suspect procedure in many cultures), as well as the need to sample their animals (also a barrier for many, as animals, whether domestic or wild, are prized commodities and sampling was sometimes seen as damaging/tainting the meat or reducing its value). Early focus group discussions helped describe practices and beliefs about disease that warranted further exploration, and also catalyzed information exchange between our teams and local experts, which often informed sites for sampling. For example, discussions with bat hunters we learned about the location of bat roosts or caves for sampling, and in conversations with bushmeat vendors, we were directed to villages where they bought hunted meat and where we could move further upstream in the bushmeat value chain.

Figure 6. Profiles of PREDICT behavioral risk team members.

TINA KUSUMANINGRUM, PREDICT/Indonesia, Field Coordinator. *"There is no doubt that joining PREDICT is one of the best decisions in my researcher career. Learning how to design and implement a surveillance project, maintain networking and professional relationships with partners, and communicate the results back to the communities and decision makers—these were all exceptional experiences that will be very useful for my future career."*

MWOKOZI MWANZALILA, PREDICT/Tanzania, Behavioral Scientist & Community Engagement Liaison, Sokoine University of Agriculture. *"PREDICT Project has helped me to create more confidence when talking in front of people. In addition, I have gained new knowledge on zoonotic diseases."*

HILARION MOUKALA NDOLO, PREDICT/Republic of Congo, Behavioral Risk Survey Investigator. *"I was hired by PREDICT to perform ethnographic interviews, focus groups and questionnaires in the communities and bushmeat markets in Brazzaville. In these studies, we discovered there are those who don't understand the concept of protected animal species, nor that handling animal species presents multiple risks of contamination with zoonotic diseases agents. I want to find ways to better educate communities and raise awareness about wildlife conservation."*



VICTORINE MAPTUE TOGEUM, PREDICT/Cameroon, Human Clinical & Behavioral Research Coordinator.

"The position I held in the PREDICT project has truly boosted my professional career. Indeed, the research carried out within the framework of this project enjoys great visibility and will be cited most often. This has helped increase my notoriety within the national and international scientific community. The Cameroonian government can turn the results of this research into concrete measures that build capacity in the health field."

Designing and implementing One Health interventions with at-risk populations

As PREDICT's laboratories detected and confirmed virus findings, including new discoveries of potentially dangerous pathogens, it became imperative to engage our host country government partners and community stakeholders to share these findings along with recommendations for continued surveillance and risk reduction. In Sierra Leone for example, PREDICT scientists discovered a new ebolavirus in bats, Bombali virus, which was the first time an ebolavirus had been detected in wildlife before causing human infection (Goldstein et al. 2018). The sampling sites for these bats were close to villages and human dwellings, as by design our surveillance sites were selected to explore risks between animal and human populations. A potentially deadly virus detected in an animal necessarily requires an empathetic and strategic human (public) health response. By using some of the contextual data about human exposure, collected through behavioral risk investigations, our team worked collaboratively with PREDICT Consortium ecology, bat biology, and virology experts to design and develop a rapid intervention strategy.

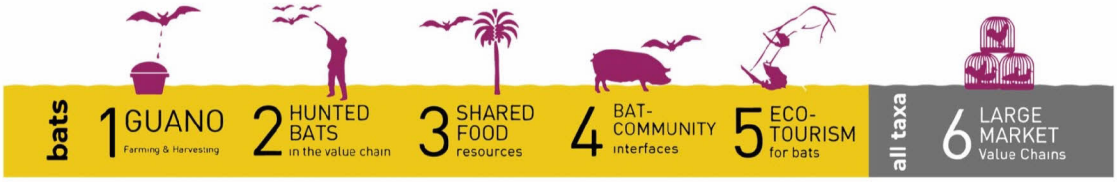
To identify the most culturally appropriate, feasible, and effective intervention resource format, our team developed a framework for assessing potential materials, channels of communications, respective audiences, and core messaging. A moderated picture book format, delivered by a trusted community leader, was selected as the best tool to put into the hands of our local team and in-country stakeholders. A communications plan was developed to ensure a well-coordinated effort and timely discussions with government and community stakeholders, following the release of the new Bombali virus finding. The resource, entitled *Living Safely with Bats (*PREDICT Consortium 2018*)*, leveraged the collective subject matter expertise of the consortium and featured illustrations from a team member trained in animal biology and visual arts ensuring accurate, consistent, and compelling visual representations. To refine and test the book format and key messages, focus groups held with project subject matter experts and feedback was solicited from project country teams. The book's content benefited from cultural vetting by 17 country teams (Bangladesh, Cambodia, Cameroon, Cote d'Ivoire, DR Congo, Ghana, Guinea, Indonesia, Lao PDR, Malaysia, Nepal, ROC, Senegal, Sierra Leone, Tanzania, Thailand, and Vietnam). Following vetting, the *Living Safely with Bats* resource was piloted in Sierra Leone and in Tanzania with feedback solicited to improve both the content and the process of delivery. A comprehensive review of the book was also conducted with the PREDICT team in Guinea.

Consortium experts, including our behavioral risk team embedded with our staff scientists in West Africa, helped train and support the implementation of the *Living Safely with Bats* resource during community outreach events in Sierra Leone, Guinea, and Liberia beginning in July and August 2018. Country teams utilized the resource in a variety of formats: official briefings with ministry partners, in-person presentations and community meetings, classroom sessions in local primary and secondary schools, and local radio broadcasts. In Guinea, radio broadcasts reached thousands of individuals across the entire Forest Region – the area where the 2014 West Africa Ebola epidemic originated, likely via a spillover event from a bat (Saez et al. 2015). This resource has been translated into 12 languages, including Amharic, Bahasa, Burmese, Dusun, English, French, Khmer, Kiswahili, Lao, Malay, Thai, and Vietnamese. The book was also adapted to share with the communities that PREDICT teams throughout Asia had engaged and worked with over time. Changes to content in this version included artistic modifications to incorporate locally salient fruits, foliage, and protective clothing items, in addition to content addressing Asia specific human-bat interfaces identified as particularly high-risk for virus spillover (date palm sap collection, bat guano farming and harvesting practices, and cave-related tourism).

Figure 7. Bat-related educational interventions

All versions of the Living Safely with Bats *resource provide talking points for moderators. These talking points cover themes such as bats as essential agents in the local ecosystem, basic ways to live safely with bats, disposal of dead bats, what to do when with them contact is unavoidable, and managing bats in and around the outside of the home.*

Figure 8. Bat-human interfaces investigated by PREDICT One Health surveillance teams.



Bat-related interfaces investigated by PREDICT's One Health surveillance team and explored in-depth through our human behavioral risk investigations included: guano farming and harvesting, hunted bats in the value chain, shared food resources with bats, bat-community interfaces, and ecotourism for bats. Large market value chains were a principal area of interest in relation to all wildlife taxa.

Sharing our findings for sustained One Health engagement

A major lesson learned towards the end of the project was managing expectations as project activities concluded. Due to our One Health surveillance design, PREDICT teams collected a vast quantity of data, an enormous and valuable archive of information that required a tremendous amount of data review for quality assurance prior to use. Taking inventory of this archive of hundreds of thousands of data points – generated from human and animal biological specimen data (including geolocation coordinates, other metadata, and virus level results) and data from behavioral questionnaires and qualitative interview transcripts – was a massive undertaking for consortium staff at both the global and country levels. Before it can be made available to the global community, this data needs to be prepared for analysis by our teams, a process requiring time, creativity, and technical skills in order to characterize the multiple dimensions of risk explored throughout the project.

Conclusions

PREDICT was a watershed One Health endeavor for its systematic inclusion of human behavioral investigations in such a large, global zoonotic disease surveillance program. The project incorporated behavioral data into a transdisciplinary analytical framework, which integrated the behavioral data with viral, human biological, animal and environmental data. Through these ongoing analyses and subsequent publications, findings from our behavioral risk investigations will contribute to the evolving One Health evidence base and will provide a model of best practices and lessons learned for those looking to further explore and understand the human drivers of zoonotic disease emergence and transmission. PREDICT successfully integrated behavioral risk investigations into country-level One Health surveillance efforts, enabling the collection of empirical and context-specific data on human activities related to disease emergence, amplification, and transmission, while also catalyzing an expanded scope of value-added activities: community outreach and trust building, sharing findings and results in an iterative feedback loop to help inform risk communications, and developing risk reduction and behavioral change communication strategies tailored to the unique contexts of affected communities.

To be successful, emerging infectious disease surveillance projects cannot focus on surveillance and detection of pathogens alone. Integrated mixed methods projects allow investigations of the specific human activities that are hypothesized to drive disease emergence, amplification, and transmission, in order to better substantiate behavioral disease drivers along with the social dimensions of infection and transmission dynamics. We encourage future programs to work with exposed communities in endemic areas on educational and capacity-building initiatives to improve community awareness of, and risk mitigation strategies for, those emerging and endemic pathogens. Involving at-risk communities in disease hotspot areas is critical, both for developing awareness of disease risk and encouraging community agency to define realistic strategies for disease mitigation for their particular community. During the last year of the project, as our country teams returned to participating villages and communities to share results, community members wanted and encouraged the team to share findings beyond just their local area, as they realized the value of the project's broader impact,and wanted to share this knowledge with other neighboring at-risk communities. They voiced appreciation of the value of One Health data and evidence, from the wildlife we captured and sampled and the viruses we detected, to the unique animal-human contexts identified as risks for infection Even though risk reduction or intervention strategies we identified might imply changes in behaviors that have been ongoing for generations, their interest and willingness to engage demonstrates the power of community buy-in for developing the foundation needed for adoption of prevention and sustained disease control efforts.

Perhaps the most positive outcome of PREDICT has been the integration of social science approaches, particularly training in participatory methods for engaging and developing long-term relationships with communities to work towards resiliency. Our global Consortium worked for over 10 years to strengthen the capacity for local scientists to safely, ethically, and humanely put One Health in action from identification of at-risk communities and sites for wildlife and human sampling activities, to collection and testing of those samples, and finally for sharing findings with our global, national, and local stakeholders. But bringing in the behavioral sciences allowed us to push toward fuller community integration and engagement. The One Health approach aims to break down barriers between silos in the scientific and health communities and importantly bridge divides between natural and social systems. PREDICT provides a model and framework for transforming theory into practice, for "socializing" One Health and taking it to scale.

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Appendix/Supplemental Materials

FOCUS GROUP GUIDE Version 2, May 1, 2015

The focus group discussion is initiated by naming all of the animals that can be found in the community. The goal of this exercise is to explore animal diversity.

The community mapping activity locates where the different kinds of animals can be found relative to the site of the focus group. It should be emphasized that this will not be an 'accurate' map. This exercise is designed to assess the distribution and overlap of animals. Prompts such as 'anywhere else?' should be used. The animal list will contain insects, reptiles and fish. Map only mammalian and avian species.

These two activities together should be limited to 10-15 minutes. The themes to be explored in the discussion are 1) contact and context, 2) illness in animals and humans, and 3) rules and restrictions. Events such as animal die-offs should be added to the map, if they are discussed.

1) Contact and context

- Which of these animals do you see the most often? The least? (Probe: where, why)
- What animals do you come into physical contact with? (Probe: where, why, how often)

- Which of these animals do you eat?
    - Where do you get them? How are they prepared? Which are for special occasions only?
- What are animals good for other than food? (probe: labor, medicinal, magic, pets, by-product uses)
- Which animals come into buildings or places where people are? Is water shared with animals?
- How are unwanted animals kept out? (probe: which animals, all methods used)
- Who takes care of the animals? (Probe: who, specific jobs, animal movements)

2) Illness in animals and humans

Animals

- What happens when animals get really sick? How are the animals cared for?
- Has this happened recently? Do people try to hide animal sickness?
- Is animal sickness reported to anyone? (probe for differences between wild and domestic animals)
- Have any animals been destroyed or killed by authorities? Describe.
- What happens to animals when they die? (probe: eaten, buried, left to rot, depends if wild or not)

Humans

- What is the most unusual or memorable sickness anyone has had? What happened?
- What are the causes of illness or sickness?
- Do you know anyone who has gotten sick from an animal? What happened?
- What do you know about animals that can give you infections or diseases?

3) Rules and restrictions

- Are there places in the community where you aren't allowed to go? Why not?
- Are there any rules about hunting or trapping animals? (Probe: cultural, legal)
- Are there any animals that you don't eat or that are avoided? Why?
- Are there official rules or laws about garbage disposal? Human waste? Animal waste?
- Is garbage a problem in this community? What's the problem?

Final question for all: If you could change one thing in your life, what would it be and how would you do it?

ETHNOGRAPHIC INTERVIEW GUIDE

Core Themes

1. Human movement
2. Socioeconomics
3. Biosecurity in human environments
4. Illness, medical care/treatment and death of humans
5. Human-animal contact

HUMAN MOVEMENT

GOAL: To understand living environment and 'home range' (e.g., how far people travel and why).

Home

Where do you live/what kind of dwelling? How many people are in the household? How many rooms? How many are children? Is everyone related? Sleeping arrangements?

How often do you move? Any seasonality of movements?—eg, for work, for food, for safety (e.g., against flood, drought, conflict)?

What are the things you do to protect your home (against predators, animals, outsiders, bad weather)?

Work

What kind of work or activities do you do? What do other household members do? Where do these activities happen?

How do you protect your activities and business interests? (e.g., grazing or crop land, business competition, hunting territory, animal stock)

Travel

How far do household members travel from home and why? (Follow up on animal related issues: shopping, selling/buying/trading, hunting, transport, etc)

How travel (by foot, bike, cart, truck, plane)? Is it ever for overnight? Where stay?

Why traveling? (work/migrant, family, religion, holidays, to sell/trade/buy animals)

Other family members in other areas of the country? Visit often?

Observed environment

Have there been any changes in the environment: new roads, more boats or ports, fields, buildings, population movement (in or out), land clearing or abandonment, new houses, other new buildings

Who is responsible for the changes? Are the changes good or bad?

SOCIOECONOMICS

GOAL: To understand a typical day and how money and social standing impact opportunity and risk.

Daily routine

Tell me about your daily routine (get description of work on a usual day, include purchasing and preparing food, timing of types of meals, responsibilities/duties related to animals, any changes by season)

How do people in the household contribute to earning money and getting food (and water)?

Where do the children play? Who takes care of the children when you are at work?

Animal responsibilities

Describe the animal related jobs and responsibilities for people at every age (i.e., young children, older children, young adults, adults, elderly).

What are the skills/knowledge needed before moving to the next stage of duties/responsibilities?

Are there differences in responsibilities between boys and girls, men and women, by ethnicity or class?

Education

How many children are currently in school? Until what age do your children go to school? (boys and girls?)

What is your level of education? Why did you stop?

Economics

Do you make more money than other people who do the same things as you? Why do you think that is?

Are there times of year when you make less money? What happens then?

Are there times when food is more expensive than others? Tell me about that (eg, different food availability, seasonal, festival related).

Do you think you and your household are better off than most people? Could you do things to make it better?

BIOSECURITY IN HUMAN ENVIRONMENTS

GOAL: To determine if any sanitation or hygiene factors could play a role in disease spillover

Water and food

Is there a central source of water? What is the source? (eg, pond, uncovered well, rainwater, taps, covered well)
Is there a water source you like better?
How far away is the water source? Do animals drink from the same source?
Do you do anything to your drinking water to clean it before you drink it?
How do you store your food? (e.g., open containers, covered, hanging, refrigerate)
Do you eat or drink things where you suspect animal contact? (e.g., teeth/scratch marks, feces or urine seen)
Do you regularly clean your food prep station/kitchen and tools? How?

Sanitation

Are there toilets, latrines or other designated areas for human waste? Are these cleaned and used regularly?
Are butchering and slaughtering areas separate? How often are they cleaned and how? Who does the cleaning?
Are there any official rules or laws about human waste and garbage disposal?
Are there any animal pest control laws? What do you do to control animal pests?

Hygiene

When are the best times to wash your hands? Do you use soap? How much does soap cost and where get it?
Do you wash your hands at home? at work?
How often and where do you and your household members bathe?

ILLNESS, MEDICAL CARE/TREATMENT, DEATH

GOAL: To identify any unusual disease experiences—signs, symptoms and sources

Household illness

Is anyone sick right now?
What do you do when someone in the household gets sick? Who takes care of that person?
The last time someone was seriously sick what happened (explore when, with what, how did they get sick, who told/consulted, anyone else get sick after, final outcome)?
Has anyone ever had an sickness that people don't usually get? What happened? Where did it come from?

Illness from animals

Do you know anyone who has gotten sick from an animal? What animal? What did they get? What happened?
Do you know any other diseases/illnesses people can get from animals? How does the animal give the illness to the person? How often does it happen?

Medical care/treatment

How sick would you have to feel to stay home and not do normal routine?
Where do you go when you are sick?
Do you prefer to use traditional medicine, western medicine or a combination?
How sick would you have to feel to go to doctor/clinic/hospital? What does that cost? (in time, lost wages/business, transport costs, etc) How far away?

Death

What is the tradition when someone dies? (Explore if reported to authorities, differ by age or gender, what happens to the body, does the community come together or is it private.)

HUMAN ANIMAL CONTACT

GOAL: To gain knowledge about interactions with animals, animal health and animal perceptions and knowledge.

Encourage but don't lead discussion about which animals. Allow respondent to name the animals. If no birds or bats are mentioned, follow up by asking specific questions about birds and bats.

Indirect contact

What kind of meat do people in your household eat? How do you get it/where does it come from? What is furthest away an animal comes from?

Is meat dead or alive when you get it? If dead(/prepared), how to tell if good/fresh?

If alive, how long are live animals kept before being sold or eaten? How do you get live animals home?

How is meat prepared (raw/undercooked)? Is meat prepared in the same place as other activities? (e.g., preparing vegetables, cleaning babies/changing diapers, where other food or drinking water is stored)

Do animals come in or near the dwelling? How do you know animals are there? Which animals?

Direct contact

Do you or someone in your household handle live animals? In what context? (e.g. ranching/animal husbandry, hunting, wet markets, work, around dwelling/other building, pets)

What are the animals that you keep/raise or sell? How many different kinds of animals? How many of each?

For how long do you have the animals?

Where do live animals come from? Where is the furthest away an animal comes from?

Who buys/trades for your live animals? Where do the animals go?

Have you been bitten, scratched or had bleeding after handling an animal? By a wild animal?

Where are live animals slaughtered? butchered? Do people buy or sell parts?

Do you travel with animals? Explore details of the process, specific routes and encounters (eg, with other animals, with animal transport supporting industries, such as holding areas, restaurants, hotels) along the way.

Explore for differences over time in animal handling, eg, seasonality, legal, religious, animal reproduction

Animal products/rituals

Other uses of animals—e.g., as pets, medicine, magic, fertilizer, for trading

Rules for children around wild animals as pets, playing with wild animals or dead animals

Animal health

How do you care for your animals: how are they fed, what do they eat, where do they eat/graze and sleep? Are they segregated or all together? Differences by season? day/night? Does anyone live or stay with the animals?

Is there a central area for animal waste? How often are animal cages, stalls, or penned areas cleaned? Who cleans them?

Do the animals get veterinary care? Vaccinations?

How do you know when an animal is sick? What's the first thing you do about a sick animal?

Have you seen an animal outbreak or die-off? What happened?

Perceptions and knowledge

What are the most unusual animals anyone can buy?—seasonal? Expensive? Who buys?

Are there any animals you avoid eating? Why? Ever heard of anyone eating/selling dead or infected animals?

Do people ever eat non-domesticated animals/wildlife? Where do they get them?

Who usually buys wildlife products? Have there been changes over time?

What do you do when you find a dead animal?

What laws about animals do you know? (eg, limiting/outlawing hunting, reporting and culling of sick animals)

From: Karen Saylors [redacted]
Sent: Thu, 26 Dec 2019 11:26:40 -0800
Subject: Re: Predict Behavioral Draft for your review
To: Jonna Mazet <jkmazet@ucdavis.edu>
Cc: David J Wolking <djwolking@ucdavis.edu>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, "Olson, Sarah" [redacted] Emily Hagan <hagan@ecohealthalliance.org>

Hi Jonna.
Thanks very much for the comments and suggestions.
I'm back working today and will incorporate your and Sarah's edits, as well as anyone else's who isn't out on holiday over the coming days. We will do some final wordsmithing and get you a final draft early on Monday, with acknowledgements and final figures.

Happy holidays y'all! :)
best,
Karen

On Thu, Dec 26, 2019 at 10:55 AM Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> Hi,
> My suggested edits are attached. Not sure who is vacationing & who is working. If working, Karen, I want to let you know that I think your (& David's) prose is eloquent and works very nicely. I had almost no comments on the first half of the paper. The second half, where we start adding in figures, is still very well-written but starts to get a little more sales-pitchy, reminiscent of content for a report or brochure, rather than written for a journal audience. So I have made more comments on that section for your consideration and a bit more substantive revision.
> Text me if you want to clarify any of it.
> Great work & I really appreciate the effort to get this great product out in the literature. I think USAID will love it, too.
> Please make sure to get the acknowledgement stuff in there.
> Under separate copy, I'll send the response to reviewers & galleys from Diego's paper in this journal for ease of reference.
> Happy Holidays everyone,
> Jonna

On Tue, Dec 24, 2019 at 8:00 AM David J Wolking <djwolking@ucdavis.edu> wrote:

> Thanks Karen!
> For those new to the conversation (mainly Chris and Peter), this is the article (an approach/perspectives piece) invited by the One Health Outlooks journal that Jonna and [redacted] are editing. The Dec. 30th deadline gets this into the review without journal fees, so we did our best to push this forward over the last 3 weeks and make the deadline. Huge thanks to Karen, Jason, Stephanie, and Emily for getting it there. We realize it's terrible timing for co-author review given the holidays...

That said, it makes great Xmas reading ;-)

David

On Tue, Dec 24, 2019 at 7:35 AM Karen Saylors <[redacted]> wrote:

> Hi everyone.
> Please find attached our team's manuscript for your review. As we are aiming for the Monday deadline of the One Health Outlook, we'd appreciate your comments and edits by Friday.

Thanks so much and happy holidays!

Best,
Karen, David and Emily

From: Ben Oppenheim <boppenheim@metabiota.com>
Sent: Wed, 15 Jan 2020 14:02:39 -0800
Subject: Re: Question re. BCA
To: Peter Daszak <daszak@ecohealthalliance.org>
Cc: [redacted] Nita Madhav <nmadhav@metabiota.com>, Dean Jamison <djamison@uw.edu>, Dennis Carroll [redacted] Jonna Mazet <jkmazet@ucdavis.edu>, Nicole Stephenson <nstephenson@metabiota.com>, Cara Chrisman <cchrisman@usaid.gov>, "nwolfe@metabiota.com" <nwolfe@metabiota.com>, Samtha Maher <maher@ecohealthalliance.org>, "erubin@metabiota.com" <erubin@metabiota.com>, Kierste Miller <kmiller@metabiota.com>

Absolutely, yes. I believe that USAID will be hosting, but would ask our USAID colleagues to confirm if that's correct
all the best,
Ben

On Wed, Jan 15, 2020 at 1:59 PM Peter Daszak <daszak@ecohealthalliance.org> wrote:

> Just wanted to check in with everyone – are we still having an in-person BCA meeting on the 12th Feb in DC?
>
> Cheers,
>
> Peter
>
> **Peter Daszak**
>
> *President*
>
> EcoHealth Alliance
>
> 460 West 34th Street – 17th Floor
>
> New York, NY 10001
>
> Tel. +1 212-380-4474
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> Website: www.ecohealthalliance.org
>
> Twitter: @PeterDaszak

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: Ben Oppenheim [mailto:boppenheim@metabiota.com]
Sent: Wednesday, January 8, 2020 12:16 AM
To: REDACTED Nita Madhav; Dean Jamison; Dennis Carroll; Jonna Mazet; Nicole Stephenson; Cara Chrisman; nwolfe@metabiota.com; Samtha Maher; Peter Daszak; erubin@metabiota.com; Kierste Miller
Subject: Re: BCA updates and two requests

Dear GVP colleagues

Happy new year -- I hope that you all had a wonderful holiday and start to 2020.

We would of course be happy to prepare a short brief about the BCA activities, as well as a few slides, around the end of January. Please let us know if you have an exact deadline, or any specs we should bear in mind (e.g., how much background would be needed on methodologies employed, such as catastrophe modeling).

Since the last meeting we have made progress on several fronts, including:

Exceedance probability estimates

- Built on existing data sets and compiled additional data on losses from historical epidemics (cases, deaths), to provide an actuarial view of risk
- Developed preliminary baseline ("no GVP") estimates for Infrequent spillover / moderate R_0 pathogens (e.g., filoviruses) and respiratory non-influenza viruses (e.g., coronaviruses), with continuing development work on other catalogs
- Developed methodology for modeling GVP impacts on exceedance probability curves (e.g., via reduced spark risk, improved time to intervention)

Characterization of GVP impact

- Research into PREDICT-driven capacity building improvements, with preliminary indications of improvement to response time.
- Synthesized research (e.g. new key informant interviews) on potential GVP benefits for new product development

Economic losses

- Finalized methodology for estimating statistical value of lives lost (saved)
- Compiled revised dataset on shocks to national income from historical epidemics

Looking forward to our call next week,

Ben (and colleagues)

On Wed, Dec 18, 2019 at 2:58 PM REDACTED wrote:

Hi Dean, Ben, and Nita,

I am reaching out with updates and two requests related to BCA. Recently, a 501(c)3 non-profit organization was formed for the Global Virome Project, and GVP will be holding its first Board meeting in mid-February 2020. During the meeting, we would like to brief board members about the BCA group's great activities to date.

Would you be able to develop **a short brief about the BCA group's activities (1-2 page max), and a couple of slides**? Our timeline would likely be around the end of January, prior to the BOD meeting. My colleagues copied here can follow up with an exact deadline.

In addition to the request above, would you be able to share quick updates (some bullet points in an email to the group cc'ed here) about the progress of the analysis since our last meeting?

Please send your response to my colleagues copied here, as I will be handing my GVP work over. Thank you very much for your hard work.

Best wishes,

REDACTED

--

Ben Oppenheim, PhD

Director, Product Development // Senior Scientist

510.501.1097

--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

510.501.1097

From: Ben Oppenheim <boppenheim@metabiota.com>
Sent: Wed, 15 Jan 2020 23:27:31 -0800
Subject: presentation for 16 January advisory call
To: Dean Jamison <djamison@uw.edu>, Stefano M Bertozzi <sbertozzi@berkeley.edu>, Paola Gadsden <paola.gadsden@cisidat.org.mx>, Nita Madhav <nmadhav@metabiota.com>, Nicole Stephenson <nstephenson@metabiota.com>, Jaclyn Guerrero <jguerrero@metabiota.com>, Dennis Carroll [REDACTED]>, Cara Chrisman <cchrisman@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, "Stephen S. Morse" <ssm20@cumc.columbia.edu>, Gavin Yamey <gavin.yamey@duke.edu>, "Boyle, Colin" <Colin.Boyle@ucsf.edu>, "Rubin, Eddy" <erubin@metabiota.com>
Advisory meeting 01162020.pdf

Dear advisors,
Attached, please find a copy of the presentation materials for tomorrow's call.
We're very much looking forward to our discussion, and to your feedback.

all the best,
Ben

--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

510.501.1097

GVP Benefit-Cost Analysis Advisory Panel Meeting

January 16, 2020

Agenda

- Progress since last meeting
- Classification and focus criteria
- Estimates of capacity building impacts
- Preliminary EP and impact analysis
- Next steps for 12 Feb meeting

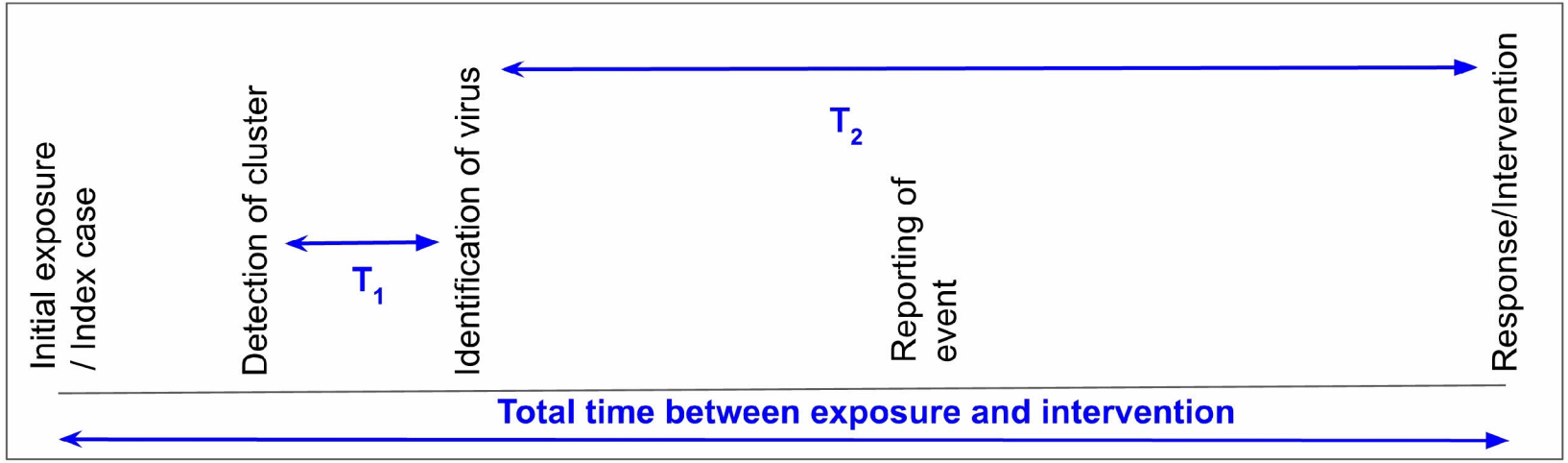
Progress to date

1. Finalized conceptual framework for GVP benefit stream
2. Completed key informant research on new product development
3. Refined and expanded historical dataset of epidemic losses
4. Refined VSL estimation and sensitivity-testing approach
5. Finalized dataset of historical GNI losses
6. Model development and parameterization
7. Continuing progress on exceedance probability estimates (preliminary results)

Proposed Mechanism for GVP benefits	Decrease frequency	Improve response time	Source
More information about the geographic and host range of known pathogens	Potential	Potential	Advisor discussions
Greater diversity of viral reagents for countermeasure development	No (based on Stef & Paola's research)	No (based on Stef & Paola's research)	Carroll et al. 2018 Supplement
Capacity building (e.g. training surveillance and lab staff, etc.)	Potential	Potential	Carroll et al. 2018 Supplement
Enhancing rapid diagnosis during outbreaks	No	Potential	Carroll et al. 2018 Supplement
Designing risk mitigation policies	Fully dependent on external parties and factors	Fully dependent on external parties and factors	Carroll et al. 2018 Supplement
Strategies to triage potentially pandemic viruses for enhanced characterization and risk mitigation policies	Fully dependent on external parties and factors	Fully dependent on external parties and factors	Carroll et al. 2018 Supplement
Early warning of future threats	Fully dependent on external parties and factors	Fully dependent on external parties and factors	Jonas and Seifman 2019
Data to improve prevention and reduction of these threats	Fully dependent on external parties and factors	Fully dependent on external parties and factors	Jonas and Seifman 2019
Inputs for advance preparation of response for unexpected outbreaks of unknown diseases	Fully dependent on external parties and factors	Fully dependent on external parties and factors	Jonas and Seifman 2019

Modeled mechanisms for GVP impact

- Decreased frequency of events (prevention of spillover)
- Decreased intervention time leading to decreased event severity
  - Improved detection time
  - Improved time to identification of the virus
  - Improved time between identification and response



Approach to GVP impact analysis

- Many of GVP's hypothesized impacts are difficult to quantify and there is a large degree of irreducible uncertainty
- A break-even analysis will provide the project team's best estimate of the likely impact, along with a range of other outcomes under different assumptions
- The project team believes that this approach will provide the most impartial and balanced view of our research and outputs

Break-even analysis process:

1. Determine the required "Break Event Point" based on the economic analysis
2. Calculate the impact of GVP (in deaths averted and GDP loss mitigated) required to reach the "Break Event Point" for the program
3. Model the impact of GVP over a range of impacted parameters (frequency of spillover and intervention time)
4. Present the evidence collected for the impact of GVP on frequency of spillover and intervention time

Classification of Viruses

Classification	Examples	Model type	Freq.	Severity	Spark map	CFR
A. Pandemic influenza		Mechanistic	Low	High	4 countries	Low
B. Infrequent spillover - Moderate R0	Ebola, Marburg, Machupo	Mechanistic	Low to Moderate	Low to High	Bat diversity and human pop	High
C. Non-Flu Respiratory	SARS, MERS	Mechanistic	Low	High	Bat and Rodent diversity	Moderate
D. Frequent spillover - low R0	Lassa, Hantaviruses	Phenomenological	High	Moderate	Rodent diversity	Low - Moderate
E. Vector-borne	Dengue, Zika, Yellow fever	Phenomenological	Moderate	Moderate - High	Vectors	Low - Moderate
F. Other	Monkeypox, Sosuga virus	Phenomenological	Low	Low to high	Hotspots	Correlated with event size

Factors facilitating GVP Impact

- Historical data from all known zoonotic pathogens from the 25 priority viral families over the past 50 years was assessed
- Following guidance from previous advisory panel meetings, we have focused further analysis on **high priority pathogens** where it is expected that **expanding knowledge** of the ecology of the disease supports prevention and response

GVP has the potential for impact when...	Counter-Examples	Explanation
There are little to no surveillance and research programs already in place to monitor for the pathogen.	Influenza	There are currently many programs specifically dedicated to monitoring for pandemic influenza. The effect of GVP specifically on influenza detection is limited compared to the current efforts
The pathogen has caused a substantial number of deaths (greater than 50 deaths ever reported).	Hendra, Lujo, Whitewater Arroyo	Since pathogens below the 50 death threshold have caused so few cases, they are not likely to be considered a high priority for decision-makers and stakeholders. Learning more about their ecology likely would not impact surveillance or mitigation efforts.
The pathogen is uncommon (does not have a high annual incidence).	Lassa, Hanta, CCHF, RVF	Since these pathogens are common, their ecology is already well known. Learning more about their ecology is unlikely to impact future efforts.
Targeted surveillance and control programs do not already exist.	Dengue, Yellow fever, Zika, Rocio	Vector-borne diseases are already well studied with specific programs targeting their surveillance and control; it is unlikely that GVP alone will significantly alter or improve vector control systems (Note: Most of these also meet an additional criteria.)

Focus Criteria

Historical data for 101 zoonotic pathogens in the 25 priority viral families were evaluated and included several thousand event records

Focus criteria represent potential GVP impact and availability of sufficient data for model development

Example Pathogens NOT meeting Focus Criteria

Pathogen	<50 Deaths Ever Reported	High Annual Incidence	Vector-borne
Monkeypox virus	FALSE	TRUE	FALSE
Influenza virus	FALSE	TRUE	FALSE
Andes virus	FALSE	TRUE	FALSE
Guanarito virus	TRUE	FALSE	FALSE
Hendra virus	TRUE	FALSE	FALSE
Sin Nombre virus	TRUE	FALSE	FALSE
Rocio virus	FALSE	FALSE	TRUE
Chikungunya virus	FALSE	TRUE	TRUE
CCHF virus	FALSE	TRUE	TRUE
RVF virus	FALSE	TRUE	TRUE
Seoul virus	TRUE	TRUE	FALSE
Sandfly fever virus	TRUE	TRUE	TRUE
Zika virus	FALSE	TRUE	TRUE

Pathogens Meeting Focus Criteria

Pathogen	Total cases	Total Deaths	# of Events	Frequency	Severity
Zaire ebolavirus	33811	14727	19	Moderate	Moderate
SARS Coronavirus	9410	924	1	Low	High
MERS Coronavirus	2503	830	5	Low	High
Marburg virus	608	491	12	Moderate	Moderate
Machupo virus	1816	438	4	Moderate	Moderate
Sudan ebolavirus	810	426	8	Moderate	Moderate
Nipah virus	685	375	25	Moderate	Moderate
Bundibugyo ebolavirus	183	70	2	Moderate	Moderate

Historical Events (subset)

Pathogen	Event Start Year	Main Affected Countries	Deaths	Cases	Death Rate (Micromort)	Case Rate (Microprobability)	Affected Population (M)
Bundibugyo ebolavirus	2007	Uganda	42	131	1.42	4.44	29.486338
MERS Coronavirus	2012	Saudi Arabia	764	2158	4.16	11.76	183.568256
Marburg virus	2004	Angola	329	375	17.54	19.99	18.758145
Marburg virus	1998	DRC	125	154	2.79	3.43	44.849967
Nipah virus	1998	Malaysia	111	283	5.02	12.80	22.114654
Nipah virus	2004	Bangladesh	61	79	0.15	0.19	410.959296
SARS Coronavirus	2002	China, HK	924	9410	0.22	2.23	4217.33494
Sudan ebolavirus	2000	Uganda	224	428	9.47	18.10	23.650172
Sudan ebolavirus	1976	South Sudan	151	299	2.51	4.96	60.253759
Zaire ebolavirus	2013	SL, LR, GN	11305	28613	58.34	147.66	193.770893
Zaire ebolavirus	2018	DRC	2240	3666	13.32	21.80	168.136182

Capacity Building - Outbreak Response

Data from the Outbreak Response Status Tracking Tool received from UCD on 11/13/2019

Included countries:

- Bangladesh
- Cameroon
- DRC
- Malaysia
- Mongolia
- Rwanda
- Sierra Leone
- Thailand
- Uganda

Specimens submitted to laboratory

	2012 - 2015	2016 - 2018
Submitted = YES	3	14
Submitted = Unknown/No	6	3

Fisher's exact test: $p = 0.03$

Interpretation: There was a significant improvement in sample submission from 2016 onwards, when compared to prior years.
Concern: Much of the data is classified as unknown, which may bias the results.

Next Steps

1. Prepare the GVP scenarios and EP curves
2. Estimate benefit-cost ratio + refining GVP break-even analysis
3. Prepare for 12 Feb meeting
    a. Confirm venue and timing (adjusting agenda around any advisors' schedule constraints)
    b. Schedule calls/briefings with any advisors who can't attend
    c. Determine materials advisors would like to have in hand prior to the meeting
4. Final report preparation

Appendix

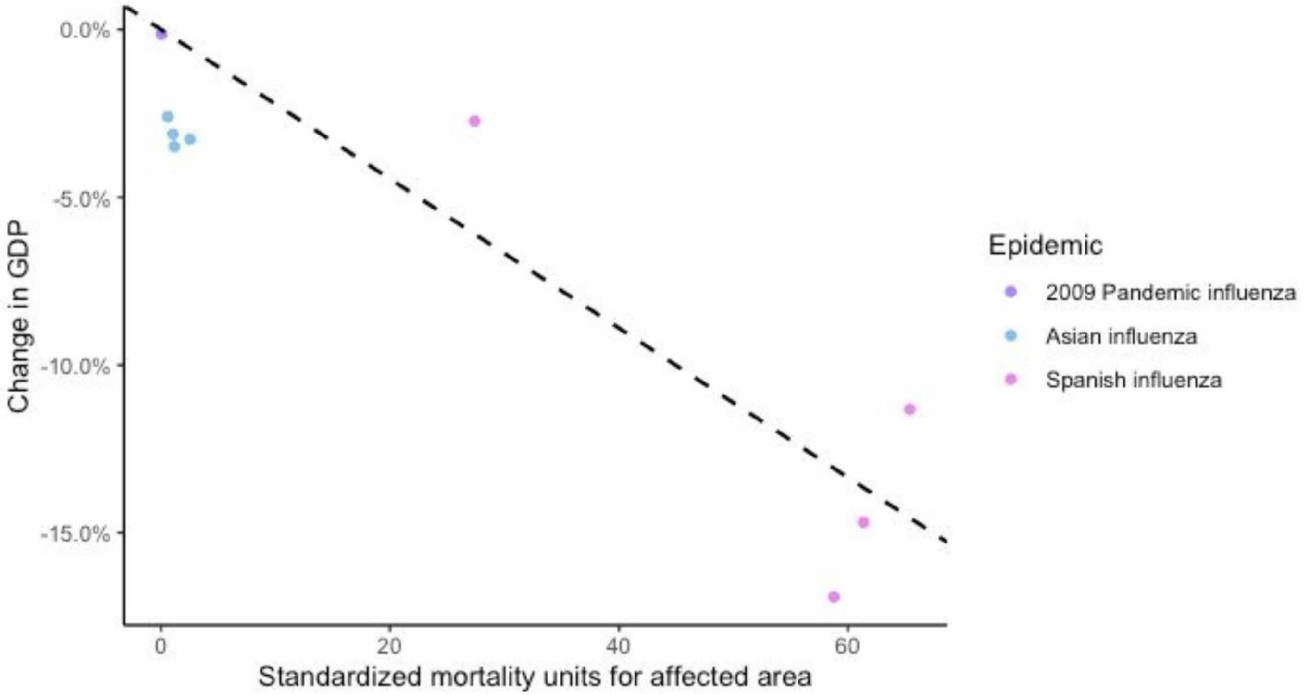
Capacity Building - Workforce

From UCD's PREDICT Y5 Global Roster (Master) obtained from UCD on 1/2/2020 (current as of Feb 2019):

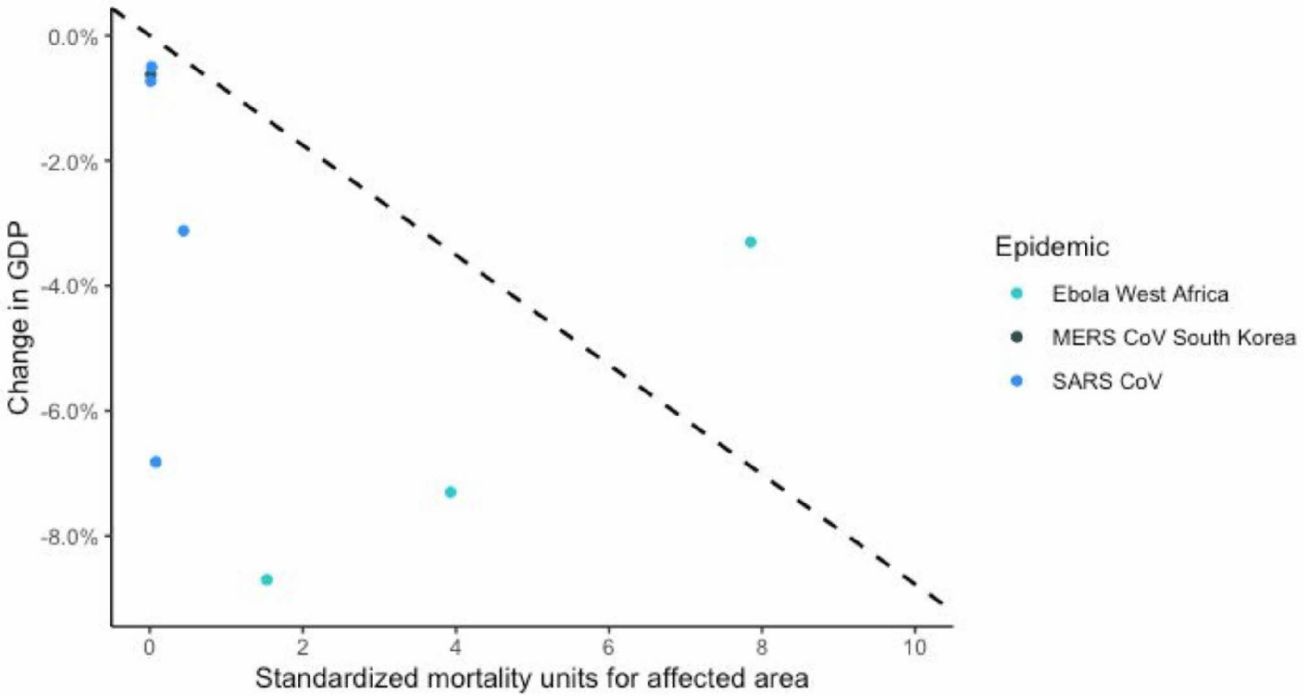
349 personnel trained outside the US/Canada/France

- 173 currently inactive (not currently working for PREDICT or implementing partner)
  - 101 currently working or studying in a health/lab/wildlife capacity
    - 97 are working or studying within the same region as they were trained
  - 54 unknown current employment
  - 18 currently not working or studying in a health/lab/wildlife capacity

Historical GNI losses – pandemic flu



Historical GNI losses – non flu viral epidemics



From: Dennis Carroll <[redacted]>
Sent: Thu, 16 Jan 2020 13:47:31 -0400
Subject: Re: presentation for 16 January advisory call
To: Ben Oppenheim <boppenheim@metabiota.com>
Cc: "Boyle, Colin" <Colin.Boyle@ucsf.edu>, Cara Chrisman <cchrisman@usaid.gov>, Dean Jamison <djamison@uw.edu>, Gavin Yamey <gavin.yamey@duke.edu>, Jaclyn Guerrero <jguerrero@metabiota.com>, Jonna Mazet <jkmazet@ucdavis.edu>, Nicole Stephenson <nstephenson@metabiota.com>, Nita Madhav <nmadhav@metabiota.com>, Paola Gadsden <paola.gadsden@cisidat.org.mx>, Peter Daszak <daszak@ecohealthalliance.org>, "Rubin, Eddy" <erubin@metabiota.com>, Stefano M Bertozzi <sbertozzi@berkeley.edu>, "Stephen S. Morse" <ssm20@cumc.columbia.edu>

Am landing a bit late at National airport. Will call in as soon as I have arrived

d

On Thu, Jan 16, 2020 at 2:28 AM Ben Oppenheim <boppenheim@metabiota.com> wrote:

> Dear advisors,
> Attached, please find a copy of the presentation materials for tomorrow's call.
> We're very much looking forward to our discussion, and to your feedback.

all the best,
Ben

--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

510.501.1097

--
Dr Dennis Carroll
Global Virome Project, Core Team
Senior Fellow, Scowcroft Institute of International Affairs at the Bush School of Government and Public Service, Texas A&M University
Counselor and Advisor to the Faculty of Tropical Medicine at Mahidol University

mobile: 202-999-6144
email: [redacted]

From: "Morse, Stephen S." <ssm20@cumc.columbia.edu>
To: Ben Oppenheim <boppenheim@metabiota.com>, Dean Jamison <djamison@uw.edu>, Stefano M Bertozzi <sbertozzi@berkeley.edu>, Paola Gadsden <paola.gadsden@cisidat.org.mx>, Nita Madhav <nmadhav@metabiota.com>, "Nicole Stephenson" <nstephenson@metabiota.com>, Jaclyn Guerrero <jguerrero@metabiota.com>, Dennis Carroll <[redacted]>, "Cara Chrisman" <cchrisman@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, "Peter Daszak" <daszak@ecohealthalliance.org>, Gavin Yamey <gavin.yamey@duke.edu>, "Boyle, Colin" <Colin.Boyle@ucsf.edu>, "Rubin, Eddy" <erubin@metabiota.com>
Subject: Re: presentation for 16 January advisory call
Sent: Thu, 16 Jan 2020 19:46:42 +0000

Many thanks for a great deal of very thoughtful work and comments. Enjoyed the discussion.

Happy New Year (just in time for the Lunar New Year next week).

Best,
Steve

From: Ben Oppenheim <boppenheim@metabiota.com>
Date: Thursday, January 16, 2020 at 2:28 AM
To: Dean Jamison <djamison@uw.edu>, Stefano M Bertozzi <sbertozzi@berkeley.edu>, Paola Gadsden <paola.gadsden@cisidat.org.mx>, Nita Madhav <nmadhav@metabiota.com>, Nicole Stephenson <nstephenson@metabiota.com>, Jaclyn Guerrero <jguerrero@metabiota.com>, Dennis Carroll <[redacted]>, Cara Chrisman <cchrisman@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, "Morse, Stephen S." <ssm20@cumc.columbia.edu>, Gavin Yamey <gavin.yamey@duke.edu>, "Boyle, Colin" <Colin.Boyle@ucsf.edu>, "Rubin, Eddy" <erubin@metabiota.com>
Subject: presentation for 16 January advisory call

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all the best,
Ben

--
Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

510.501.1097

From: Andrew Clements <aclements@usaid.gov>
Sent: Tue, 21 Jan 2020 10:44:13 -0800
Subject: Re: Reminder: PREDICT MT Call - Tuesday January 21, 2020 @ 8:30AM
To: Tracey Goldstein <tgoldstein@ucdavis.edu>
Cc: David J Wolking <djwolking@ucdavis.edu>, Alisa Pereira Emerging Threats Division <apereira@usaid.gov>, Amalhin Shek <ashek@usaid.gov>, "Cara J. Chrisman" <cchrisman@usaid.gov>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, PREDICTMGT <predictmgt@usaid.gov>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>

Thanks. Great work!

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jan 21, 2020, at 6:28 PM, Tracey Goldstein <tgoldstein@ucdavis.edu> wrote:

Dear All,

Please find attached the proofs of the Marburg paper - just a reminder this is not the final version and that we are under embargo until Friday noon when it is released. We will share the press release as soon as we finalize it for your comments and input.

Best Tracey

On Mon, Jan 20, 2020 at 3:49 PM David J Wolking <djwolking@ucdavis.edu> wrote:

Hi there,
Below is the agenda for tomorrow's call.

Talk soon,

David

PREDICT Management Team Meeting Agenda
Tuesday, January 21, 2020
8:30-9:30AM PST/11:30-12:30pm EST
Zoom link: [redacted]
Additional Zoom info below agenda

USAID Updates

1. Administrative items

- March 2020 meeting updates (confirming dates, plans and preparation, etc.)
- GAO GHSA audit news (Viet Nam and Indonesia visits)?

2. Novel CoV Wuhan outbreak

- PREDICT assistance to country govts, genetic analyses, and modeling efforts reported to date

3. On close-out - standing item

- *Review/discussion of USAID close-out tracker & Predict tracking tools*
- *Media library and content curation* (plans for making available media, images, etc. as a resource; best platforms, etc.) - new standing item
- *Feedback on data sharing platforms (DDL flexibility & Open Science Framework)*

4. Final report updates

5. Mission, partner communications & country roundup essentials

- Nepal meeting read-out
- Others?

6. Publication, media, and conference updates

- 19th International Congress on Infectious Diseases, Kuala Lumpur (February 20-23, 2020)

- PMAC, Bangkok, Thailand (January 28-31, 2020)

7. AOB

Zoom Call-in info
Zoom link: [redacted]
Or iPhone one-tap :
US: +16468769923,, REDACTED or +16699006833,, REDACTED
Or Telephone:
Dial(for higher quality, dial a number based on your current location):
US: +1 646 876 9923 or +1 669 900 6833
Meeting ID: REDACTED

On Fri, Jan 17, 2020 at 12:32 PM David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi there,
> Just a reminder about next week's PREDICT management team call (Zoom link: REDACTED

I'll follow-up early next week with the agenda. In the meantime if there's anything in particular you want to discuss, send it my way and I'll build it it.

Best,

David

--
Tracey Goldstein, PhD
Associate Director, Professor
One Health Institute
School of Veterinary Medicine
University of California
Davis, CA 95616
Phone: (530) 752-0412
Fax: (530) 752-3318
E-mail: tgoldstein@ucdavis.edu

<41467_2020_14327_Author _proofs.pdf>

From: Dennis Carroll <[redacted]>
Sent: Thu, 23 Jan 2020 13:24:50 -0500
Subject: Fwd: Explanatory Statement
To: Eddy Rubin <[redacted]>, Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, Samtha Maher <maher@ecohealthalliance.org>
[Untitled].pdf

---------- Forwarded message ---------
From: **Rieser, Tim (Appropriations)** <Tim_Rieser@appro.senate.gov>
Date: Thu, Dec 19, 2019 at 1:31 PM
Subject: Explanatory Statement
To: Dennis Carroll <[redacted]>

--
Dr Dennis Carroll
Global Virome Project, Core Team
Senior Fellow, Scowcroft Institute of International Affairs at the Bush School of Government and Public Service, Texas A&M University
Counselor and Advisor to the Faculty of Tropical Medicine at Mahidol University

mobile: 202-999-6144
email: [redacted]

The Secretary of State shall not carry out the directive under this heading in the House report regarding a determination.

GAVI.—The agreement includes $290,000,000 for a contribution to The GAVI Alliance and expects the United States to maintain this level of commitment for the next replenishment cycle.

Global Health Security.—The agreement includes $100,000,000 for Global Health Security, including for programs to strengthen public health capacity in countries where there is a high risk of zoonotic disease. Funds should also be made available to support the collection and analysis of data on unknown viruses, and should be made available, on a matching basis with other donors, to support a coordinating mechanism for the sharing of data on unknown viruses with zoonotic potential among countries, following consultation with the Committees on Appropriations.

Not later than 45 days after enactment of the Act, the USAID Administrator shall submit a report to the Committees on Appropriations on the proposed uses of Global Health Security funds, which shall comply with the directives described under this heading in the House and Senate reports.

Global Fund.—The agreement includes $1,560,000,000 for a contribution to the Global Fund to Fight AIDS, Tuberculosis, and Malaria and affirms the United States share of 33 percent as included in section 202(d) of the United States Leadership Against HIV/AIDS, Tuberculosis, and Malaria Act of 2003, as amended.

Global Health and Women's Economic Empowerment Programing Coordination.—The USAID Administrator shall not carry out the directives under the heading "Global Health and Women's Economic Empowerment Programing Coordination" under this heading in the Senate report. No funds are included in the agreement for the pilot project described under such heading.

DEVELOPMENT ASSISTANCE

The agreement provides $3,400,000,000 for Development Assistance. Funds for certain programs under this heading are allocated according to the following table and subject to section 7019 of the Act:

From: Ben Oppenheim <boppenheim@metabiota.com>
Sent: Thu, 30 Jan 2020 20:17:55 -0800
Subject: Re: Question re. BCA
To: Cara Chrisman <cchrisman@usaid.gov>, Mary Radford <maradford@ucdavis.edu>
Cc: Dennis Carroll [redacted], Dean Jamison <djamison@uw.edu>, [redacted]
Jonna Mazet <jkmazet@ucdavis.edu>, Kierste Miller <kmiller@metabiota.com>, Nicole Stephenson <nstephenson@metabiota.com>, Nita Madhav <nmadhav@metabiota.com>, Peter Daszak <daszak@ecohealthalliance.org>, Samtha Maher <maher@ecohealthalliance.org>, Stefano M Bertozzi <sbertozzi@berkeley.edu>

hi Cara
Mary Raford on Jonna's team just sent in a booking request for a room at UCDC, but I believe it hasn't been confirmed that. If we can convene at USAID, I think it's probably worth squeezing in a bit to save the funds (and besides, it's a friendly crowd.)
Thank you very much for circling back on this and providing the option (and Mary, thank you also for your help in securing space!)

all the best,
Ben

On Thu, Jan 30, 2020 at 6:48 PM Cara Chrisman <cchrisman@usaid.gov> wrote:

> Hi All,
> Where did this land? I was able to secure at room at USAID (500 D Street SW) that technically fits 8 people for 9-5pm on the 12th, but I think should be fine with the 10-12 people. I'll try and check it out to tomorrow to make sure. Let me know if this is still needed and I'll also figure out what the procedure are in the new building for guests - think it's quite straight forward.
>
> Best,
> Cara
>
> Cara J. Chrisman, PhD
> Deputy Division Chief
> Emerging Threats Division
> Office of Infectious Disease, Bureau for Global Health
> U.S. Agency for International Development (USAID)
> Desk: (202) 916-2065
> Cell: (202) 674-3231
> E-mail: cchrisman@usaid.gov

On Fri, Jan 17, 2020 at 6:46 PM Dennis Carroll [redacted] wrote:

> Great location. Cara, any thoughts on USAID availability- or should we accept the UCDC option?

On Fri, Jan 17, 2020 at 6:18 PM Ben Oppenheim <boppenheim@metabiota.com> wrote:

> Stef mentioned that the UC Washington DC building (UCDC). That seems ideal to me.. very well located, and I remember there being a few good medium-sized conference rooms.
> **Jonna / Stef:** would it be possible for either of you to book via your institutions? I'm also happy to reach out, but not sure if non-UC people can make a booking request

On Thu, Jan 16, 2020 at 11:19 AM Jonna Mazet <jkmazet@ucdavis.edu> wrote:

> National Academies (Keck Center) is an option, but we will have to pay for the room. It would be worth you checking

into options for room rental at a hotel or flex space, as well. I don't think CDC is a great option, just because we don't have major involvement from them on this piece at this point.
Let me know what option you and costs

On Wed, Jan 15, 2020 at 2:36 PM Ben Oppenheim <boppenheim@metabiota.com> wrote:

hi Cara
I think we're looking at approx. 10-12 people in person, with 3-4 people dialing in remotely.

All: any suggestions re: backup locations? UCDC and the Nat'l Academies come to mind
all the best,
Ben

On Wed, Jan 15, 2020 at 2:30 PM Cara Chrisman <cchrisman@usaid.gov> wrote:

Hi All,
My apologies, the logistics have been a bit of a challenge with finding a room within USAID. Could you confirm the exact time and expected number of attendees? As folks are still moving into this new building, we don't yet have access to some of the larger rooms and there are some issues with the rooms being booked for partial days. While I continue to look at this, I would suggest we also consider backup options just in case I can't find something.

Best,
Cara

Cara J. Chrisman, PhD
Deputy Division Chief
Emerging Threats Division
Office of Infectious Disease, Bureau for Global Health
U.S. Agency for International Development (USAID)
Desk: (202) 916-2065
Cell: (202) 674-3231
E-mail: cchrisman@usaid.gov

On Wed, Jan 15, 2020 at 5:28 PM Peter Daszak <daszak@ecohealthalliance.org> wrote:

Great – thanks.

Cheers,

Peter

Peter Daszak

President

EcoHealth Alliance

460 West 34th Street – 17th Floor

New York, NY 10001

Tel. +1 212-380-4474

Website: www.ecohealthalliance.org

Twitter: @PeterDaszak

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: Ben Oppenheim [mailto:boppenheim@metabiota.com]
Sent: Wednesday, January 15, 2020 5:03 PM
To: Peter Daszak
Cc: REDACTED Nita Madhav; Dean Jamison; Dennis Carroll; Jonna Mazet; Nicole Stephenson; Cara Chrisman; nwolfe@metabiota.com; Samtha Maher; erubin@metabiota.com; Kierste Miller
Subject: Re: Question re. BCA

Absolutely, yes. I believe that USAID will be hosting, but would ask our USAID colleagues to confirm if that's correct

all the best,

Ben

On Wed, Jan 15, 2020 at 1:59 PM Peter Daszak <daszak@ecohealthalliance.org> wrote:

> Just wanted to check in with everyone – are we still having an in-person BCA meeting on the 12th Feb in DC?

Cheers,

Peter

Peter Daszak

President

EcoHealth Alliance

460 West 34th Street – 17th Floor

New York, NY 10001

Tel. +1 212-380-4474

Website: www.ecohealthalliance.org

Twitter: @PeterDaszak

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

From: Ben Oppenheim [mailto:boppenheim@metabiota.com]
Sent: Wednesday, January 8, 2020 12:16 AM
To: REDACTED Nita Madhav; Dean Jamison; Dennis Carroll; Jonna Mazet; Nicole Stephenson; Cara Chrisman; nwolfe@metabiota.com; Samtha Maher; Peter Daszak; erubin@metabiota.com; Kierste Miller
Subject: Re: BCA updates and two requests

Dear GVP colleagues

Happy new year -- I hope that you all had a wonderful holiday and start to 2020.

We would of course be happy to prepare a short brief about the BCA activities, as well as a few slides, around the end of January. Please let us know if you have an exact deadline, or any specs we should bear in mind (e.g., how much background would be needed on methodologies employed, such as catastrophe modeling).

Since the last meeting we have made progress on several fronts, including:

Exceedance probability estimates

- Built on existing data sets and compiled additional data on losses from historical epidemics (cases, deaths), to provide an actuarial view of risk
- Developed preliminary baseline ("no GVP") estimates for Infrequent spillover / moderate R_0 pathogens (e.g., filoviruses) and respiratory non-influenza viruses (e.g., coronaviruses), with continuing development work on other catalogs
- Developed methodology for modeling GVP impacts on exceedance probability curves (e.g., via reduced spark risk, improved time to intervention)

Characterization of GVP impact

- Research into PREDICT-driven capacity building improvements, with preliminary indications of improvement to response time.
- Synthesized research (e.g. new key informant interviews) on potential GVP benefits for new product development

Economic losses

- Finalized methodology for estimating statistical value of lives lost (saved)
- Compiled revised dataset on shocks to national income from historical epidemics

Looking forward to our call next week,

Ben (and colleagues)

On Wed, Dec 18, 2019 at 2:58 PM [REDACTED] wrote:

Hi Dean, Ben, and Nita,

I am reaching out with updates and two requests related to BCA. Recently, a 501(c)3 non-profit organization was formed for the Global Virome Project, and GVP will be holding its first Board meeting in mid-February 2020. During the meeting, we would like to brief board members about the BCA group's great activities to date.

Would you be able to develop **a short brief about the BCA group's activities (1-2 page max), and a couple of slides**? Our timeline would likely be around the end of January, prior to the BOD meeting. My colleagues copied here can follow up with an exact deadline.

In addition to the request above, would you be able to share quick updates (some bullet points in an email to the group cc'ed here) about the progress of the analysis since our last meeting?

Please send your response to my colleagues copied here, as I will be handing my GVP work over. Thank you very much for your hard work.

Best wishes,

REDACTED

--

Ben Oppenheim, PhD

Director, Product Development // Senior Scientist

510.501.1097

--

Ben Oppenheim, PhD

Director, Product Development // Senior Scientist

510.501.1097

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Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

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Ben Oppenheim, PhD
Director, Product Development // Senior Scientist

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Dr Dennis Carroll
Global Virome Project, Core Team
Senior Fellow, Scowcroft Institute of International Affairs at the Bush School of Government and Public Service, Texas A&M University
Counselor and Advisor to the Faculty of Tropical Medicine at Mahidol University

mobile: 202-999-6144
email: REDACTED

--
Ben Oppenheim, PhD
Senior Director, Product Development // Senior Scientist

510.501.1097

From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Andrew Clements <aclements@usaid.gov>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, predict Sympa List <predict@ucdavis.edu>, Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, Alisa Pereira <apereira@usaid.gov>, Amalhin Shek <ashek@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>
Subject: PREDICT Y6Q1 Expend by Country/Category Report
Sent: Fri, 14 Feb 2020 21:47:18 +0000
PREDICT Quarterly Financial Report_By Country-Category_Y6Q1_final.pdf

Hi Andrew. Please find attached the PREDICT Y6Q1 Expenditure by Country and Category report for October-December 2019. If you have any questions, please let me know.

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
REDACTED *(cell)*
530-754-9034 (office)
Skype: ealeasure

PREDICT-2 Expenses Quarter 1 Year 6 (10/01/2019-12/31/2019) - Combined (Core + Ebola)

Cost Category	US Central	Bangladesh	Cambodia	Cameroon	China	Cote d'Ivoire	DRC	Egypt	Ethiopia
Salaries	743	63,801	44,079	10,770	0	30,759	-14,234	85,121	39,978
Fringe	347	25,298	18,023	4,406	0	11,964	-6,616	33,987	18,782
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	1,524	158	103	0	0	21	0	209	0
Foreign Travel	0	4,447	5,587	1,677	0	2,270	-639	6,157	8,348
Services	0	15,088	3,612	6,729	0	83,922	520	39,625	3,645
Supplies	117	3,532	431	108	0	579	0	3,747	108
Other	0	1,621	19,318	11,547	0	-5,120	6,859	1,052	35,024
Indirects	1,557	35,375	49,013	8,630	-983	16,361	-7,852	50,384	52,995
Total Costs	**$4,287**	**$149,319**	**$140,166**	**$43,866**	**-$983**	**$140,756**	**-$21,961**	**$220,283**	**$158,880**

Cost Category	Gabon	Ghana	Guinea	India	Indonesia	Jordan	Kenya	Lao PDR	Liberia
Salaries	0	30,302	3,535	10,633	63,908	31,954	6,508	23,374	64,786
Fringe	0	13,509	831	4,216	25,810	12,905	2,674	9,053	23,823
Equipment	0	0	0	0	0	0	16,726	0	0
Domestic Travel	0	0	0	26	155	78	0	0	0
Foreign Travel	0	1,241	2,429	741	4,903	2,451	11,894	67	2,639
Services	0	1,302	149	723	255,814	79,249	6,387	33,415	23,746
Supplies	0	54	106	589	1,608	804	19,593	25	106
Other	0	31,677	20,998	270	-596	-298	2,764	18,976	-191
Indirects	0	40,962	16,050	4,504	45,905	22,952	11,463	33,146	25,102
Total Costs	**$0**	**$119,047**	**$44,098**	**$21,703**	**$397,508**	**$150,095**	**$78,010**	**$118,056**	**$140,011**

Cost Category	Malaysia	Mongolia	Myanmar	Nepal	RoC	Rwanda	Senegal	Sierra Leone	South Sudan
Salaries	63,908	29,174	-3,589	59,188	2,127	68,330	33,173	3,076	0
Fringe	25,810	11,431	-1,290	19,818	843	24,082	13,927	1,231	0
Equipment	0	0	0	0	0	0	0	28,730	0
Domestic Travel	155	6,810	0	103	5	103	1,057	0	0
Foreign Travel	4,903	1,916	0	3,420	148	5,588	13,153	9,812	0
Services	5,058	-13,845	13,377	3,612	145	3,612	3,645	149	0
Supplies	1,608	216	0	457	118	431	13,969	554	0
Other	-596	1,457	5,681	10,004	54	39,271	7,937	8,385	0
Indirects	45,905	18,277	3,882	46,685	115	77,664	24,670	13,290	0
Total Costs	**$146,752**	**$55,436**	**$18,061**	**$143,287**	**$3,554**	**$219,081**	**$111,533**	**$65,227**	**$0**

Cost Category	Sudan	Tanzania	Thailand	Uganda	Vietnam
Salaries	0	22,178	59,207	12,870	34,221
Fringe	0	6,524	23,842	5,300	14,361
Equipment	0	0	0	0	0
Domestic Travel	0	-421	129	0	106
Foreign Travel	0	4,136	4,162	3,443	3,400
Services	0	3,645	4,335	3,645	0
Supplies	0	160	1,020	108	428
Other	0	35,387	-866	336	7,925
Indirects	0	27,816	43,037	10,523	28,010
Total Costs	**$0**	**$99,425**	**$134,865**	**$36,224**	**$88,451**

$3,025,040 **Y6Q1 PREDICT-2 Costs (Combined)** **$134,062,397 Obligated to Date**

$4,459,651 **Balance Remaining** *($77.64M Core for YR 1-6 + $56.42M Ebola for YR 2-6)*

PREDICT-2 Expenses Quarter 1 Year 6 (10/01/2019-12/31/2019) - CORE

Cost Category	US Central	Bangladesh	Cambodia	Cameroon	China	Cote d'Ivoire	DRC	Egypt	Ethiopia
Salaries	743	63,801	44,079	8,244	0	16,750	0	85,121	15,458
Fringe	347	25,298	18,023	3,426	0	6,799	0	33,987	7,856
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	0	158	103	0	0	21	0	209	0
Foreign Travel	0	4,447	5,587	687	0	1,280	0	6,157	687
Services	0	15,088	3,612	903	0	35,242	0	39,625	903
Supplies	0	3,532	431	108	0	579	0	3,747	108
Other	0	1,621	19,318	16,426	0	-68	12,143	1,052	27,929
Indirects	621	35,375	49,013	7,008	-983	11,397	6,921	50,384	23,378
Total Costs	**$1,711**	**$149,319**	**$140,166**	**$36,802**	**-$983**	**$72,001**	**$19,063**	**$220,283**	**$76,320**

Cost Category	Gabon	Ghana	Guinea	India	Indonesia	Jordan	Kenya	Lao PDR	Liberia
Salaries	0	4,122	1,670	10,633	63,908	31,954	5,990	23,374	1,145
Fringe	0	1,713	60	4,216	25,810	12,905	2,475	9,053	46
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	0	0	0	26	155	78	0	0	0
Foreign Travel	0	344	0	741	4,903	2,451	525	67	0
Services	0	451	149	723	255,814	79,249	451	33,415	149
Supplies	0	54	106	589	1,608	804	81	25	106
Other	0	22,501	11,075	270	-596	-298	5,275	18,976	33
Indirects	0	13,236	7,489	4,504	45,905	22,952	4,990	33,146	887
Total Costs	**$0**	**$42,421**	**$20,549**	**$21,703**	**$397,508**	**$150,095**	**$19,788**	**$118,056**	**$2,366**

Cost Category	Malaysia	Mongolia	Myanmar	Nepal	RoC	Rwanda	Senegal	Sierra Leone	South Sudan
Salaries	63,908	29,174	-3,589	59,188	2,127	68,330	9,311	1,145	0
Fringe	25,810	11,431	-1,290	19,818	843	24,082	3,707	46	0
Equipment	0	0	0	0	0	0	0	0	0
Domestic Travel	155	6,810	0	103	5	103	0	0	0
Foreign Travel	4,903	1,916	0	3,420	148	5,588	687	0	0
Services	5,058	-13,845	13,377	3,612	145	3,612	903	149	0
Supplies	1,608	216	0	457	118	431	108	106	0
Other	-596	1,457	5,681	10,004	54	39,271	10,856	33	0
Indirects	45,905	18,277	3,882	46,685	115	77,664	7,776	887	0
Total Costs	**$146,752**	**$55,436**	**$18,061**	**$143,287**	**$3,554**	**$219,081**	**$33,348**	**$2,366**	**$0**

Cost Category	Sudan	Tanzania	Thailand	Uganda	Vietnam
Salaries	0	10,237	59,207	8,244	34,221
Fringe	0	4,650	23,842	3,426	14,361
Equipment	0	0	0	0	0
Domestic Travel	0	0	129	0	106
Foreign Travel	0	687	4,162	687	3,400
Services	0	903	4,335	903	0
Supplies	0	108	1,020	108	428
Other	0	33,499	-866	5,286	7,925
Indirects	0	18,574	43,037	7,008	28,010
Total Costs	**$0**	**$68,660**	**$134,865**	**$25,662**	**$88,451**

$2,426,692 **Y6Q1 PREDICT-2 Costs (CORE)** **$77,642,397 Obligated to Date**

$3,750,465 **Balance Remaining** *($13.6M/YR for YR 1-2 + $16.3M Y3 + $17.05M Y4 + $16.49M Y5 + $600K Jordan)*

PREDICT-2 Expenses Quarter 1 Year 6 (10/01/2019-12/31/2019) - Ebola

Cost Category	*US Central*	*Cameroon*	*Cote d'Ivoire*	*DRC*	*Ethiopia*	*Ghana*	*Guinea*	*Kenya*	*Liberia*
Salaries	*0*	*2,526*	*14,009*	*-14,234*	*24,519*	*26,181*	*1,865*	*518*	*63,642*
Fringe	*0*	*979*	*5,165*	*-6,616*	*10,926*	*11,796*	*771*	*199*	*23,778*
Equipment	*0*	*0*	*0*	*0*	*0*	*0*	*0*	*16,726*	*0*
Domestic Travel	*1,524*	*0*	*0*	*0*	*0*	*0*	*0*	*0*	*0*
Foreign Travel	*0*	*990*	*990*	*-639*	*7,660*	*897*	*2,429*	*11,369*	*2,639*
Services	*0*	*5,825*	*48,680*	*520*	*2,742*	*851*	*0*	*5,936*	*23,597*
Supplies	*117*	*0*	*0*	*0*	*0*	*0*	*0*	*19,512*	*0*
Other	*0*	*-4,879*	*-5,052*	*-5,283*	*7,095*	*9,175*	*9,924*	*-2,511*	*-224*
Indirects	*935*	*1,621*	*4,963*	*-14,773*	*29,617*	*27,726*	*8,561*	*6,472*	*24,215*
Total Costs	**$2,576**	**$7,064**	**$68,755**	**-$41,024**	**$82,560**	**$76,626**	**$23,550**	**$58,222**	**$137,645**

Cost Category	*Senegal*	*Sierra Leone*	*Tanzania*	*Uganda*
Salaries	*23,863*	*1,931*	*11,940*	*4,626*
Fringe	*10,220*	*1,186*	*1,874*	*1,874*
Equipment	*0*	*28,730*	*0*	*0*
Domestic Travel	*1,057*	*0*	*-421*	*0*
Foreign Travel	*12,466*	*9,812*	*3,449*	*2,755*
Services	*2,742*	*0*	*2,742*	*2,742*
Supplies	*13,862*	*448*	*52*	*0*
Other	*-2,919*	*8,351*	*1,888*	*-4,950*
Indirects	*16,894*	*12,403*	*9,242*	*3,515*
Total Costs	**$78,185**	**$62,861**	**$30,765**	**$10,562**

$598,348 **Y6Q1 PREDICT-2 Costs (Ebola)** **$56,420,000 Obligated to Date**

$709,185 **Balance Remaining**

From: Andrew Clements <aclements@usaid.gov>
Sent: Tue, 18 Feb 2020 22:09:24 +0100
Subject: Re: PREDICT Y6Q1 Expend by Country/Category Report
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, predict Sympa List <predict@ucdavis.edu>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Alisa Pereira <apereira@usaid.gov>, Amalhin Shek <ashek@usaid.gov>, Cara Chrisman <cchrisman@usaid.gov>

Thanks!

Andrew Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
E-mail: aclements@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

On Tue, Feb 18, 2020 at 10:08 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Yes.
>
> *Elizabeth Leasure*
>
> *Financial Operations Manager*
>
> *One Health Institute*
>
> REDACTED *(cell)*
>
> *530-754-9034 (office)*
>
> *Skype: ealeasure*
>
> **From:** Andrew Clements <aclements@usaid.gov>
> **Sent:** Tuesday, February 18, 2020 12:53 PM
> **To:** Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
> **Cc:** Jonna Mazet <jkmazet@ucdavis.edu>; predict Sympa List <predict@ucdavis.edu>; Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>; Alisa Pereira <apereira@usaid.gov>; Amalhin Shek <ashek@usaid.gov>; Cara Chrisman <cchrisman@usaid.gov>
> **Subject:** Re: PREDICT Y6Q1 Expend by Country/Category Report
>
> # On track to complete by 3/31/20?
>
> Andrew Clements, Ph.D.
> Senior Scientific Advisor
> Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
>
> U.S. Agency for International Development
>
> Mobile phone: 1-571-345-4253
> E-mail: aclements@usaid.gov

On Tue, Feb 18, 2020 at 6:22 PM Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Andrew. As of the Y6Q1 report, we have $108K left in cost share to certify in order to fulfill our LOP cost share obligation of $3.7M for PREDICT.
>
> Thanks,
>
> Liz

Elizabeth Leasure

Financial Operations Manager

One Health Institute

REDACTED *cell)*

530-754-9034 (office)

Skype: ealeasure

From: Andrew Clements <aclements@usaid.gov>
Sent: Saturday, February 15, 2020 12:54 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>; predict Sympa List <predict@ucdavis.edu>; Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>; Alisa Pereira <apereira@usaid.gov>; Amalhin Shek <ashek@usaid.gov>; Cara Chrisman <cchrisman@usaid.gov>
Subject: Re: PREDICT Y6Q1 Expend by Country/Category Report

Thanks, Liz.

Can you provide a status update on Predict's progress meeting the cost share? (I don't regularly get the standard form that includes this information.)

Andrew P. Clements, Ph.D.

Senior Scientific Advisor

Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health

U.S. Agency for International Development

Mobile phone: 1-571-345-4253

Email: aclements@usaid.gov

On Feb 14, 2020, at 10:47 PM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Andrew. Please find attached the PREDICT Y6Q1 Expenditure by Country and Category report for October-December 2019. If you have any questions, please let me know.
>
> Thanks,
>
> Liz
>
> *Elizabeth Leasure*
>
> *Financial Operations Manager*
>
> *One Health Institute*
>
> REDACTED *(cell)*
>
> *530-754-9034 (office)*
>
> *Skype: ealeasure*
>
> <PREDICT Quarterly Financial Report_By Country-Category_Y6Q1_final.pdf>

From: Andrew Clements <aclements@usaid.gov>
Sent: Thu, 20 Feb 2020 02:19:41 -0500
Subject: Re: SARS-CoV-2 synthesis
To: "Anthony, Simon J." <sja2127@cumc.columbia.edu>
Cc: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, "Wells, Heather" <hlw2124@cumc.columbia.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>, Tracey Goldstein <tgoldstein@ucdavis.edu>

Thanks, Simon. Will take a look.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Feb 19, 2020, at 8:04 PM, Anthony, Simon J. <sja2127@cumc.columbia.edu> wrote:

> Hi Andrew –
>
> Just sharing this with you in case it is useful. Obviously, things change by the day, but this is nonetheless intended to help summarize where we are currently with the SARS-CoV-2 epidemic.
>
> Heather – thanks for putting this together.
>
> S.
>
> ---
> Simon J Anthony, D.Phil
> Assistant Professor, Columbia University
> 722 West 168th Street, 17th Floor, NY, NY, 10032
> Email: sja2127@cumc.columbia.edu
> Mobile: [redacted]
> Office: 212-342-0558
> <The epidemiology and genetic composition of 2019-nCoV.pdf>

From:	Woutrina A Smith <wasmith@ucdavis.edu>
To:	Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
CC:	Oladele Ogunseitan <oladele.ogunseitan@uci.edu>;Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh" <Karesh@ecohealthalliance.org>;mr84@columbia.edu <mr84@columbia.edu>;alexandra zuber <alexandrazuber@atahealthstrategies.com>;Matthew Blake <mblake@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Terra Kelly <trkelly@ucdavis.edu>;Jaber Amine Belkhiria <jabelkhiria@ucdavis.edu>;Elizabeth Leasure <ealeasure@UCDAVIS.EDU>;Jonna Mazet <jkmazet@ucdavis.edu>;McNeil, Carrie S. <csmcnei@sandia.gov>;Jutta Lehmer <JLehmer@salud.unm.edu>;Omar Romero-hernandez <oromero@haas.berkeley.edu>;Bruce Baird Struminger <BStruminger@salud.unm.edu>;Federico Castillo <f.castillo@berkeley.edu>;Ndola PRATA <ndola@berkeley.edu>;Tiffany Harris, PhD, MS" <th2604@columbia.edu>;Costa, Cristiane <co123@cumc.columbia.edu>;Amaya, Idalia M. <ima2107@cumc.columbia.edu>;Sam Halabi <sfh9@georgetown.edu>;onehealthnextgen Sympa List <onehealthnextgen@ucdavis.edu>
Sent:	2/20/2020 9:09:52 AM
Subject:	Re: Reminder: OHW-NG - Executive Board Call February 12th Cancelled

Hi OHW-NG Executive Board,

A few quick updates here since we aren't having an EB call until next week:

- The AFROHUN Kampala meetings went well last week, it was tremendously helpful to have some facetime with the Secretariat team to allay anxiety about change in general and to have discussions about launching Year 1 activities.

- Year 1 Work Plan revisions are underway and will be submitted back to USAID this week. Thank you to all who provided quick turnaround info requests to be responsive to USAID clarification requests.

- Planning is underway for the strategic planning workshops with AFROHUN at the end of March and with SEAOHUN at the end of April. More details to come on this.

- The Consortium of Universities for Global Health Conference in in Washington DC starting April 18, 2020. If folks will be in the area and want to get together for a OHW-NG afternoon working meeting and/or dinner meeting on Saturday, April 18, please let me know. Not critical but it would be nice to overlap and discuss plans if folks are interested and will be in the area. I'll mention this on EB call next week when we should then make a decision on scheduling.

- We submitted a coronavirus emergency response funds concept on launching a SEAOHUN and and AFROHUN Outbreak Response ECHO platform last week and it is being circulated at USAID. No update yet on whether it will move forward.

Best wishes, Woutrina

Woutrina Smith, DVM, MPVM, PhD
Professor of Infectious Disease Epidemiology
Associate Director, UCD One Health Institute
Technical Director, USAID One Health Workforce - Next Gen
Co-Director, UCGHI Planetary Health Center of Expertise
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1089 Veterinary Medicine Dr
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wasmith@ucdavis.edu
+1 530 219-1369

On Feb 4, 2020, at 10:17 AM, Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU> wrote:

Dear all,

Please note we are cancelling next week's OHW-NG EB call (February 12th). We will resume these fantastic

discussions on February 26th but please feel free to reach out to me or onehealthnextgen@ucdavis.edu with any questions.

Regards,

Corina Monagin, MPH, DrPH
Project Scientist
One Health Institute
School of Veterinary Medicine
University of California Davis
1089 Veterinary Medicine Drive
Davis, CA 95616, USA

Mobile: +1.415.741.6996

From: David J Wolking <djwolking@ucdavis.edu>
To: Ava Sullivan <sullivan@ecohealthalliance.org>
CC: Tammie O'Rourke <torourke@metabiota.com>;David Wolking <djwolking@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh <karesh@ecohealthalliance.org>;Kevin Olival <Olival@ecohealthalliance.org>;Jon Epstein <epstein@ecohealthalliance.org>;Alice Latinne <latinne@ecohealthalliance.org>;Emily Hagan <hagan@ecohealthalliance.org>;Aleksei Chmura <chmura@ecohealth.net>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 3/10/2020 4:18:08 PM
Subject: Re: [predict] Re: Urgent: Government reports requiring approval for public release of data

Whoop!

On Tue, Mar 10, 2020 at 4:13 PM Ava Sullivan <sullivan@ecohealthalliance.org> wrote:
Another great update!
The reports for CIV have been approved.

Many thanks,
Ava

Ava Sullivan
PREDICT-2 Operations Coordinator
Country Liaison, India

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001
607-280-7669 (mobile)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

On Mar 9, 2020, at 11:17 AM, Tammie O'Rourke <torourke@metabiota.com> wrote:

Thank-you so much Ava, I have updated EIDTH with the releases for Jordan & Egypt.
I will get the Liberia final report published sometime today.
Tammie

On Mon, Mar 9, 2020 at 8:12 AM Ava Sullivan <sullivan@ecohealthalliance.org> wrote:
Hi David!
Thanks for the message and the support. We are actively working on all of these reports with the country teams. Three fantastic updates as we whittle this list down:

The Jordan reports have been approved for release
The Egypt reports have been approved for release
The Liberia report can be made into a final draft and Jim is ready to share with Gov. contacts.

I CC'd Tammie so she can make these changes in EIDITH. Tammie, forgive me if I should be sending this info to someone else.

Thanks!,
Ava

Ava Sullivan
PREDICT-2 Operations Coordinator
Country Liaison, India

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

607-280-7669 (mobile)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

On Mar 6, 2020, at 4:47 PM, David J Wolking <djwolking@ucdavis.edu> wrote:

--
Tammie O'Rourke
Metabiota
Senior Information Management Developer
Emerging Pandemic Threats - PREDICT Program
tel +1-250-618-2460

From:	Tammie O'Rourke <torourke@metabiota.com>
To:	Ava Sullivan <sullivan@ecohealthalliance.org>
CC:	David Wolking <djwolking@ucdavis.edu>;Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh <karesh@ecohealthalliance.org>;Kevin Olival <Olival@ecohealthalliance.org>;Jon Epstein <epstein@ecohealthalliance.org>;Alice Latinne <latinne@ecohealthalliance.org>;Emily Hagan <hagan@ecohealthalliance.org>;Aleksei Chmura <chmura@ecohealth.net>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent:	3/12/2020 6:48:18 AM
Subject:	[predict] Re: Urgent: Government reports requiring approval for public release of data

Great news, thanks Ava. I have updated EIDITH.

On Tue, Mar 10, 2020 at 4:13 PM Ava Sullivan <sullivan@ecohealthalliance.org> wrote:
Another great update!
The reports for CIV have been approved.

Many thanks,
Ava

Ava Sullivan
PREDICT-2 Operations Coordinator
Country Liaison, India

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607-280-7669 (mobile)
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Metabiota
Senior Information Management Developer
Emerging Pandemic Threats - PREDICT Program
tel +1-250-618-2460

From: Murray, Suzan <MurrayS@si.edu>
To: maher@ecohealthalliance.org <maher@ecohealthalliance.org>;Peter Daszak <daszak@ecohealthalliance.org>
CC: Galicia, Veronica <GaliciaV@si.edu>;jkmazet@ucdavis.edu" <jkmazet@ucdavis.edu>
Sent: 3/23/2020 10:04:29 AM
Subject: GVP

Dear Samantha and Peter

We recognize that this is a very busy time but wanted to see if there's anything we can do to facilitate putting the lawyers in touch. I would very much like to participate with GVP but unfortunately may not do so until our legal team has granted permission.

Peter, is it OK for us to work directly with Samantha to get this organized?

Many thanks,

Suzan

From:	alexandra zuber <alexandrazuber@atahealthstrategies.com>
To:	oromero@haas.berkeley.edu <oromero@haas.berkeley.edu>;Federico Castillo <f.castillo@berkeley.edu>;Elizabeth Leasure <ealeasure@ucdavis.edu>;Matthew Blake <mblake@ucdavis.edu>;Sam Halabi <sfh9@georgetown.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Woutrina A Smith <wasmith@ucdavis.edu>;Terra Kelly <trkelly@ucdavis.edu>;daszak@ecohealthalliance.org" <daszak@ecohealthalliance.org>;William B. Karesh" <karesh@ecohealthalliance.org>
CC:	Carolyn Forlee <cforlee@ucdavis.edu>
Sent:	3/31/2020 12:24:34 PM
Subject:	Doodle for participation in OCA, SWOT, and NUPAS calls with AFROHUN

Dear Obj 3 Benchmarking and Business Planning Group (BPG), Jonna, Woutrina, and Terra, Tomorrow in our Objective 3 call with AFROHUN I'll be discussing the dates for our three proposed two hour Zoom calls with AFROHUN, for which proposed a window between April 8-17. The time window for these calls are 7:00 am- 9:00 am PST/ 10:00 am- 12:00 pm EST.

Before our 10 am EST call tomorrow, can you populate the Doodle Poll with all of your windows of availability for these three calls? That way I will know if there are any days that really don't work well for us. You are the core folks I envision being on these calls from the global team (we can discuss adding people as needed, also considering feasibility).

Note- I removed April 9th as a possible date, given their ECHO COVID planned for that same time.

I'd like to start with just one meeting the week of April 7th, so we have time to debrief on what worked or didn't work from the call format, before we hold the subsequent two. I think it's best to start with SWOT, and then have OCA and NUPAS in the following week.

Thanks all,

Alexandra Zuber, MPP, DrPH
Founder and CEO, Ata Health Strategies, LLC
Email: alexandrazuber@atahealthstrategies.com
Phone: +1 (617) 680-3950
LinkedIn: alexandrazuber/
Website: www.atahealthstrategies.com
Twitter: @alexandrazuber

From: Andrew Clements <aclements@usaid.gov>
Sent: Wed, 1 Apr 2020 12:21:19 -0700
Subject: Extension work plan
To: djwolking@ucdavis.edu
Cc: predictmgt@usaid.gov, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Attachment
PREDICT COVID-19 Workplan (USAID draft)_v3_APC.docx

Hi David,
Made a few edits (see attached). If okay with you all, please accept all changes, attach the budget breakout, send me a copy, and consider it AOR approved.

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

Begin forwarded message:

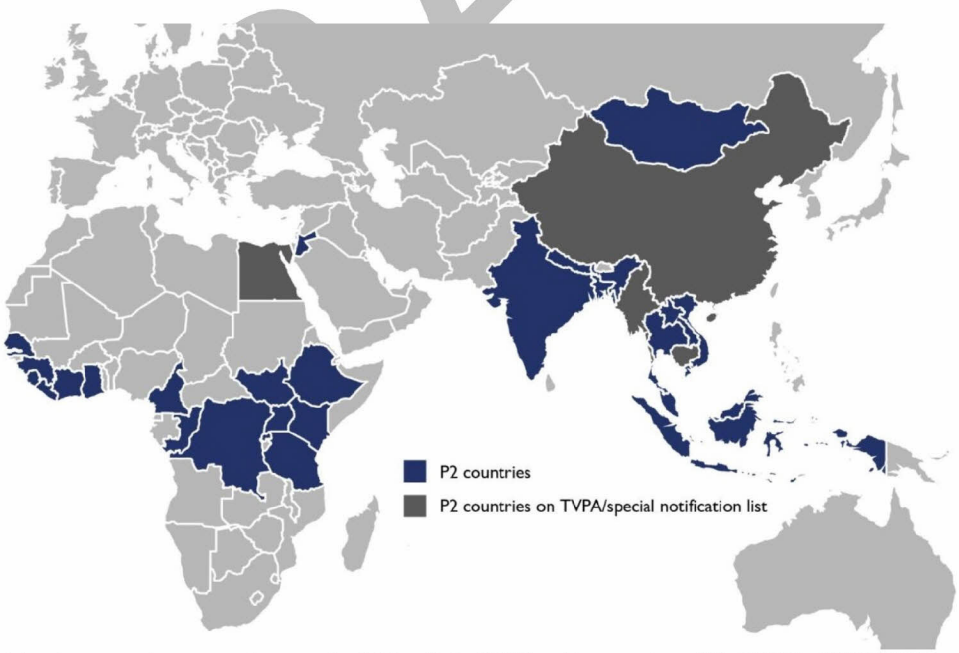
From: "Andrew P. Clements" <REDACTED
Date: April 1, 2020 at 9:15:16 PM GMT+2
To: Andrew Clements <aclements@usaid.gov>

PREDICT-2 COVID-19 Workplan
Emergency Support for the SARS CoV-2 Pandemic

As a USAID-funded development project, over the past 10 years, PREDICT has aimed to strengthen the capacity of host country partners in the health security sector, especially for infectious disease prevention and surveillance, as well as outbreak preparedness. Our approach to capacity strengthening has worked to establish the essential infrastructure and provide hands-on experiences for the One Health workforce in surveillance and pathogen detection. PREDICT has dedicated the most recent portion of this second phase (2014-2019) to ensuring that host country partners are well positioned to lead One Health surveillance through the transfer of knowledge, skills, capabilities, and technologies.

On December 31, 2019, China reported a cluster of atypical pneumonia of unknown cause. Since that time, a novel coronavirus has been characterized with likely zoonotic origins and potential involvement of a live animal market in the initial outbreak in China. This new virus, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS CoV-2) has been confirmed as the agent causing Coronavirus Disease 2019 (COVID-19) in people, and the World Health Organization (WHO) officially declared a COVID-19 pandemic on March 11, 2020. The primary concern is an informed and effective global response to the COVID-19 pandemic, and there is also a need for investigation into likely animal source(s) of this pandemic to better prepare for future SARS CoV-2 or SARS-like outbreaks.

PREDICT's Global Network



During this six-month extension period (April 1, 2020 – September 30, 2020), PREDICT will use its technical expertise, data, and biological specimens to assist countries through the

project's existing global network (see map above). Specifically, we will provide technical assistance with detection and characterization of human and animal SARS CoV-2 cases to inform pandemic response. As possible, we will also investigate the animal source(s) of this virus and other potential intermediate hosts.

Scope of Work

Note: the following represents the 6-month work plan of April 1, 2020. However, due to the dynamic pandemic environment (e.g. changes in virus spread, travel and shipping constraints, and expansion of efforts by other donors and development partners to assist affected countries), it is possible that country needs may shift over the next 6 months. As a results, changes may be necessary to the work plan. Any changes to activities or country budgets will be submitted to the AOR for approval.

Objective 1: Support initial detection of SARS CoV-2 to inform public health response

Activities (as feasible and appropriate during a pandemic):

- Based on emergency needs assessments at the start of the pandemic, work with PREDICT-2 global collaborating laboratories (up to 28 countries in Africa, Asia, and the Middle East that previously conducted work under PREDICT-2[1]) to evaluate technical, personnel, and resource demands for pandemic response.
- Provide technical and resource assistance to laboratories for initial detection[2] of SARS CoV-2 in collaborating laboratories; assistance could include external technical and commodity support such as specific SARS CoV-2 primers, probes, positive controls, updated protocols, and training; funding for personnel; knowledge and technology transfer; or other assistance as needs emerge.

Timeline: April – June 2020

Expected outcomes: Demand-driven assistance to countries supporting pandemic response and conduct of rapid and high-quality in-country testing for SARS CoV-2 to inform control measures.

Objective 2: Conduct investigations to characterize potential animal source(s) of SARS CoV-2 and previous spillover of SARS-like viruses

Activities (as feasible and appropriate during a pandemic):

- In participating countries, participate in technical discussions at the global, regional, and/or country level to plan and prioritize retrospective and prospective (if possible) research towards identifying SARS CoV-2 animal source(s) of and intermediate hosts(s).

[1] To conduct work in China, Cambodia, Egypt, and Myanmar, special notification and TVPA waivers are required.

[2] Limited to "jump starting" detection after the virus is introduced to countries. Not intended to support widespread testing as the virus spreads rapidly.

- Identify relevant data and samples collected by PREDICT-2 in South and Southeast Asia[3] that could provide insight into the possible animal host(s) of SARS CoV-2.
- Conduct testing for SARS-like viruses using previously collected PREDICT-2 samples (animals and humans) in South and Southeast Asia[2] to evaluate a) potential reservoir host(s) and intermediate host(s), and b) evidence for prior spillover events among humans in the region.
- Conduct additional analyses of existing project data from markets in mainland Southeast Asia with a focus on live animal markets, including but not limited to human behaviors, types of animals present, value chains and networks, and other risks for virus spillover and spread at high-risk hypothesized SARS CoV-2 interfaces.

Timeline: April – September 2020 (global analysis and planning); May – September 2020 (testing and analyses)

Outcomes: Prioritized list of data and samples for analysis; investigations aimed at identifying animal hosts for SARS CoV-2; insights shared that enable countries in the South and Southeast Asia region (and beyond) to design and target prevention strategies to reduce the risk of future spillovers of SARS CoV-2 and related viruses from animals to people.

Objective 3: Managing and Coordinating Operations

Activities:

- Implement the workplan and strategy.
- Effectively execute, monitor, and close-out the Cooperative Agreement and any sub-award agreements, sub-contracts, and service agreements while ensuring compliance.
- Respond to all requests for information.
- Submit financial and technical reports, including the Cooperative Agreement final report (which will include work conducted during this extension).
- Release data into USAID's Data Development Library for public access and use.
- Assure compliance with all federal regulations and host country laws and regulations.
- Hold separate biweekly coordination meetings with USAID Management Team and the project Executive Board.
- Assure professional and effective communications with USAID and all partners and stakeholders.
- Hold the end of project briefing for USAID (which was postponed in March 2020) to showcase achievements, findings, impact, and recommendations to inform future directions for pandemic prevention, surveillance, detection, and response.

Timeline: April – September 2020

Outcomes: Implementation of workplan; ensured compliance with USG policies and regulations and with host country policy and regulations; timely submission of all reports and response to

[3] Currently planned for Indonesia, Laos, Malaysia, Nepal, Thailand, and Viet Nam as data and evidence dictate, as well as Cambodia and other countries in the region pending special notification.

data call requests; compilation and submission of final project report; successful out-briefing and project wrap-up meeting.

Total Budget: up to **$3.0 M**

Budget Breakout by Objectives and Countries:

From:	Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>
To:	Woutrina A Smith <wasmith@ucdavis.edu>;Oladele Ogunseitan <oladele.ogunseitan@uci.edu>;Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh <Karesh@ecohealthalliance.org>;mr84@columbia.edu" <mr84@columbia.edu>;alexandra zuber <alexandrazuber@atahealthstrategies.com>;Matthew Blake <mblake@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Terra Kelly <trkelly@ucdavis.edu>;Jaber Amine Belkhiria <jabelkhiria@ucdavis.edu>;Elizabeth Leasure <ealeasure@UCDAVIS.EDU>;Jonna Mazet <jkmazet@ucdavis.edu>;McNeil, Carrie S. <csmcnei@sandia.gov>;Jutta Lehmer <JLehmer@salud.unm.edu>;Omar Romero-hernandez <oromero@haas.berkeley.edu>;Bruce Baird Struminger <BStruminger@salud.unm.edu>;Federico Castillo <f.castillo@berkeley.edu>;Ndola PRATA <ndola@berkeley.edu>;Tiffany Harris, PhD, MS" <th2604@columbia.edu>;Costa, Cristiane <co123@cumc.columbia.edu>;Amaya, Idalia M. <ima2107@cumc.columbia.edu>;Sam Halabi <sfh9@georgetown.edu>
CC:	onehealthnextgen Sympa List <onehealthnextgen@ucdavis.edu>
Sent:	4/3/2020 7:06:01 AM
Subject:	Re: [onehealthnextgen] OHW-NG One Health ECHO Session Series - SAVE THE DATE!

My apologies – I forgot the attachment. Late night email…

C

From: on behalf of Corina Grigorescu Monagin
Date: Thursday, April 2, 2020 at 8:30 PM
To: Woutrina A Smith , Oladele Ogunseitan , Peter Daszak , "'William B. Karesh, D.V.M'" , "mr84@columbia.edu" , alexandra zuber , Matthew Blake , Tracey Goldstein , David J Wolking , Terra Kelly , Jaber Amine Belkhiria , Liz Leisure , Jonna Mazet , "McNeil, Carrie S." , Jutta Lehmer , Omar Romero-hernandez , Bruce Baird Struminger , Federico Castillo , Ndola PRATA , "Tiffany Harris, PhD, MS" , "Costa, Cristiane" , "Amaya, Idalia M." , Sam Halabi
Cc: onehealthnextgen Sympa List
Subject: [onehealthnextgen] OHW-NG One Health ECHO Session Series - SAVE THE DATE!

Hello OHW-NG EB team,

Please see attached for next week's ECHO session *Save the Date* flyer. This is the beginning of a series that will run every two weeks with varied topics. The next sessions are on April 8-9th (one each for the Africa and Asia time zones) and will focus on COVID-19 community surveillance topics.

For internal information, this flyer does not specifically state COVID-19 because we are waiting on approval from USAID for updated activity tracking. We expect the approval to come through by early next week, in which case we are then free to advertise COVID-19 focus on all documents going forward. We will have an updated announcement early next week with the detailed agenda for the session. Please remember to register in advance!

Any questions, please let us know.

Stay safe and healthy,

Corina

Corina Monagin, MPH, DrPH
Project Scientist
One Health Institute
School of Veterinary Medicine
University of California Davis
1089 Veterinary Medicine Drive

Davis, CA 95616, USA

Mobile: +1.415.741.6996

USAID
FROM THE AMERICAN PEOPLE

HCEA
Championing One Health

SEAOHUN
Southeast Asia One Health University Network

ONE HEALTH UPDATES

ECHO biweekly sessions for AFROHUN & SEAOHUN members and stakeholders

NEXT SESSION: APRIL 8-9, 2020

SESSION TOPIC:

COMMUNITY SURVEILLANCE

AGENDA COMING SOON!

AFROHUN
AFRICA ONE HEALTH UNIVERSITY NETWORK

SEAOHUN
SOUTHEAST ASIA ONE HEALTH UNIVERSITY NETWORK

AFRICA SESSION [90 minutes]
Thursday, April 9
US: 9:30 am EDT | 7:30 am MDT | 6:30 am PDT
Africa: 1:30 pm GMT | 2:30 pm WAT | 3:30 pm CAT and SAST | 4:30 pm EAT

SOUTHEAST ASIA SESSION [90 minutes]
Wednesday, April 8 (USA)/Thursday, April 9 (SE Asia)
US: 9 pm EDT, 7 pm MDT, 6 pm PDT
Southeast Asia: 8 am ICT, 9 am MYT, 9 am PHT

Visit our website for free pre-registration and connection information at ohwng.org

Questions? Contact onehealthnextgen@ucdavis.edu

UCDAVIS One Health Institute School of Veterinary Medicine
EcoHealth Alliance
Ata Health Strategies
ICAP Columbia University Mailman School of Public Health
Berkeley University of California
Project ECHO
UCI University of California, Irvine

From:	Peter Daszak <daszak@ecohealthalliance.org>
To:	Andrew Clements <aclements@usaid.gov>;Jonna Mazet <jkmazet@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;djwolking@ucdavis.edu" <djwolking@ucdavis.edu>;William B. Karesh <karesh@ecohealthalliance.org>
CC:	predictmgt@usaid.gov <predictmgt@usaid.gov>
Sent:	4/3/2020 4:12:11 PM
Subject:	RE: Trump ended coronavirus detection pandemic program - Los Angeles Times

I agree the headline for this story is unfortunate, but as you know something we can't control. Behind that, the story is actually not too unbalanced.

We're in a bit of catch-22 here because the journalists saw the news that PREDICT has an extension (good news), but decided to focus on the closure. I certainly gave them quotes about how successful PREDICT has been and how important it was to dealing with COVID-19, but they went with a different angle.

Bottom line, I think it is important that we are voices in these stories – it wouldn't look good to have them say "we reached out for comment but there was no response." It would also be really bad if they interviewed people who reinforced the political angle, which we didn't, and won't.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Andrew Clements
Sent: Friday, April 3, 2020 11:09 AM
To: Jonna Mazet ; Christine Kreuder Johnson ; djwolking@ucdavis.edu; Peter Daszak ; William B. Karesh
Cc: predictmgt@usaid.gov
Subject: Trump ended coronavirus detection pandemic program - Los Angeles Times

Hi all,

Just read the following article:

https://www.latimes.com/science/story/2020-04-02/coronavirus-trump-pandemic-program-viruses-detection

Can I respectfully request that, from now on, all people associated with Predict resist from providing any quotes to media that have anything to do with the ending of Predict? So no public speculating on why it

ended and no public lamenting that it's ended. Yes, it's unfortunate that the work will not continue, but I think the point has been made enough times now.

A more-helpful alternative (which some of you have used) is to talk about all the great things that were accomplished by Predict and how USAID was visionary in supporting this kind of work when no one else did and in the face of many critics. So more of "we had a great run for 10 years" and less of "it should have run for another 10 years.

As always, any questions about why Predict is ending or the future of the EPT program should be referred to USAID. As noted in the article, USAID is planning a new project to reduce spillover which is a natural transition of part of the portfolio. Unfortunately, many of the articles about Predict ending neglect to say there are other continuing and new investments under EPT.

Thanks for your understanding. Please let me know if you have any questions.

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

From: David J Wolking <djwolking@ucdavis.edu>
Sent: Mon, 6 Apr 2020 12:41:23 -0700
Subject: Re: Extension work plan
To: Andrew Clements <aclements@usaid.gov>
Cc: David J Wolking <djwolking@ucdavis.edu>, PREDICTMGT <predictmgt@usaid.gov>, Amalhin Shek <ashek@usaid.gov>, Alisa Pereira Emerging Threats Division <apereira@usaid.gov>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, Elizabeth Leasure <ealeasure@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>
PREDICT COVID-19 Workplan (FINAL)_v2.docx

I sure can, is this what you had in mind?
David

On Mon, Apr 6, 2020 at 12:33 PM Andrew Clements <aclements@usaid.gov> wrote:

> Hi David,
>
> Since you have 3 objectives in the narrative, but only 2 in the budget table, would it be possible to remove the mention of objective 3 and add a sentence that states that the costs of those management-like activities are included in the objective 1 and 2 costs?
>
> Andrew

Andrew Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
E-mail: aclements@usaid.gov

For more information on USAID's Emerging Pandemic Threats program, see: http://www.usaid.gov/ept2

On Sun, Apr 5, 2020 at 11:29 PM David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi Andrew,
> Please find attached the updated workplan with budget breakdown.
>
> Let us know if you have any questions or concerns, happy to clarify but hopefully this version is on target.
>
> Best,
>
> David
>
> On Wed, Apr 1, 2020 at 12:43 PM David J Wolking <djwolking@ucdavis.edu> wrote:
>
> > Thanks Andrew, working on it this afternoon with the team!
> > David
> >
> > On Wed, Apr 1, 2020 at 12:21 PM Andrew Clements <aclements@usaid.gov> wrote:
> >
> > > Hi David,
> > > Made a few edits (see attached). If okay with you all, please accept all changes, attach the budget breakout, send me a copy, and consider it AOR approved.
> > >
> > > Andrew
> > >
> > > *Andrew P. Clements, Ph.D.*
> > > *Senior Scientific Advisor*

Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

Begin forwarded message:

From: "Andrew P. Clements" REDACTED
Date: April 1, 2020 at 9:15:16 PM GMT+2
To: Andrew Clements <aclements@usaid.gov>

PREDICT-2 COVID-19 Workplan
Emergency Support for the SARS CoV-2 Pandemic

As a USAID-funded development project, over the past 10 years, PREDICT has aimed to strengthen the capacity of host country partners in the health security sector, especially for infectious disease prevention and surveillance, as well as outbreak preparedness. Our approach to capacity strengthening has worked to establish the essential infrastructure and provide hands-on experiences for the One Health workforce in surveillance and pathogen detection. PREDICT has dedicated the most recent portion of this second phase (2014-2019) to ensuring that host country partners are well positioned to lead One Health surveillance through the transfer of knowledge, skills, capabilities, and technologies.

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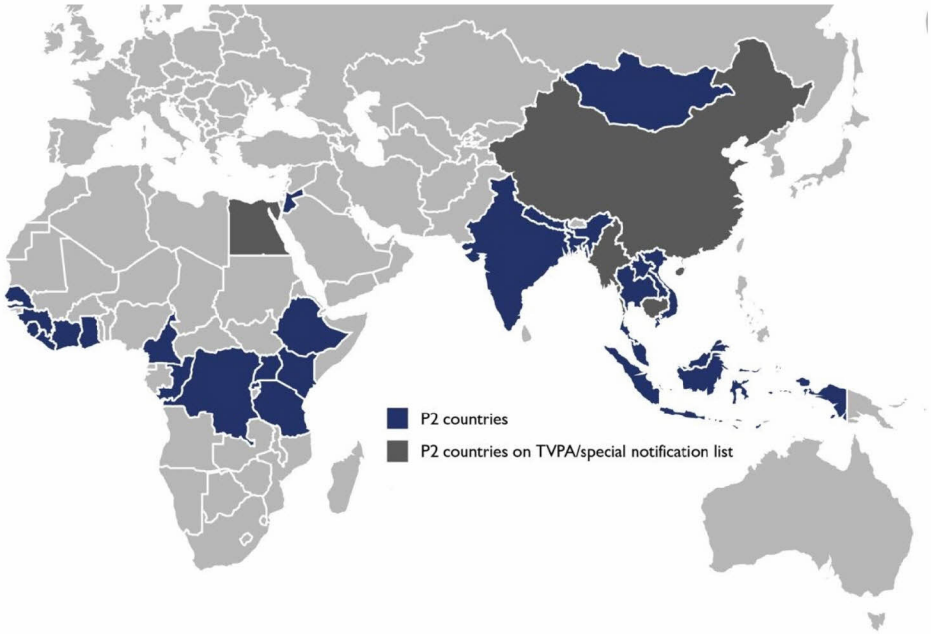
PREDICT's Global Network



During this six-month extension period (April 1, 2020 – September 30, 2020), PREDICT will use its technical expertise, data, and biological specimens to assist countries through the project's existing global network (see map above). Specifically, we will provide technical assistance with detection and characterization of human and animal SARS CoV-2 cases to inform pandemic response. As possible, we will also investigate the animal source(s) of this virus and other potential intermediate hosts.

Scope of Work

Note: the following represents the 6-month work plan of April 1, 2020. However, due to the dynamic pandemic environment (e.g. changes in virus spread, travel and shipping constraints, and expansion of efforts by other donors and development partners to assist affected countries), it is possible that country needs may shift over the next 6 months. As a result, changes may be necessary to the work plan. Any changes to activities or country budgets will be submitted to the AOR for approval.

Managing and Coordinating Operations

Activities:

- Implement the workplan and strategy.
- Effectively execute, monitor, and close-out the Cooperative Agreement and any sub-award agreements, sub-contracts, and service agreements while ensuring compliance.
- Respond to all requests for information.
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- Hold the end of project briefing for USAID (which was postponed in March 2020) to showcase achievements, findings, impact, and recommendations to inform future directions for pandemic prevention, surveillance, detection, and response.

Timeline: April – September 2020

Outcomes: Implementation of workplan; ensured compliance with USG policies and regulations and with host country policy and regulations; timely submission of all reports and response to data call requests; compilation and submission of final project report; successful out-briefing and project wrap-up meeting.

Objective 1: Support initial detection of SARS CoV-2 to inform public health response

Activities (as feasible and appropriate during a pandemic):

- Based on emergency needs assessments at the start of the pandemic, work with PREDICT-2 global collaborating laboratories (up to 28 countries in Africa, Asia, and the Middle East that previously conducted work under PREDICT-2[1]) to evaluate technical, personnel, and resource demands for pandemic response.
- Provide technical and resource assistance to laboratories for initial detection[2] of SARS CoV-2 in collaborating laboratories; assistance could include external technical and commodity support such as specific SARS CoV-2 primers, probes, positive controls, updated protocols, and training; funding for personnel; knowledge and technology transfer; or other assistance as needs emerge.

Timeline: April – June 2020

Expected outcomes: Demand-driven assistance to countries supporting pandemic response and conduct of rapid and high-quality in-country testing for SARS CoV-2 to inform control measures.

Objective 2: Conduct investigations to characterize potential animal source(s) of SARS CoV-2 and previous spillover of SARS-related viruses

Activities (as feasible and appropriate during a pandemic):

- In participating countries, participate in technical discussions at the global, regional, and/or country level to plan and prioritize retrospective and prospective (if possible) research towards identifying SARS CoV-2 animal source(s) of and intermediate hosts(s).
- Identify relevant data and samples collected by PREDICT-2 in South and Southeast Asia[3] that could provide insight into the possible animal host(s) of SARS CoV-2.
- Conduct in-depth analysis of PREDICT-2 coronavirus findings and conduct additional testing for SARS-related viruses using previously collected PREDICT-2 samples (animals and humans) in South and Southeast Asia[2] as needed to evaluate a) potential reservoir host(s) and intermediate host(s), and b) evidence for prior spillover events among humans in the region.
- Conduct additional analyses of existing project data from markets in mainland Southeast Asia with a focus on live animal markets, including but not limited to human behaviors, types of animals present, value chains and networks, and other risks for virus spillover and spread at high-risk hypothesized SARS CoV-2 interfaces.

Timeline: April – September 2020 (global analysis and planning); May – September 2020 (testing and analyses)

Outcomes: Prioritized list of data and samples for analysis; investigations aimed at identifying animal hosts for SARS CoV-2; insights shared that enable countries in the South and Southeast

[1] To conduct work in China, Cambodia, Egypt, and Myanmar, special notification and TVPA waivers are required.
[2] Limited to "jump starting" detection after the virus is introduced to countries. Not intended to support widespread testing as the virus spreads rapidly.
[3] Currently planned for Indonesia, Laos, Malaysia, Nepal, Thailand, and Viet Nam as data and evidence dictate, as well as Cambodia and other countries in the region pending special notification.

Asia region (and beyond) to design and target prevention strategies to reduce the risk of future spillovers of SARS CoV-2 and related viruses from animals to people.

Total Budget: up to **$3.0 M**

Budget Breakout by Country and Objective

Country	Total	Total Obj. 1	Total Obj. 2
Bangladesh	$41,328	$41,328	$0
Cambodia	$0	$0	$0
Cameroon	$41,328	$41,328	$0
China	$0	$0	$0
Cote d'Ivoire	$41,328	$41,328	$0
DR Congo	$41,328	$41,328	$0
Egypt	$0	$0	$0
Ethiopia	$18,902	$18,902	$0
Ghana	$41,328	$41,328	$0
Guinea	$41,328	$41,328	$0
India	$15,904	$15,904	$0
Indonesia	$174,116	$18,902	$155,214
Jordan	$15,904	$15,904	$0
Kenya	$41,328	$41,328	$0
Lao PDR	$171,117	$15,904	$155,214
Liberia	$41,328	$41,328	$0
Malaysia	$326,331	$15,904	$310,427
Mongolia	$18,902	$18,902	$0
Myanmar*	$0	$0	$0
Nepal	$326,331	$15,904	$310,427
Republic of Congo	$18,902	$18,902	$0
Rwanda	$41,328	$41,328	$0
Senegal	$38,330	$38,330	$0
Sierra Leone	$41,328	$41,328	$0
Tanzania	$41,328	$41,328	$0
Thailand (RDMA)	$310,427	$0	$310,427
Uganda	$41,328	$41,328	$0
Viet Nam	$326,331	$15,904	$310,427
Total	**$2,257,437**	**$705,301**	**$1,552,136**

Note: Costs for managing and coordinating operations are incorporated into Objectives 1 and 2.

From: alexandra zuber <alexandrazuber@atahealthstrategies.com>
To: Sam Halabi <sfh9@georgetown.edu>;daszak@ecohealthalliance.org" <daszak@ecohealthalliance.org>;William B. Karesh" <karesh@ecohealthalliance.org>;Terra Kelly <trkelly@ucdavis.edu>;Jonna Mazet <jkmazet@ucdavis.edu>;Matthew Blake <mblake@ucdavis.edu>;Elizabeth Leasure <ealeasure@ucdavis.edu>;f.castillo@berkeley.edu" <f.castillo@berkeley.edu>;Omar Romero-Hernandez <oromero@haas.berkeley.edu>;margaritamartins@berkeley.edu <margaritamartins@berkeley.edu>
Sent: 4/14/2020 11:13:07 AM
Subject: Please make sure to review: AFROHUN OCA self assessment

Dear BPG,
I've sent this a couple times, but I know a lot is swirling right now, so I wanted to be sure you had this at the ready for our Thursday OCA workshop with AFROHUN. They will send an agenda and will be presenting to us (domains that scored less than 4 is their recent plan).

Please take a moment to review before our call together. Per our last discussion, here is my recommended areas of focus below. I would suggest this person be ready to respond first after AFROHUN presents these domains, but all are welcome to chime in.

- Governance: Sam
- Administration: Matt/ Liz
- Human Resources: Matt
- Financial Management: Liz
- Organizational Management: Omar/ Margarita
- Program Management: Liz
- Project Performance Management: Federico/ Alex

Thanks all again for your incredible dedication to Obj 3 and AFROHUN this month!

Alexandra Zuber, MPP, DrPH
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From: Agnes Yawe
Sent: Friday, March 20, 2020 3:04 PM
To: alexandra zuber
Cc: Terra Kelly ; Irene Naigaga ; Sarah Nannyanzi
Subject: AFROHUN OCA self assessment

Dear Alexandra,

As promised please receive attached AFROHUN preliminary OCA self assessment. In addition to the scale, we made some comments that give some details on what needs improvement either internally (i.e. AFROHUN can handle with internal capacity) or externally (AFROHUN needs external support).
Happy to provide some more clarity where it may be required.
Regards.

Agnes


Organizational Capacity Assessment Tool: Participant's Copy

For Organizations Funded by USAID

New Partners Technical Assistance Initiative (NuPITA) Project

December 2012

The New Partners Initiative Technical Assistance (NuPITA) project is funded by the United States Agency for International Development (USAID) through Contract No: GHS-I-00-07-00002-00. The Technical Assistance Project to New Partners Initiative (TA-NPI) project is funded by the United States Department of Health and Human Services—Centers for Disease Control and Prevention through Contract No: 200-2004-05316/Task Order 002. Both projects are implemented by John Snow, Inc. in collaboration with Initiatives Inc.

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Organizational Capacity Assessment Tool

Goal:
The goal of this tool is to assist organizations in assessing the critical elements for effective organizational management, and identifying those areas that need strengthening or further development.

Purpose:
The OCA tool was designed to enable organizations to define a capacity-building improvement plan, based on self-assessed need. This Organizational Capacity Assessment (OCA) was initially designed to measure overall capacity of organizations funded by President's Emergency Plan for AIDS Relief (PEPFAR) under the New Partners Initiative (NPI). This OCA tool provides organizations with a set of criteria to assess their current management capacity to implement quality health programs, to identify key areas that need strengthening. Although many capacity assessments exist, the structure and process of this tool distinguishes it from others. Multi-level and multi-department involvement fosters team building and organizational learning. Inclusion of management, compliance, and program components ensure a holistic understanding of the organization's strengths and challenges and the guided self-assessment by skilled facilitators instills ownership on the part of the organization for its improvement plan.

The OCA tool assesses technical capacity in seven domains, and each domain has a number of sub-areas.

OCA Domains
1. Governance
2. Administration
3. Human Resources
4. Financial Management
5. Organizational Management
6. Program Management
7. Project Performance Management

Using This Tool
This Organizational Capacity Assessment tool is designed to enable organizational learning, foster team sharing, and encourage reflective self-assessment within organizations.

Recognizing that organizational development is a process, the use of the OCA tool results in concrete action plans to provide organizations with a clear organizational development road map. The OCA can be repeated on an annual basis to monitor the effectiveness of previous actions, evaluate progress in capacity improvement, and identify new areas in need of strengthening.

The OCA is an interactive self-assessment process that should bring together staff from all departments at implementing organizations, both at headquarters and in the field, for the two- to three-day assessment. Not intended to be a scientific method, the value of the OCA is in its collaborative, self-assessment process. The framework offers organizations a chance to reflect on their current status against recognized best practices. Lively discussions are also an opportunity for management, administration, and program staff to learn how each functions, strengthening the team and reinforcing the inter-relatedness of the seven OCA components.

Each page of this tool examines one area. A range of examples of services available is provided along a continuum, from 1-4.

The methodology is a guided self-assessment that encourages active participation. The facilitator and participants meet and discuss each area to determine where the organization sits along the continuum of implementation. Facilitators ask open-ended, probing questions to encourage group discussion, and take notes on participant responses. These notes are later used for the action planning.

Sample questions which might help the facilitator to probe further into the content areas are presented on each page.

The scores that are arrived at are designed to set priorities for the actions and are not used to judge performance. Facilitators use the information from the scoring and rationale sheets to define the issues and actions. The organization reviews or adjusts the problem statement and builds on the suggested actions to define action steps, responsibilities, timeframe, and possible technical assistance needs.

The ability to identify areas to be addressed will strengthen the organization and in subsequent years, enable it to view improvement and note where progress is still needed.

Table of Contents

Governance

Objective: To assess the organization's motivation and stability by reviewing its guiding principles, structure and oversight.

Vision/Mission

Subsection Objective: To review the organization's vision and/or mission statements, learn what drives the organization, how the statements reflect what it does and how they are communicated and understood by staff.

Resources: vision and/or mission statements, anonymous staff and board questionnaires (see Facilitator's Guide)

Vision/Mission ●			
1	**2**	**3**	**4**
The vision and/or mission is • Not a clearly stated description of what the organization aspires to achieve or become	The vision and/or mission is • A moderately clear or specific understanding of what the organization aspires to become or achieve • Not widely held • Rarely used to direct actions or to set priorities	The vision and/or mission is • A clear, specific statement of what the organization aspires to become or achieve • Well-known to most but not all staff • Sometimes used to direct actions and to set priorities	The vision and/or mission is • A clear, specific and forceful understanding of what the organization aspires to become or to achieve • Well-communicated and broadly held within the organization • Consistently used to direct actions and to set priorities

Organizational Structure

Subsection Objective: To determine if the organization's structure—most often depicted in an organogram but also perhaps in a narrative—is in line with its mission, goals and programs and if systems exist to ensure strong coordination among departments or functions.

Resources: organizational diagram, organogram or narrative

Organizational Structure ●			
1	**2**	**3**	**4**
The organization has • No formal structure • An unclear description of its departments and their functions	The organization has • A basic structure, but it is incomplete and/or undocumented • A structure that is not aligned with its mission/goals and programs • Unclear definitions of department functions • Somewhat clear lines of responsibility and communication among departments	The organization has • A well-designed structure (e.g., organogram) relevant to its mission/goals and programs • Identified the functions and responsibilities of departments • Clearly defined and appropriate lines of responsibility and communication among departments	The organization has • A well-defined structure relevant to its mission/goals and programs • Clearly defined and appropriate functions and responsibilities of departments • Clear, appropriate lines of communication and coordination among departments • A narrative description of the structure if appropriate

Board Composition and Responsibilities

Subsection Objective: To assess the board's composition, terms of reference (TOR), procedures and oversight to ensure that the board is capable of providing adequate guidance to the organization.

Resources: board membership, board TOR, board meeting minutes, anonymous board questionnaire

Board Composition and Responsibility ●			
1	**2**	**3**	**4**
The board • Is drawn from a narrow spectrum; members have little or no relevant experience • Has term limits that are not defined or are unreasonably long or short • Has no process for electing officers • Has infrequent or poorly attended and undocumented meetings • Does not have TOR or a clear understanding of its key functions	The board • Is drawn from a somewhat broad spectrum; some members have relevant experience • Has term limits that are not defined or are unreasonable • Has no process for electing officers • Has well-planned meetings at regular intervals, but attendance and/or documentation is irregular • Has TOR, but they are incomplete and/or do not provide appropriate separation of roles from the executive management team • Has some understanding of its functions as defined in the TOR, but they are inconsistently carried out • Is rarely or not at all involved in strategic planning/policy formulation	The board • Is drawn from a broad spectrum; all members have relevant experience • Has term limits that are defined and reasonable • Informally elects officers • Has well-planned, documented meetings held at regular intervals with good attendance • Has clear TOR reflecting appropriate separation of roles from the executive management team • Has a good understanding of its functions as defined in the TOR and mostly carries them out • Is involved in strategic planning/policy formulation, but participation is not always consistent	The board • Is drawn from a broad spectrum; all members have relevant experience • Has term limits that are defined and reasonable • Has officers elected/appointed according to board procedures • Has regular, well-planned, documented meetings with good attendance • Has clear TOR and a good understanding of its functions, all of which are consistently carried out with appropriate separation from the executive management team • Displays willingness and a proven track record to learn about the organization, to participate in strategic planning/policy formulation and to address organizational issues

Legal Status

Subsection Objective: To assess the organization's legal standing—and therefore sustainability—by checking legal registration and compliance with local tax and labor laws.

Resources: registration, where possible and feasible, local tax laws, local labor laws

Legal Status ●			
1	**2**	**3**	**4**
The organization is • Not legally registered, registration has expired, or the organization does not know its legal status and local labor laws • Not aware of its tax status and/or is not paying taxes • Not aware of statutory audit and reporting requirements	The organization is • Not currently a legally recognized entity in the country in which it operates but has applied for legal status • Aware of its tax status and local labor laws but is not fully compliant • Aware of statutory audit and reporting requirements but is not fully compliant	The organization is • Legally registered and aware of its tax status • Not always compliant with tax obligations and/or labor laws • Not always compliant with statutory audit and reporting requirements	The organization is • Legally registered and aware of its tax status • Fully complies with tax obligations and labor laws • Fully complies with statutory audit and reporting requirements

Succession Planning

Subsection Objective: To assess the organization's ability to continue smooth operations and to manage programs in the event of an absence of, or shift in, leadership.

Resources: job descriptions of senior management, succession plan, organizational chart

Succession Planning ●			
1	**2**	**3**	**4**
The organization • Is highly dependent on the chief executive officer (CEO)/executive director (ED) • Would cease to exist or function without the CEO/ED • Has no plan for how it would continue if the CEO/ED left	The organization • Is dependent on the CEO/ED • Would continue to exist without the CEO/ED but most likely in a very different form, or with significantly less capability and reduced program quality • Has a very basic succession plan describing how the organization will continue if the CEO/ED leaves	The organization • Has limited dependence on CEO/ED; s/he does not have sole control of, for example, finances and planning • Would continue in a similar way without the CEO/ED, but fundraising and/or program quality would suffer significantly • Has a documented plan for how it would continue should the CEO/ED leave, but no member of management could take on the CEO/ED role	The organization • Is reliant but not dependent on the CEO/ED • Has a clear, documented succession plan • Has the potential for a smooth transition to a new leader; fundraising and program quality would not be major problems • Would handle transition by having a senior management team fill in or one or more members of the management team would take on the CEO/ED role

Administration

Objective: To assess the organization's capacity to develop and apply policies and procedures, the existence and quality of its administrative systems and its staff knowledge of the systems.

Operational Policies, Procedures, and Systems

Subsection Objective: To assess the availability of and adherence to operational policies.

Resources: policy and procedures manual, anonymous staff questionnaires, related payment vouchers

Operational Policies, Procedures, and Systems ●			
1	**2**	**3**	**4**
The organization has • No documented operational policies and procedures	The organization has • Documented some operational policies and procedures, but they are incomplete or not compliant with national and donor regulations • Policies and procedures that are not consistently adhered to • Not oriented or trained staff in the policies and procedures	The organization has • Documented most or all operational policies and procedures and they are compliant with national and donor regulations • Policies and procedures that are known but not consistently adhered to • Oriented or trained staff in the policies and procedures • No process for regularly reviewing and updating operational policies and procedures	The organization has • Complete and appropriate operational policies and procedures • Policies and procedures that are known and understood by staff • Policies and procedures that are consistently adhered to, reviewed and updated

Travel Policies and Procedures

Subsection Objective: To assess the availability of and adherence to travel policies and procedures, especially compliance with donor rules and regulations.

Resources: travel manual, staff questionnaires, related payment vouchers

Travel Policies and Procedures ★			
1	**2**	**3**	**4**
The organization has • No documented travel procedures (i.e., per diem levels, forms, approval procedures)	The organization has • Documented some travel policies and procedures, but they are incomplete or noncompliant with donor requirements • Policies and procedures that are not well-known or understood by staff and not consistently adhered to	The organization has • Documented most or all travel policies and procedures, and they comply with donor requirements • Policies and procedures that are generally known and understood by staff but not consistently adhered to	The organization has • Complete and appropriate travel policies and procedures that comply with donor requirements • Policies and procedures that are known and understood by staff • Policies and procedures that are consistently adhered to, reviewed and updated

Procurement

Subsection Objective: To assess the availability of and adherence to procurement policies and procedures.

Resources: procurement policies, procurement files, related payment vouchers, procurement plan

Procurement ★			
1	**2**	**3**	**4**
The organization has • No documented procurement procedures • No documented procurement plan	The organization has • Documented some procurement policies and procedures, but they are incomplete or inappropriate • Policies and procedures that are not well-known or understood by staff and inconsistently adhered to • No documented procurement plan, but is aware of procurement regulations	The organization has • Documented most or all procurement policies and procedures, and they are appropriate • Policies and procedures that are generally known and understood by staff but inconsistently adhered to • A documented procurement plan	The organization has • Complete and appropriate procurement policies and procedures that incorporate donor-specific policies as required • Policies and procedures that are known and understood by staff • Policies and procedures that are consistently adhered to, reviewed and updated • A documented procurement plan that is annually revised/updated

Fixed-Asset Control

Subsection Objective: To assess the availability of and adherence to policies and systems for managing fixed assets.

Resources: fixed-asset policies, fixed-asset register, physical inventory reports

Fixed-Asset Control ★			
1	**2**	**3**	**4**
The organization has • No documented fixed-asset procedures (i.e., inventory of assets and systems for stock control) • No fixed-asset register	The organization has • Documented some fixed-asset policies and procedures, but they are incomplete or inappropriate • Policies and procedures that are not well-known or understood by staff and not consistently adhered to • A fixed-asset register that is not complete	The organization has • Documented most or all fixed-asset policies and procedures, and they are appropriate • Policies and procedures that are known and understood by staff but inconsistently adhered to • A fixed-asset register that is complete but not regularly updated	The organization has • Complete and appropriate fixed-asset policies and procedures that incorporate donor policies as required • Policies and procedures that are known and understood by staff • Policies and procedures that are consistently adhered to, reviewed and updated • A fixed-asset register that is regularly updated and confirmed through a physical inventory at least every two years

Information Systems

Subsection Objective: To assess the functionality of the organization's information systems and its documentation of information system policies and procedures.

Resources: information system policies and procedures, staff interviews

Information Systems ●			
1	**2**	**3**	**4**
The organization has • No documented information system policies and procedures • An insufficient information system to manage operations and/or programs • No one designated to manage the information system	The organization has • Documented some information system policies and procedures, but they are incomplete or inappropriate • An information system that supports operations and programs at basic levels of functionality • No one designated to manage the information system	The organization has • Documented most or all information system policies and procedures • An information system that adequately supports operations and programs at a good level of functionality without major inputs • A staff member (or outside provider) designated to manage the information system	The organization has • Complete and appropriate information system policies and procedures • An information system that effectively and efficiently supports operations and programs at a high level of functionality and maintenance • A staff member (or outside provider) designated to manage the information system

Human Resources Management

Objective: To assess the organization's ability to maintain a satisfied and skilled workforce, to manage operations and staff time and to implement quality programs.

Job Descriptions

Subsection Objective: To review the systems for developing, disseminating, following and updating job descriptions (JDs) to ensure that staff roles and responsibilities are clearly defined and understood and that they are relevant to the needs of the organization.

Resources: sample job descriptions for each position or level (depending on size of organization)

Job descriptions ●			
1	**2**	**3**	**4**
The organization has • No JDs for staff, volunteers or interns	The organization has • JDs for each staff member, but not all key sections are covered • Staff, volunteers and interns who are not aware of or do not have copies of their JDs	The organization has • Clear JDs for each staff member that include all sections • Staff, volunteers and interns with copies or access to copies of their JDs • JDs that are not respected/adhered to, reviewed or regularly updated	The organization has • JDs for each staff member that cover all sections • Staff, volunteers and interns with copies of or access to their JDs • JDs that are respected/adhered to, reviewed and updated

Recruitment

Subsection Objective: To assess the organization's systems for recruiting staff and consultants including confirming and documenting professional and salary history.

Resources: recruitment manual/guidelines or policy, recruitment guidelines, documentation of employment history, personnel manual

Recruitment ●			
1	**2**	**3**	**4**
The organization has • Neither guidelines nor a consistent approach to recruiting staff • No system for verifying employment history for staff or consultants	The organization has • Basic guidelines for recruitment, but they are not consistently applied or reviewed • No process for verifying staff or consultants' employment history • Not oriented or trained HR staff in applying the guidelines • Not provided opportunities for career advancement	The organization has • Clear, transparent recruitment guidelines, but they are neither consistently applied nor regularly reviewed • Has a process for verifying employment history but does not file or update the information • Not consistently oriented or trained HR staff in applying the guidelines • Not provided opportunities for career advancement	The organization has • Clear, transparent recruitment guidelines that are consistently applied and reviewed • A process for verifying, updating and filing employment history • Consistently oriented and regularly trained/updated HR staff in applying the guidelines • Provided opportunities for career advancement

Staffing Levels

Subsection Objective: To assess the organization's management of staffing—positions available, positions filled, vacancies—for the program and for the organization as a whole and the means for ensuring staffing levels are and remain adequate.

Resources: staffing plan and/or organizational diagram, vacancy and turnover data, attendance information, retention policy

Staffing Levels ●			
1	**2**	**3**	**4**
The organization has • No formal staffing plan • Positions/vacancies that are not documented • Many key management and technical positions open or filled by staff without the right qualifications or skills • No system to ensure that positions are filled quickly • High turnover and severe problems with staff attendance affecting program implementation • No retention procedures	The organization has • A formal staffing plan • Documented positions and vacancy data • Some key positions filled with qualified and skilled staff • No system to ensure that positions are filled quickly • High turnover rate or staff attendance problems affecting program implementation • Not conducted or documented exit interviews	The organization has • A formal staffing plan • Documented and available vacancy data • Qualified and skilled staff in all key positions (technical, administrative, finance) • A system to ensure that positions are filled quickly • Moderate turnover or minor attendance problems • Conducted and documented exit interviews	The organization has • A formal staffing plan • Documented positions and vacancy data • Qualified and skilled staff in all positions • Active recruitment to fill gaps • A system for rapidly filling new positions where staff turnover is high • Minimal turnover and no attendance problems • Conducted and documented exit interviews and used the information

Personnel Policies

Subsection Objective: To ensure that personnel policies document and verify staff time and that best practices in managing personnel are adhered to.

Resources: personnel manual, staff time records, work schedule policies, 2–3 personnel files, payment vouchers

Personnel Policies ★			
1	**2**	**3**	**4**
The organization has • No personnel policy manual	The organization has • Basic personnel policies that include either a drug-free workplace policy, nondiscrimination policies (for US organizations), or timekeeping policy • Inconsistently applied the polices • Not disseminated the policies to all staff and/or required signature statements • No process for updating personnel policies, manuals or staff time records	The organization has • Comprehensive and donor compliant personnel policies including a drug-free workplace policy, discrimination policies (for US organizations), and timekeeping policy, at a minimum • Polices that are adhered to and aligned with HR practices • Not disseminated the policies to all staff or required signature statements • Not updated personnel policies and manuals or time records	The organization has • Comprehensive and donor compliant personnel policies • Policies that are adhered to and correspond to HR practices • Disseminated policies to all staff and required and filed signature statements • Regularly reviewed and updated policies, manuals and staff time records

Staff Salaries and Benefits

Subsection Objective: To review the organization's systems for setting and managing salaries and benefits.

Resources: salary grades and ranges, 2–3 personnel files from different levels

Staff Salaries and Benefits ★			
1	**2**	**3**	**4**
The organization has • No clear rationale/structure for staff salaries such as pay grades and ranges or salary history • Not clearly documented benefits in a policy manual • Salaries and benefits that are not equitably applied and/or do not conform to national labor requirements	The organization has • A clear rationale/structure for staff salaries, such as pay grades and ranges and salary history • A process for documenting salary history • Not consistently applied the rationale or reviewed or updated it • Clearly documented benefits in a policy manual • Benefits of which staff are aware, but they are neither equitably applied nor conform to national labor requirements	The organization has • A clear rationale/structure for staff salaries such as pay grades and ranges and salary history • A process for documenting salary history • Consistently applied the rationale to all staff, but does not review or update salaries regularly • Benefits that are clearly documented in a policy manual • Benefits of which staff are aware, that are equitably applied and conform with national labor requirements	The organization has • A clear rationale/structure for staff salaries such as pay grades and ranges and salary history • A process for documenting salary history • A rationale for salaries that is consistently applied to all staff, reviewed and updated annually • Pay increases that follow the salary framework and/or policy • Benefits that are clearly documented in a policy manual, equitably applied and conform to national labor laws • Pay increases coordinated with performance reviews

Staff Performance Management

Subsection Objective: To review the organization's systems for managing staff performance including performance appraisals.

Resources: samples of completed performance appraisals or a blank form

Staff Performance Management ●			
1	**2**	**3**	**4**
The organization has • No process for regularly assessing staff performance • No probationary period or review process for new staff • Not updated or filed changes in staff work status, salary and benefits	The organization has • A process for assessing staff performance, but it does not include setting objectives, listing responsibilities/tasks, supervision or professional development • A three-month probationary period for new staff but no formal review • A process that is not participatory and follows an auditing rather than a supportive approach • Inconsistently filed or updated changes in staff work status, salary and benefits	The organization has • A process for assessing staff performance that includes setting objectives, listing responsibilities/ tasks, assessing performance on past activities, supervision and professional development • A performance review process for new staff that is not timely or consistently done • A participatory process regularly used for performance appraisals • Conducted appraisals for some, but not all, staff • Consistently filed and updated changes in staff work status, salary and benefits	The organization has • A process for assessing staff performance that includes setting objectives, listing responsibilities/ tasks, assessing performance on past activities, supervision and professional development • Regularly conducted appraisals for all staff at least once a year • Regularly reviews new staff performance after the probationary period • Consistently filed, updated and made changes in staff work status, salary and benefits

Volunteers and Interns

Subsection Objective: To review the organization's systems for managing field and office volunteers and interns.

Resources: volunteer/intern policy, samples of completed performance appraisals

Volunteers/Interns ●			
1	**2**	**3**	**4**
The organization has • No policy for selecting or managing volunteers/interns • No training program for volunteers or interns • No job descriptions • No performance standards or feedback process • No supervisory guidance to support volunteers/interns	The organization has • A basic volunteer/intern policy that includes guidance on selection, supervision and support • Job descriptions • Orientation and/or training for volunteers that is not consistent • No performance standards or regular review of performance • Inconsistent or irregular supervision • High volunteer turnover that affects program implementation	The organization has • A comprehensive volunteer/intern policy that includes guidance on selection, supervision and support • Job descriptions • Volunteers/interns appropriately trained for their tasks • Performance standards but no performance review • Provided regular, consistent supervision and feedback • Moderate turnover	The organization has • A comprehensive volunteer/intern policy that includes guidance on selection, supervision and support • Volunteers/interns who are appropriately and consistently trained for their tasks • Performance standards and regular performance reviews • Provided regular, consistent supervision and feedback • Minimal turnover

Financial Management

Objective: To assess the quality of the organization's financial system and policies and procedures and the staff's knowledge of the system.

Financial Systems

Subsection Objective: To assess the existence and use of the financial system, especially its ability to respond to management needs and donor requirements.

Resources: financial manual, accounting journals, chart of accounts, payment vouchers, staff training plan/curricula, staff interviews

Financial Systems ★			
1	**2**	**3**	**4**
The organization has • No formal financial system • Transactions that are either not recorded or are recorded on an ad hoc basis • A filing system that maintains only invoices/receipts for all expenditures and incoming funds	The organization has • A basic financial system, but it is incomplete and/or not compliant with accounting standards • Systems that are not consistently adhered to • Not oriented or trained financial staff on systems	The organization has • A good financial system with most or all required components • A computerized accounting system that is not fully operational • Systems that are consistently adhered to • Oriented or trained financial staff on systems • No process for reviewing and updating the financial system • Not included a narrative description of its financial system in its financial manual	The organization has • A complete and appropriate financial system • A fully operational, computerized accounting system • Systems that are consistently adhered to, reviewed and updated • Systems known and understood by trained staff • A narrative description of its financial system in its financial manual

Financial Policies and Procedures

Subsection Objective: To assess the existence and use of financial policies and procedures and their ability to respond to management needs and donor requirements.

Resources: financial manual, accounting journals, chart of accounts, staff interviews, payment vouchers, staff training plan/curricula

Financial Policies and Procedures ★			
1	**2**	**3**	**4**
The organization has • No documented financial policies and procedures	The organization has • Some documented financial policies and procedures, but they are incomplete and/or do not comply with donor requirements • Policies and procedures that are inconsistently adhered to • Not oriented or trained staff in the policies and procedures	The organization has • Documented most or all financial policies and procedures and they are compliant • Policies and procedures that are consistently adhered to • Oriented or trained staff in the policies and procedures • No process for regularly reviewing and updating financial policies and procedures	The organization has • Complete and appropriate financial policies and procedures • Policies and procedures that are known and understood by staff • Policies and procedures that are consistently adhered to, reviewed and updated

Internal Controls

Subsection Objective: To assess if internal controls adequately safeguard the organization's assets, manage internal risk and ensure the accuracy and reliability of accounting data.

Resources: financial manual, signatory policy/authority matrix, payment vouchers, staff interviews, audit reports on internal controls, insurance policies

Internal Controls ★			
1	**2**	**3**	**4**
The organization has • No documented internal controls • Improper segregation of duties and checks and balances (1–2 people are responsible for all steps in financing or procurement)	The organization has • Some documented internal controls, but they are incomplete and inappropriate • Procedures not well-known and understood by staff and not consistently adhered to • Inadequate segregation of duties	The organization has • Most or all documented appropriate internal controls • Procedures that are generally known by staff but not consistently adhered to • Adequate segregation of duties • No process for reviewing and updating internal controls or for assessing financial risk	The organization has • Complete and appropriately documented financial controls • Procedures known and understood by trained staff • Internal controls that are consistently adhered to, reviewed and updated • A process for assessing financial risk

Financial Documentation

Subsection Objective: To assess if record keeping is adequate and if financial files are audit ready.

Resources: financial files, finance manual, staff interviews

Financial Documentation ★			
1	**2**	**3**	**4**
The organization has • No written financial documentation procedures • No filing system, and financial files are not readily available • No one designated to manage the financial files	The organization has • Some written financial documentation procedures, but they are incomplete and/or inappropriate • Procedures that are not consistently adhered to and/or are not known to staff • A basic filing system, but financial files are not complete • No one designated to manage the financial files	The organization has • Financial documentation procedures that are mostly or completely documented in writing and appropriate • Procedures that are generally adhered to, known and understood by staff • Financial documentation files that are not regularly updated or secure • A staff member designated to manage the financial files	The organization has • Complete and appropriate financial documentation procedures • Procedures that are known and understood by staff • Procedures that are consistently adhered to, reviewed and updated • Up-to-date financial files in a secure location • A staff member designated to manage the financial files

Budgeting

Subsection Objective: To assess the organization's financial planning and if there is a system for monitoring budgets and determining additional funding requirements.

Resources: organization's budget, project budgets, budget worksheet, chart of accounts, budget tracking worksheet

Budgeting ●			
1	**2**	**3**	**4**
The organization has • No formal master budget • No core-cost budget • Project budgets, but they are not clear and/or not aligned with project needs • Not included core costs in its project budgets	The organization has • A basic master budgeting process, but it is incomplete • A core-cost budget, but it is not aligned with the strategic plan and/or is not regularly reviewed to address shortfalls • Project budgets, but they are not always clear and not consistently aligned with project needs • An inconsistent methodology for including core costs in its project budgets	The organization has • A good master budgeting process that includes most or all required components • A core-cost budget that is generally aligned with the strategic plan, but is not regularly reviewed to address shortfalls • Project budgets that are clear, but not reviewed regularly nor consistently aligned with project needs • A consistent methodology for including core costs in project budgets, but the methodology is not documented and does not ensure full cost recovery	The organization has • A complete and appropriate master budget • A core-cost budget that is aligned with the strategic plan and regularly reviewed; any shortfalls are addressed • Clear project budgets that are reviewed regularly by senior management and adapted to align with project needs and donor requirements • A consistent methodology for including core costs in project budgets that is documented and ensures full cost recovery

Financial Reporting

Subsection Objective: To assess whether the organization's routine financial reporting system allows it to meet statutory and donor requirements and stakeholders' needs for information.

Resources: annual financial statements, financial reports to donors, donor grant agreements, management reports, senior management meeting minutes, board meeting minutes

Financial Reporting ★			
1	**2**	**3**	**4**
The organization has • No routine system for financial reporting • No recent financial statements • Not yet submitted a financial report to a donor and/or other stakeholders • No one designated to prepare or approve reports or financial statements	The organization has • A basic system for financial reporting, but reporting requirements and deadlines are not adhered to • Designated staff to prepare and approve reports and financial statements • Inconsistently delivered financial reports to stakeholders (donor, budget holders, senior management, board members) • Irregular reviews of financial reports by senior staff .	The organization has • A good financial reporting system; reporting requirements and deadlines are generally adhered to • Regularly delivered financial reports to stakeholders (donors, budget holders, senior management, board members), but they are not always accurate and/or complete • Sporadic reviews of financial reports by senior staff • Some documented financial reporting procedures	The organization has • A complete and appropriate financial reporting system; reporting requirements and deadlines are consistently adhered to • Regularly delivered accurate and complete financial reports to stakeholders (donors, budget holders, senior management, board members) • A system for senior staff to review financial reports at least every three months and to use the reports to make decisions • Complete and appropriately documented financial reporting procedures regularly reviewed and updated

Audits

Subsection Objective: To assess whether the organization undergoes routine audits that meet statutory and donor requirements and has a system for addressing audit findings.

Resources: financial audit reports, post-audit management plans, financial manual staff interviews

Audits ★			
1	**2**	**3**	**4**
The organization has • No internal or external auditing system • Not complied with statutory and/or donor auditing requirements	The organization has • A basic audit/review system, but auditing requirements and deadlines are not adhered to • Completed a recent statutory and/or donor audit, but the scope of the audit does not meet requirements • Not implemented previous audit report recommendations • Not shared audit reports with board members and other stakeholders	The organization has • A good system for managing audits; audit findings and recommendations are generally addressed • Consistently complied with its statutory and donor audit requirements in a timely manner • No internal audit function that regularly assesses risk or reviews and updates financial management systems to reflect the changing environment • Not shared audit reports with board members and other stakeholders	The organization has • A complete and appropriate system for managing audits; audit findings and recommendations are systematically addressed • A written narrative of its audit systems in the finance manual • Consistently complied with its statutory and donor audit requirements in a timely manner • An internal audit function that assesses risk and updates financial management systems as needed • Consistently shared audit reports with board members and other stakeholders

Cost Share

Subsection Objective: To assess whether the organization has systems to track, report, and document cost share in compliance with donor regulations.

Resources: approved grant agreements/budgets, cost-sharing plan and procedures, cost-share vouchers

Cost Share ★			
1	**2**	**3**	**4**
The organization has • No documented cost-sharing procedures • No cost-share plan	The organization has • Documented some cost-share procedures • Procedures that are incomplete and/or inappropriate • An inconsistent accounting system for entering and reporting on cost share • No cost-share plan	The organization has • Documented most or all cost-share procedures, and they are appropriate • Procedures that are not known to staff • Procedures that are inconsistently adhered to • An inconsistent accounting system for entering and reporting on cost share • A cost-share plan	The organization has • Complete and appropriately documented cost-share procedures • Procedures known and understood by staff • Procedures consistently adhered to, reviewed and updated • A consistent accounting system for entering and reporting on cost share • A cost-share plan

Financial Sustainability

Subsection Objective: To assess the organization's finance strategy and its ability to secure a diversified revenue base, to generate reserves and to sustain its operations without donor funds.

Resources: organization's budget, annual financial statements, strategic plan, finance strategy (business plan)

Financial Sustainability ●			
1	**2**	**3**	**4**
The organization has • Full dependence on one external donor • No unrestricted funds • Not enough liquidity to pay all outstanding financial obligations • No documented finance strategy	The organization has • Almost full dependence on external donor funds (more than one donor) • Limited unrestricted funds • Not enough liquidity to pay all outstanding financial obligations • A finance strategy that is not fully documented	The organization has • A somewhat diversified funding base, but is too reliant on restricted income • Limited reserves to operate without donor grants • Enough liquidity to pay all outstanding financial obligations • A documented finance strategy that is not fully in line with the strategic plan and is not reviewed regularly	The organization has • A diversified funding base with strong stakeholder relationships • Income-generating activities and/or unrestricted sources of income • Enough liquidity to pay all outstanding financial obligations • Enough reserves to run for a few months without any donor funding • A written policy for building/maintaining reserves • A documented finance strategy in line with the strategic plan and reviewed regularly

Organizational Management

Objective: To assess the organization's planning, management of external relations and information and means of identifying and capitalizing on new opportunities.

Strategic Planning

Subsection Objective: To assess the organization's ability to realize its mission and goals by reviewing its strategic plan.

Resources: strategic plan

Strategic Planning ●			
1	**2**	**3**	**4**
The organization has • No strategic plan	The organization has • A basic strategic plan that does not reflect its vision, mission and values • A plan that is not based on an analysis of strengths and weaknesses, the external environment and clients' needs • A plan that does not include priorities, measurable objectives or clear strategies • Not used the plan for management decisions or operational planning • No process for regularly reviewing the plan • Not defined its resource needs	The organization has • A comprehensive, written strategic plan that reflects its mission, vision and values • Based the plan on a review of strengths and weaknesses, the external environment and clients' needs • Included priorities, measurable objectives and clear strategies • Not used the plan for management decisions or operational planning • No process for regular reviews • Not defined resource needs or does not have a corresponding budget	The organization has • A comprehensive, written strategic plan that reflects its mission, vision and values • Based the plan on a review of strengths and weaknesses, the external environment and clients' needs • Included priorities and measurable objectives • Referred to the plan for management decisions and operational planning • Regularly reviewed the plan • Clear resource needs and a corresponding budget

Resource Mobilization

Subsection Objective: To assess the organization's ability to identify and capitalize on new business opportunities through grants and partnerships.

Resources: business development plan, resource development plan, funding strategy

Resource Mobilization ●			
1	**2**	**3**	**4**
The organization has • No business plan or funding strategy • Not estimated its future resource needs • Taken no steps to identify additional local, national or international resources or opportunities to support its programs and activities, either directly or through partnerships • Not created a communication strategy for resource mobilization	The organization has • A business plan and has taken preliminary steps to estimate future resource needs based on an analysis of its programs and/or its strategic plan • Identified additional resource providers or opportunities and their interests and potential for support • Not created a communication strategy to attract resources	The organization has • A business plan based on an analysis of its programs and resource needs and the activities in its strategic plan • Identified resource providers • Created a communication strategy for resource mobilization • Received support from at least one source or has a clear plan for fundraising or proposal writing • Insufficient funds to support its activities	The organization has • A business plan based on an analysis of its programs and resource needs and the activities in its strategic plan • Identified resource providers • Created a communication strategy for resource mobilization • Successfully bid for resources from one or more sources • Sufficient funds to support its activities

Operational Plan Development

Subsection Objective: To assess the contents, approval and reviews of the annual operational plan.

Resources: operational plan

Operational Plan ●			
1	**2**	**3**	**4**
The organization has • No operational plan	The organization has • An annual operational plan • Included goals, measurable objectives and strategies, but no timelines, responsibilities or indicators • Not linked the operational plan to project or program workplans and budgets • Not developed the operational plan with staff participation • Not set dates for quarterly reviews • Not submitted the plan on time to HQ or donors (if required)	The organization has • An annual operational plan • Included goals, measurable objectives, strategies, timelines, responsibilities and indicators • Linked the plan to project/program workplans and budgets • Not developed the operational plan with staff participation • No dates for quarterly reviews • Not submitted the plan on time to HQ or donors (if required)	The organization has • An annual operational plan • Included goals, measurable objectives, strategies, timelines, responsibilities and indicators • Linked the plan to program/project workplans and budget • Developed the plan with staff participation • Set dates for quarterly reviews • Submitted the plan on time to HQ or donors (if required)

Communication Strategy

Subsection Objective: To assess the comprehensive, completeness and effectiveness of the organization's communication strategy.

Resources: communication strategy, sample USAID-funded and non-USAID-funded publications

Communication Strategy ●			
1	**2**	**3**	**4**
The organization has • No strategy for identifying audiences, channels, materials, and dissemination for promotion of technical/best practice innovation and overall achievements • No one assigned responsibility for developing/overseeing communication strategy and products (written, oral and/or online) • No process/tools for testing the materials/messages • No branding/marking policies or procedures for documents or equipment	The organization has • An incomplete strategy, lacking objectives, responsibility, timelines and dissemination mechanisms • Assigned responsibility for communication strategy development • No process/tools for testing materials/messages • Developed branding/marking policies for projects as required by USAID but does not have an organizational branding/marking policy	The organization has • A complete communication strategy, • Tasked staff member(s) with communication strategy management including documentation oversight • A process for testing materials/messages and revising based on test results • Developed its own branding policy (including appropriate USAID branding/marking requirements) and oriented staff, but it is inconsistently adhered to • Created templates for documents and a style guide	The organization has • A comprehensive communication strategy • Tasked staff member(s) with communication strategy management, including documentation development and oversight • A process for testing and revising materials/messages based on test results • Developed its own branding policy (including appropriate USAID branding/marking requirements), oriented staff, and instituted a system to monitor compliance • Created templates and a style guide and trained staff on their use

Change Management

Subsection Objective: To assess the organization's sustainability and relevance by reviewing its systems and processes for responding to internal or external emerging situations, reviewing programs and analyzing needs.

Resources: policy review plan or timeline

Change Management ●			
1	**2**	**3**	**4**
The organization has • No process for responding to internal changes (staffing, leadership and budget issues) • No process for planning for or responding to external changes (government policies or donor priorities/funding)	The organization has • Basic processes for reviewing internal changes, such as policy reviews or the funding environment • No process for planning for or responding to external changes, such as regular reviews of the operational plan and budget monitoring • Inconsistently involved staff in reviewing the effectiveness of new/revised management systems and policies • Significant delays or problems encountered in response to change	The organization has • Established processes for reviewing internal change • Processes for planning for and responding to external change • Consistently involved staff in reviewing the effectiveness of new/revised management systems and policies, processes, programs • Few delays or major problems encountered in response to change	The organization has • Established effective and consistent routines for planning and reviewing and responding to internal and external change • Consistently involved staff in reviewing the effectiveness of new/revised management systems and policies • Systems for monitoring whether changes are implemented and lead to improvements • Ways to gauge staff comfort with the way change is introduced and addressed

Knowledge Management

Subsection Objective: To assess the organization's ability to link with other organizations (government, national, international, community, technical, academic) and its system for sharing knowledge, experiences, technical expertise and best practices with staff.

Resources: listing of association memberships and linkages with external organizations, staff reports on meetings attended, organizational newsletters

Knowledge Management ●			
1	**2**	**3**	**4**
The organization has • No technical linkages with other organizations to share best practices or program experiences • No process for ensuring staff are continuously updated on best practices	The organization has • Basic technical linkages with other organizations to share best practices or program experiences • Staff who are updated on best practices, but not regularly • No process for ensuring learning is applied to the program or shared with stakeholders	The organization has • Essential and appropriate links with other organizations to share best practices or program experiences • A process for routine staff sharing of best practices and lessons learned • Not applied new knowledge or best practices to ongoing programs or shared them with stakeholders • Has no process for reviewing/integrating new/current knowledge and best practices in annual planning	The organization has • Active links with appropriate organizations to share best practices or program experiences • A process for routinely sharing technical expertise and experiences with staff and stakeholders • Applied best practices to its program and shares information with stakeholders and appropriate staff • Annual planning that includes reviews and integration of new/current knowledge and best practices

Stakeholder Involvement

Subsection Objective: To assess the organization's ability to coordinate programs and to involve stakeholders.

Resources: list of key stakeholders, stakeholder report

Stakeholder Involvement ●			
1	**2**	**3**	**4**
The organization has • No information about key stakeholders and service providers in the same geographic and/or technical areas in which it operates	The organization has • Some information about stakeholders and service providers in the same geographic and/or technical areas in which it operates • Information that is incomplete and out of date	The organization has • Current information about stakeholders working in the same geographic and technical areas • Identified where stakeholders are, what they do, their expectations and how/if they can collaborate • No regular meetings with stakeholders	The organization has • Complete and up-to-date information about all stakeholders working in the same geographic and technical areas and, if appropriate, collaborative agreements with them • Regular (at least annually) meetings with stakeholders to review relevant activities and their impact on the organization's area of operations

Internal Communication

Subsection Objective: To review the organization's approach to internal communication.

Resources: staff questionnaires (Facilitator's Guide)

Internal Communication ●			
1	**2**	**3**	**4**
The organization has • Limited communication between and among management and staff • Few structured opportunities to exchange ideas or to discuss management, program or technical issues • Not encouraged staff ideas or input • Staff who feel uncomfortable raising issues	The organization has • Limited communication between and among management and staff • Opportunities for discussions between and among management and staff, but they are rarely used • Sometimes encouraged staff ideas and input • Staff who feel uncomfortable raising issues	The organization has • Open communication between and among management and staff • Regular opportunities for discussing management, program or technical areas • Encouraged staff ideas and input • Staff who are comfortable raising issues but find it more difficult to raise challenging ones	The organization has • Open communication between and among management and staff • Regular opportunities for exchanging ideas or discussing management, program or technical issues • Consistently encouraged and incorporated staff ideas and input • Staff who feel comfortable initiating discussions, contributing ideas and raising issues

Decision Making

Subsection Objective: To assess how the organization makes decisions, who is involved, and how decisions are communicated.

Resources: staff questionnaires (Facilitator's Guide)

Decision Making ●			
1	**2**	**3**	**4**
The organization has • Not included staff in the decision-making process • Not communicated or explained decisions that affect the organization • Staff who feel excluded	The organization has • An unclear process for seeking and including staff ideas in the decision-making process • Inconsistently communicated or explained decisions to staff • Staff who feel they play a minor role in making decisions	The organization has • Encouraged staff ideas but seldom incorporated them into decisions • Communicated and explained decisions to staff • Not fully included staff participation in making decisions	The organization has • Sought, respected and incorporated staff ideas into decision-making • Communicated and explained decisions to staff • Staff who feel a sense of responsibility, accountability and ownership of decision-making

Program Management

Objective: To assess the organization's ability to implement comprehensive programs that respond to local needs and priorities by reviewing compliance with donor requirements, management of sub-grants with partners, technical reporting and whether its comprehensive health services meet the needs of specific target populations.

Donor Compliance

Objective: To assess the organization's capability to respond to USG donor requirements; thereby ensuring the effective implementation of its USG-funded programs.

Resources: copy of the USAID A-122 Cost Principles, staff interviews (Facilitator's Guide)

Donor Compliance ★			
1	**2**	**3**	**4**
The organization • Is not familiar with the terms of the cooperative agreement, A-122 Cost Principles (i.e., reasonable, allocable, and allowable) or Standard Provisions • Has not listed and assigned responsibility for all donor requirements	The organization • Is knowledgeable of the terms of the cooperative agreement, A-122 Cost Principles and Standard Provisions • Is aware of donor requirements, has assigned responsibility, but does not have systems in place to ensure compliance	The organization • Is knowledgeable of the terms of the cooperative agreement, A-122 Cost Principles and Standard Provisions • Has systems in place to ensure compliance with donor requirements • Does not comply consistently	The organization • Is knowledgeable of the terms of the cooperative agreement, A-122 Cost Principles, and Standard Provisions • Has systems in place to ensure compliance with donor requirements • Complies consistently

Sub-grant Management

Subsection Objective: To assess the organization's ability to subcontract with other organizations, and monitor technical implementation and financial management of sub-grants.

Resources: sub-grants management and monitoring manual or written procedures, partner agreements, staff interviews, USAID approval documentation, technical reports from grantees, supervisory trip reports, financial reports from grantees, financial tracking of grantees

Sub-grant Management ★			
1	**2**	**3**	**4**
The organization has • No policies and procedures to guide sub-grant management and support • No formal sub-grants with partner organizations	The organization has • Some documented sub-grant management policies and procedures, but these are incomplete or non-compliant • Formal sub-grants with some partners, but they have not been oriented to their responsibilities • Sub-grantees who do not submit regular financial and technical reports in accordance with their agreements • Basic policies and guidance for supervising and supporting sub-grantees • No regularly scheduled supervisory visits	The organization has • Most or all documented and compliant sub-grant management policies and procedures • Formal sub-grants with all partners; some sub-grantees are oriented to their responsibilities • Sub-grantees who do not consistently submit financial and technical reports • Policies and guidance for supervising and supporting sub-grantees, but not all staff are aware of or utilize the guidance • Conducted infrequent supervisory visits	The organization has • Complete and appropriate sub-grant management policies and procedures • Formal sub-grants with all partners, and they are oriented to their responsibilities • Sub-grantees who submit all required reports in a timely manner • Solid policies and guidance for providing regularly scheduled supervision and support • Regular supervisory visits to assess inventory and financial records and implementation; feedback is shared with partners and used for follow-up visits.

Technical Reporting

Subsection Objective: To review the organization's ability to document technical activities and results for donors, program planning and program development.

Resources: most recent technical report, workplan

Technical Reporting ★			
1	**2**	**3**	**4**
The organization • Does not document quantitative or qualitative progress on its workplan or its objectives and strategies, facilitating factors or barriers • Does not identify lessons learned and/or best practices • Does not report on donor, government or other program indicators • Does not use information to review/revise its strategy with staff and stakeholders	The organization • Documents qualitative progress on its workplan, including objectives and strategies, facilitating factors and barriers • Does not identify lessons learned or best practices • Does not report on government, donor or other program indicators • Does not use information to review/revise strategies with staff or stakeholders	The organization • Documents both qualitative and quantitative workplan progress and reviews objectives and strategies, facilitating factors and barriers • Documents lessons learned and best practices • Reports on donor, government or other program indicators • Does not use information to review/revise strategies with staff and stakeholders	The organization • Documents both quantitative and qualitative workplan progress, and reviews objectives and strategies, facilitating factors and barriers • Documents lessons learned and best practices • Reports on donor, government and other program indicators • Uses information to review/revise strategies with staff and stakeholders

Refer

Subsection Objective: To assess the organization's systems and processes for directing clients to other providers, ensuring those providers offer quality services and monitoring clients' access to services.

Resources: referral plan, memoranda of understanding with referral sites, referral reports or data

Referral ●			
1	**2**	**3**	**4**
The organization has • Not mapped referral sites • Not established links for referring clients for HIV and AIDS treatment or other health/support services	The organization has • Mapped referral sites • No agreements with government, private or NGO health or social service providers to ensure that clients requiring HIV and AIDS treatment or other health or support services have access to them	The organization has • A clear referral process with government, private or NGO health or social service providers to ensure that clients requiring HIV and AIDS treatment or other health or support services have access to them • A process for following clients and monitoring quality of care • Clients who are not always appropriately referred or who encounter problems at referral sites	The organization has • A clear referral process system and strong linkages with government, private or NGO health or social service providers to ensure that clients requiring HIV and AIDS treatment or other health or support services have access to them • A process for following clients and monitoring quality of care • Clients who are consistently referred to appropriate locations and who do not encounter problems at referral sites

Community Involvement

Subsection Objective: To ensure the organization's programs respond to and address community needs by reviewing how they involve community members in planning and decision-making.

Resources: community participation and/ or mobilization plan; if not documented, discuss approach with appropriate staff

Community Involvement ●			
1	**2**	**3**	**4**
The organization • Orients communities on its programs, but does not actively include them • Does not involve affected families and communities in planning and decision-making	The organization • Orients communities on its program and discusses its approach with community leaders • Inconsistently involves affected families and communities in planning and decision-making	The organization • Orients communities and leaders on its program and actively engages them in the activities • Involves affected families and communities in planning and decision-making and sometimes integrates their ideas into program design and revision	The organization • Orients communities and leaders on its program and actively engages them in activities and service provision • Involves affected families and communities in planning and decision-making and consistently integrates their views into program design and revision

Culture and Gender

Subsection Objective: To evaluate the organization's systems for assessing culture and gender issues among the populations it serves and for integrating cultural and gender concerns into its programs.

Resources: community or client assessments, program plans

Culture and Gender ●			
1	**2**	**3**	**4**
The organization does • Not consider local cultural or gender issues in programming • Not have tools for assessing local cultural or gender issues • Not discuss the role of local culture and gender norms in program design with staff	The organization does • Consider local cultural or gender issues in its programming • Not have tools for assessing local cultural or gender issues relevant to programs • Discuss the role of local culture and gender norms in program design with staff	The organization does • Consider local cultural or gender concerns in its programming • Have tools for assessing cultural and gender issues • Have guidelines for culturally relevant and gender based approaches and programming • Not train staff on how to use the tools or findings	The organization does • Consider local culture or gender concerns in its programming • View culture and gender as integral to program success • Have tools for assessing cultural and gender issues • Have guidelines for culturally relevant and gender-based approaches and programming • Train staff on the tools, interpreting findings and incorporating elements of culture and gender in program design

Project Performance Management

Objective: To assess the organization's systems for overseeing field activities, setting standards and monitoring actual performance against them, and setting indicators and monitoring progress toward achieving outcomes.

Field Oversight Activities

Subsection Objective: To assess the organization's systems for overseeing field activities.

Resources: field oversight policies and procedures, trip reports, management meeting minutes

Field Oversight ●			
1	**2**	**3**	**4**
The organization • Has no formal procedures and processes for overseeing field administrative and programmatic operations	The organization • Has some documented field oversight policies, but they are incomplete • Reviews annual workplans and progress reports, but irregularly • Monitors compliance with program and donor requirements	The organization • Has most or all documented oversight policies and procedures • Approves annual workplans on a regular basis • Monitors compliance with program and donor requirements • Reviews and approves field-level HR and finance manuals • Reviews quarterly project M&E data and progress reports • Provides technical and administrative guidance • Makes irregular supervision visits	The organization • Has documented and comprehensive field oversight policies and procedures • Approves workplans and provides feedback • Reviews data and progress reports and provides feedback • Monitors compliance with program and donor requirements • Reviews and approves field-level HR and finance manuals • Provides technical and administrative guidance • Makes at least semi-annual supervisory visits, and results are discussed with management and technical staff

Standards

Subsection Objective: To assess the organization's application of recognized standards in service delivery.

Resources: standards/guidelines used, monitoring reports

Standards ●			
1	**2**	**3**	**4**
The organization has • No standards for service delivery	The organization has • Minimal standards for service delivery • Not made staff aware of the standards • Not applied the standards appropriately	The organization has • A good system for using standards for service delivery • Made staff aware of the standards • Appropriately trained staff to apply and monitor the standards • A process for monitoring standards, but it is not applied comprehensively	The organization has • Solid standards for service delivery • Made staff aware of the standards and has trained staff to apply them • A process for monitoring adherence to standards that is consistently adhered to • A process for improving adherence to standards

Quality Assurance

Subsection Objective: To assess the organization's ability to identify and address gaps in meeting performance standards.

Resources: quality monitoring tools (could be part of M&E tools)

Quality Assurance ●			
1	**2**	**3**	**4**
The organization has • Unclear performance expectations • No process for monitoring the quality of services it provides, either through program evaluations, quality monitoring or supervision	The organization has • Performance expectations, but no process to assess performance against standards	The organization has • Performance expectations and a process that assesses performance against standards • Taken client satisfaction into consideration • Included an analysis of gaps or weaknesses • Not developed an improvement plan	The organization has • Performance expectations and a system that assesses performance against standards • Taken client satisfaction into consideration • Analyzed gaps or weaknesses to identify root causes • Identified a plan to address root causes • An improvement plan to address gaps or weaknesses • Studied and incorporated the results into the program

Supervision

Subsection Objective: To assess the organization's systems for supportive review of and feedback on staff performance and program activities.

Resources: supervision plan or guidelines, supervisors' reports

Supervision ●			
1	**2**	**3**	**4**
The organization has • Not developed a supervision plan or approach • Not clarified supervisory responsibilities • Not trained supervisors or provided tools • No process for carrying out supervision	The organization has • A supervision plan but no approach • Detailed supervisory responsibilities, but they are not followed • Not trained supervisors or provided tools • An unclear process for supervision • No process for reviewing findings with staff and management	The organization has: • A clear supervision plan with a supportive approach • Detailed supervisory responsibilities that are followed • Trained supervisors and provided them with tools • Logistical and program barriers to providing regular supervision • No process for documenting or discussing findings with staff and management	The organization has • A detailed supervision plan with a supportive approach • Detailed supervisory responsibilities that are followed • Trained supervisors and provided them with tools • A mechanism for carrying out visits according to the timeline • A process for documenting and discussing findings with staff and management • A process for following and addressing issues

Monitoring and Evaluation (M&E)

Subsection Objective: To assess how the organization collects and uses data to plan, monitor and evaluate its programs.

Resources: M&E plan, M&E tools, M&E reports

Monitoring and Evaluation ★			
1	**2**	**3**	**4**
The organization has • No M&E plan • No process for monitoring program implementation • Not identified indicators to monitor • No system for data processing: tools, trained data collectors, data quality review or a plan for analyzing and using information	The organization has • A basic M&E plan • Identified outcome indicators • Developed data collection tools • Trained staff in M&E • No system for regularly collecting, analyzing or reporting data • No review of data quality • No process for reporting progress against targets	The organization has • A well-defined M&E plan • Process and outcome indicators • Trained staff to collect data, and data collection is consistently done • A process for consistently using data/findings for follow-up monitoring, support or planning and reporting against targets • No process for sharing results with field and stakeholders	The organization has • A well-defined M&E plan • Process and outcome indicators • A process for using data for follow-up monitoring, program adjustments, planning and determining progress towards achieving targets • A process for data quality review • A strategy for reporting on progress against targets and involving staff and data collectors in reviewing and using findings • A strategy for regularly sharing information with stakeholders, including the community

From: Woutrina A Smith <wasmith@ucdavis.edu>
To: Corina Grigorescu Monagin <cgmonagin@UCDAVIS.EDU>;Oladele Ogunseitan <oladele.ogunseitan@uci.edu>;Peter Daszak <daszak@ecohealthalliance.org>;William B. Karesh <Karesh@ecohealthalliance.org>;mr84@columbia.edu" <mr84@columbia.edu>;alexandra zuber <alexandrazuber@atahealthstrategies.com>;Matthew Blake <mblake@ucdavis.edu>;Tracey Goldstein <tgoldstein@ucdavis.edu>;David John Wolking <djwolking@ucdavis.edu>;Terra Kelly <trkelly@ucdavis.edu>;Elizabeth Leasure <ealeasure@UCDAVIS.EDU>;Jonna Mazet <jkmazet@ucdavis.edu>;McNeil, Carrie S. <csmcnei@sandia.gov>;Jutta Lehmer <JLehmer@salud.unm.edu>;Omar Romero-hernandez <oromero@haas.berkeley.edu>;Bruce Baird Struminger <BStruminger@salud.unm.edu>;Federico Castillo <f.castillo@berkeley.edu>;Ndola PRATA <ndola@berkeley.edu>;Tiffany Harris, PhD, MS" <th2604@columbia.edu>;Costa, Cristiane <co123@cumc.columbia.edu>;Amaya, Idalia M. <ima2107@cumc.columbia.edu>;Sam Halabi <sfh9@georgetown.edu>
CC: onehealthnextgen Sympa List <onehealthnextgen@ucdavis.edu>
Sent: 4/17/2020 10:20:32 AM
Subject: OHW-NG flyer for One Health COVID-19 ECHO sessions next week

Hi OHW-NG Executive Board,

Here is the flyer announcement for the next OHW-NG One Health COVID-19 ECHO sessions next Wed/Thurs, April 22/23, for the AFROHUN and SEAOHUN regions. The topic is "What's working and what's not for COVID-19 response strategies around the world". The more detailed flyers including future session topics will be out early next week once we have Secretariat confirmation. Feel free to share this flyer with your networks as you like. French translation will be offered for the AFROHUN session as before. Faculty, students, and stakeholders are welcome. Previous recordings and the FAQ website are available through our ohwng.org website.

Best wishes, Woutrina

Woutrina Smith, DVM, MPVM, PhD
Professor of Infectious Disease Epidemiology
Associate Director, UCD One Health Institute
Technical Director, USAID One Health Workforce - Next Gen
Co-Director, UCGHI Planetary Health Center of Expertise
School of Veterinary Medicine, UC Davis
1089 Veterinary Medicine Dr
Davis, CA 95616
wasmith@ucdavis.edu
+1 530 219-1369 c

USAID FROM THE AMERICAN PEOPLE

HCEA Championing One Health

SEAOHUN Southeast Asia One Health University Network

ONE HEALTH UPDATES

ECHO biweekly sessions for AFROHUN & SEAOHUN members and stakeholders

NEXT SESSION: APRIL 22-23, 2020

SESSION TOPIC:

WHAT'S WORKING & WHAT'S NOT FOR COVID-19 RESPONSE STRATEGIES AROUND THE WORLD

AGENDA COMING SOON!

AFROHUN
AFRICA ONE HEALTH UNIVERSITY NETWORK

SEAOHUN
SOUTHEAST ASIA ONE HEALTH UNIVERSITY NETWORK

AFRICA SESSION [90 minutes]
Thursday, April 23
US: 9:30 am EDT | 7:30 am MDT | 6:30 am PDT
Africa: 1:30 pm GMT | 2:30 pm WAT | 3:30 pm CAT and SAST | 4:30 pm EAT

SOUTHEAST ASIA SESSION [90 minutes]
Wednesday, April 22 (USA)/Thursday, April 23 (SE Asia)
US: 9 pm EDT, 7 pm MDT, 6 pm PDT
Southeast Asia: 8 am ICT, 9 am MYT, 9 am PHT

Visit our website for free pre-registration and connection information at ohwng.org

Questions? Contact onehealthnextgen@ucdavis.edu

UCDAVIS One Health Institute School of Veterinary Medicine · EcoHealth Alliance · Ata Health Strategies · ICAP Columbia University Mailman School of Public Health · Berkeley University of California · Project ECHO · UCI University of California, Irvine

From: Peter Daszak <daszak@ecohealthalliance.org>
To: David A Relman <relman@stanford.edu>, "Kristian G. Andersen" <[redacted]>
Cc: Diane Griffin <dgriffi6@jhmi.edu>, "Shore, Carolyn" <CShore@nas.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: Quick votes?
Sent: Thu, 30 Apr 2020 02:16:26 +0000

OK – will do now..

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

---

From: David A Relman <relman@stanford.edu>
Sent: Wednesday, April 29, 2020 8:15 PM
To: Kristian G. Andersen <[redacted]>
Cc: Diane Griffin <dgriffi6@jhmi.edu>; Peter Daszak <daszak@ecohealthalliance.org>; Shore, Carolyn <CShore@nas.edu>; Jonna Mazet <jkmazet@ucdavis.edu>; David A Relman <relman@stanford.edu>
Subject: Re: Quick votes?

Hi Kristian-
Yes, but...we will incorporate all votes no matter when they are received! And besides, nothing is written in stone. All topics are available to the sponsors and to the full committee, so there will be opportunity to re-direct or re-define efforts.
David

From: "Kristian G. Andersen" <[redacted]>
Date: Wednesday, April 29, 2020 at 4:38 PM
To: David A Relman <relman@stanford.edu>
Cc: Diane Griffin <dgriffi6@jhmi.edu>, Peter Daszak <daszak@ecohealthalliance.org>, "Shore, Carolyn" <CShore@nas.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: Quick votes?

Hey David - are these the ones Lisa just emailed around? Looks like they already listed the 'priority' ones? Sorry, I'm confused by all the emails flying around... ;).

K

On Wed, Apr 29, 2020 at 3:46 PM David A Relman <relman@stanford.edu> wrote:

Hi Diane, Kristian, Peter—

We're about to finalize the viral WG selections of topics for consideration tomorrow morning. Do you want to (can you) send us your top 3 choices? No need to elaborate…

Best,

David

From: Peter Daszak <daszak@ecohealthalliance.org>
To: David A Relman <relman@stanford.edu>, "Kristian G. Andersen" <REDACTED
Cc: Diane Griffin <dgriffi6@jhmi.edu>, "Shore, Carolyn" <CShore@nas.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: RE: Quick votes?
Sent: Thu, 30 Apr 2020 02:22:13 +0000

OK – sorry to be late, as usual. I'm totally happy with the top 3 priorities the group's chosen here.

If I were to vote, I would have gone with A1, A3, A5 (host range). I feel that A2 has a ton of attention anyway, and that the results of the genetic analyses are so widely and rapidly debated online, usually without too much controversy, that our opinion and consensus is not as useful. I also feel that, while many believe A5 (host range) is not a pressing issue, I think we're going to come across potentially intractable problems if this virus gets into livestock, or if it is circulating in the very extensive mixed wildlife-livestock farms of S. China.

Again – very happy with the 3 choices as they stand.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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Sent: Wednesday, April 29, 2020 8:15 PM
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Cc: Diane Griffin <dgriffi6@jhmi.edu>; Peter Daszak <daszak@ecohealthalliance.org>; Shore, Carolyn <CShore@nas.edu>; Jonna Mazet <jkmazet@ucdavis.edu>; David A Relman <relman@stanford.edu>
Subject: Re: Quick votes?

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<CShore@nas.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
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> David

From: Diane Griffin <dgriffi6@jhmi.edu>
To: David A Relman <relman@stanford.edu>, "Kristian G. Andersen" <[redacted], Peter Daszak <daszak@ecohealthalliance.org>
Cc: "Shore, Carolyn" <CShore@nas.edu>, Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Re: Quick votes?
Sent: Thu, 30 Apr 2020 11:49:56 +0000

Sorry to be slow - too many deadlines . .
My top 3 (in order) are:
3, 4, 1

Diane

Diane E. Griffin, MD PhD
Vice President, National Academy of Sciences
University Distinguished Service Professor
W. Harry Feinstone Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health
615 N. Wolfe St, Rm E5636
Baltimore, MD 21205
410-955-3459
dgriffi6@jhu.edu

From: David A Relman <relman@stanford.edu>
Sent: Wednesday, April 29, 2020 6:46 PM
To: Diane Griffin <dgriffi6@jhmi.edu>; Kristian G. Andersen <[redacted]; Peter Daszak <daszak@ecohealthalliance.org>
Cc: David A Relman <relman@stanford.edu>; Shore, Carolyn <CShore@nas.edu>; Jonna Mazet <jkmazet@ucdavis.edu>
Subject: Quick votes?

Hi Diane, Kristian, Peter—
We're about to finalize the viral WG selections of topics for consideration tomorrow morning. Do you want to (can you) send us your top 3 choices? No need to elaborate…
Best,
David

From: Ben Oppenheim <boppenheim@metabiota.com>
Sent: Tue, 9 Jun 2020 22:22:28 -0700
Subject: Re: GVP BCA draft paper
To: Dennis Carroll <[redacted], Cara Chrisman <cchrisman@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, Stefano M Bertozzi <sbertozzi@berkeley.edu>, "Stephen S. Morse" <ssm20@cumc.columbia.edu>, Gavin Yamey <gavin.yamey@duke.edu>, "Boyle, Colin" <Colin.Boyle@ucsf.edu>, Nicole Stephenson <nstephenson@metabiota.com>, Jaclyn Guerrero <jguerrero@metabiota.com>, Nita Madhav <nmadhav@metabiota.com>, Paola Gadsden <paola.gadsden@cisidat.org.mx>, Dean Jamison <djamison@uw.edu>, "Rubin, Eddy" <erubin@metabiota.com>

Dear advisors,

I hope that you're all doing well. A quick follow-up on the status of the draft: we're beginning to incorporate edits, and if you could provide your comments in about 2 weeks (circa 23 June) that would help us prepare to submit the manuscript, ideally in early-mid July.

all the best,
Ben

On Fri, May 29, 2020 at 10:01 PM Ben Oppenheim <boppenheim@metabiota.com> wrote:

> Dear advisors
>
> I hope this note finds you and yours healthy and safe.
> Our last meeting in February seems rather distant now given the pace of events. But we've used the intervening time to refine our analysis and develop a draft paper, which you'll find attached here, along with technical appendices.
>
> Our goal is to revise and submit this draft to a journal as soon as possible, while it can most usefully inform policy discussions and resource allocation. But there is work to be done on the draft, and your feedback and questions on both the substance and presentation of the material would be terrific. Given everyone's schedule, I expect that emails or bilateral calls would be easiest, but I'm happy to coordinate a group conference call if that is more desirable.
>
> The basic headline we presented in DC is unchanged. We think that GVP's key impacts are likely to be in the areas of spillover risk reduction and capacity building, and that the magnitude of those impacts are likely to yield a favorable benefit-cost ratio. We think it important that readers have tools to estimate their own BRC, based on their assumptions, and we've worked to provide those.
>
> all the best,
> Ben

--
Ben Oppenheim, PhD
Vice President, Product, Policy and Partnerships

510.501.1097

--
Ben Oppenheim, PhD
Vice President, Product, Policy and Partnerships

510.501.1097

From: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
To: Andrew Clements <aclements@usaid.gov>
Cc: David John Wolking <djwolking@ucdavis.edu>, Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, Jonna Mazet <jkmazet@ucdavis.edu>, PREDICTMGT <predictmgt@usaid.gov>
Subject: RE: VAT Exemption for USAID/Egypt for PREDICT-2
Sent: Thu, 9 Jul 2020 16:05:23 +0000

Hi Andrew. The PREDICT-funded activities in Egypt have ceased, so should probably just drop it at this point.

Thanks,
Liz

Elizabeth Leasure
Financial Operations Manager
One Health Institute
REDACTED *(cell)*
530-754-9034 (office)
Skype: ealeasure

From: Andrew Clements <aclements@usaid.gov>
Sent: Thursday, July 9, 2020 8:11 AM
To: Elizabeth Leasure <ealeasure@UCDAVIS.EDU>
Cc: David John Wolking <djwolking@ucdavis.edu>; Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>; Jonna Mazet <jkmazet@ucdavis.edu>; PREDICTMGT <predictmgt@usaid.gov>
Subject: VAT Exemption for USAID/Egypt for PREDICT-2

Hi Liz,

My understanding is that the Egypt VAT issue was never resolved. Is it still worth following up on or should we drop it? Thanks!

Andrew

From: David J Wolking <djwolking@ucdavis.edu>
Sent: Fri, 31 Jul 2020 14:14:16 -0700
Subject: Reminder: P2 EB Call Monday August 3 @ 11AM Pacific
To: Aleksei Chmura <chmura@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>, Amanda Fine [redacted], Ava Lee Sullivan <sullivan@ecohealthalliance.org>, Brian Bird <bhbird@ucdavis.edu>, Carolina Chrurchill [redacted], Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>, Dawn Zimmerman <Zimmermand@si.edu>, Elizabeth Leasure <ealeasure@ucdavis.edu>, Jon Epstein <epstein@ecohealthalliance.org>, Karen Saylors [redacted] Kevin Olival <Olival@ecohealthalliance.org>, "Murray, Suzan" <MurrayS@si.edu>, Nicole Gardner <nrgardner@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, "predict@ucdavis.edu" <predict@ucdavis.edu>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, "Prof. Woutrina Smith" <wasmith@ucdavis.edu>, Sarah Olson <[redacted] Simon Anthony <sja2127@columbia.edu>, "Tammie O'Rourke" <[redacted] Tracey Goldstein <tgoldstein@ucdavis.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>

Hi there,
Just a reminder about next week's P2 Executive Board call at the usual time (Monday August 3rd @ 11AM Pacific). Zoom info and the agenda will follow soon.

Enjoy the weekend,

David

--
David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

From: David J Wolking <djwolking@ucdavis.edu>
Sent: Mon, 3 Aug 2020 11:34:54 -0700
Subject: Re: Reminder: P2 EB Call Monday August 3 @ 11AM Pacific
To: David J Wolking <djwolking@ucdavis.edu>
Cc: Aleksei Chmura <chmura@ecohealthalliance.org>, Alison Andre <andre@ecohealthalliance.org>, Amanda Fine [redacted], Ava Lee Sullivan <sullivan@ecohealthalliance.org>, Brian Bird <bhbird@ucdavis.edu>, Carolina Chrurchill [redacted], Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Corina Grigorescu Monagin <cgmonagin@ucdavis.edu>, Dawn Zimmerman <Zimmermand@si.edu>, Elizabeth Leasure <ealeasure@ucdavis.edu>, Jon Epstein <epstein@ecohealthalliance.org>, Karen Saylors [redacted] Kevin Olival <Olival@ecohealthalliance.org>, "Murray, Suzan" <MurrayS@si.edu>, Nicole Gardner <nrgardner@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>, "predict@ucdavis.edu" <predict@ucdavis.edu>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, "Prof. Woutrina Smith" <wasmith@ucdavis.edu>, Sarah Olson <[redacted]>, Simon Anthony <sja2127@columbia.edu>, "Tammie O'Rourke" [redacted], Tracey Goldstein <tgoldstein@ucdavis.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>

Hi EB,
Here is a link to the DRAFT P2 5-year report we shared with USAID on Friday. We'll be talking through this with USAID tomorrow on our senior management team call.

Thanks for helping us cross that bridge!

David

On Sun, Aug 2, 2020 at 2:03 PM David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi there,
> Below is the agenda and Zoom link for tomorrow's call.

Best,

David

PREDICT Executive Board Meeting
Monday, August 3, 2020
11:00AM-12:00PM PDT/2:00-3:00pm EDT
Zoom link: [redacted]
Additional Zoom info below agenda

1. Brief operations updates
Status of awards and planning for closeout (<60 days!)
Capturing/curating photo/film content for reports and media
Updates on publications and group author/acknowledgements list?

- Reminder to please update this Google Sheet - thoughts on "Pending" tab also welcome for continued discussion...

2. Final Report
Draft 5-year CoAg report submitted to USAID Friday July 31, 2020
Country reports now online at https://p2.predict.global/country-reports
Vol 1 - Global report updates on chapter drafts (deadline was July 30th) - link to working outline...

- Disease X: status and updates?
- Coronaviruses: draft evolving and under Jonna's review
  - Infographic on COVID-19 support - reminder to contribute feedback to Nistara
- Capacity: status and updates - draft complete
- Discovery - draft evolving with Simon and Tracey (aiming for end of month target)
- EHP: drafted
- Predicting spillover - drafted
  - Reminder to review select Emerging Disease Insights: only reviewed and finalized EDIs are available online at https://p2.predict.global/insights
- Frontiers of emergence chapter: drafted

- Human behaviors and spillover risk at wildlife human interface - drafted
- Wildlife value chain - drafted
- Non-viral pandemic threats (AMR and beyond): drafted
- ASL 2050: drafted
- Outbreak response: status and updates?
- Conclusion: status and updates?

3. Data sharing plans

DDL status - open data September 2020; all of the reports below need to be final by end of September.
Status of government reports and approvals as of August 2, 2020...

Country	Report	Notes/updates
Bangladesh	Pending	3 reports - human, domestic animal, wildlife; human is with Arif; the rest are influenza subtyping and are with Simon now for input; updates?
Indonesia	ID-001-P1P2	Updates? Still pending...
Indonesia	ID-002-P2 wildlife	
Indonesia	ID-004-P2 wildlife	
Indonesia	ID-005-P2 wildlife	
Indonesia	ID-006-P2 human	
Indonesia	ID-007-P2 wildlife	
Indonesia	ID-008-P2 human	
Malaysia	MP-007-P2 wildlife	Updates?
Thailand	TH-008-P2 human	Updates?

4. Extension SOW Status Updates

PCR testing
Serological testing

Standing items (time permitting)

5. Media, publication and conference updates

6. Upcoming funding opportunities?

7. Consortium author list

- Link to Google Sheet (on authorship vs. acknowledgements)

Zoom Call-in info
Topic: PREDICT EB Call
Join Zoom Meeting: [redacted]

Meeting ID: [redacted]

One tap mobile
[redacted] (San Jose)
(New York)

Dial by your location
[redacted] (San Jose)
(New York)
Meeting ID: [redacted]

On Fri, Jul 31, 2020 at 2:14 PM David J Wolking <djwolking@ucdavis.edu> wrote:

> Hi there,
> Just a reminder about next week's P2 Executive Board call at the usual time (Monday August 3rd @ 11AM Pacific).
> Zoom info and the agenda will follow soon.

Enjoy the weekend,

David

--
David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
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Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: John Mackenzie <J.Mackenzie@curtin.edu.au>
CC: Peter Daszak <daszak@ecohealthalliance.org>
Sent: 8/31/2020 11:18:25 AM
Subject: Re: NYTimes.com: U.S. Will Revive Global Virus-Hunting Effort Ended Last Year

Thanks, John -- devil's in the details, as it really isn't renewing or reviving as it stands now, but the future looks promising.
Stay tuned!
Hope you are doing okay.
Really nice to hear from you,
Jonna

On Sun, Aug 30, 2020 at 5:13 PM John Mackenzie <J.Mackenzie@curtin.edu.au> wrote:

Great news from The New York Times:

U.S. Will Revive Global Virus-Hunting Effort Ended Last Year. I'm thrilled to read this!

A federal agency is resurrecting a version of Predict, a scientific network that for a decade watched for new pathogens dangerous to humans. Joe Biden has also vowed to fund the effort.

https://www.nytimes.com/2020/08/30/health/predict-pandemic-usaid.html?smid=em-share

From: David J Wolking <djwolking@ucdavis.edu>
Sent: Mon, 31 Aug 2020 11:29:06 -0700
Subject: Re: Reminder: PREDICT Management Team Call - Tuesday September 1, 2020 @ 8:30AM Pacific
To: Cara Chrisman <cchrisman@usaid.gov>
Cc: David J Wolking <djwolking@ucdavis.edu>, Aleksei Chmura <chmura@ecohealthalliance.org>, Alisa Pereira Emerging Threats Division <apereira@usaid.gov>, Alison Andre <andre@ecohealthalliance.org>, Amalhin Shek <ashek@usaid.gov>, Ava Lee Sullivan <sullivan@ecohealthalliance.org>, Catherine Machalaba <Machalaba@ecohealthalliance.org>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, "Clements, Andrew (GH/HIDN)" <AClements@usaid.gov>, Elizabeth Leasure <ealeasure@ucdavis.edu>, Karen Saylors <[redacted]>, Peter Daszak <daszak@ecohealthalliance.org>, "predict@ucdavis.edu" <predict@ucdavis.edu>, PREDICTMGT <predictmgt@usaid.gov>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>

Thanks Cara, should we try to reschedule? Not sure if the majority of USAID team is also part of that review.
Best,

David

On Mon, Aug 31, 2020 at 11:11 AM Cara Chrisman <cchrisman@usaid.gov> wrote:

> Hi David & All,
> I have to miss this week as we have an internal review of our portfolio with GH leadership. Since I won't be on the call and since so many people on the call are involved, I just wanted to say a huge CONGRATULATIONS on the NIH/CREID announcement! Really exciting to hear and look forward to following it as it goes forward!

If there's anything out of the management meeting that I can follow up on, please let me know.

Best,
Cara

Cara J. Chrisman, PhD
Deputy Division Chief
Emerging Threats Division
Office of Infectious Disease, Bureau for Global Health
U.S. Agency for International Development (USAID)
Desk: (202) 916-2065
Cell: [redacted]
E-mail: cchrisman@usaid.gov

On Sat, Aug 29, 2020 at 5:42 PM 'David J Wolking' via PREDICTMGT <predictmgt@usaid.gov> wrote:

> Hi there,
> Just a reminder about next week's PREDICT Management Team Call (Tuesday September 1, 2020 @ 8:30AM Pacific). Zoom details are the same as always and below for quick reference. I'll send the agenda along early next week, so if there is anything in particular you would like to discuss, please send it along before Monday COB.

Enjoy the weekend,

David

Zoom Call-in info
Zoom link: [redacted]
Or iPhone one-tap :
US: +1[redacted]
Or Telephone:
Dial(for higher quality, dial a number based on your current location):

US: +REDACTED
Meeting ID: REDACTED

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David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

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David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

From: David J Wolking <djwolking@ucdavis.edu>
Sent: Tue, 1 Sep 2020 07:04:40 -0700
Subject: Re: Reminder: PREDICT Management Team Call - Tuesday September 1, 2020 @ 8:30AM Pacific
To: Andrew Clements <aclements@usaid.gov>
Cc: David J Wolking <djwolking@ucdavis.edu>, Cara Chrisman <cchrisman@usaid.gov>, Aleksei Chmura <chmura@ecohealthalliance.org>, Alisa Pereira Emerging Threats Division <apereira@usaid.gov>, Alison Andre <andre@ecohealthalliance.org>, Amalhin Shek <ashek@usaid.gov>, Ava Lee Sullivan <sullivan@ecohealthalliance.org>, Catherine Machalaba <Machalaba@ecohealthalliance.org>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Elizabeth Leasure <ealeasure@ucdavis.edu>, Karen Saylors <[redacted]>, Peter Daszak <daszak@ecohealthalliance.org>, "predict@ucdavis.edu" <predict@ucdavis.edu>, PREDICTMGT <predictmgt@usaid.gov>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>

Noted, we had the same discussion with our Executive Board yesterday...
Great minds ;-)

David

On Tue, Sep 1, 2020 at 3:13 AM Andrew Clements <aclements@usaid.gov> wrote:

> Thanks, David.
> Let's discuss timing/frequency of these calls after 9/30/2020. Specifically, do we keep the same schedule or dial it back.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Sep 1, 2020, at 12:01 AM, David J Wolking <djwolking@ucdavis.edu> wrote:

> Great!
> Below is the agenda, talk soon...

David

PREDICT Management Team Meeting Agenda
Tuesday, September 1, 2020
8:30-9:30AM PDT/11:30-12:30pm EDT
Zoom link: [redacted]
Additional Zoom info below agenda...

USAID Updates

1. Administrative items
Award close-out updates (as needed)
M&E - life of project
PREDICT data updates

2. Final Report updates
Wrapping up the CoAg 5-year report - link here: Open Link
Country report and engagement updates (https://p2.predict.global/country-reports)
Strategies and plans for report dissemination (printing, sharing etc.)
Legacy report updates

3. Extension updates

Mission communications updates (if any)
COVID-19 support tracking and updates
Reservoir testing and serology updates - Excel sheet coming soon as PCR test results due to UC Davis August 31st

4. Media, meetings, and public engagement updates

5. AOB
Zoom Call-in info
Zoom link: [redacted]
Or iPhone one-tap :
US: +[redacted]
Or Telephone:
Dial(for higher quality, dial a number based on your current location):
US: +[redacted]
Meeting ID: REDACTED

On Mon, Aug 31, 2020 at 1:57 PM Cara Chrisman <cchrisman@usaid.gov> wrote:

> False alarm, it just got rescheduled so I'll speak with you all tomorrow!

Sent from my iPhone

> On Aug 31, 2020, at 3:47 PM, Andrew Clements <aclements@usaid.gov> wrote:
>
> I'll be on the call tomorrow.

Andrew P. Clements, Ph.D.
Senior Scientific Advisor
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
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On Aug 31, 2020, at 8:11 PM, Cara Chrisman <cchrisman@usaid.gov> wrote:

> Hi David & All,
> I have to miss this week as we have an internal review of our portfolio with GH leadership. Since I won't be on the call and since so many people on the call are involved, I just wanted to say a huge CONGRATULATIONS on the NIH/CREID announcement! Really exciting to hear and look forward to following it as it goes forward!

If there's anything out of the management meeting that I can follow up on, please let me know.

Best,
Cara

Cara J. Chrisman, PhD
Deputy Division Chief
Emerging Threats Division
Office of Infectious Disease, Bureau for Global Health
U.S. Agency for International Development (USAID)

Desk: (202) 916-2065
Cell: REDACTED
E-mail: cchrisman@usaid.gov

On Sat, Aug 29, 2020 at 5:42 PM 'David J Wolking' via PREDICTMGT <predictmgt@usaid.gov> wrote:

> Hi there,
> Just a reminder about next week's PREDICT Management Team Call (Tuesday September 1, 2020 @ 8:30AM Pacific). Zoom details are the same as always and below for quick reference. I'll send the agenda along early next week, so if there is anything in particular you would like to discuss, please send it along before Monday COB.

Enjoy the weekend,

David

Zoom Call-in info
Zoom link: REDACTED
Or iPhone one-tap :
US: +REDACTED
Or Telephone:
Dial(for higher quality, dial a number based on your current location):
US: +REDACTED
Meeting ID: REDACTED

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David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

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David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

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David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

From:	David J Wolking <djwolking@ucdavis.edu>
To:	Peter Daszak <daszak@ecohealthalliance.org>;Aleksei Chmura <chmura@ecohealthalliance.org>;Ava Sullivan <sullivan@ecohealthalliance.org>
CC:	Johnson Christine Kreuder (ckjohnson@ucdavis.edu) <ckjohnson@ucdavis.edu>;Prof. Jonna Mazet <jkmazet@ucdavis.edu>;Eunah Regina Cho <eecho@ucdavis.edu>
Sent:	9/4/2020 10:54:56 AM
Subject:	Re: China files for PREDICT report

Hi Peter and Ava,

Here is the proof of the China report and the two special features. The report has an extensive reference list but these are not linked in the report text. If you could read through and let us know where to put them, that would be great, otherwise perhaps we just rename them from references to "Publications" or something if they are all China specific?

If you have any other changes please let us know ASAP. We plan to book this with the other reports in our volume 2 package and want to share with USAID early next week to complete the CoAg report requirements.

Thanks,

David

On Fri, Aug 28, 2020 at 8:13 AM David J Wolking <djwolking@ucdavis.edu> wrote:
Thanks Peter, received.

David

On Thu, Aug 27, 2020 at 10:34 PM Peter Daszak <daszak@ecohealthalliance.org> wrote:

Apologies for delay – just digging through the pile to get to it eventually

Cheers,

Peter

Peter Daszak

President

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USA

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Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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David J. Wolking
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University of California, Davis

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PREDICT

EMERGING DISEASE INSIGHTS

Understanding the Cross-Species Transmission of Bat Coronaviruses in China

Over the past decade, PREDICT China's surveillance efforts have generated a rich database with over 500 bat coronavirus (CoV) sequences. This includes alphacoronavirus sequences from 41 bat species and betacoronavirus sequences (the group that includes SARS-related CoVs) from 31 bat species. Our team has used these data to analyze the evolutionary origins and potential for cross-species transmission of bat CoVs in China.

This work showed that SARS-related CoVs have an evolutionary origin of diversity in Southwest China, particularly Yunnan province, and that the alphacoronaviruses (including Swine acute diarrhea syndrome coronavirus, SADS-CoV) likely diversified out of an evolutionary hotspot in Guangdong province. This has important implications for public health because many of the bats present in these regions are also found in neighboring countries, and even throughout Southeast Asia. This includes the reservoir hosts of the two virus sequences most closely related to SARS-CoV-2, and points to a critical region for further surveillance.

Our analysis also provides critical data on the origin of SARS-CoV-2. It shows that two sequences reported from bats belonging to the genus *Rhinolophus* are the closest relatives of the virus causing COVID-19, and that CoVs from pangolins are not from the clade that led to the origin of COVID-19. It supports the hypothesis that pangolin viruses include genes from bat-CoVs that recombined with other viruses already present in pangolins.

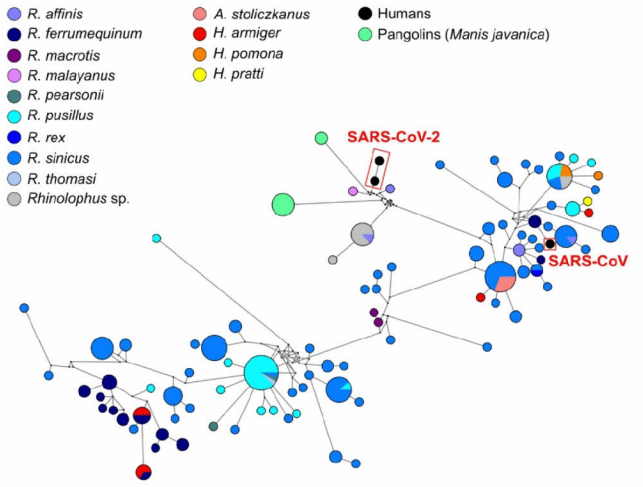

FIGURE 1. Median-joining network of 202 RNA-dependent RNA polymerase (*RdRp*) sequences of bat SARS-related CoVs, including two SARS-CoV-2, one SARS-CoV, and eight Malayan pangolin (*Manis javanica*) CoV sequences. Colors represent the host species corresponding to each CoV. Circle size is proportional to the number of identical sequences found. Branch length represents how closely related different strains are.

REFERENCES

Latinne A, Hu B, Olival KJ, Zhu G, Zhang L, Li H, Chmura AA, Field HE, Zambrana-Torrelio C, Epstein JH, Li B, Zhang W, Wang L-F, Shi Z-L, Daszak P (2020) Origin and cross-species transmission of bat coronaviruses in China. *Nature Communications* 11: 4235

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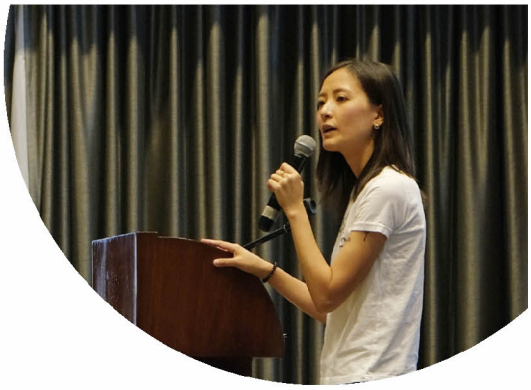


PREDICT
EMERGING DISEASE INSIGHTS

Enhancing China-US Collaboration on Emerging Infectious Diseases Research

To counter the significant global health threat that emerging infectious diseases (EIDs) represent, China and the US have been leading efforts in preparedness with unparalleled resources, widespread engagement, and national and geopolitical imperatives to contribute to global health security. This commitment has been essential to the advancement of our understanding of pandemic threats. Even though the US and China have both invested in EID research, integrated scientific studies with strong ecological and evolutionary components are not well-supported yet. Designing these integrated programs will help to better understand the risk of spillover and spread of pathogens in humans and animals, as well as to achieve a complete understanding of disease emergence to develop risk-mitigation strategies.

To further address this challenge, the PREDICT project participated in workshops co-hosted by the US National Science Foundation and National Natural Science Foundation of China in Kunming, China (2012); Shenzhen, China (2018); and Berkeley, US (2018). The workshops included reports on EID research taking place in China and the US, and facilitated a discussion of critical priorities to reduce risk of pandemics and promote global health.

Experts at the workshop agreed to increase efforts to address the drivers of EIDs, including:

- Landscape Change
- Migration, Transportation, and Trade
- Economic Development and Food Preference
- Climate Variability and Change

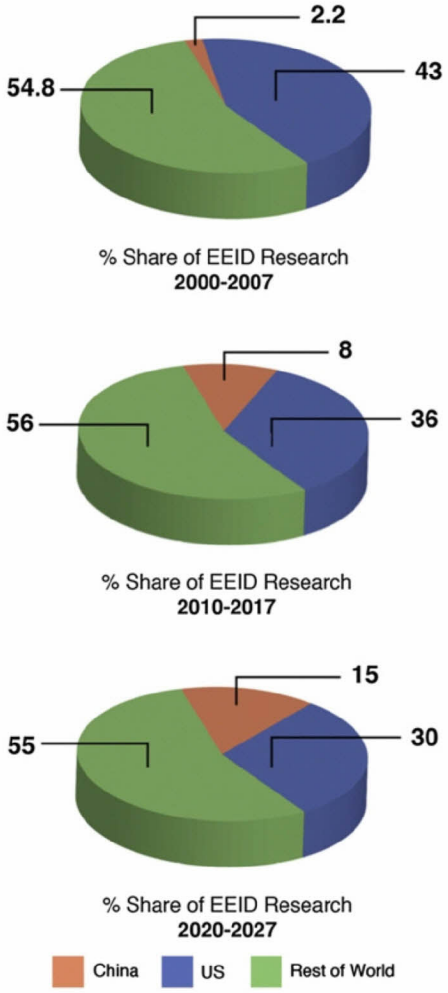


FIGURE 1. Current and projected future contributions to research involving the ecology and evolution of infectious diseases (EEID) from China, the U.S., and the rest of the world based on the published literature.

The meetings included highlights of China-US collaboration on EID surveillance and data collection conducted by PREDICT China over the past decade, a collaboration which has benefited the global community. Workshop outcomes included publication of the following key recommendations in two scientific papers (Mazet et al. 2015; Evans et al. 2019):

- Investments in training for disease ecology, eco-evolutionary dynamics, study design natural system, disease modeling, and complex data analysis
- Capacity building for EID research. This involves extending ecological and analytical training in less developed countries, where pathogens are most likely to emerge—moving beyond efforts limited to field sampling and pathogen detection
- New approaches to integrate ecological training and accelerate EID preparedness, including broadening data collection to reduce uncertainties and improving analytical techniques to identify regions at highest risk for EIDs
- Strengthening public health infrastructures in EID hotspots to reduce the number of outbreaks
- Substantial decade-long US–China joint funding mechanisms for integrated multidisciplinary EID research projects, which are needed to accomplish cross-training and meet the research objectives discussed above

The workshops were considered a success in that they led to the announcement of a jointly-funded program launched by NSF-China and the US NSF in their "Ecology and Evolution of Infectious Diseases" program.

REFERENCES

1. Mazet JA, Wei Q, Zhao G, Cummings DA, Desmond JS, Rosenthal J, King CH, Cao W, Chmura AA, Hagan EA, Zhang S. Joint China-US call for employing a transdisciplinary approach to emerging infectious diseases. *Ecohealth*. 2015 Dec 1;12(4):555-9.
2. Evans TS, Shi Z, Boots M, Liu W, Olival KJ, Xiao X, Vandewoude S, Brown H, Chen JL, Civitello DJ, Escobar L. Synergistic China–US Ecological Research is Essential for Global Emerging Infectious Disease Preparedness. *EcoHealth*.:1-4.

CHINA

In the highly biodiverse southern region of China, interactions among humans, wildlife, and livestock are increasing as a result of agricultural intensification, population movements, and urbanization. These changes provide a favorable context for the emergence of zoonotic disease, posing a public health threat particularly to the rural communities where frequent contact with animals occurs, but disease prevention measures are inadequate.

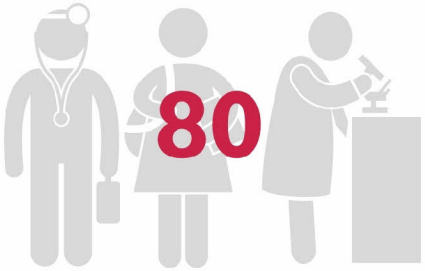
PREDICT China has worked with scientists, communities, and policy makers to discover zoonotic viruses among animal populations before emerging and causing potential pandemics. The project has allowed for an improved understanding of the pathogenesis of zoonotic viruses and the risk of emergence among human communities with the goal of developing targeted approaches to preventing and responding to zoonotic diseases.

During the past 10 years, the PREDICT project increased capacity of a One Health approach for emerging infectious disease prevention and response. The PREDICT team conducted concurrent virus surveillance among wild animals and human populations in high-risk regions in China, focusing on southern China, which is considered a "hotspot" for emerging zoonotic diseases in areas undergoing continuous land use change and overexploitation of natural resources. The PREDICT China team also collected human behavioral data to understand the risk factors for zoonotic disease emergence and identify appropriate social and behavioral interventions to reduce risk.

The PREDICT team worked with local laboratory partners to carry out virus characterization and pathogenesis studies to assess the zoonotic potential of detected viruses from surveillance, and developed serological assays for select bat coronaviruses. With support from the PREDICT modeling team, PREDICT China was able to use data collected over the past 10 years to better understand the virus evolution, host-pathogen dynamics, and general ecology of disease emergence.

LOCAL PARTNERS

- Chinese Center for Disease Control and Prevention
- Guangdong Provincial Center for Disease Control and Prevention
- Guangdong Provincial Institute of Public Health
- Institute of Microbiology, Chinese Academy of Sciences
- School of Health Sciences, Wuhan University
- Wuhan Institute of Virology, Chinese Academy of Sciences
- Yunnan Provincial Institute of Endemic Disease Control

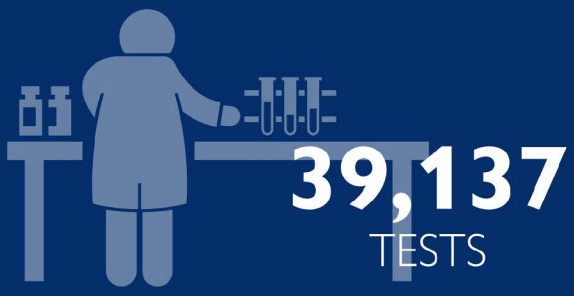


DEVELOPED the One Health Workforce by training 80 people in China.

OPERATIONALIZED One Health surveillance and sampled over 7.3K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.

LABORATORY STRENGTHENING

- Wuhan Institute of Virology of Chinese Academy of Sciences
- Institute of Microbiology of Chinese Academy of Sciences



DETECTED 108 unique viruses in both animal and human populations.

GUANGJIAN ZHU

Country Coordinator, *EcoHealth Alliance*

"During the past decade I worked for PREDICT, I have seen many scientists join the field for emerging infectious disease research. I hope my work through PREDICT can help set a gold standard for wildlife emerging infectious diseases field research practices in China."

ACHIEVEMENTS

PREDICT China demonstrated that bats are hosts of hundreds of coronavirus (CoV) strains, including SARS-related CoVs, some of which can infect human cells, cause disease in the lab mouse model for SARS, and evade candidate SARS vaccines and monoclonal therapeutics. Some of the virus sequences we identified were used to demonstrate Remdesivir's broad efficacy against SARS-CoV and 'pre-pandemic' bat-CoVs. We also found serological evidence of spillover of these viruses in rural populations, suggesting that communities in rural Southeast Asia could be exposed to bat coronaviruses each year, irrespective of their involvement in the wildlife trade. We showed that bat-origin CoVs are also responsible for a new disease that killed over 25,000 pigs in south China, and that the virus causing this disease, SADS-CoV, is also able to infect human cells in the laboratory. Finally, our collaborative team in China discovered the closest known relative of the virus causing COVID-19 (SARS-CoV-2). Throughout this work, we repeatedly raised awareness with the Chinese Government, the US Embassy, USG agencies, the WHO, and the public on the likelihood of a coronavirus-induced pandemic, similar to COVID. As the COVID pandemic unfolded, we have continued to communicate widely on the value of the PREDICT project in identifying its likely origin.

ONE HEALTH SURVEILLANCE

To promote One Health collaboration in emerging zoonotic disease surveillance, PREDICT China worked with the China Centers for Disease Control and Prevention and its provincial departments, National Forestry and Grassland Administration, FAO China, agricultural universities, and hospitals/clinics to conduct virus surveillance in animal and human populations. Two sites were selected as the sampling sites for concurrent animal and human surveillance (Table 1).

PREDICT China organized joint training on animal surveillance, conducted concurrent field sampling in animals and people, and established a communication and coordination network among multisectoral partners for timely results-sharing. PREDICT China's work has helped developed a culture of One Health collaboration in China that receives strong support from the government.

TABLE 1. Animals and humans sampled at concurrent community surveillance sites.

	NO. OF SAMPLING EVENTS	NO. OF ANIMALS SAMPLED	NO. OF HUMANS SAMPLED
CONCURRENT SITE 1	7	578	200
CONCURRENT SITE 2	8	473	300

VIRUS DETECTION

The PREDICT project's strategy for virus detection included screening samples using broadly reactive consensus PCR (cPCR) for priority virus families, including ccoronaviruses, filoviruses, flaviviruses, paramyxoviruses, and influenza virus. Viruses detected via these assays were sequenced to investigate their relationship to known pathogens, and samples were prioritized for further characterization based on these results. This approach allows for detection of both known and novel viruses and improves our understanding of the potential for the virus to cause disease in humans and/or animals.

This approach led to the discovery of a remarkable diversity of viruses in bats, particularly coronaviruses, including close relatives of SARS-CoV and SARS-CoV-2. Our work provides further evidence that both of these human pathogens originated in bats, and that there is substantial potential for further spillover. Working in collaboration with NIAID-funded partners, we demonstrated that some of the newly discovered bat-CoVs were able to bind to human cells, infect them in vitro, and cause SARS-like disease in a lab animal model. Our findings led to the discovery that Remdesivir – the only drug currently known to have efficacy against COVID – could also disrupt replication of bat-CoVs that are on the cusp of emergence.

PREDICT China also discovered a range of paramyxoviruses in bats and both paramyxoviruses and CoVs in rodents. The team sampled wild and captive bred bamboo rats (a widely farmed and consumed species) to assess whether wildlife farming amplified virus prevalence and therefore risk of spillover. We found no evidence that it did, but the sample size was small for wild rodents given their widespread hunting.

Of the 29 CoVs detected during PREDICT-2, 26 were found in bat hosts while two species of commensal rodent, the Norway rat and Oriential house rat, were found to host three known CoVs: Murine CoV, Rodent CoV, and Longquan Aa mouse CoV. Insectivorous bats, primarily members of the genera *Hipposideros*, *Rhinolophus*, *Miniopterus*, and *Myotis*, were host to 23 of the 26 (88.5%) bat-CoVs, seven of which are novel viruses detected as a result of PREDICT project surveillance. Members of the fruit bat family, Pteropodidae, hosted five CoVs, two of which are novel viruses. Furthermore, two CoVs were found in both insectivorous and fruit bat species, demonstrating the ability of these viruses to infect a diversity of bat hosts.

Paramyxovirus (PMV) diversity was also high – a total of 20 unique viruses (three known and 17 novel) were detected in bats and rodents throughout PREDICT-2. Similar to CoV findings, insectivorous bats were the dominant hosts (18 of 20 viruses). However, bat-PMV abundance was relatively low, as each virus was only detected 1-2 times in contrast to bat-CoVs, where we detected each virus an average of 16 times (range: 1 – 69). In addition to the insectivorous bat-PMV findings, one novel virus, PREDICT_PMV-123, was found in a single fruit bat (Dawn bat; *Eonycteris spelaea*) and multiple Norway rats tested positive for the known Beilong virus.

The only virus to be detected in humans was Influenza A, a well-known pathogen of humans and animals, found in an adult male. This single detection was a result of syndromic surveillance efforts in Guangdong Province.

TABLE 2. Virus heatmap for bats and rodents/shrews and by disease transmission interface

Viral Test Type

	Coronaviruses	Filoviruses	Flaviviruses	Influenzas	Paramyxoviruses
Aselliscus (bats)	0.9% (1236)	0% (618)	0% (216)	0% (834)	0.3% (618)
Chaerephon (bats)	0% (128)	0% (64)	0% (50)	0% (114)	0% (64)
Eonycteris (bats)	15% (520)	0% (260)	0% (260)	0% (520)	0.4% (260)
Hipposideros (bats)	1.6% (812)	0% (406)	0% (388)	0% (794)	0.5% (406)
Ia (bats)	0% (72)	0% (36)	0% (32)	0% (68)	8.3% (36)
Megaderma (bats)	0% (60)	0% (30)	0% (30)	0% (60)	0% (30)
Miniopterus (bats)	16.8% (956)	0% (478)	0% (294)	0% (760)	1% (478)
Myotis (bats)	10.8% (1356)	0% (678)	0% (300)	0% (978)	0.4% (678)
Rhinolophus (bats)	10.2% (1916)	0% (958)	0% (756)	0% (1714)	0.4% (958)
Rousettus (bats)	6.5% (260)	0% (130)	0% (98)	0% (228)	0% (130)
Tadarida (bats)	0% (136)	0% (68)	0% (62)	0% (130)	0% (68)
Taphozous (bats)	0% (580)	0% (290)	0% (290)	0% (580)	1% (290)
Tylonycteris (bats)	0% (288)	0% (144)	0% (144)	0% (288)	0% (144)
Apodemus (rodents/shrews)	0% (8)	0% (4)		0% (4)	0% (4)
Crocidura (rodents/shrews)	0% (48)	0% (24)		0% (24)	0% (24)
Eothenomys (rodents/shrews)	0% (24)	0% (12)		0% (12)	0% (12)
Mus (rodents/shrews)	0% (160)	0% (80)		0% (80)	0% (80)
Niviventer (rodents/shrews)	0% (76)	0% (38)		0% (38)	0% (38)
Rattus (rodents/shrews)	4.2% (1392)	0% (696)		0% (696)	2.7% (696)
Rhizomys (rodents/shrews)	0% (516)	0% (258)		0% (258)	0% (258)
Tupaia (rodents/shrews)	0% (44)	0% (22)		0% (22)	0% (22)
Unknown (rodents/shrews)	0% (12)	0% (6)		0% (6)	0% (6)

	Coronaviruses	Filoviruses	Flaviviruses	Influenzas	Paramyxoviruses
animal production	0% (560)	0% (280)		0% (280)	0% (280)
crop production	0% (80)	0% (40)		0% (40)	0% (40)
crop production; dwellings	0% (56)	0% (28)	0% (28)	0% (56)	0% (28)
crop production; dwellings; natural areas	3.7% (3528)	0% (1764)	0% (398)	0% (2162)	0.2% (1764)
crop production; natural areas	9.9% (4316)	0% (2158)	0% (1758)	0% (3916)	0.8% (2158)
dwellings	9.2% (1060)	0% (530)	0% (236)	0% (754)	3.6% (530)
dwellings; natural areas	4.5% (516)	0% (258)	0% (258)	0% (516)	0.8% (258)
natural areas	0% (484)	0% (242)	0% (242)	0% (484)	0% (242)

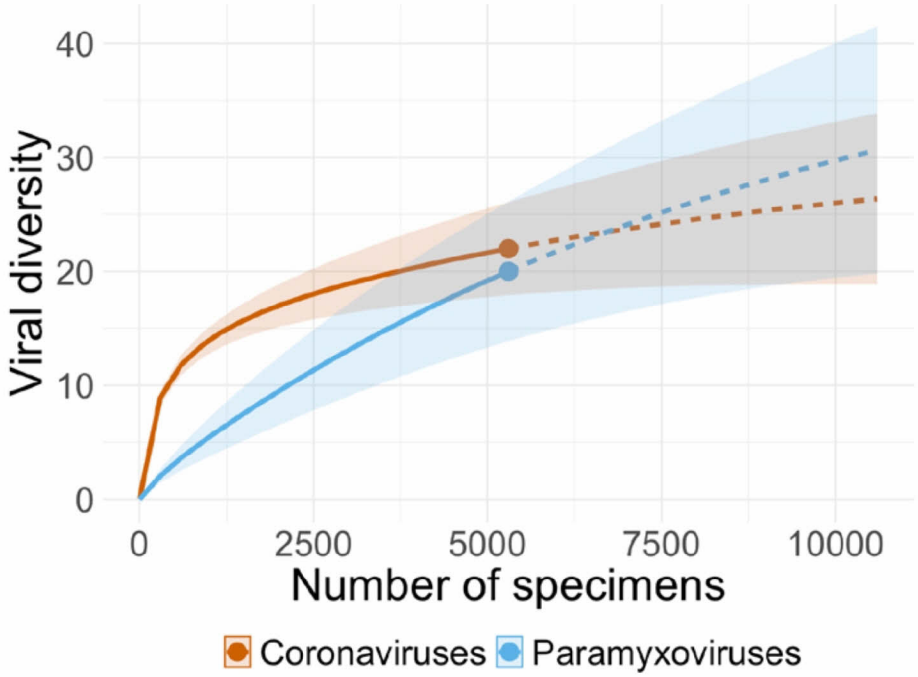


FIGURE 1. Virus discovery in China. The extensive sampling of bats in China led to evidence of the beginning of saturation of the discovery curve for coronaviruses. This suggests that it would be possible to identify the majority of currently unknown CoVs in China, given relatively unsubstantial further sampling and testing.

VIRUS TABLE

VIRUS FAMILY	VIRUS	SPECIES	SAMPLING LOCATION	# OF POSITIVE INDIVIDUALS
Coronavirus	PREDICT_CoV-22	Dawn Bat, Leschenault's Rousette	Xishuangbanna	43
	PREDICT_CoV-23	Dawn Bat	Xishuangbanna	1
	PREDICT_CoV-53	Intermediate Roundleaf Bat	Guilin	2
	PREDICT_CoV-60	Chinese Water Myotis	Chuxiong	17
	PREDICT_CoV-79	Least Horseshoe Bat	Guilin	37
	PREDICT_CoV-95	Intermediate Roundleaf Bat	Guilin	2
	PREDICT_CoV-107	Rickett's Big-Footed Bat	Chuxiong	3
	PREDICT_CoV-108	Himalayan Whiskered Myotis, Least Horseshoe Bat	Guilin	7
	PREDICT_CoV-111	Chinese Water Myotis	Chuxiong	1
	Bat coronavirus 1	Schreiber's Long-Fingered Bat, Small Long-Fingered Bat	Guangzhou, Jinning	69
	Bat coronavirus 512/2005	Rickett's Big-Footed Bat	Chuxiong	1
	Bat coronavirus Anlong 57/43	Himalayan Whiskered Myotis	Guilin	1

	Bat coronavirus HKU2	Chinese Horseshoe Bat, Himalayan Whiskered Myotis, Intermediate Horseshoe Bat, Least Horseshoe Bat, Stoliczka's Trident Bat, Thomas's Horseshoe Bat	Chuxiong, Guandong, Guilin, Jinning, Xishuangbanna	77
	Bat coronavirus HKU6	Chinese Water Myotis, Daubenton's Myotis, Himalayan Whiskered Myotis, Rickett's Big-Footed Bat, Small Long-Fingered Bat	Chuxiong, Guandong, Guilin, Jinning	62
	Bat coronavirus HKU8	Schreiber's Long-Fingered Bat	Guangzhou, Jinning	7
	Bat coronavirus HKU9	Dawn Bat, Intermediate Roundleaf Bat, Leschenault's Rousette	Chuxiong, Guilin, Xishuangbanna	11
	Bat coronavirus HKU10	Large-Eared Roundleaf Bat, Stoliczka's Trident Bat	Guilin, Xishuangbanna	6
	Bat coronavirus RS3376	Chinese Horseshoe Bat	Jinning	1
	Bat coronavirus RS4125/4259	Thomas's Horseshoe Bat	Xishuangbanna	1
	Hipposideros bat alphacoronavirus MJ/67C	Intermediate Horseshoe Bat, Stoliczka's Trident Bat	Xishuangbanna	6
	Myotis alphacoronavirus	Fringed Long-Footed Myotis	Chuxiong	1
	Rhinolophus/Hipposideros alphacoronavirus	Intermediate Horseshoe Bat	Xishuangbanna	4
	Rousettus bat coronavirus GCCDC1/346/356	Chinese Horseshoe Bat, Dawn Bat, Leschenault's Rousette	Jinning, Xishuangbanna	36
	Rousettus bat coronavirus/NRC-2	Leschenault's Rousette	Chuxiong	1
	SARS-related bat coronavirus RsSHC014	Intermediate Horseshoe Bat	Chuxiong	1
	SARS-related betacoronavirus Rp3/2004	Chinese Horseshoe Bat, Intermediate Horseshoe Bat, Thomas's Horseshoe Bat	Chuxiong, Guangzhou, Jinning, Xishuangbanna	17
	Longquan Aa mouse coronavirus	Norway Rat	Guangzhou	3
	Murine coronavirus	Norway Rat, Oriental House Rat	Guangzhou, Xishuangbanna	17
	Rodent coronavirus	Norway Rat	Guangzhou	14
Paramyxovirus	PREDICT_PMV-47	Great Evening Bat	Chuxiong	2
	PREDICT_PMV-49	Black-Bearded Tomb Bat, Unidentified Taphozous Bat	Guilin	2
	PREDICT_PMV-88	Intermediate Horseshoe Bat	Xishuangbanna	1
	PREDICT_PMV-89	Chinese Horseshoe Bat	Jinning	1
	PREDICT_PMV-90	Black-Bearded Tomb Bat	Guilin	1
	PREDICT_PMV-123	Dawn Bat	Xishuangbanna	1
	PREDICT_PMV-129	Chinese Horseshoe Bat	Guangzhou	1
	PREDICT_PMV-130	Fringed Long-Footed Myotis	Chuxiong	1
	PREDICT_PMV-134	Chinese Horseshoe Bat	Guilin	1
	PREDICT_PMV-135	Stoliczka's Trident Bat	Xishuangbanna	1
	PREDICT_PMV-136	Unidentified Taphozous Bat	Guilin	1
	PREDICT_PMV-157	Schreiber's Long-Fingered Bat	Jinning	2
	PREDICT_PMV-158	Schreiber's Long-Fingered Bat	Jinning	2
	PREDICT_PMV-162	Schreiber's Long-Fingered Bat	Jinning	1
	PREDICT_PMV-164	Stoliczka's Trident Bat	Xishuangbanna	1
	PREDICT_PMV-165	Chinese Water Myotis	Chuxiong	1
	PREDICT_PMV-166	Chinese Water Myotis	Jinning	1
	Bat paramyxovirus BtHp-ParaV/GD2012	Intermediate Roundleaf Bat	Guilin	2
	Bat paramyxovirus/B16-40	Schreiber's Long-Fingered Bat	Jinning	1
	Beilong virus	Norway Rat	Guangzhou	19
Influenza virus	Influenza A	Human	The 1st Affiliated Hospital of Shantou University	1
Total				**493**

EPIDEMIOLOGIC & BEHAVIORAL RISK

For PREDICT-2, our team in China conducted surveillance in both community and clinical settings by employing an integrated biological-behavioral surveillance approach. Through this approach, PREDICT China aimed to assess spillover potential of emerging zoonotic viruses at high-risk, human-animal interfaces and to use an evidence-based approach to identify behavioral risk factors associated with those interfaces. Ultimately this surveillance resulted in development of risk-mitigation strategies tailored to local contexts, including community education around our *Living Safely with Bats* risk reduction and behavior change communication resource.

DEMOGRAPHIC CHARACTERISTICS OF STUDY PARTICIPANTS

Variable		Community (n=500)		Hospital (n=218)	
		n	%	n	%
Gender	Female	280	56	103	47
	Male	220	44	115	53
Age	Under 18 years	1	0	116	53
	18-44 years	108	22	30	14
	45-64 years	280	56	42	19
	65 or older	111	22	30	14
Residence time	< 1 month	0	0	2	1
	> 1 month - 1 year	0	0	7	3
	> 1 - 5 years	4	1	96	44
	> 5 -10 years	22	4	16	7
	> 10 years	474	95	97	44
Education	None	92	18	103	47
	Primary	255	51	32	15
	Secondary	141	28	53	24
	College/University	10	2	30	14
Livelihood	Crop production	440	88	0	0
	Labor work	25	5	8	4
	Homemaker	7	1	7	3
	Animal production	9	2	3	1
	Non-animal business	8	2	44	20
	Children/Student		0	117	54
	Medical worker	1	0	2	1
	Unemployed	8	2	37	17
Self-report unusual symptoms in the past 12 months	Fever with headache and severe fatigue or weakness (encephalitis)	73	15	11	5
	Fever with cough and shortness of breath or difficulty breathing (SARI)	54	11	48	22
	Fever with muscle aches, cough, or sore throat (ILI)	69	14	68	31
	Fever with bleeding or bruising not related to injury (hemorrhagic fever)	2	0	1	0
	Fever with diarrhea or vomiting	10	2	15	7
	Others	23	5	7	3
	None	378	76	85	39

PREDICT China conducted biological-behavioral surveillance among rural residents in Yunnan, Guangxi, and Guangdong districts of Southern China, where the team had previously identified SARS-related CoVs in bats. In addition to the samples collected for virus detection, the PREDICT team collected serum samples from people that were evaluated for antibodies against four bat-borne coronaviruses (using a new ELISA assay based on selected nucleocapsid proteins). Surveys were administered to collect data on human-animal contact and zoonotic disease spillover risk. In this

research, almost 20% of participants reported severe acute respiratory infections (SARI) and/or influenza-like illness (ILI) symptoms in the past year. Risk factors associated with these self-reported symptoms included poultry, carnivore, rodent/shrew, or bat contact along with socioeconomic factors, such as income and district of residence. Nine participants (0.6%) tested positive for antibodies against bat coronaviruses, suggesting bat coronavirus spillover in individuals in these communities. These results highlight the utility of an hypothesized early-warning system under non-outbreak conditions to detect the spillover event of emerging zoonotic diseases by extending the traditional clinical-based surveillance to at-risk communities.

The decade-long PREDICT project allowed the team to establish a biobank and database which will enable cost-effective future surveillance programs and in-depth studies for zoonotic disease prevention and control.

BEHAVIORAL RISK INVESTIGATIONS

PREDICT China also conducted ethnographic interviews and field studies in the rural communities of Yunnan, Guangxi, and Guangdong provinces. Data were analyzed to identify both risk and protective factors for zoonotic disease emergence at the individual, community, and policy levels (Figure 2). A total of 88 ethnographic interviews and 55 field observations were conducted at nine sites. The study provides evidence of frequent human-animal interactions in these communities and identifies key behavioral risk factors that can be targeted for mitigation strategies to reduce the risk of disease emergence. Existing local programs and policies around human and animal health, community development, and conservation are considered effective resources for developing cost-effective strategies to mitigate zoonotic disease risks.

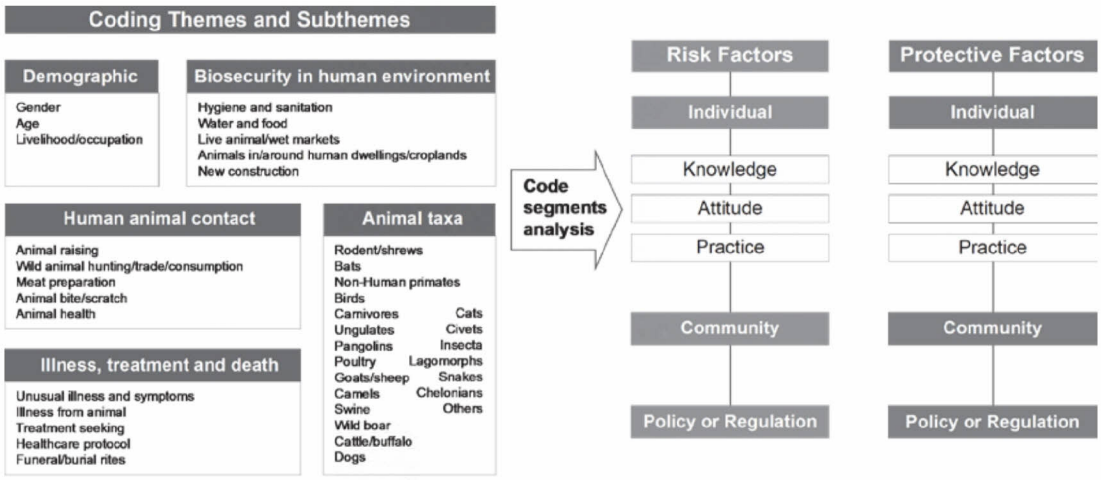


FIGURE 2. Qualitative method to identify the risk factors of zoonotic disease emergence.

Given the likely large number of undiscovered zoonotic pathogens currently in circulation in China, measures to reduce human-wildlife contact due to specific behaviors are urgently needed. This is particularly important for rural communities where close contact with bats and rodents was reported and zoonotic pathogens have been detected in animal populations. Enforcement of current wildlife protection policies coupled with capacity building in local clinics would likely significantly reduce high-risk contact between humans, wildlife, and livestock and risk for disease emergence and spread.

COMMUNITY ENGAGEMENT & RISK COMMUNICATION

PREDICT China presented the results of surveillance actitivities to agency leads from the China CDC, Provincial and city CDCs in Yunnan, Guangdong, Beijing, and Shanghai. Behavioral risk surveys at all sites included presentation of results to communities where sampling and analysis took place.

CAPACITY STRENGTHENING

Although a national emerging infectious disease surveillance and reporting system was established in China following the SARS outbreak in 2002, the clinical-based effort is reaction-driven versus a proactive approach. PREDICT China worked with Chinese researchers and the government to expand surveillance to animals for early detection and proactive prevention. By working with both humans and animals, PREDICT China built communication and collaboration platforms which brought multisectoral stakeholders together for more effective and efficient surveillance.

In addition, the PREDCT China field team has significantly contributed to increased capacity for in-country field practices by providing training to different ecology, zoology, and virology research groups on field biosafety and humane animal sampling. Through the in-country partners, training was conducted for broad external partners from African and Asian countries.

OUTBREAK PREPAREDNESS & RESPONSE

A novel bat-origin coronavirus, swine acute diarrhea syndrome coronavirus (SADS-CoV), caused fatal swine disease outbreaks in Guangdong Province, during 2016-2018, leading to the death of more than 25,000 pigs. PREDICT China worked closely with agricultural researchers to identify the pathogen and investigate the ecology of transmission to provide recommendations for prevention measures. In the two years following the outbreak, PREDICT China has conducted regular surveillance among bat populations around farms in Guangdong Province, and worked with the global modeling team to assess the potential for future spillover from bats to pigs across China.

PRACTICAL IMPLICATIONS

- Identification of hundreds of bat-origin CoV sequences
- Discovery of a large diversity of CoVs closely related to SARS-CoV and SARS-CoV-2
- Identification of bat-CoVs with clear potential to emerge directly in people
- Identification of a novel bat-origin virus, SADS-CoV, causing widespread outbreak in pigs in Southern China

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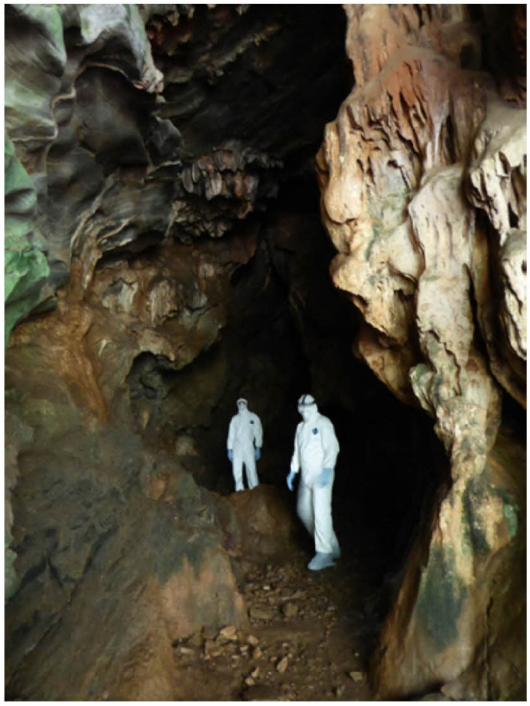
SPECIAL FEATURES

ONE HEALTH ACTION RESPONDING TO THE FATAL SWINE ACUTE DIARRHEA (SADS) SYNDROME OUTBREAKS

From October 2016, a fatal swine disease outbreak was observed in a pig farm in Guangdong province, China, causing severe acute diarrhea and vomiting, leading to death in newborn piglets (younger than five days) with a mortality of 90%. By May 2017, the disease has caused 24,693 piglet deaths at four farms. The clinical signs and preliminary lab testing suggested it was a novel disease caused by coronaviruses.

Learn more at **p2.predict.global/insights**



UNDERSTANDING THE CROSS-SPECIES TRANSMISSION OF BAT CORONAVIRUSES IN CHINA

Over the past decade, PREDICT China's surveillance efforts have generated a rich database with over 500 bat coronavirus (CoV) sequences. This includes alphacoronavirus sequences from 41 bat species and betacoronavirus sequences (the group that includes SARS-related CoVs) from 31 bat species. Our team has used these data to analyze the evolutionary origins and potential for cross-species transmission of bat CoVs in China.

Learn more at **p2.predict.global/insights**

ENHANCING THE CHINA-US COLLABORATION ON THE ECOLOGY & EVOLUTION OF EMERGING INFECTIOUS DISEASES (EEID) RESEARCH

To counter the significant global health threat that emerging infectious diseases (EIDs) represent, China and the US have been leading efforts in preparedness with unparalleled resources, widespread engagement, and national and geopolitical imperatives to contribute to global health security. This commitment has been essential to the advancement of our understanding of pandemic threats. Even though the US and China have both invested in EID research, integrated scientific studies with strong ecological and evolutionary components are yet well-supported.

Learn more at **p2.predict.global/insights**

USAID FROM THE AMERICAN PEOPLE
UCDAVIS VETERINARY MEDICINE One Health Institute
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EcoHealth Alliance
METABIOTA™
Smithsonian Institution

UCDUSR0008007

From: Ava Sullivan <sullivan@ecohealthalliance.org>
Subject: Re: China files for PREDICT report
Sent: Tue, 8 Sep 2020 09:20:30 -0400
Cc: Peter Daszak <daszak@ecohealthalliance.org>, Aleksei MacDurian <chmura@ecohealthalliance.org>, "Johnson Christine Kreuder (ckjohnson@ucdavis.edu)" <ckjohnson@ucdavis.edu>, Jonna Mazet <jkmazet@ucdavis.edu>, Eunah Regina Cho <eecho@ucdavis.edu>
To: David Wolking <djwolking@ucdavis.edu>

Thanks David,
Well received. We are working to get this back ASAP.
Ava

Ava Sullivan
Project Manager and Research Assistant

EcoHealth Alliance
520 Eighth Avenue – Suite 1200
New York, NY 10018
607-280-7669 (mobile)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

> On Sep 7, 2020, at 7:23 PM, David J Wolking <djwolking@ucdavis.edu> wrote:
>
> Hi Peter and team,
> Just making sure you received this message and understand the urgency. We really need to wrap up the country volume to dedicate our team to the final push for the global report.

Thanks, we really appreciate your efforts for a quick turnaround,

David

> On Fri, Sep 4, 2020 at 10:54 AM David J Wolking <djwolking@ucdavis.edu> wrote:
>
> Hi Peter and Ava,
> Here is the proof of the China report and the two special features. The report has an extensive reference list but these are not linked in the report text. If you could read through and let us know where to put them, that would be great, otherwise perhaps we just rename them from references to "Publications" or something if they are all China specific?

If you have any other changes please let us know ASAP. We plan to book this with the other reports in our volume 2 package and want to share with USAID early next week to complete the CoAg report requirements.

Thanks,

David

On Fri, Aug 28, 2020 at 8:13 AM David J Wolking <djwolking@ucdavis.edu> wrote:

> Thanks Peter, received.
> David

On Thu, Aug 27, 2020 at 10:34 PM Peter Daszak <daszak@ecohealthalliance.org> wrote:

> Apologies for delay – just digging through the pile to get to it eventually

Cheers,

Peter

Peter Daszak

President

EcoHealth Alliance

520 Eighth Avenue, Suite 1200

New York, NY 10018-6507

USA

Tel.: +1-212-380-4474

Website: www.ecohealthalliance.org

Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
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Senior Manager, PREEMPT Project
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David J. Wolking
Senior Manager, Global Programs, One Health Institute
Global Operations Officer, PREDICT Project of USAID Emerging Threats Division
Senior Manager, PREEMPT Project
School of Veterinary Medicine
University of California, Davis

From: "Tammie O'Rourke" [redacted]
Sent: Mon, 28 Sep 2020 08:57:23 -0700
Subject: Re: Embargo for China
To: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>

No problem - I have sent a message to the data team to clarify how embargos work. They are usually quick at responding.
Tammie

On Sun, Sep 27, 2020 at 2:57 PM Christine Kreuder Johnson <ckjohnson@ucdavis.edu> wrote:

> Thanks Tammie, v helpful. It would be good to understand the duration of the embargo and what our options are for this, esp if we select 'unk'/
>
> Appreciate your incredible fortitude in managing all of these late changes.
>
> /ckj

From: Tammie O'Rourke <[redacted]
Date: Friday, September 25, 2020 at 3:16 PM
To: Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>
Subject: Embargo for China

Hi Chris,

As discussed, below is an excerpt from the DDL documentation on requesting an Embargo. I noticed when creating the data asset they have the option to choose "unknown" for the proposed embargo date, not sure if that means you can go beyond a year? I could send a message to the USAID data team to clarify if we need to use that option.

I hope this helps, please let me know if you have any questions,

Tammie

Embargo Section

Embargo Requested?

Select "yes" if you are requesting a temporary delay (an embargo) in making this data public. Please be aware that the embargo will be granted contingent upon approval.

Proposed Embargo Date

Please select or enter the earliest date on which you would like this data to be released. An embargo may last up to and including 12 months after the award completion date.

Embargo Request Rationale

Please describe the reasons for requesting the embargo. The main permissible reasons for granting an embargo are for a pending publication or pending patent application. Additional guidance can be found in ADS 579.3.3.3, page 18.

The ADS reference states:

579.3.4.3 Embargos on Data Publication Effective Date: 10/01/2014

USAID may embargo, or temporarily withhold from public release for a reasonable period (e.g. 12 months), a Dataset resulting from federally funded research while the Dataset is the subject of a pending publication or pending patent application. Implementing partners must still submit the Dataset to USAID, and with agreement of the Contract or Agreement Officer, it can be held as non-public until the conclusion of the embargo period.

--

Tammie O'Rourke

Labyrinth Global Health

Systems Integrator

Emerging Pandemic Threats - PREDICT Program

tel +1-250-618-2460

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From: Peter Daszak <daszak@ecohealthalliance.org>
To: Tammie O'Rourke [redacted] Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>, Hongying Li <li@ecohealthalliance.org>, Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: RE: Embargo for China
Sent: Tue, 29 Sep 2020 00:05:25 +0000

Please request a 12 month embargo. It will likely take that long.

The language should be "The embargo is requested pending approval of publications by the appropriate government authorities in China".

Thanks for doing this.

The genetic sequences will be uploaded to Genbank by collaborators in Wuhan, once publications are in press.

Cheers,

Peter

Peter Daszak
President

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USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Tammie O'Rourke [redacted]
Sent: Monday, September 28, 2020 12:28 PM
To: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Cc: Jonna Mazet <jkmazet@ucdavis.edu>; Peter Daszak <daszak@ecohealthalliance.org>
Subject: Re: Embargo for China

Hi Chris,
Below is the data team's further comments on embargos. Our plan was to publish the China data in separate datasets under the PREDICT data asset, but based on what they said we will have to create a separate data asset for China. This is not ideal because it would be easy for someone to entirely miss China's data since it would be separate in the DDL. We could put something in the ReadMe file to explain this however.
Tammie

The embargo would have to apply to the entire data asset, since we clear and publish submissions at the asset level. In other words, the entire data asset would not be published until the embargo has passed. Embargoes are generally approved by our clearance officials and are usually honored. Once a submission with an embargo has been cleared, someone from the curation team will contact you to confirm that the data can be published once the embargo date has passed.

If you choose "unknown" for the embargo date, our team or the risk assessment team will contact you during or after the clearance process to see if you have a better idea of when it will be okay to publish the data.

On Sun, Sep 27, 2020 at 2:57 PM Christine Kreuder Johnson <ckjohnson@ucdavis.edu> wrote:

Thanks Tammie, v helpful. It would be good to understand the duration of the embargo and what our options are for this, esp if we select 'unk'/

Appreciate your incredible fortitude in managing all of these late changes.

/ckj

From: Tammie O'Rourke [REDACTED]
Date: Friday, September 25, 2020 at 3:16 PM
To: Christine Kreuder Johnson <ckjohnson@UCDAVIS.EDU>, Jonna Mazet <jkmazet@ucdavis.edu>, Peter Daszak <daszak@ecohealthalliance.org>
Subject: Embargo for China

Hi Chris,

As discussed, below is an excerpt from the DDL documentation on requesting an Embargo. I noticed when creating the data asset they have the option to choose "unknown" for the proposed embargo date, not sure if that means you can go beyond a year? I could send a message to the USAID data team to clarify if we need to use that option.

I hope this helps, please let me know if you have any questions,
Tammie

Embargo Section

Embargo Requested?
Select "yes" if you are requesting a temporary delay (an embargo) in making this data public. Please be aware that the embargo will be granted contingent upon approval.
Proposed Embargo Date
Please select or enter the earliest date on which you would like this data to be released. An embargo may last up to and including 12 months after the award completion date.
Embargo Request Rationale
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The ADS reference states:
579.3.4.3 Embargos on Data Publication Effective Date: 10/01/2014
USAID may embargo, or temporarily withhold from public release for a reasonable period (e.g. 12 months), a Dataset resulting from federally funded research while the Dataset is the subject of a pending publication or pending patent application. Implementing partners must still submit the Dataset to USAID, and with agreement of the Contract or Agreement Officer, it can be held as non-public until the conclusion of the embargo period.

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From: Lisa Kramer <lkramer@usaid.gov>
Sent: Thu, 19 Jan 2017 07:48:26 +0300
Subject: Re: Update from Rwanda
To: Jonna Mazet <jkmazet@ucdavis.edu>
Cc: "AOTR/Grant Manager Andrew Clements" <AClements@usaid.gov>, Alisa Pereira <apereira@usaid.gov>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, Brian Bird <bhbird@ucdavis.edu>, Tracey Goldstein <tgoldstein@ucdavis.edu>, Kirsten Gilardi <kvgilardi@ucdavis.edu>, David J Wolking <djwolking@ucdavis.edu>

Thank you very much Jonna.

Lisa Kramer
Regional Emerging Pandemic Threats Advisor
USAID/Kenya and East Africa
+254-20-862-2107 (O)
+2 REDACTED (C)

On Thu, Jan 19, 2017 at 3:52 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

FYI -- update from Julius below,
Jonna

The ROHSC met this morning (Rwanda Agriculture Board,Rwanda Biiomedical Center (Ministry of Health), P&R,and PREDICT) and left Kigali for Rusizi. Both Julius and Jean Claude are part of the team (along with Jean Felix Kinani working for P&R, and a senior technician from RBC). At 4 pm they were interviewed by Voice of America Radio (Kinyarwanda version) for an hour, with locals calling in and ROHSC members helping Isidore Gafarasi, Director of Veterinary Services for RAB, to respond to questions. They got to Rusizi late this evening, and Gafarasi did another interview with National Radio of Rwanda (Rusizi Branch) with the District Veterinary Officer in Rusizi. Tomorrow morning early they will head out to the Bugarama sector of the Rusizi River to investigate reported wild birds mortalities.

PS: No new updates from Uganda today.

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: Kramer, Lisa <lkramer@usaid.gov>;Alisa Pereira <apereira@usaid.gov>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>;David J Wolking <djwolking@ucdavis.edu>
Sent: 1/24/2017 7:57:23 AM
Subject: Re: Cameroon

Thanks. I've heard the same via FAO.

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jan 24, 2017, at 4:53 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:

Looks like Cameroon also involved now (bird deaths in North, but not yet official). No Predict response yet requested.
We'll keep you posted,
J

Sent: Thu, 26 Jan 2017 22:39:38 -0800
Subject: Re: Jerry Garteh's Work at the FDA
From: Jonna Mazet <jkmazet@ucdavis.edu>
To: "William B. Karesh" <karesh@ecohealthalliance.org>

Thanks!
J

On Thu, Jan 26, 2017 at 6:55 PM, William B. Karesh <karesh@ecohealthalliance.org> wrote:

> Thanks.
>
> Jon, the emails go back months but I can't see that they ever communicated their questions or concerns with us, nor do they mention that the US Forest Service Contract stipulates the Mr Garcia is free to work on other contractual agreements.
>
> Let's discuss in person when you have chance.
>
> **William B. Karesh, D.V.M**
> *Executive Vice President for Health and Policy*
>
> EcoHealth Alliance
> 460 West 34th Street - 17th Floor
> New York, NY 10001 USA
>
> +1.212.380.4463 (direct)
> +1.212.380.4465 (fax)
> www.ecohealthalliance.org
>
> President, OIE Working Group on Wildlife
>
> Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group
>
> EPT Liaison - USAID Emerging Pandemic Threats - PREDICT 2 program
>
> ***EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.***
>
> On Jan 25, 2017, at 7:19 PM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
>
> > FYI
> > J
> >
> > ---------- Forwarded message ----------
> > From: **Kendra Chittenden** <kchittenden@usaid.gov>
> > Date: Tue, Jan 24, 2017 at 10:07 AM
> > Subject: Fwd: Jerry Garteh's Work at the FDA
> > To: Alisa Pereira <apereira@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>
> >
> > Just found the initial email chain
> > ---------- Forwarded message ----------
> > From: **Kendra Chittenden** <kchittenden@usaid.gov>
> > Date: Mon, Oct 24, 2016 at 9:20 AM
> > Subject: Re: Jerry Garteh's Work at the FDA
> > To: Monica Dea <mdea@usaid.gov>

Thanks!

On Mon, Oct 24, 2016 at 9:14 AM, Monica Dea <mdea@usaid.gov> wrote:

> Dear Kendra, please see the information from Adam regarding Jerry Garteh's employment by USAID US Forest Services.
> thanks.

---------- Forwarded message ----------
From: **Keith Metzner** <kmetzner@usaid.gov>
Date: Wed, Oct 19, 2016 at 7:22 PM
Subject: Fwd: Jerry Garteh's Work at the FDA
To: Jennifer Tikka <jtikka@usaid.gov>
Cc: Leslie Flagg USAID <lflagg@usaid.gov>, Monica Dea <mdea@usaid.gov>

Jennifer,

You may wish to consult with Monica about how to proceed from here.

According to Monica Mr. Jerry Garteh has been working part-time with PREDICT since April or May of 2016 and has been the full-time PREDICT Liberia Country Coordinator since 1 Oct.

Something is strange here?

Keith

Keith Metzner

Natural Resources Officer
USAID | **LIBERIA**
Office of Economic Growth
Embassy of the United States of America
502 Benson Street, Monrovia, Liberia

kmetzner@usaid.gov
Tel: (+231) 77- 677-7000 Ext. 7414
Mobile: REDACTED

---------- Forwarded message ----------
From: **Welti, Adam J -FS** <adamjwelti@fs.fed.us>
Date: Wed, Oct 19, 2016 at 7:11 PM
Subject: RE: Jerry Garteh's Work at the FDA
To: Keith Metzner <kmetzner@usaid.gov>
Cc: Jennifer Tikka <jtikka@usaid.gov>, Leslie Flagg USAID <lflagg@usaid.gov>, "Sheridan, Kathleen A -FS" <kathleenasheridan@fs.fed.us>

Hi Keith,

Jerry is under contract with our office via METI and is full time. At this time, his contract runs through December 2016 but as we finalize our work plan for the coming months, our goal would be to extend his contract through September 2017 to support further activities. He and I are working on the draft work plan for this next phase and will submit for your review in the coming days. I am attaching here, prior documentation on the survey and follow on associated efforts (including report on 1st phase work plan as well as 2nd phase work plan).

Please let me know of any additional questions.

Kindly,

Adam Welti

Africa and Middle East Program

US Forest Service, International Programs

From: Keith Metzner [mailto:kmetzner@usaid.gov]
Sent: Wednesday, October 19, 2016 2:43 PM
To: Welti, Adam J -FS <adamjwelti@fs.fed.us>
Cc: Jennifer Tikka <jtikka@usaid.gov>; Leslie Flagg USAID <lflagg@usaid.gov>
Subject: Jerry Garteh's Work at the FDA

Hi Adam,

Can you please share something about Jerry Garteh's contract and his work at the FDA.

Is he part or full-time and for how long?

Thanks,

Keith

Keith Metzner

Natural Resources Officer

USAID | LIBERIA

Office of Economic Growth

Embassy of the United States of America

502 Benson Street, Monrovia, Liberia

kmetzner@usaid.gov

Tel: (+231) 77- 677-7000 Ext. 7414

Mobile: REDACTED

--

Monica N. Dea
Sr. Public Health Advisor
Health Team
USAID Liberia
502 Benson Street, Monrovia
Tel (Reception): +(231) 77 677 7000
Tel (Direct): +(231) 77 677 7226
Mobile: + REDACTED

--

Kendra Chittenden, Ph.D. | Senior Infectious Disease Advisor| USAID | mobile (703-209-5424) |KChittenden@usaid.gov

--

Kendra Chittenden, Ph.D. | Senior Infectious Disease Advisor| USAID | mobile (703-209-5424) |KChittenden@usaid.gov

From: Jonna Mazet <jkmazet@ucdavis.edu>
To: Zandra Andre <zandre@usaid.gov>
CC: Alisa Pereira <apereira@usaid.gov>;AOTR/Grant Manager Andrew Clements <AClements@usaid.gov>;David J Wolking <djwolking@ucdavis.edu>
Sent: 1/27/2017 7:37:19 AM
Subject: Re: FW: [predict] Continued issues with PREDICT transition

Thanks so much -- you have a good weekend, too,
Jonna

On Fri, Jan 27, 2017 at 1:50 AM, Zandra Andre <zandre@usaid.gov> wrote:
Hi Jonna,

Thanks for following up.

I've asked her time and again to deal with Metabiota directly. I have actively tried not be be engaged with this but have been dragged in it. For the last two days, she and I attended the same workshop so every coffee break she took the opportunity to continue on with this. She seems to be a reasonable person and maintains an acceptable level of professionalism for the most part but you're right, as this continues, doubts will start to percolate.
I appreciate your focused attention on this and I hope that we can move past all of this soon.

I don't intend on being engaged at this level with issue from this point.

Have a good weekend,
Zandra

Dr. Zandra Hollaway ANDRE
DVM, MPH, ACVPM
Senior One Health Team Lead
U.S. AGENCY FOR INTERNATIONAL DEVELOPMENT
US Embassy - Abidjan, Côte d'Ivoire
T: +225 22 49 43 35 M:+225 04 89 27 36
From the US: (301) 985-8627 x 4335
USAID.gov | ZAndre@usaid.gov | @USAIDWestAfrica

On Fri, Jan 27, 2017 at 6:02 AM, Jonna Mazet <jkmazet@ucdavis.edu> wrote:
Dear Zandra, Alisa, and Andrew,
As a follow-up to Karen's email detailing all of the issues regarding Marie-Josiane's employment issues, I want to confirm that I am in receipt of the invoice that she submitted to Metabiota for her hours in January, slated to be paid on her regular pay day (at the end of the month). There has been no break in employment or compensation, though she did receive a termination letter in order to proceed with her hiring at IPCI.
Of course, this begs the question as to why she would engage or complain about her situation at all. I remain distressed about communication issues and have been assured that she will be deterred from disturbing you in the future. I would appreciate your assistance in dissuading inappropriate communications regarding her employment situation with anyone other than her employer and any other unprofessional behavior. If any such behavior continues, we will have no choice but to question her ability to communicate professionally and represent the project in any capacity.
I also remain in constant contact with Metabiota and am monitoring their communication strategies and management plan in this difficult transition.
Thank you for your support,
Jonna

From: Andrew Clements <aclements@usaid.gov>
Sent: Mon, 30 Jan 2017 12:39:25 +0700
Subject: Re: D&F form for new PREDICT-2 subcontract to procure services from Rwanda Biomedical Center
To: Elizabeth Leasure <ealeasure@ucdavis.edu>
Cc: PREDICTMGT <predictmgt@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>, David John Wolking <djwolking@ucdavis.edu>

Thanks

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

On Jan 30, 2017, at 8:00 AM, Elizabeth Leasure <ealeasure@ucdavis.edu> wrote:

> Hi Andrew. The D&F document you requested for the RBC subcontract is attached. Please let me know if you need anything else to proceed with approving this subcontract.
>
> Thanks,
> Liz
>
> Elizabeth Leasure
> One Health Institute
> University of California, Davis
> 530-754-9034 (office)
> REDACTED (cell)
>
> --
> You received this message because you are subscribed to the Google Groups "PREDICTMGT" group.
> To unsubscribe from this group and stop receiving emails from it, send an email to predictmgt+unsubscribe@usaid.gov.
> To post to this group, send email to predictmgt@usaid.gov.
> To view this discussion on the web visit https://groups.google.com/a/usaid.gov/d/msgid/predictmgt/BL2PR08MB1166F894480EECB2D85ACDDA24B0%40BL2PR08MB116.namprd08.prod.outlook.com.
>
> <Determination and findings NRL-RBC_1-29-17.doc>

From: Peter Daszak <daszak@ecohealthalliance.org>
To: Cara Chrisman <cchrisman@usaid.gov>, Nathan Wolfe <nwolfe@metabiota.com>, Eddy Rubin <erubin@metabiota.com>, Jonna Mazet <jkmazet@ucdavis.edu>, "Brooke Watson" <watson@ecohealthalliance.org>, Hongying Li <li@ecohealthalliance.org>
Cc: Amalhin Shek <ashek@usaid.gov>, Dennis Carroll <dcarroll@usaid.gov>, Alison Andre <andre@ecohealthalliance.org>, Rebecca Benmahdi <rbenmahdi@metabiota.com>, Elizabeth S Chase <eschase@ucdavis.edu>, "Taylor Elnicki" <telnicki@metabiota.com>
Subject: RE: Request: GVP Update for Newsletter, Due COB Feb. 27th
Sent: Wed, 22 Feb 2017 17:26:26 +0000

Will do...

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

+1.212.380.4473 (direct)
+1.212.380.4465 (fax)
www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Cara Chrisman [mailto:cchrisman@usaid.gov]
Sent: Tuesday, February 21, 2017 4:13 PM
To: Nathan Wolfe; Eddy Rubin; Jonna Mazet; Peter Daszak; Brooke Watson; Hongying Li
Cc: Amalhin Shek; Dennis Carroll; Alison Andre; Rebecca Benmahdi; Elizabeth S Chase; Taylor Elnicki
Subject: Request: GVP Update for Newsletter, Due COB Feb. 27th

Dear GVP Colleagues,

We would like to request your assistance in developing short blurbs for the next GVP newsletter. Would you please provide a short blurb on the items below by **COB Monday, February 27th** to Amalhin Shek (cc'ed)?

- Chan-Zuckerberg BioHub: Nathan
- Legacy Ventures: Nathan
- Illumina: Eddy
- Genomics Meeting: Eddy
- Science Philanthropy Alliance: Jonna
- University of Minnesota Presentation: Jonna
- Chinese Natl Virome Project Meeting: Peter/Brooke/Hongying
- CAS International Affairs Meeting: Peter/Hongying

While other items will be featured, any assistance with the items above would be greatly appreciated (and please let us know if we've missed anything). Please note that items in the newsletter are designed for public consumption, so should be written as such.

Thanks,

Cara

Cara J. Chrisman, PhD
Senior Infectious Diseases Technical Advisor
Emerging Threats Division
Office of Infectious Disease
Bureau for Global Health
U.S. Agency for International Development (USAID)

Desk: (202) 712-1161
Cell: [redacted]
E-mail: cchrisman@usaid.gov

From: David J Wolking <djwolking@ucdavis.edu>
Sent: Thu, 23 Feb 2017 02:18:19 +0000
To: "abekiri@ucdavis.edu" <abekiri@ucdavis.edu>, "ckilonzo@ucdavis.edu" <ckilonzo@ucdavis.edu>, "djwolking@ucdavis.edu" <djwolking@ucdavis.edu>, "gmwangoka@ihi.or.tz" <gmwangoka@ihi.or.tz>, [redacted], "predict@ucdavis.edu" <predict@ucdavis.edu>, [redacted]
Cc: Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, "Prof. Jonna Mazet" <jkmazet@ucdavis.edu>, Taylor Gabourie <tagabourie@ucdavis.edu>, William Karesh <karesh@ecohealthalliance.org>
Subject: [predict] Re: Request by 3/3- Information on Zoonotic Disease Illnesses or Outbreaks in Tanzania

Hi Tanzania team,

We didn't touch on this on the call today but since we have now received the official request for information from CDC, it's time to begin planning and preparing an information packet to share, similar to the example I sent along to you all from Uganda.

With teams in the Lake Zone or preparing for departure now I suggest Abel and Chris as the best POCs for helping organize information.

Abel would you be willing to act as lead since you have been engaged in these meetings?

Let's make a plan very soon and identify the best combo of global, regional, and country specific resources that highlight our work and the importance of zoonotic viruses (known and emerging) as well as the risk of spillover from wildlife, etc so these themes are recognized by the planning committee and given fair attention at the workshop.

Please let me know how you would like to organize the preparation and Taylor and I will do whatever we can to assist.

Best,

David

On Wed, Feb 22, 2017 at 07:29 One Health (CDC) <onehealth@cdc.gov> wrote:

> Dear partners,
>
> CDC and USAID are collaborating with the government of Tanzania to conduct a One Health Zoonotic Disease Prioritization (OHZDP) workshop. CDC has developed a One Health Zoonotic Disease Prioritization Tool (OHZDPT) which allows a country to bring together multisectoral, One Health representatives to prioritize endemic and emerging zoonoses of greatest national concern using equal input from all represented sectors including human, animal (livestock and wildlife), and environmental health. Having a list of prioritized zoonoses allows a country to focus limited financial and personnel resources to build laboratory capacity, strengthen surveillance in humans and animals, develop joint outbreak response plans, and to create joint prevention and control strategies. Specific details are in the attachment titled, "CDC One Health Zoonotic Disease Prioritization Workshop Overview." The prioritization of zoonotic diseases is a key component of GHSA and GHSA roadmaps and helps to set priorities for further systems capacity building in line with GHSA and JEE. Tanzania's National One Health Platform is hosting the workshop.
>
> Beginning about 60 days before the desired workshop date, trained CDC workshop facilitators work with in country partners to develop a list of endemic and emerging zoonoses of concern for prioritization during the workshop and to identify multisectoral partners, both voting members and observers, for participation in the workshop.
>
> The OHZDP tool is semi-quantitative and relies on facilitators, in collaboration with stakeholders, generating a list of zoonoses in advance of workshop discussions. Before the stakeholders come together, developing a list of endemic and

emerging zoonotic diseases that each ministry would like to discuss during the prioritization workshop is needed. This list is developed from both published and unpublished information sources. A team approach should be used to develop the list of about 30-40 endemic and emerging zoonotic diseases for prioritization during the workshop. The CDC One Health Office has started with a list of 32 endemic and emerging zoonotic diseases that have been identified either as reportable diseases in Tanzania's National One Health Strategy Plan, and/or were deemed important in the report of the expert group selected to prioritize zoonotic diseases in Tanzania, October-December 2016. Please find the list of 32 diseases attached.

CDC facilitators coordinate the creation of this list and literature review by working with in-country partners, including CDC and USAID staff. We would like to give partners the opportunity to share information and data on zoonotic diseases in Tanzania that may be beneficial to have during the workshop. We are asking partners to share any available information such as reports, publications, or other materials regarding zoonotic disease illnesses or outbreaks in Tanzania. If you have any additional information you'd like to share on any of the zoonoses on the existing list, or on zoonoses that are not listed, but are present in Tanzania, please let us know by **Friday, March 3rd**. **Send all information to onehealth@cdc.gov and CDC facilitators Karen Alroy (nfu1@cdc.gov) and Carrie Eggers (xfy1@cdc.gov).**

Thank you for your partnership in preparing for Tanzania's One Health Zoonotic Disease Prioritization Workshop. If you have any questions, please let us know.

Kerri Simone, MPH *on behalf of*

CDC One Health Office

cdc.gov/onehealth

 **Click on the icon to subscribe to One Health updates from CDC.**

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From: Abel Ekiri <abekiri@ucdavis.edu>
To: "One Health (CDC)" <onehealth@cdc.gov>, "lkramer@usaid.gov" <lkramer@usaid.gov>, [redacted] "nkabir@usaid.gov" <nkabir@usaid.gov>, "Zelalem.Tadesse@fao.org" <Zelalem.Tadesse@fao.org>, [redacted], "lparish@usaid.gov" <lparish@usaid.gov>, "Clements, Andrew (CDC usaid.gov)" <AClements@usaid.gov>, [redacted], "gmwangoka@ihi.or.tz" <gmwangoka@ihi.or.tz>, David John Wolking <djwolking@ucdavis.edu>, Christopher kilonzo <ckilonzo@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>, "Clements, Andrew (CDC usaid.gov)" <AClements@usaid.gov>, "apereira@usaid.gov" <apereira@usaid.gov>, [redacted] "janetrix.amuguni@tufts.edu" <janetrix.amuguni@tufts.edu>, "irwego@umn.edu" <irwego@umn.edu>, "ayawe@ohcea.org" <ayawe@ohcea.org>, "pelicank@umn.edu" <pelicank@umn.edu>, "mcrane@usaid.gov" <mcrane@usaid.gov>
Cc: "Barton Behravesh, Casey (CDC/OID/NCEZID)" <dlx9@cdc.gov>, "Eggers, Carrie (CDC/CGH/DGHP)" <xfy1@cdc.gov>, "Alroy, Karen (CDC/OID/NCIRD)" <nfu1@cdc.gov>, "Salyer, Stephanie J. (CDC/CGH/DGHP)" <wig9@cdc.gov>, "Gatei, Wangeci (CDC/CGH/DGHP)" <wgg3@cdc.gov>, Sarah Paige <spaige@usaid.gov>, Ashna Kibria <akibria@usaid.gov>, Ricardo Echalar <rechalar@usaid.gov>, "emwijarubi@usaid.gov" <emwijarubi@usaid.gov>, [redacted] "pswai@usaid.gov" <pswai@usaid.gov>, "jdavis@usaid.gov" <jdavis@usaid.gov>, "emily.s.kelley2.civ@mail.mil" <emily.s.kelley2.civ@mail.mil>, "Judd, Kelsie N CTR (US)" <kelsie.n.judd.ctr@mail.mil>
Sent: Fri, 24 Feb 2017 18:06:39 +0000
Subject: [predict] Re: Request by 3/3- Information on Zoonotic Disease Illnesses or Outbreaks in Tanzania

Dear Kerri,

Thanks for inviting the PREDICT-Tanzania team to share information and data on zoonotic diseases in preparation for the Tanzania OHZDP workshop. We'll be sharing the requested information shortly, and will be happy to contribute to and participate in the OHZDP workshop in capacity deemed relevant by the organising team.

Kind regards,

Abel

Abel B. Ekiri, BVM, MS, PhD, Dipl. ACVPM

Project Scientist
One Health Institute
School of Veterinary Medicine
University of California, Davis
California, USA

Research Associate
Faculty of Veterinary Medicine
Sokoine University of Agriculture

Morogoro, Tanzania

From: One Health (CDC) <onehealth@cdc.gov>
Sent: Wednesday, February 22, 2017 7:29:04 AM
To: lkramer@usaid.gov; [redacted] nkabir@usaid.gov; [redacted] lparish@usaid.gov; Clements, Andrew (CDC usaid.gov); [redacted] gmwangoka@ihi.or.tz; David John Wolking; Abel Ekiri; Christopher kilonzo; predict@ucdavis.edu; Clements, Andrew (CDC usaid.gov); apereira@usaid.gov; [redacted] janetrix.amuguni@tufts.edu; irwego@umn.edu; ayawe@ohcea.org; pelicank@umn.edu; mcrane@usaid.gov
Cc: One Health (CDC); Barton Behravesh, Casey (CDC/OID/NCEZID); Eggers, Carrie (CDC/CGH/DGHP); Alroy, Karen (CDC/OID/NCIRD);

Salyer, Stephanie J. (CDC/CGH/DGHP); Gatei, Wangeci (CDC/CGH/DGHP); Sarah Paige; Ashna Kibria; Ricardo Echalar; emwijarubi@usaid.gov; [redacted]pswai@usaid.gov; jdavis@usaid.gov; emily.s.kelley2.civ@mail.mil; Judd, Kelsie N CTR (US)

Subject: Request by 3/3- Information on Zoonotic Disease Illnesses or Outbreaks in Tanzania

Dear partners,

CDC and USAID are collaborating with the government of Tanzania to conduct a One Health Zoonotic Disease Prioritization (OHZDP) workshop. CDC has developed a One Health Zoonotic Disease Prioritization Tool (OHZDPT) which allows a country to bring together multisectoral, One Health representatives to prioritize endemic and emerging zoonoses of greatest national concern using equal input from all represented sectors including human, animal (livestock and wildlife), and environmental health. Having a list of prioritized zoonoses allows a country to focus limited financial and personnel resources to build laboratory capacity, strengthen surveillance in humans and animals, develop joint outbreak response plans, and to create joint prevention and control strategies. Specific details are in the attachment titled, "CDC One Health Zoonotic Disease Prioritization Workshop Overview." The prioritization of zoonotic diseases is a key component of GHSA and GHSA roadmaps and helps to set priorities for further systems capacity building in line with GHSA and JEE. Tanzania's National One Health Platform is hosting the workshop.

Beginning about 60 days before the desired workshop date, trained CDC workshop facilitators work with in country partners to develop a list of endemic and emerging zoonoses of concern for prioritization during the workshop and to identify multisectoral partners, both voting members and observers, for participation in the workshop.

The OHZDP tool is semi-quantitative and relies on facilitators, in collaboration with stakeholders, generating a list of zoonoses in advance of workshop discussions. Before the stakeholders come together, developing a list of endemic and emerging zoonotic diseases that each ministry would like to discuss during the prioritization workshop is needed. This list is developed from both published and unpublished information sources. A team approach should be used to develop the list of about 30-40 endemic and emerging zoonotic diseases for prioritization during the workshop. The CDC One Health Office has started with a list of 32 endemic and emerging zoonotic diseases that have been identified either as reportable diseases in Tanzania's National One Health Strategy Plan, and/or were deemed important in the report of the expert group selected to prioritize zoonotic diseases in Tanzania, October-December 2016. Please find the list of 32 diseases attached.

CDC facilitators coordinate the creation of this list and literature review by working with in-country partners, including CDC and USAID staff. We would like to give partners the opportunity to share information and data on zoonotic diseases in Tanzania that may be beneficial to have during the workshop. We are asking partners to share any available information such as reports, publications, or other materials regarding zoonotic disease illnesses or outbreaks in Tanzania. If you have any additional information you'd like to share on any of the zoonoses on the existing list, or on zoonoses that are not listed, but are present in Tanzania, please let us know by **Friday, March 3rd**. **Send all information to onehealth@cdc.gov and CDC facilitators Karen Alroy (nfu1@cdc.gov) and Carrie Eggers (xfy1@cdc.gov).**

Thank you for your partnership in preparing for Tanzania's One Health Zoonotic Disease Prioritization Workshop. If you have any questions, please let us know.

Kerri Simone, MPH *on behalf of*
CDC One Health Office
cdc.gov/onehealth

Click on the icon to subscribe to One Health updates from CDC.

From: Andrew Clements <aclements@usaid.gov>
To: Jonna Mazet <jkmazet@ucdavis.edu>
CC: sgillette@usaid.gov <sgillette@usaid.gov>;Alisa Pereira <apereira@usaid.gov>;Elizabeth Leasure <ealeasure@ucdavis.edu>;djwolking@ucdavis.edu <djwolking@ucdavis.edu>;Christine Kreuder Johnson <ckjohnson@ucdavis.edu>
Sent: 3/1/2017 3:50:08 AM
Subject: Call to discuss future of surveillance with change to FAO scope

Hi Jonna,

Hope your trip to Africa went well.

When you are caught up, can we schedule a call with the people on this email to talk about how Predict moves forward with surveillance following the proposed changes to FAO's scope in Africa. This would include EHP and triangulated surveillance (but not MERS since we don't expect that to be affected).

Let us know when you and your team are available. Thursday and Friday this week work for me, but next week is also good.

Thanks!

Andrew

Andrew P. Clements, Ph.D.
Senior Scientific Adviser
Emerging Threats Division/Office of Infectious Diseases/Bureau for Global Health
U.S. Agency for International Development
Mobile phone: 1-571-345-4253
Email: aclements@usaid.gov

From:	David McIver <dmciver@metabiota.com>
To:	David John Wolking <djwolking@ucdavis.edu>;predict@ucdavis.edu" <predict@ucdavis.edu>
CC:	Beth Edison <bedison@metabiota.com>;Karen Saylors <ksaylors@metabiota.com>
Sent:	3/2/2017 9:51:28 AM
Subject:	[predict] Fwd: China_ 2017 Country implementation plan

Hi David,

We received the below e-mail regarding CIPs from Sudarat at RDMA Bangkok. What would you advise our response to be? Happy to contribute towards this CIP with our operations in China if that's the direction.

Thanks a lot,
Dave

—
David McIver, PhD
PREDICT Asia Regional Coordinator | Epidemiologist
Metabiota

e: dmciver@metabiota.com
c: +1 778-269-2965

Begin forwarded message:

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Subject: Fwd: China_ 2017 Country implementation plan
Date: March 2, 2017 at 12:38:41 AM PST
To: Jon Epstein <epstein@ecohealthalliance.org>, Hongying Li <li@ecohealthalliance.org>, <zlshi@wh.iov.cn>
Cc: <nliang@metabiota.com>, Daniel Schar <dSchar@usaid.gov>, "David McIver, dmciver@metabiota.com c: 778-269-2965" <dmciver@metabiota.com>

Dear PREDICT China team,

Attachment is a draft CIP for China. Please provide update including timeline for the planned activities. And if some activities are missed, please include them in. Please update and submit 2017 to us by March 8, COB.

Thank you very much.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

Produced in Native Format

From: David J Wolking <djwolking@ucdavis.edu>
To: Alisa Pereira Emerging Threats Division <apereira@usaid.gov>;Clements, Andrew (GH/HIDN) <AClements@usaid.gov>;Shana Gillette <sgillette@usaid.gov>;PREDICTMGT <predictmgt@usaid.gov>;predict@ucdavis.edu <predict@ucdavis.edu>
Sent: 3/3/2017 8:02:21 AM
Subject: [predict] Fwd: China_ 2017 Country implementation plan

Hi there,

Just sharing this CIP request received by our PREDICT/China team from RDMA. We are planning to compete this by the assigned deadline and simply wanted you all to be aware in case you have any concerns.

Best,

David

---------- Forwarded message ----------
From: **Molly Turner** <turner@ecohealthalliance.org>
Date: Thu, Mar 2, 2017 at 6:46 AM
Subject: Fwd: China_ 2017 Country implementation plan
To: David John Wolking <djwolking@ucdavis.edu>, Nicole Ureda <nureda@ucdavis.edu>
Cc: Evelyn Luciano <luciano@ecohealthalliance.org>, Ava Sullivan <sullivan@ecohealthalliance.org>, Hongying Li <li@ecohealthalliance.org>, Aleksei Chmura <chmura@ecohealthalliance.org>

Hi David and Nicole,

Just keeping you guys in the loop in the latest CIP request, this time from RDMA with regards to our China work.

Thanks,
Molly
---------- Forwarded message ----------
From: **EcoHealth Alliance** <li@ecohealthalliance.org>
Date: Thu, Mar 2, 2017 at 7:08 AM
Subject: Fwd: China_ 2017 Country implementation plan
To: Aleksei Chmura <chmura@ecohealthalliance.org>, Evelyn Luciano <luciano@ecohealthalliance.org>, Molly Turner <turner@ecohealthalliance.org>, Ava Sullivan <sullivan@ecohealthalliance.org>

FYI...formal request for the timeline?

Begin forwarded message:

From: Sudarat Damrongwatanapokin <sdamrongwatanapokin@usaid.gov>
Date: March 2, 2017 at 3:38:41 AM EST
To: Jon Epstein <epstein@ecohealthalliance.org>, Hongying Li <li@ecohealthalliance.org>, zlshi@wh.iov.cn
Cc: nliang@metabiota.com, Daniel Schar <dSchar@usaid.gov>, "David McIver, dmciver@metabiota.com c: 778-269-2965" <dmciver@metabiota.com>

Subject: Fwd: China_ 2017 Country implementation plan

Dear PREDICT China team,

Attachment is a draft CIP for China. Please provide update including timeline for the planned activities. And if some activities are missed, please include them in. Please update and submit 2017 to us by March 8, COB.

Thank you very much.

Best regards,
Sudarat Damrongwatanapokin, D.V.M., Ph.D.
Regional Animal Health Advisor
USAID Regional Development Mission Asia
Bangkok, 10330
E-mail: sdamrongwatanapokin@usaid.gov
Tel: +662-257-3243, Fax:+662 -2573099

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Molly Turner
Federal Grants Coordinator

EcoHealth Alliance
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Produced in Native Format

From: Abel Ekiri <abekiri@ucdavis.edu>
To: "One Health (CDC)" <onehealth@cdc.gov>, "lkramer@usaid.gov" <lkramer@usaid.gov>, [redacted] "nkabir@usaid.gov" <nkabir@usaid.gov> [redacted] "lparish@usaid.gov" <lparish@usaid.gov>, "Clements, Andrew (CDC usaid.gov)" <AClements@usaid.gov>, [redacted] "gmwangoka@ihi.or.tz" <gmwangoka@ihi.or.tz>, David John Wolking <djwolking@ucdavis.edu>, Christopher kilonzo <ckilonzo@ucdavis.edu>, "predict@ucdavis.edu" <predict@ucdavis.edu>, "Clements, Andrew (CDC usaid.gov)" <AClements@usaid.gov>, "apereira@usaid.gov" <apereira@usaid.gov>, [redacted] "janetrix.amuguni@tufts.edu" <janetrix.amuguni@tufts.edu>, "irwego@umn.edu" <irwego@umn.edu>, "ayawe@ohcea.org" <ayawe@ohcea.org>, "pelicank@umn.edu" <pelicank@umn.edu>, "mcrane@usaid.gov" <mcrane@usaid.gov>, Jonna Mazet <jkmazet@ucdavis.edu>
Cc: "Barton Behravesh, Casey (CDC/OID/NCEZID)" <dlx9@cdc.gov>, "Eggers, Carrie (CDC/CGH/DGHP)" <xfy1@cdc.gov>, "Alroy, Karen (CDC/OID/NCIRD)" <nfu1@cdc.gov>, "Salyer, Stephanie J. (CDC/CGH/DGHP)" <wig9@cdc.gov>, "Gatei, Wangeci (CDC/CGH/DGHP)" <wgg3@cdc.gov>, Sarah Paige <spaige@usaid.gov>, "Ashna Kibria" <akibria@usaid.gov>, Ricardo Echalar <rechalar@usaid.gov>, "emwijarubi@usaid.gov" <emwijarubi@usaid.gov> [redacted] "pswai@usaid.gov" <pswai@usaid.gov>, "jdavis@usaid.gov" <jdavis@usaid.gov>, "emily.s.kelley2.civ@mail.mil" <emily.s.kelley2.civ@mail.mil>, "Judd, Kelsie N CTR (US)" <kelsie.n.judd.ctr@mail.mil>
Subject: Re: Request by 3/3- Information on Zoonotic Disease Illnesses or Outbreaks in Tanzania: PREDICT Part 2
Sent: Fri, 3 Mar 2017 19:34:36 +0000
Emerging viral threats and VHFs - East-Central Africa region.zip

And here is part 2 with the other folder: Emerging viral threats and viral hemorrhagic fevers (VHFs) – East-Central Africa region.

Sincerely,

Abel Ekiri, BVM, MS, PhD, DACVPM

Research Scientist

USAID PREDICT project

One Health Institute

University of California, Davis

aekiri@ucdavis.edu

From: Abel Ekiri
Sent: Friday, March 3, 2017 11:30 AM
To: One Health (CDC); lkramer@usaid.gov; [redacted] nkabir@usaid.gov; [redacted] lparish@usaid.gov; Clements, Andrew (CDC usaid.gov); [redacted] gmwangoka@ihi.or.tz; David John Wolking; Christopher kilonzo; predict@ucdavis.edu; Clements, Andrew (CDC usaid.gov); apereira@usaid.gov; [redacted] janetrix.amuguni@tufts.edu; irwego@umn.edu; ayawe@ohcea.org; pelicank@umn.edu; mcrane@usaid.gov; Jonna Mazet
Cc: Barton Behravesh, Casey (CDC/OID/NCEZID); Eggers, Carrie (CDC/CGH/DGHP); Alroy, Karen (CDC/OID/NCIRD); Salyer, Stephanie J. (CDC/CGH/DGHP); Gatei, Wangeci (CDC/CGH/DGHP); Sarah Paige; Ashna Kibria; Ricardo Echalar; emwijarubi@usaid.gov; [redacted] pswai@usaid.gov; jdavis@usaid.gov; emily.s.kelley2.civ@mail.mil; Judd, Kelsie N CTR (US)
Subject: Re: Request by 3/3- Information on Zoonotic Disease Illnesses or Outbreaks in Tanzania: PREDICT Part 1

Dear Kerri,

The PREDICT-Tanzania team has been involved in surveillance activities for emerging and unknown viral zoonotic pathogens in Tanzania over the last 7 years. We sharing two compressed files containing materials related to PREDICT surveillance activities and viral findings as well as select publications on what we consider to be critical zoonotic disease threats to Tanzania, including endemic diseases and transboundary threats from the greater East/Central Africa region and beyond. We would like to emphasize the importance of considering both known and emerging (including newly discovered or introduced) zoonotic diseases in the workshop and are proponents of broadening the discussion beyond specific pathogens to potentially include groups of dangerous zoonotic disease threats with similar signs and symptoms, for example viral hemorrhagic fevers.

We hope these resources will contribute to and inform the discussion at the upcoming OHZDP Workshop.

Contents of the two compressed folders are detailed below. Due to large file size, will send these in two parts (Part 1 & 2) so you can download them easily.

PREDICT Data and Resources folder:

1) The PREDICT-1 Tanzania Final Report along with a map and list of viral findings from the first phase of the project (2009-2014). This information is also publically available in an interactive platform at http://data.predict.global/

2) A selection of publications from PREDICT Consortium partners and from joint work conducted by the collaborative Sokoine University of Agriculture, Ifakara Health Institute, and UC Davis Health for Animals and Livelihood Improvement (HALI) project (haliproject.org). These publications were selected as they describe work on known and emerging zoonotic disease threats in Tanzania and the greater region.

Emerging viral threats and viral hemorrhagic fevers (VHFs) – East-Central Africa region folder:

A selection of publications demonstrating the risk of influenza and viral hemorrhagic fevers with particular emphasis on zoonotic disease threats from wildlife (e.g., Ebola, Marburg, CCHF, HPAI, RVF, and novel viral threats such as arenavirues and henipaviruses). These publications were selected as they provide evidence for these threats within Tanzania's borders and in the greater region.

Please don't hesitate to contact us if we can provide further information that may be useful for the workshop.

Sincerely,

Abel B. Ekiri, BVM, MS, PhD, DACVPM

Research Scientist

USAID PREDICT project

One Health Institute

University of California, Davis

aekiri@ucdavis.edu

From: One Health (CDC) <onehealth@cdc.gov>
Sent: Wednesday, February 22, 2017 7:29:04 AM
To: lkramer@usaid.gov; [redacted]; nkabir@usaid.gov; [redacted] lparish@usaid.gov; Clements, Andrew (CDC usaid.gov); [redacted] gmwangoka@ihi.or.tz; David John Wolking; Abel Ekiri; Christopher kilonzo; predict@ucdavis.edu; Clements, Andrew (CDC usaid.gov); apereira@usaid.gov; [redacted] [redacted] janetrix.amuguni@tufts.edu; irwego@umn.edu; ayawe@ohcea.org; pelicank@umn.edu; mcrane@usaid.gov
Cc: One Health (CDC); Barton Behravesh, Casey (CDC/OID/NCEZID); Eggers, Carrie (CDC/CGH/DGHP); Alroy, Karen (CDC/OID/NCIRD); Salyer, Stephanie J. (CDC/CGH/DGHP); Gatei, Wangeci (CDC/CGH/DGHP); Sarah Paige; Ashna Kibria; Ricardo Echalar; emwijarubi@usaid.gov; [redacted] pswai@usaid.gov; jdavis@usaid.gov; emily.s.kelley2.civ@mail.mil; Judd, Kelsie N CTR (US)
Subject: Request by 3/3- Information on Zoonotic Disease Illnesses or Outbreaks in Tanzania

Dear partners,

CDC and USAID are collaborating with the government of Tanzania to conduct a One Health Zoonotic Disease Prioritization (OHZDP) workshop. CDC has developed a One Health Zoonotic Disease Prioritization Tool (OHZDPT) which allows a country to bring together multisectoral, One Health representatives to prioritize endemic and emerging zoonoses of greatest national concern using equal input from all represented sectors including human, animal (livestock and wildlife), and environmental health. Having a list of prioritized zoonoses allows a country to focus limited financial and personnel resources to build laboratory capacity, strengthen surveillance in humans and animals, develop joint outbreak response plans, and to create joint prevention and control strategies. Specific details are in the attachment titled, "CDC One Health Zoonotic Disease Prioritization Workshop Overview." The prioritization of zoonotic diseases is a key component of GHSA and GHSA roadmaps and helps to set priorities for further systems capacity building in line with GHSA and JEE. Tanzania's National One Health Platform is hosting the workshop.

Beginning about 60 days before the desired workshop date, trained CDC workshop facilitators work with in country partners to develop a list of endemic and emerging zoonoses of concern for prioritization during the workshop and to identify multisectoral partners, both voting members and observers, for participation in the workshop.

The OHZDP tool is semi-quantitative and relies on facilitators, in collaboration with stakeholders, generating a list of

zoonoses in advance of workshop discussions. Before the stakeholders come together, developing a list of endemic and emerging zoonotic diseases that each ministry would like to discuss during the prioritization workshop is needed. This list is developed from both published and unpublished information sources. A team approach should be used to develop the list of about 30-40 endemic and emerging zoonotic diseases for prioritization during the workshop. The CDC One Health Office has started with a list of 32 endemic and emerging zoonotic diseases that have been identified either as reportable diseases in Tanzania's National One Health Strategy Plan, and/or were deemed important in the report of the expert group selected to prioritize zoonotic diseases in Tanzania, October-December 2016. Please find the list of 32 diseases attached.

CDC facilitators coordinate the creation of this list and literature review by working with in-country partners, including CDC and USAID staff. We would like to give partners the opportunity to share information and data on zoonotic diseases in Tanzania that may be beneficial to have during the workshop. We are asking partners to share any available information such as reports, publications, or other materials regarding zoonotic disease illnesses or outbreaks in Tanzania. If you have any additional information you'd like to share on any of the zoonoses on the existing list, or on zoonoses that are not listed, but are present in Tanzania, please let us know by **Friday, March 3rd**. **Send all information to onehealth@cdc.gov and CDC facilitators Karen Alroy (nfu1@cdc.gov) and Carrie Eggers (xfy1@cdc.gov).**

Thank you for your partnership in preparing for Tanzania's One Health Zoonotic Disease Prioritization Workshop. If you have any questions, please let us know.

Kerri Simone, MPH *on behalf of*

CDC One Health Office

cdc.gov/onehealth

Click on the icon to subscribe to One Health updates from CDC.

REVIEW

Global Patterns of Influenza A Virus in Wild Birds

Björn Olsen,[1,2] Vincent J. Munster,[3] Anders Wallensten,[4,5] Jonas Waldenström,[6] Albert D. M. E. Osterhaus,[3] Ron A. M. Fouchier[3]*

The outbreak of highly pathogenic avian influenza of the H5N1 subtype in Asia, which has subsequently spread to Russia, the Middle East, Europe, and Africa, has put increased focus on the role of wild birds in the persistence of influenza viruses. The ecology, epidemiology, genetics, and evolution of pathogens cannot be fully understood without taking into account the ecology of their hosts. Here, we review our current knowledge on global patterns of influenza virus infections in wild birds, discuss these patterns in the context of host ecology and in particular birds' behavior, and identify some important gaps in our current knowledge.

Influenza A viruses have been isolated from many species, including humans, pigs, horses, mink, felids, marine mammals, and a wide range of domestic birds, but wildfowl and shorebirds are thought to form the virus reservoir in nature. The influenza A virus genome consists of eight segments of negative-stranded RNA, which code for 11 proteins. Influenza viruses are classified on the basis of two of these proteins expressed on the surface of virus particles; the hemagglutinin (HA) and neuraminidase (NA) glycoproteins (*1*). In wild birds and poultry throughout the world, influenza viruses representing 16 HA and 9 NA antigenic subtypes have been detected (*2*), which can be found in numerous combinations (also called subtypes, e.g., H1N1, H16N3).

The HA protein is initially synthesized as a single polypeptide precursor (HA0), which is cleaved into HA_1 and HA_2 subunits by proteases. The mature protein mediates binding of the virus to host cells, followed by fusion with endosomal membranes (*1*). Influenza viruses of subtypes H5 and H7, but not other HA subtypes, may become highly pathogenic after introduction into poultry and can cause outbreaks of highly pathogenic avian influenza (HPAI, formerly termed "fowl plague"). The switch from a low pathogenic avian influenza (LPAI) virus phenotype, common in wild birds and poultry, to the HPAI virus phenotype is achieved by the introduction of basic amino acid residues into the HA0 cleavage site, which facilitates systemic virus replication. HPAI isolates have been obtained primarily from commercially raised poultry (*3*).

In the past decade, HPAI outbreaks have occurred frequently, caused by influenza viruses of subtype H5N1 in Asia, Russia, the Middle East, Europe, and Africa (ongoing since 1997); H5N2 in Mexico (1994), Italy (1997), and Texas (2004); H7N1 in Italy (1999); H7N3 in Australia (1994), Pakistan (1994), Chile (2002), and Canada (2003); H7N4 in Australia (1997); and H7N7 in the Netherlands (2003) (*3*, *4*).

Migratory Birds as a Natural Reservoir of LPAI Viruses

LPAI viruses have been isolated from at least 105 wild bird species of 26 different families (Table 1) (*5*). All influenza virus subtypes and most HA/NA combinations have been detected in the bird reservoir and poultry, whereas relatively few have been detected in other species. Although many wild bird species may harbor influenza viruses, birds of wetlands and aquatic environments such as the Anseriformes (particularly ducks, geese, and swans) and Charadriiformes (particularly gulls, terns, and waders) constitute the major natural LPAI virus reservoir (*1*). Anseriformes and Charadriiformes are distributed globally, except for the most arid regions of the world (*6*).

In birds, LPAI viruses preferentially infect cells lining the intestinal tract and are excreted in high concentrations in their feces. It has been shown that influenza viruses remain infectious in lake water up to 4 days at 22°C and more than 30 days at 0°C (*7*), and the relatively high virus prevalence in birds living in aquatic environments may be due in part to efficient transmission through the fecal-oral route via surface waters (*1*, *7*).

Migration is a common strategy for birds occupying seasonal habitats and may range from short local movements to intercontinental migrations. Migratory birds can carry pathogens, particularly those that do not significantly affect the birds' health status and consequently interfere with migration. Many Anseriformes and Charadriiformes are known to perform regular long-distance migrations (*6*), thereby potentially distributing LPAI viruses between countries or even continents. Birds breeding in one geographic region often follow similar migratory flyways, e.g., the East Asian–Australian flyway from eastern Siberia south to eastern Asia and Australia (Fig. 1A). However, the major flyways are simplifications, and there are numerous exceptions where populations behave differently from the common patterns (*6*, *8*). Within the large continents and along the major flyways, migration connects many bird populations in time and space, either at common breeding areas, during migration, or at shared nonbreeding areas (Fig. 1). As a result, virus-infected birds can transmit their pathogens to other populations that subsequently may bring the viruses to new areas.

It is important to realize that the transmission of the viruses and their geographical spread is dependent on the ecology of the migrating hosts. For instance, migrating birds rarely fly the full distance between breeding and nonbreeding areas without stopping over and "refueling" along the way. Rather, birds make frequent stopovers during migration and spend more time eating and preparing for migration than actively performing flights (*9*). Many species aggregate at favorable stopover or wintering sites, resulting in high local densities. Such sites may be important for transmission of LPAI viruses between wild and captive birds and between different species.

Influenza Viruses in Ducks

Extensive surveillance studies of wild ducks in the Northern Hemisphere have revealed high LPAI virus prevalence primarily in juvenile—presumably immunologically naïve—birds with a peak in early fall before southbound migration. In North America, the prevalence falls from ~60% in ducks sampled at marshalling sites close to the Canadian breeding areas in early fall, to 0.4 to 2% at the wintering grounds in the southern U.S.A., and ~0.25% on the ducks' return to the breeding grounds in spring. Similar patterns have been observed in Northern Europe, but influenza virus detection during spring migration can be significantly higher, up to 6.5%. Surveillance of the nesting grounds of ducks in Siberia before winter migration revealed the presence of influenza viruses in up to 8% of birds (*10*).

Such year-round prevalence raises the possibility that LPAI virus can persist in ducks alone. This hypothesis complements earlier ones, in which additional host species or preservation of infectious influenza viruses in frozen lakes over the winter play a role in the perpetuation of avian influenza viruses (*1*, *7*).

All HA and NA subtypes, with the exception of H13 to H16, circulate in wild ducks in North America and Northern Europe. In a 26-year longitudinal study performed in Canada, influenza viruses of subtypes H3, H4, and H6 were isolated from ducks most frequently; H1, H2, H7, H10,

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and H11 less frequently; and H5, H8, H9, and H12 only sporadically. Although in other North American and European studies, influenza viruses of subtypes H3, H4, and H6 were also detected frequently, the detection of other virus subtypes was not significantly different (*4*, *11*). Thus, the prevalence of influenza virus in general, as well as the specific distribution of subtypes, may vary between different surveillance studies depending on species, time, and place.

In the Canadian studies, cyclic patterns of influenza virus subtypes were reported: Peaks in virus isolation of an HA subtype were followed 1 to 2 years later by reduced rates of isolation of this subtype. This observation awaits confirmation in other surveillance studies but is of particular interest in relation to findings for other infectious diseases: Cyclic patterns described for measles and whooping cough in humans have provided new insights in the role of spatial factors, herd immunity, and population age-structure on epidemiology (*12*). Cycling of influenza virus in wild birds could provide similar new insights into the ecology of influenza viruses in their natural hosts.

Influenza virus surveillance of ducks has been performed in Japan since the late 1970s. As in other studies, influenza virus prevalence and isolated subtypes varied between years and locations (*5*). The prevalence of influenza virus in wild birds elsewhere in Asia is largely unknown, but several studies have been conducted in live bird markets, where most HA and NA subtypes were found in poultry (*1*, *13*). It is plausible that the circulation of the LPAI virus subtypes in poultry at least partially reflects that in wild birds, but no direct connection has yet been established.

Dabbling ducks of the *Anas* genus, with Mallards (*Anas platyrhynchos*) as the most extensively studied species, have been found to be infected with influenza viruses more frequently than other birds, including diving ducks (Table 1) (*5*). Differences in virus prevalence between ecological guilds of ducks are likely in part related to behavior. Dabbling ducks feed primarily on food in surface waters; diving ducks forage at deeper depths and more often in marine habitats (*6*). Dabbling ducks display a propensity for abmigration, the switching of breeding grounds between years, which is in part due to mate choice (*6*). This behavior could provide an opportunity for influenza viruses to be transmitted between different host subpopulations. LPAI virus infection generally causes no major clinical signs in dabbling ducks, and experimental infections indicate that animals only produce a transient, low-level humoral immune response, which may be sufficient to provide partial protection against reinfection with viruses of the same subtype but is unlikely to confer protection against heterologous reinfections (*14*). Different influenza virus subtypes can also infect ducks concomitantly, creating the opportunity for genetic mixing (*15*).

Table 1. Prevalence of influenza A virus in wild birds. Influenza virus prevalence in specific species is given only if tests on >500 birds have been reported; lower numbers in individual species are included in the total. See (*5*) for additional comments and original data. Of the 36 species of ducks, 28,955 were dabbling ducks and 1011 were diving ducks, with influenza virus prevalence of 10.1 and 1.6%, respectively.

Family	Species	Sampled	Positive	
			(*n*)	(%)
Ducks	36 species	34,503	3275	9.5
	Mallard (*Anas platyrhynchos*)	15,250	1965	12.9
	Northern Pintail (*Anas acuta*)	3,036	340	11.2
	Blue-winged Teal (*Anas discors*)	1,914	220	11.5
	Common Teal (*Anas crecca*)	1,314	52	4.0
	Eurasian Wigeon (*Anas penelope*)	1,023	8	0.8
	Wood Duck (*Aix sponsa*)	926	20	2.2
	Common Shelduck (*Tadorna tadorna*)	881	57	6.5
	American Black Duck (*Anas rubripes*)	717	130	18.1
	Green-winged Teal (*Anas carolinensis*)	707	28	4.0
	Gadwall (*Anas strepera*)	687	10	1.5
	Spot-billed Duck (*Anas poecilorhyncha*)	574	21	3.7
Geese	8 species	4,806	47	1.0
	Canada Goose (*Branta canadensis*)	2,273	19	0.8
	Greylag Goose (*Anser anser*)	977	11	1.1
	White-fronted Goose (*Anser albifrons*)	596	13	2.2
Swans	3 species	5,009	94	1.9
	Tundra Swan (*Cygnus columbianus*)	2,137	60	2.8
	Mute Swan (*Cygnus olor*)	1,597	20	1.3
	Whooping Swan (*Cygnus cygnus*)	930	14	1.5
Gulls	9 species	14,505	199	1.4
	Ring-billed gull (*Larus delawarensis*)	6,966	136	2.0
	Black-tailed Gull (*Larus crassirostris*)	1,726	17	1.0
	Black-headed Gull (*Larus ridibundus*)	770	17	2.2
	Herring Gull (*Larus argentatus*)	768	11	1.4
	Mew Gull (*Larus canus*)	595	0	0.0
Terns	9 species	2,521	24	0.9
	Common Tern (*Sterna hirundo*)	961	16	1.7
Waders	10 species	2,637	21	0.8
Rails	3 species	1,962	27	1.4
	Eurasian Coot (*Fulica atra*)	1,861	23	1.2
Petrels	5 species	1,416	4	0.3
	Wedge-tailed Shearwater (*Puffinus pacificus*)	794	4	0.5
Cormorants	1 species	4,500	18	0.4
	Great Cormorant (*Phalacrocorax carbo*)	4,500	18	0.4

Little is known about the prevalence of influenza viruses in wild ducks in the Southern Hemisphere or potential transmission between the hemispheres. There is little connectivity between northern and southern Anatidae species, and most species stay year round within each breeding continent. The Blue-winged Teal (*Anas discors*) is one of the few North American species that has a winter distribution that includes South America (Fig. 1C) (*6*). There are several other duck species that could serve as hosts for influenza virus in South America (*6*), but surveillance data are not available. Similarly, only 6 of 39 Anatidae species breeding in Eurasia winter with at least part of the population south of the Sahara desert in Africa, e.g., the Garganey (*Anas querquedula*) (Fig. 1C) and the Northern Pintail *(Anas acuta)*, each have African winter populations in excess of one million birds (*16*). As in South America, none of the 22 Anatidae species that breed in sub-Saharan Africa spend the nonbreeding season outside the continent. However, there are several species with large, widespread populations in Africa (*16*), and some migrate within Africa (*17*). Potential areas for mixing of Eurasian and African ducks are in West Africa, near the Senegal and Niger Rivers, the floodplains of the Niger River in Nigeria and Mali, and Lake Chad (*16*), and influenza viruses in African Anatidae populations may thus be linked to Eurasia through migrating species. Anatidae of Oceania are mainly resident and do not perform regular seasonal migrations (*6*).

Influenza Viruses in Gulls and Terns

The first recorded isolation of influenza virus from wild birds was from a Common Tern (*Sterna*

hirundo) in 1961. This HPAI H5N3 virus was responsible for an outbreak in South Africa where at least 1300 of these birds died (*3*). The most frequently detected LPAI virus subtype in gulls is H13, a subtype rarely found in other birds. Recently, a "novel" virus subtype (H16), related to H13, was described in Black-headed Gulls (*Larus ridibundus*) in Sweden. The genes of H13 and H16 viruses are genetically distinct from those of influenza viruses from other hosts, which suggests they have been genetically isolated for sufficient time to allow genetic differentiation (*2*). This concurs with the observation that gull influenza viruses do not readily infect ducks when they are inoculated experimentally (*1*). Although other influenza virus subtypes are also occasionally detected in terns and gulls (Table 1) (*5*), it is plausible that the viruses that are genetically indistinguishable from viruses of other avian hosts are most likely not endemic in gulls and terns.

Influenza viruses can be detected in a small proportion of gulls, with the highest virus prevalence reported in late summer and early fall. Most gull species breed in colonies (*6*), with adults and juveniles crowded in a small space, creating good opportunities for virus spread. This situation contrasts with that in dabbling ducks that do not breed in dense colonies (*6*), and epizootics could be more easily initiated when birds congregate in large numbers during molt, migration, or wintering.

Influenza Viruses in Waders

Waders in the Charadriidae and Scolopacidae families are adapted to either marine or freshwater wetland areas and often live side-by-side with ducks (*18*). Long-term influenza virus surveillance studies are still sparse, but data from North America suggest a distinct role of these birds in the perpetuation of certain virus subtypes. Influenza viruses of subtypes H1 to H12 have been isolated in birds migrating through the eastern U.S.A., with a high prevalence of certain HA subtypes (H1, H2, H5, H7, H9 to H12) and a larger variety of HA/NA combinations as compared with ducks in Canada, suggesting that waders maintain a wider spectrum of viruses. Moreover, the seasonal prevalence of influenza viruses in waders seems to be reversed as compared with ducks, with higher virus prevalence (~14%) during spring migration (*19*). This has led to the hypothesis that different families of wetland birds are involved in perpetuation of LPAI virus and suggests a role for waders, which may carry the virus north to the duck breeding grounds in spring. Recent genetic analyses have not revealed striking differences between influenza viruses from ducks and waders in the Americas, suggesting that these viral gene pools are not separated (*20*, *21*). Although the wader-duck link may be a plausible scenario based on the North American data, studies in waders in Northern Europe have failed to produce similar results. Nevertheless, many wader species of the Northern Hemisphere are long-distance intercontinental migrants (*8*) and may, therefore, have the potential to distribute influenza viruses around the globe.

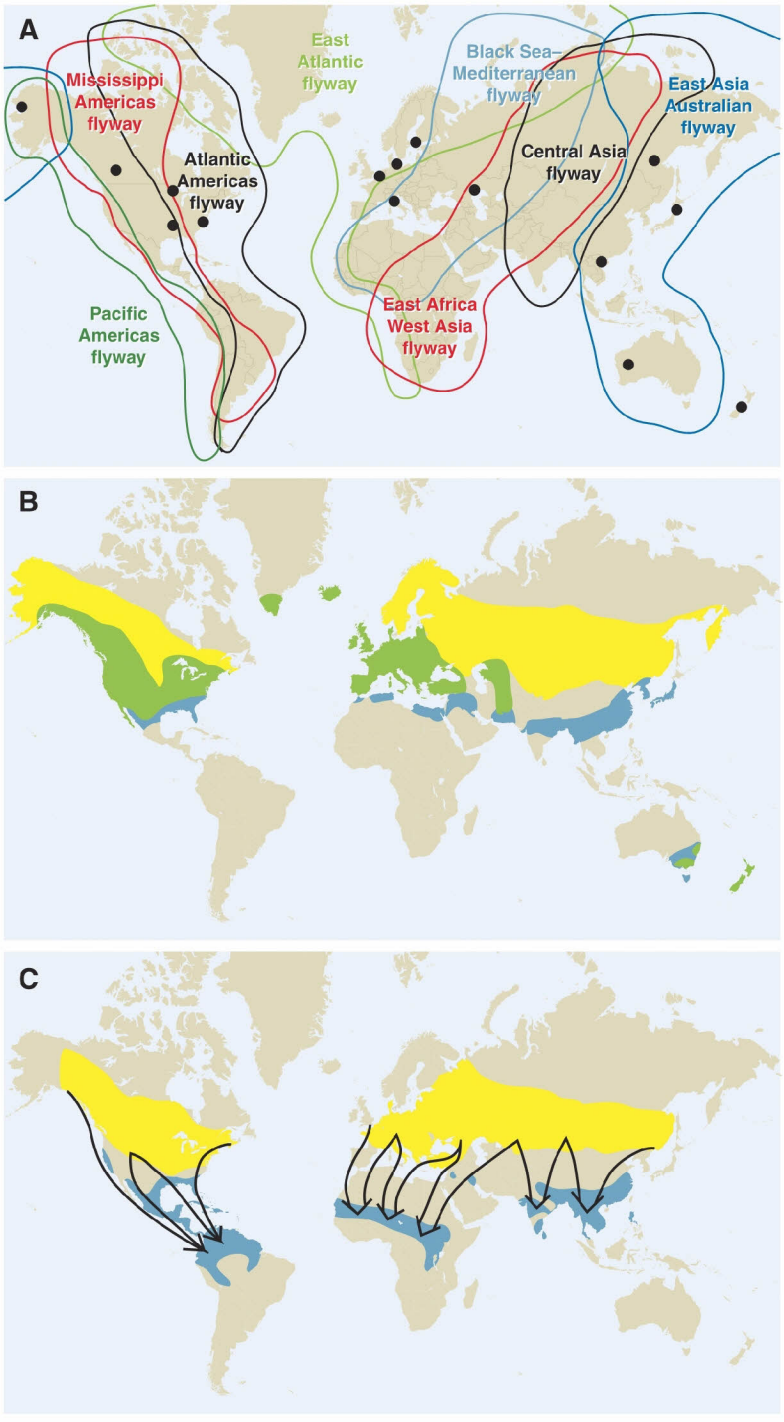

Fig. 1. Migratory flyways of wild bird populations. A world map with the main general migratory flyways of wild bird populations is shown (adapted from information collected and analyzed by Wetlands International). (**A**) Black dots indicate the locations of historical and current influenza virus surveillance sites from which data have been used in this manuscript. These global migration flyways are simplifications, and there are situations where populations behave differently from the common patterns. Migration patterns of Mallard (*Anas platyrhynchos*) (**B**) and Garganey (*Anas querquedula*) in Eurasia and Africa and Blue-winged Teal (*Anas discors*) in the Americas (**C**) (right and left parts of the map, respectively) are provided. Yellow color indicates breeding areas in which species are absent during winter, green indicates areas in which species are present around the year, and blue indicates areas in which species are only present in winter and do not breed. Arrows indicate the seasonal migration patterns.

Influenza Viruses in Other Wild Birds

LPAI viruses can be found in numerous other bird species (Table 1) (*5*), but it is unclear in which of these species influenza viruses are endemic and in which the virus is a temporary pathogen. Species in which influenza viruses are endemic share the same habitat at least part of the year with other species in which influenza viruses are frequently detected, including geese, swans, rails, petrels, and cor-

morants. In these birds and others (*5*), influenza virus prevalence seems to be lower than in dabbling ducks (Table 1), but it should be noted that studies on these species are limited, and it is possible that peak prevalence has been missed because of its seasonal nature or location.

As for ducks, gulls, and waders, their behavior and ecology may be an important determinant of their role as host species. For instance, geese are mainly herbivorous and often congregate in large flocks for grazing in pastures and agricultural fields, especially during the nonbreeding season. Such flocks may reach tens of thousands of birds in optimal areas and often contain several different species. Colonial breeding occurs in some goose species, but most are solitary nesters or nest in loose groups with little interaction between pairs. Given that wild geese and ducks are the ancestors of today's domestic goose and duck species and that these domestic animals in parts of the world are frequently kept alongside chickens, wild geese and ducks may form the bridge for influenza viruses between wild and domestic birds.

Genetic Variation of Influenza Viruses in Wild Birds

Evolution of avian influenza viruses in their natural hosts is slow, but not negligible. Avian influenza viruses can be divided into two lineages, Eurasian and American (Fig. 2), probably as a result of long-term ecological and geographical separation of hosts. However, the avifauna of North America and Eurasia are not completely separated; some ducks and shorebirds cross the Bering Strait during migration or have breeding ranges that include both the Russian Far East and northwestern North America (*6*). The majority of tundra shorebirds from the Russian Far East winter in Southeast Asia and Australia, but some species winter along the west coast of the Americas (*22*). The overlap in distribution of ducks is not as profound as that of shorebirds, but a few species (e.g., Northern Pintail, *Anas acuta*) are common in both North America and Eurasia (*6*) and could also provide an intercontinental bridge for influenza virus. Indeed, influenza viruses carrying a mix of genes from the American and Eurasian lineages have been isolated, indicating that allopatric speciation is only partial (*23*–*25*). The partial ecological isolation of influenza virus hosts seems sufficient to facilitate divergent evolution of separate gene pools, but allows occasional spillover of gene segments from one gene pool to the other.

Within each genetic lineage, multiple sublineages of viral genes cocirculate, but there appear to be no consistent temporal or spatial correlations. Moreover, genetic data from duck and shorebird influenza virus isolates from the Americas suggest an active interplay between these host species (*20*, *21*). Although certain HA subtypes are reported to be more prevalent in either shorebirds or ducks in North America, this also does not seem to have resulted in differences in the genetic composition of influenza viruses obtained from these two reservoirs (*19*, *26*).

The segmented nature of the influenza virus genome enables evolution by a process known as genetic reassortment, i.e., the mixing of genes from two or more influenza viruses. A recent study of 35 influenza virus isolates obtained from ducks in Canada indicates that genetic "sublineages" do not persist, but frequently reassort with other viruses (*27*). Influenza viruses of a particular subtype do not necessarily have the same genetic make-up, even within a single year or a single host species. The high prevalence of influenza virus in some wild bird species and the sporadic detection of concomitant infections in single birds (*15*) support the notion that reassortment may occur in nature. Gaining information on the actual frequency of reassortment in the wild bird reservoir and the impact of these events on LPAI virus evolution will be of considerable interest.

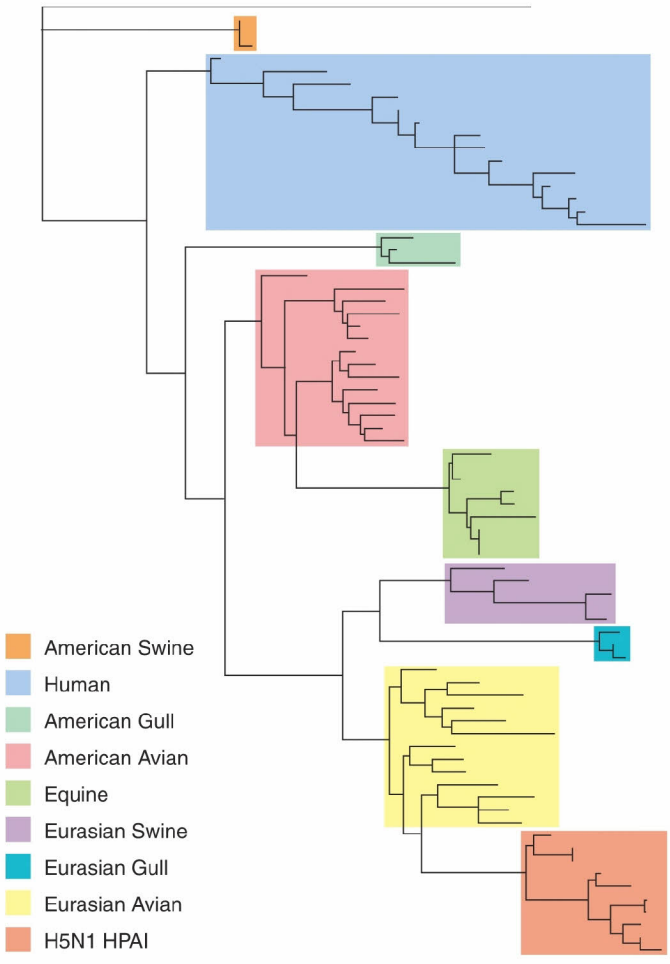

Fig. 2. Phylogenetic tree for the matrix gene of influenza A viruses from a variety of hosts. Nucleotide sequences were selected from public databases and aligned, after which a maximum likelihood tree was generated using influenza virus A/Equine/Prague/57 (H7N7) as outgroup. Sequences were selected from each host to reflect the longest possible time frame and variation in locations of virus isolation. The avian influenza viruses are divided in an American lineage (pink) and a Eurasian lineage (yellow), and there are no clear patterns of host, temporal, or spatial correlation within these lineages. In contrast, the human influenza A virus lineage (light blue), the Eurasian swine lineage (purple), and the HPAI H5N1 lineage (orange) display clear temporal patterns of virus evolution.

HPAI H5N1 Viruses in Wild Birds

In 1997, an HPAI outbreak caused by H5N1 influenza virus occurred in chicken farms and the live bird markets of Hong Kong, which also resulted in the first reported case of human influenza and fatality attributable directly to avian influenza virus (*28*). The H5N1 HPAI virus reappeared in 2002 in waterfowl at two parks in Hong Kong and was also detected in other captive and wild birds (*29*). It resurfaced again in 2003 and has devastated the poultry industry in large parts of Southeast Asia since 2004. In 2005, the virus was isolated during an outbreak among migratory birds in Qinghai Lake, China, affecting large numbers of wild birds (*30*). This single epizootic caused an estimated 10% decrease of the global population of Bar-headed Geese (*Anser indicus*), highlighting the potential devastating effects on vulnerable wildlife. Subsequently, the virus has appeared across Asia, Europe and the Middle East, and in several African countries. Wild bird deaths have been reported in several of these countries, in Europe, particularly affecting Mute Swans (*Cygnus olor*) and Whooper Swans (*Cygnus cygnus*), but mortality has also been recorded in other waterfowl species, and occasionally in raptors, gulls, and herons. So far, the HPAI H5N1 strain that originated in poultry in Southeast Asia has caused mortality in >60 wild bird species (*29*–*31*). In addition, during the devastating outbreaks in poultry, the H5N1 virus was transmitted to 175 humans, leading to 95 deaths (as of 6 March 2006), and has also

been isolated from pigs, cats, tigers, and leopards.

It is most likely that the H5N1 virus has circulated continuously in domestic birds in Southeast Asia since 1997 and, as a consequence, has evolved substantially (Fig. 2). Surveillance studies in Mainland China from 1999 onward indicated that H5N1 viruses have become endemic in domestic birds in the region and that multiple genetic lineages of the virus are cocirculating (*32*, *33*). Poultry trade and mechanical movement of infected materials are likely modes for spreading HPAI in general (*3*). For the H5N1 virus, it is without doubt that domestic waterfowl, specific farming practices, and agroecological environments played a key role in the occurrence, maintenance, and spread of HPAI for many affected countries (*34*, *35*). Although numerous wild birds have also become infected, it has been much debated whether they play an active role in the geographic spread of the disease. It has been argued that infected birds would be too severely affected to continue migration and thus unlikely to spread the H5N1 virus. Although this may be true for some wild birds, it has been shown that, in experimental infections, several bird species survive infection and shed the H5N1 virus without apparent disease signs (*31*, *32*, *36*). In addition, many wild birds may be partially immune owing to previous exposures to LPAI influenza viruses, as has been shown for chickens (*37*). Finally, recent studies suggest that HPAI viruses may become less pathogenic to ducks infected experimentally, while retaining high pathogenicity for chickens (*32*, *36*, *38*). The present situation in Europe, where infected wild birds have been found in several countries that have not reported outbreaks among poultry, suggests that wild birds can indeed carry the virus to previously unaffected areas. Although swan deaths have been the first indicator for the presence of the H5N1 virus in several European countries, this does not necessarily imply a role as predominant vectors; they could merely have functioned as sentinel birds infected via other migrating bird species.

Prospects

Despite the relatively intense surveillance studies that have been performed for many years in North America and Eurasia, our understanding of the global distribution of LPAI viruses in wild bird populations is still limited. Serological evidence indicates that influenza viruses occasionally circulate in Antarctica (*39*), and it is reasonable to assume that influenza viruses are distributed globally, wherever competent host species are present. It is possible that some subtypes are rare or not detected annually in current surveillance studies. Simply because of the limitations of our studies, we are currently biased toward species that are easy to sample during migration or wintering. Second, to understand the global patterns of LPAI viruses in wild birds, it will be crucial to integrate virus and host ecology with long-term surveillance studies to provide more insight on the year-round perpetuation of influenza viruses in wild birds. Possible intercontinental contacts among ducks and shorebirds in areas where migrating birds from the northern and southern latitudes mix are of particular interest. Can influenza viruses be perpetuated in ducks alone, or does the interface between ducks and shorebirds, as seems to occur in North America (*19*), also occur on other continents? With high-throughput sequencing technology, it should be possible to gain more insight into the genetic variability and evolution of LPAI viruses in wild birds and to integrate this information with epidemiology and virus-host ecology.

The recent H5N1 outbreaks in Eurasia have identified additional gaps in our knowledge of avian influenza viruses in wild birds in general. It should be realized that our knowledge of LPAI viruses in wild birds cannot simply be extrapolated to HPAI viruses; for instance, the most important host species or routes of transmission may be quite different (Table 1) (*29*–*31*, *38*). It is clear that influenza virus surveillance of wild birds could provide "early warning" signals for the introduction of HPAI H5N1 virus in new regions and may provide access to strains for characterization. For proper risk assessment studies, however, we also need a better understanding of the interface between wild and domestic birds, the possible transmission of influenza viruses between these populations, bird behavior, age-structures of populations, and detailed migration routes. We further need better understanding of the transmission and pathogenesis of H5N1 virus in wild birds, as well as identification of virus-permissive host species and their relative likelihood to develop disease, patterns of virus secretion, and temporal and spatial variations in virus prevalence.

With our current limited knowledge on HPAI in wild birds, there is no solid basis for including wild birds in control strategies beyond the physical separation of poultry from wild birds. Even in areas with significant outbreaks in poultry, virus prevalence in wild birds is low (*32*), and the role of these wild birds in spreading the disease is unclear. It is clear that the H5N1 problem originated from outbreaks in poultry and that the outbreaks and their geographical spread probably cannot be stopped without implementation of proper control measures in the global poultry industry. However, there is at present no scientific basis for culling wild birds to control the outbreaks and their spread, and this is further highly undesirable from a conservationist perspective.

The current increased interest in influenza virus surveillance in wild and domestic birds provides a unique opportunity to increase our understanding not only of HPAI epidemiology but also of the ecology of LPAI viruses in their natural hosts, at the same time and for the same cost.

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40. We apologize to the scientists whose original contributions have not been cited here due to space restrictions. We thank G. Rimmelzwaan, D. Smith, T. Piersma, J. de Jong, and E. de Wit for fruitful discussions and helpful comments.

Supporting Online Material

www.sciencemag.org/cgi/content/full/312/5772/384/DC1
Table S1
References and Notes

10.1126/science.1122438

Global Patterns of Influenza A Virus in Wild Birds

Björn Olsen, Vincent J. Munster, Anders Wallensten, Jonas Waldenström, Albert D. M. E. Osterhaus and Ron A. M. Fouchier

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REVIEW ARTICLE

A systematic review of Rift Valley Fever epidemiology 1931–2014

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Background: Rift Valley Fever (RVF) is a mosquito-borne viral zoonosis that was first isolated and characterized in 1931 in Kenya. RVF outbreaks have resulted in significant losses through human illness and deaths, high livestock abortions and deaths. This report provides an overview on epidemiology of RVF including ecology, molecular diversity spatiotemporal analysis, and predictive risk modeling.

Methodology: Using the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) guidelines, we systematically searched for relevant RVF publications in repositories of the World Health Organization Library and Information Networks for Knowledge (WHOLIS), U.S Centers for Disease Control and Prevention (CDC), and Food and Agricultural Organization (FAO). Detailed searches were performed in Google Scholar, SpringerLink, and PubMed databases and included conference proceedings and books published from 1931 up to 31st January 2015.

Results and discussion: A total of 84 studies were included in this review; majority (50%) reported on common human and animal risk factors that included consumption of animal products, contact with infected animals and residing in low altitude areas associated with favorable climatic and ecological conditions for vector emergence. A total of 14 (16%) of the publications described RVF progressive spatial and temporal distribution and the use of risk modeling for timely prediction of imminent outbreaks. Using distribution maps, we illustrated the gradual spread and geographical extent of disease; we also estimated the disease burden using aggregate human mortalities and cumulative outbreak periods for endemic regions.

Conclusion: This review outlines common risk factors for RVF infections over wider geographical areas; it also emphasizes the role of spatial models in predicting RVF enzootics. It, therefore, explains RVF epidemiological status that may be used for design of targeted surveillance and control programs in endemic countries.

Keywords: *Rift Valley Fever*; *spatiotemporal*; *modeling*; *epidemiology*

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Rift Valley Fever (RVF) is an arthropod-borne viral zoonosis with evidence of widespread occurrence in humans and animals in Africa and the Arabian Peninsula. Major epidemics have been reported most notably in Egypt (1977, 2003), Kenya (1997–1998, 2006–2007), Tanzania (2007), Somalia (2007), Saudi Arabia and Yemen (2000–2001), Sudan (2007), Mayotte (2008), and Mauritania (2010, 2012) (1–11). The RVF virus (RVFV) is a Phlebovirus belonging to the *Bunyaviridae* family of viruses (12). RVFV has been isolated from over 30 species of mosquitoes in six genera (13, 14). RVF outbreaks are associated with the occurrence of the warm phase of the El Niño/Southern Oscillation (ENSO) phenomenon causing floods, increased greenness of vegetation index, and emergence of mosquito vectors that infect susceptible ruminant hosts (15–17). According to the

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World Organization for Animal Health (OIE), RVFV is an OIE high-impact transboundary pathogen with potential for bioterrorism and a setback to international livestock trade (18). Here, we present a comprehensive review that provides an update on RVF with a focus on understanding the epidemiology of RVF, including ecology and risk factors as well as molecular diversity, spatiotemporal epidemiology, and risk modeling for disease endemic regions.

Methodology

Search strategy

Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) (19) guidelines were used to search for published literature from 1931 up to 31st January 2015 in PubMed, SpringerLink, WHOLIS, Food and Agricultural Organization (FAO), and U.S Centers for Disease Control and Prevention (CDC) databases. To maximize the completeness of the search and reduce selection bias, the search was restricted to English articles using the medical subject heading (MESH) search terms "rift valley fever" AND "epidemiology" OR "spatio-temporal" OR "modelling". A generalized search was performed using Google Scholar to identify relevant documents not published in peer-reviewed journals using similar terms as above. During the initial search, studies were selected based on a review of titles and abstracts. All abstracts identified from the indexed databases were screened for eligibility, and the full text of relevant articles was reviewed. Review articles on RVF were examined to identify non-indexed articles fitting the eligibility criteria (Fig. 1).

Eligibility and inclusion criteria

Studies included in this review described replicable findings on the epidemiology and geographical extent of RVF, molecular and genetic diversity, human and animal risk factors associated with ecological and climatic conditions, and spatiotemporal and predictive risk modeling for RVF.

Exclusion criteria

We excluded RVF reports on sero-epidemiological surveys that reported negative results and risk factor studies

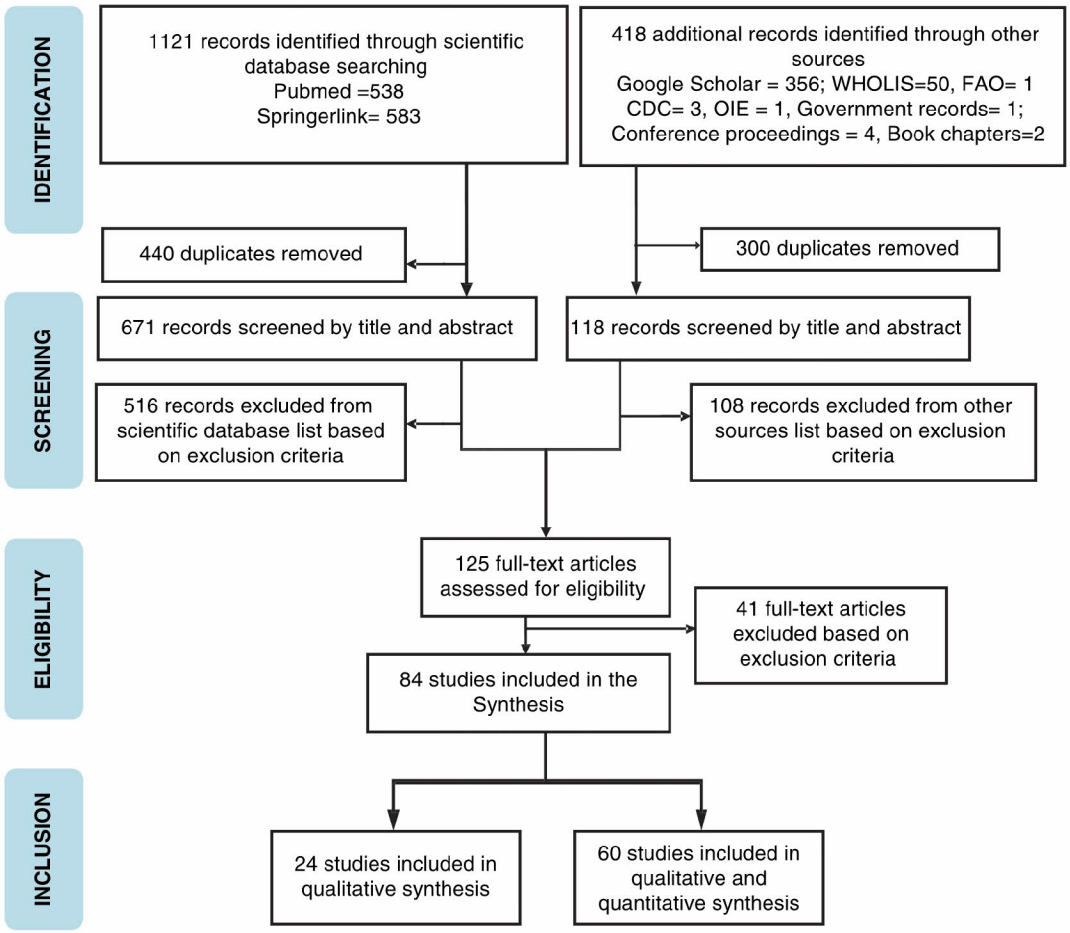

Fig. 1. PRISMA flow chart diagram describing the studies selection process for inclusion in this review [adapted and modified from (19)].

Citation: Infection Ecology and Epidemiology 2015, **5**: 28024 - http://dx.doi.org/10.3402/iee.v5.28024

that had no clear case definition or that had an extremely low sample size (<100). We developed a specific criteria based on subject matter expertise which excluded secondary reports, editorial opinions, personal communications, and studies published in scientific conferences that were purely descriptive with no quantitative or qualitative inferences, as illustrated in Fig. 1.

Results

The data

Using the key search terms, 1121 records were retrieved from indexed scientific databases [PubMed (538) and SpringerLink (583)], while 418 non-indexed reports were obtained from generalized searches in Google Scholar (356), WHOLIS (50), FAO/CDC (7), government reports (1), and conference proceedings (4). All records were imported in to Microsoft Excel, and articles presenting duplicate titles/findings were removed to obtain 800 records. Further screening was done by title and abstract focusing on studies reporting the epidemiology of RVF including ecology and risk factors as well as molecular diversity, spatial–temporal epidemiology, and risk modeling. Six hundred and seventy five articles (675) were eliminated based on the general exclusion criteria to remain with a subset of 125 publications that were assessed for eligibility by reading the full text. Furthermore, 41 articles were removed by the subject matter exclusion criteria; limiting this review to 84 publications where 60 had quantitative and qualitative inferences, while 24 had qualitative but replicable findings (Fig. 1).

Maps: spatiotemporal distribution of RVF occurrence

The descriptive geography of the epizootic or endemic status of RVFV was illustrated using GIS software (ArcView® 10.2.2) to produce distribution maps (Figs. 2 and 3). The input data were extracted from the relevant cited publications. The aggregate number of outbreaks in months as reported at country level was confirmed by clinical diagnosis or serological evidence in livestock and humans. From available records, we calculated the cumulative human case fatalities in 13 African and two Arabian countries from 1977 to 2012. More details are available in Fig. 2.

The epidemic focus of RVFV was contained in Kenya in 1912 (20) until three decades later, before spreading to neighboring Tanzania in the late 1940s (21). Intensive outbreaks in Southern Africa in the 1950s were evident in South Africa, Namibia, Zimbabwe, and Zambia forming secondary epidemic foci (22) (Fig. 2). The proximity of the Arabian Peninsula to the Horn of Africa and associated livestock trade may be responsible for the geographical spread of the virus to Saudi Arabia and Yemen (23) as indicated in Fig. 2.

An epidemiologic shift was evident in the West African pocket in the late 1980s, and may have been associated with climate variability, leading to aggressive emergence and dispersal of competent mosquito vectors of *Aedes* and *Culex* species to the large ruminant populations in Mauritania and Senegal. Southern Africa and West Africa have reported the longest RVF outbreak periods with South Africa and Mauritania (24) sustaining longer outbreaks compared to the rest of the Horn of Africa as detailed in Fig. 3.

Epidemiology, ecology and risk factors for RVF occurrence

RVF epizootics and epidemics in livestock and humans have occurred periodically with the initial geographic range restricted to sub-Saharan Africa, but since 2000 it has spread to the Arabian Peninsula. An enzootic hepatitis in sheep was observed as early as 1912, but the first clinical report was among sheep, cattle, and humans in areas near Lake Naivasha in Kenya in 1930 (25). Since that time, recurrent epidemics have been reported for the last 60 years in South Africa (26), Zimbabwe (27), Mauritania (9–11), Senegal (28), Zambia, Namibia, Gabon, Burkina Faso, Madagascar, East Africa, and more recently in Mayotte, Yemen, and Saudi Arabia (1–7, 29, 30) (Fig. 2 and Table 1).

The South African epizootic of 1951 led to deaths of over 100,000 sheep and half a million livestock abortions (25). In Egypt, a notable human epidemic was reported in 1977 causing an estimated 600 deaths and significant livestock abortions and mortalities. This first report of RVF in Egypt may have been associated with introduction of the virus through livestock trade from the Horn of Africa and aggressive emergence of mosquitoes from the flooded Nile River (32). An additional 45 RVF cases were reported in farmers in Seedy Salim district, where up to 17 human deaths were confirmed in the Egyptian Kafr Al-Sheikh Governorate (33).

A retrospective cohort study conducted in 1989 in Senegal assessed risk factors among 273 people aged >5 years. Increased seropositivity was associated with advanced age. Nursing sick people while being in contact with sick animals had a six-fold risk of infection, and male animal attendants had five-fold risk of contracting RVF as compared to females (34) (Table 1). In the Horn of Africa, epidemics have been closely associated with El Niño-related flooding resulting in a large outbreak in 1997–1998 that led to thousands of livestock deaths and estimated 500 human deaths (2, 35). In 2000, the first RVF outbreak in Saudi Arabia was investigated among 800 patients with a case fatality rate of about 14%. RVF IgM, detected in $>50\%$ persons, was indicative of active infection. The majority of cases were males over 40 years old (36). During the same period, another prospective study reported mortalities of up to 34% in 165 seropositive patients (37) (Fig. 2 and Table 1).

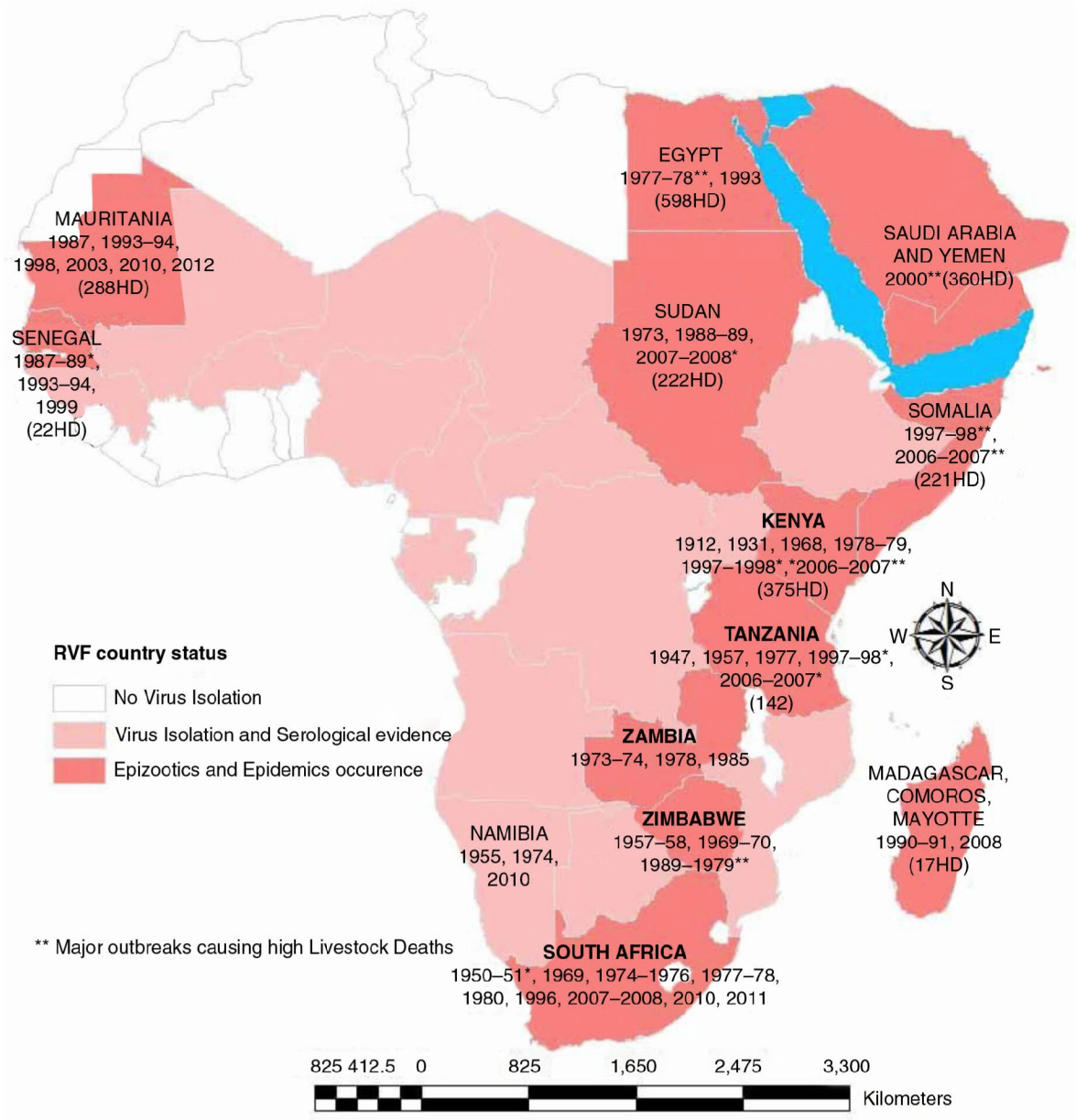

Fig. 2. Map of Africa and Arabian Peninsula illustrating the spatial and temporal distribution of Rift Valley status from the first suspected case in 1912. Total number of human deaths (HD) is indicated for selected countries for all outbreak periods. Based on (2, 5–7, 10–12, 14, 16, 22, 23, 25, 40, 46, 54, 75, 80).

In 2006–2007 the outbreak that affected Sudan, Kenya, Somalia, and Tanzania led to substantial losses of livestock and over 900 human deaths (6, 38–41). In 2000, sustained heavy rainfall in the Arabian Peninsula led to flooding and the first outbreak of RVF in Saudi Arabia and Yemen (42), which resulted in over 200,000 human infections with an estimated 250 human deaths and thousands of livestock deaths (5, 43, 44) (Fig. 2 and Table 1).

In East Africa, high-risk areas for RVFV activity have been identified based on ecological receptiveness for the vector, historical presence of virus or proximity to known infected areas, and areas experiencing increased rainfall and flooding. High incidence has been reported in areas having soil with poor drainage and flat landforms with low altitudes below 500 m (21, 45, 46). Human and animal prevalence studies focus on description of risk factors for outbreak using OR as a measure of association of factors in prevalence studies. Most of the studies examined human–animal contact or consumption of animal products (47). After the 2006–2007 RVF outbreak in Kenya, a randomized household cluster survey was conducted in two RVF outbreak foci areas – one among 248 individuals

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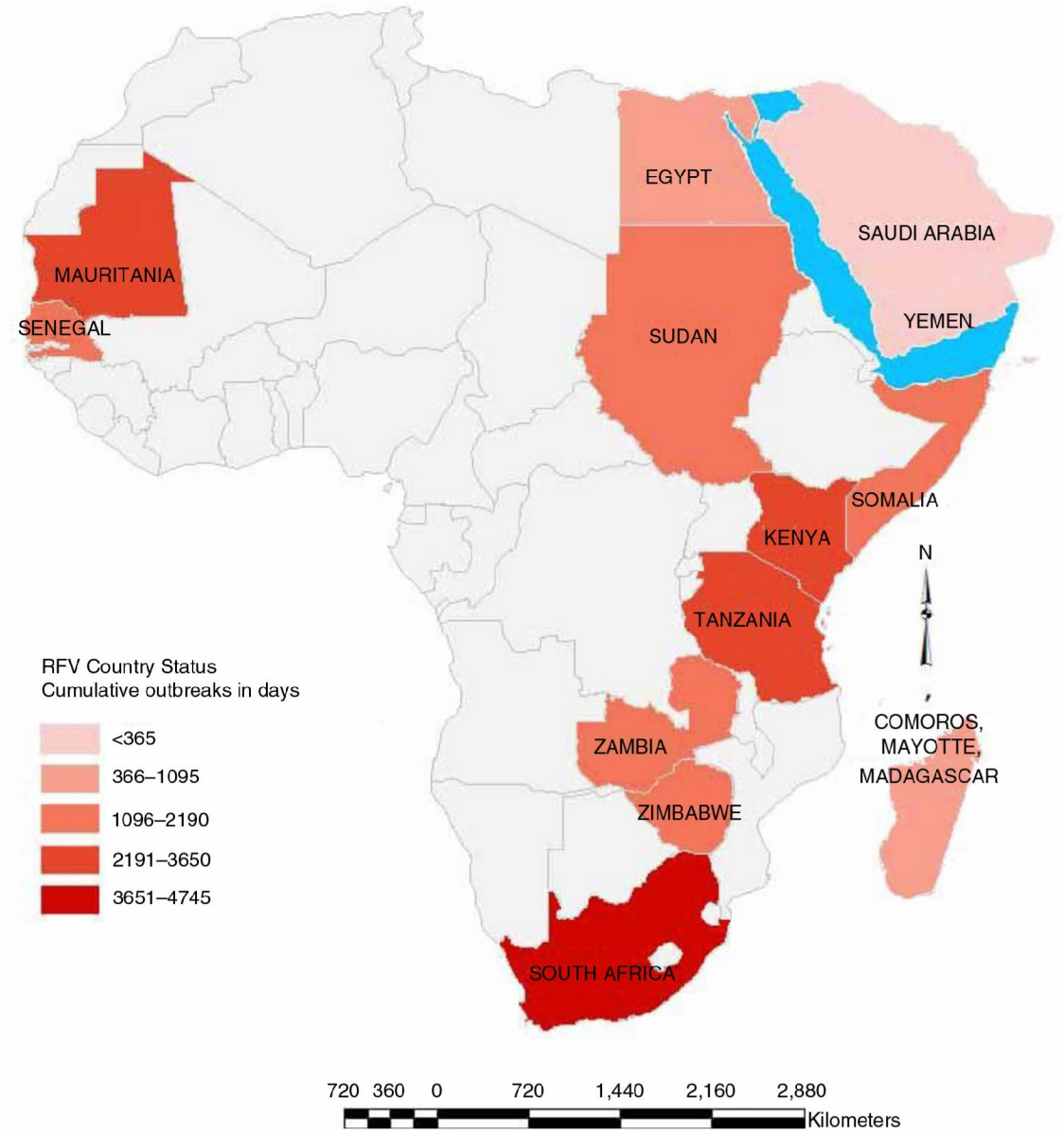

Fig. 3. Map of Africa and the Arabian Peninsula illustrating the spatial and temporal distribution of Rift Valley cumulative outbreaks in days from 1977 to 2012 (2, 5–7, 10–12, 22, 23, 25, 40, 46, 80).

and another population-based serological survey in three foci among 861 individuals in over 400 households (39, 48).

Both studies reported higher infection with RVF among male herders, and common risk factors were touching or disposing aborted fetuses or being exposed to mosquitoes. Other risk factors include consuming or handling products from sick animals, contact with livestock as herdsmen and handling of aborted fetuses, milking, skinning, slaughtering, sleeping with animals, touching blood, and caring for animals during birthing (39, 48).

Movement of livestock during the viremic phase of infection to areas with high mosquito density and naïve livestock populations poses a high risk of human infection especially among persons handling livestock (39, 49). A multispecies sero-epidemiological survey was conducted in the Sahrawi territory which is a cluster of refugee camps in Tindouf province of Algeria. Less than 1% of the 982 ruminant samples tested positive for IgG antibodies against RVFV with two clusters of high seroprevalence in Mehaires (7.14%) and Tifariti (7.69%) regions. The proximity of this region to RVF endemic countries like Mauritania and Senegal that engage in large livestock trade may have been responsible for the frequency of RVF outbreaks in 2008, where goats and older animals had higher seropositivity (50).

Table 1. Characteristics of the eligible studies investigating RVF epidemiology, ecology, risk factors, and spatial modeling 1931–2012

				Morbidity and mortality estimates					
				Animals		Humans			
Year(s)	Geographic distribution	Study design	Research questions/objectives	Reported cases	Deaths	Reported cases	Deaths	Estimated impact in US$ ($\times 10^6$)	References
1931	Kenya	Cross-sectional	Risk factors and ecology	nd	4,700	nd	nd	nd	(25)
1950–1951	South Africa	Cross-sectional	Epidemiology and spatial modeling	600,000	100,000	nd	nd	nd	(22, 26, 31)
1977–1978	Egypt	Cross-sectional	Epidemiology and socioeconomics	nd	nd	200,000	598	115	(1, 32, 81)
1978	Zimbabwe	Cross-sectional	Risk factors	70,000	10,000	nd	nd	nd	(27, 31)
1988	Mauritania	Case–control	Risk factors	nd	nd	nd	224	nd	(9)
1987–1989	Senegal	Cohort	Molecular epidemiology	1,715	nd	273	16	nd	(28, 34)
1997–1998	Kenya	Cross-sectional	Ecology, risk factors and	89,000	478	160,000	450	250[c]	(2, 35, 82)
	Somalia		socioeconomics	nd	nd	28,000	170	378[c]	
	Tanzania			nd	nd	89,000	478	nd	
1998	Mauritania	Cross-sectional	Sero-epidemiology, entomology and virology	343	nd	90	1		(30)
2000	Saudi Arabia	Cross-sectional	Risk factors and ecology	>10,000	1,000	883	245	10	(36, 37)
2000–2001	Yemeni	Cross-sectional	Risk factors and socioeconomics	22,000	6,000	1,328	166	107	(5, 42, 81)
2003	Egypt	Cross-sectional	Risk factors and virology	nd	nd	45	17	nd	(33)
2007–2008	Sudan	Cross-sectional	Risk factors and ecology	nd	nd	75,000* (698)	222	nd	(6, 79, 80)
2008–2009	Madagascar	Cross-sectional	Epidemiology and socioeconomics	nd	nd	10,000 (712)	26	nd	(84)
2006–2007	Somalia	Cross-sectional	Risk factors, predictive modeling and	nd	nd	35,000* (114)	51	541[c]	(21, 29, 39,
	Tanzania		ecology	32,000	4,200	40,000* (264)	109		40, 48, 49, 52)
	Kenya			nd	nd	75,000* (684)	158		
2010–2011	South Africa	Cross-sectional	Spatial and predictive modeling	14,342	8,877	242	26	nd	(22, 75, 84)
2012	Mauritania	Cross-sectional	Risk factors, molecular diversity	nd	343	41	17	nd	(8, 10, 11)

nd = no documented estimates; c = combined estimates.
*Estimated cases in brackets are the reported.

In 2007–2008, a large cross-sectional seroprevalence survey among 17,000 people in Tanzania revealed a higher seroprevalence of 29.3% in persons living near water bodies. Seropositivity was also associated with increased age, owning livestock, and poverty. It further showed a high correlation of increased risk in areas with dense vegetation, hence, favoring mosquito emergence and large cattle populations (51). Similarly a clinical epidemiological study of 511 RVF suspect cases in Tanzania during the 2007 outbreak revealed major signs of infection such as fever, encephalopathy, retinopathy, and hemorrhages with a high case fatality rate of about 30% in 186 laboratory-confirmed cases. Increased infection was highly associated with contact or consumption of foods of animal origin (52) (Table 1).

In 2011, a random cross-sectional survey was conducted on about 1600 livestock in Kilombero Valley, Tanzania. It showed that younger animals born after the 2007 outbreak had a lower prevalence (5.5%) compared to older animals ($>22.7\%$), but a large difference was observed in female animals having a three-fold increased risk compared to male animals (53). Grazing within 5 km of water bodies had little influence on the presence of antibodies compared to animals grazing >15 km from water bodies; this is in contrast to the expected increase in vector density at breeding sites where hosts aggregate. However, a related human study in Mbeya region of Tanzania reported a higher correlation between altitude and increased seroprevalence among 1,228 residents (51).

Despite the proximity of Uganda to Kenya and Tanzania, RVF outbreaks have never been reported in Uganda in either humans or animals. Magona et al. (54) tested 2,700 European and local goat breeds in 30 farms across four Ugandan districts and recorded a 10% seroprevalence of antiRVF IgG antibodies. Similarly in Djibouti located in the Horn of Africa, Andayi et al. (55) assessed the risk factors and sero-epidemiology of arbovirus and detected an RVF prevalence of 2.2% in 1,000 humans. This confirms the presence of subclinical virus circulation in non-epidemic areas and calls for continued virus and vector surveillance in anticipation of outbreaks.

In Mayotte, a risk factor assessment conducted in 2011 among 1,420 individuals and 198 seronegative ruminants in 33 herds (56) found that high human seroprevalence was associated with increased age (≥ 15 years), being male, proximity to water bodies, farming, and low education levels. While animal risk factors were similar to reports in East Africa, a major risk factor for both humans and animals was exposure to competent mosquito vectors (56). The 2012 outbreak in southern Mauritania reported 17 human deaths among 41 confirmed cases (10, 11). Phylogenetic analysis indicated that outbreaks may have remerged from enzootic foci with isolates having a close relationship with the strains responsible for the 2010 outbreak in the northern part of Mauritania (8, 10).

Analysis of ecological factors associated with RVF infection in Gabon from 2005 to 2007 was conducted in 4,323 individuals covering 10% of national households. Despite the lower overall seroprevalence (3.3%), individuals living around the lake region had higher seropositivity (8.3%) than those residing in forested and savannah areas (2.9 and 2.2%, respectively). This study reaffirms the role played by water bodies leading to rapid turnover of competent vectors (57) to establish RVF endemic status as also evidenced in Mbeya, Tanzania (51). The influence of sex on RVF infection rates was described by a hospital based case control study that was conducted on 290 febrile patients during the 2007 outbreak in Sudan. One hundred and twenty two (82%) of 149 patients were RVFV IgG seropositive with a reported three-fold risk of being seropositive for males (OR = 2.8, 95% CI = 1.0–7.6) (58).

In Saudi Arabia, a seroprevalence survey of 275 small ruminants examined the contribution of environmental and animal risk factors to RVF outbreaks and demonstrated a positive association of disease occurrence and increased precipitation (OR = 2), presence of water bodies (OR = 2.2), high vector density (OR = 4.2), with high disease occurrence (59); the findings were closely related to other studies in Gabon and Tanzania (51, 57). Caminade et al. (60) investigated the relationship between rainfall and greening vegetation triggering RVF outbreaks in Mauritania from 1990 to 2012. Whereas intra-season variability of weeklong rainless periods, then heavy precipitation was observed to be critical in the onset of outbreaks, this finding was contrary to the effect of total seasonal levels precipitation or normalized differential vegetative index (NDVI) responsible for East African outbreaks (15, 61).

Molecular epidemiology and genetic diversity of RVFV

Phylogenetic analysis of samples isolated from 1944 to 2000 in 10 African countries and Saudi Arabia revealed that seven main viral lineages were categorized as A, B, C, D, E, F, and G among the 33 viruses (62). Despite the A–D lineages existing in most African countries, enzootic circulation was consistent in Central Africa. There is potential of virus transportation outside endemic regions which may have been associated with the outbreak in Egypt (1977–1979) due to introduction of genotypes from endemic sub-Saharan Africa. Five more lineages (B, F, H, I, and M) were described; this high variability may be due introduction of virus by the live Smithburn vaccines used to combat the outbreaks of South Africa (1951–1968) and Zimbabwe (1969–1970) (63).

There is evidence of widespread circulation of multiple lineages B, C, K, and L, with C being isolated from outbreaks in Zimbabwe (1978), Madagascar (1991), Horn of Africa 1997–1998, Saudi Arabia (2000–2001), Kenya (2007), and South Africa (2008–2009). However, the

genetic similarity in isolates of 1977, 1983, and the 1997–1998, 2006–2007 in Kenya may indicate virus introduction through vaccination using live vaccines (63). Genetic analysis of S, M, and L segments of RVF isolates from the Arabian Peninsula outbreak in 2001 indicated striking similarity to isolates associated with RVF epidemics in Kenya (1997) and Madagascar (1991). This may rule out the genetic reassortment associated with the emergence of RVFV in the Arabian Peninsula but suggest concurrent virus circulation and genetic evolution of during the inter-epidemic period (64). Phylogenetic analysis of 2007 and 2010 outbreak samples from Sudan revealed a closer lineage with the Kenyan RVFV variants during the 2006–2007 outbreak, suggesting a common ancestry and multiple viral introductions from East Africa (65).

Common genetic ancestry was demonstrated by Faye et al. (66) from human and animal outbreak strains in Mauritania (2003) whose phylogenetic lineages were similar to isolates from Madagascar (1991), Kenya (1997), Chad (2001), and Saudi Arabia (2001). Whole genome sequencing using 12 strains of viruses isolated for over 50 years (1944–2001) from six African countries and Saudi Arabia indicated that *Aedes vexans arabiensis* was responsible for the 2000 in Saudi Arabia. These cases occurred after heavy rainfall, hence, agreeing with East African dynamics of disease emergence based on favorable ecological variables for vector emergence (66, 67). Genomic analysis of over 3,000 animal specimens collected in Kenya during the 2006–2007 outbreak demonstrated concurrent circulation and genetic reassortment of multiple virus lineages in 31 RVFV isolates. The 2006/2007 outbreak viruses had the same ancestry as the 1997/1998 outbreak strains. The coverage of all genome segments was confirmed by serology and, therefore, confirms enzootic circulation and wider geographical distribution of similar RVFV strains (38).

In West Africa, phylodynamics of RVFV has been evaluated by Bayesian models using 48 RVFV isolates collected over 65 years from 18 sites in Senegal and Mauritania, and 15 other countries (24). They demonstrated a geographic pattern with high temporal coherence matching the earlier reported cases in East Africa. There were five distinct introductions routes in Senegal and Mauritania, stretching from South Africa, Zimbabwe, hence, confirming the serological and entomological surveys that Barkedji coastal area of West Africa may be a vital entry point of RVFV in Senegal and Mauritania (24).

In East Africa, a whole genome phylogenetic analysis of 16 RVF viruses isolated from humans, livestock, and mosquitoes during the 2006–2007 outbreak revealed three distinct lineages, which in comparison had similarity to the Kenyan isolates of 1980, 1998 and the Saudi Arabia isolate of 2000 but had no genetic similarity with other isolates including Entebbe 44 and Kenya 1965 (68). This strongly suggest the possibility of focal '*de-novo*' reemergence of viruses and spontaneous release of resident virus maintained inter-epidemically in desiccated *Aedes* eggs which hatch during flooding.

During the Kenyan 2006–2007 RVF outbreak, virus isolates were analyzed for genetic diversity in three outbreak regions. The eight human isolates had up to 99.6% nucleotide sequence identity with each other across the M segment of the genome. They had high homology with the RVF strains involved in the 1996–1997 RVF outbreak in Kenya and 2000 outbreak in Saudi Arabia (49). The outbreaks of RVF in Arabian Peninsula in 2000 may be associated virus introduction from disease endemic areas through transboundary livestock trade of infected animals and migration of sick persons, these may be supported by the genetic similarity of the Arabian Peninsula strains to Kenyan isolates during the 1997/1998 RVF outbreak (23).

Spatial temporal epidemiology and predictive modeling of RVF

Earlier predictive studies by Linthicum et al. (69) used satellite derived NDVI and rainfall to assess the potential for RVFV activity in two ecologically distinct RVF enzootic areas in Kenya which indicated a positive correlation between NDVI and high mosquito population, hence the high likelihood of RVF occurrence. Using a 19-year-old NDVI data, a mask was created to identify areas where RVF was more likely to occur in the savannah ecosystems of Africa. In East Africa, there was a strong correlation between predicted risk areas and observed outbreaks of RVF from 1981 to 2000; these outbreaks were more likely to occur during warm ENSO events in East Africa while cold ENSO events in Southern Africa triggered RVF outbreaks (70).

A climatic RVF risk-monitoring model was proposed in predicting the potential spatial and temporal distribution by using NDVI anomaly and elevated sea surface temperature (SST). The model retrospectively detected previous three outbreaks (1982–83, 89 and 1997–98) which correlated with positive SST and NDVI anomalies and also predicted, almost accurately, the areas for 2006–2007 outbreak areas in East Africa (13). Despite high success in predicting outbreak areas times and areas, the coarse resolution of 8 km may overgeneralize the risk and it was, therefore, useful for small-scale areas as countries and not continental scales.

Spatiotemporal analysis employing climatic and environmental variables was used in combination with vector surveillance data to predict potential outbreaks in Horn of Africa, Sudan, and Southern Africa with suitable areas of eminent epidemics identified with a lead time of 2–4 months. Accurate prediction timelines by optimal model performance were enhanced with precise animal and human disease data (14). Using time series analysis of NDVI from September 1997 to April 1998, RVF suitable

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areas were identified in Kenya with a lead time of 5 months, these received anomalous rainfall which led to favorable conditions for emergence of RVFV vectors. This has been supported by recent studies by Anyamba et al. whose improved methods led to first the prospective prediction of RVFV circulation enabling accurate prediction with lead times of 2–4 months before outbreaks (14, 15, 71).

A large-scale continental estimate of RVF prevalence in Africa using serological data has been explored by a spatially explicit Bayesian logistic-regression model (72). There were correlated high-prevalence RVF clusters in areas that had previously experienced epidemics including Kenya's North Eastern region and Somalia. This study and others form a framework for estimating the seroprevalence where no accurate serological data are available (72, 73).

Using knowledge driven spatial modeling, RVF endemicity suitability maps for Africa were developed by Clements et al. (74). Most of sub-Saharan Africa had high predicted suitability of RVF occurrence; moderate suitability was predicted for Morocco, Algeria, and Tunisia while the whole of the Sahara desert was unsuitable. This was corroborated with overlay of observed serological prevalence for suitability for RVF in Senegal, thus providing wider applications where serological data are available.

Metras et al. (75) reported five major cycles of RVF outbreaks in South Africa from 2008 to 2011 with the 2010 cases having elaborate spatiotemporal interactions and supporting the role of other factors in the spread of disease beyond active vector dispersal. This study, however, described human patients who may have acquired infection by close contact with infected animals or who were infected directly from mosquito bites (74, 75). A comprehensive temporal and spatial distribution of RVF outbreaks in South Africa from 1950 to 2011 was described by Pienaar et al. (22) using more accurate records from smaller but extensive outbreaks in livestock and humans. These studies indicated higher cumulative outbreaks periods in South Africa despite low human and livestock mortalities (Figs. 2 and 3 and Table 1).

Previous retrospective sero-epidemiological studies in Kenya using wildlife data correlate well with spatial predictions and the epidemiological sequence of RVFV transmission providing a future window of improving RVF transmission risk models (76). Sindato et al. (46) in Tanzania examined the distribution of RVF outbreaks from 1930 to 2007. Heterogeneity in outbreaks was observed as well as increased likelihood of occurrence in areas receiving rainfall above 400 mm and areas with clay or loam soils. Previous spatial analysis of non-clinical RVF cases in Tanzania indicated the existence of multiple ruminant hosts that were potential reservoirs of RVFV during inter-epidemic period and increased the likelihood of outbreaks in animals located at elevations less than 1,000 m (21), confirming observations of influence of elevation on outbreaks in Kenya (45).

In Kenya, Hightower et al. (45) utilized geo-referenced locations of human RVF cases during the 2006–2007 outbreak combined with geological and climatological attributes to estimate incidence of RVF disease. A correlation of altitude and disease outbreak was evident with areas at $\leq$1,100 meters consistently having epidemics. This finding was in agreement with the Tanzanian study that indicated high intra-village seroprevalence of IgG in domestic and wild ruminants and higher risk at low altitudes (53).

Discussion and conclusion

This review describes RVF epidemiologic characteristics, predisposing factors, and potential geographical spread of RVFV that should be considered in light of other favorable parameters influencing outbreaks with emphasis on host susceptibility, environmental and climatic conditions. It describes the impacts of outbreaks such as case fatality and morbidity and also highlights socio-economic factors that may elevate the risks of infection among vulnerable populations.

Molecular epidemiology is a useful tool in understanding the genetic diversity of concurrent circulation of RVF related virus lineages between Africa and Arabian Peninsula, and there may be two modes of circulation: distant spread across countries or continents and endemic circulation as observed in Senegal. The role of wildlife maintenance of the RVFV in the interepizootic period has since been demonstrated in Kenya (62, 77, 78) (Fig. 2).

Spatiotemporal evidence indicates a progressive spread of RVFV from initial foci in East Africa to the entire continent and further geographical spread to Arabian Peninsula. This may be attributed to the movement of viremic livestock through transboundary livestock trade. It may be precipitated by favorable climatic conditions for aggressive vector emergence and virus dispersal. Despite the scarce data available for livestock and human mortalities, here we have attempted to report human deaths associated with RVF outbreaks over specific time periods where records were available. These maps should, therefore, be interpreted with caution as they may not accurately represent the true burden of disease (Figs. 2 and 3).

Predictive models and mapping potential risk of RVF outbreaks in endemic areas using disease occurrence data, vector population dynamics, anomalous climatic conditions, and surrogate environmental variables provide a foreseeable public health strategy for RVF surveillance (13, 14, 69, 72). The use of seroprevalence data in spatial and temporal prediction of RVF risk provides an opportunity to validate previously suggested prospective models that map areas at risk of RVFV transmission in endemic regions (76).

Despite climatic factors being a major contributor to outbreaks, other ecological and host parameters should be considered for use of spatiotemporal predictive models for cost-effective surveillance. The combination of spatial and temporal predictions of RVF risk with targeted serological and entomological surveillance can be useful and cost-effective tool capable of identifying the areas with the highest probability of an outbreak.

A comparison of RVF outbreaks in Saudi Arabia (2000) and Sudan (2007) by Hassan et al. (79) described a 'One Health' framework with similar economic impacts related to the outbreaks in both countries, and suitable ecological or environmental variables for disease emergence despite the large geographic separation (> 1,900 km). The findings of this study can be replicated in other endemic regions by improving epidemiological surveillance systems which will result in better preparedness, earlier detection, and mitigate spread of the outbreak.

RVF episodes have a predictable cyclic occurrence based on climatic forecasts and models with precise applications to the East African and Horn of Africa scenarios (14). However, recent models have failed to accurately pinpoint the location and timing of the next epidemic. This calls for collaborative research efforts that attempt to combine serological, climatic, and ecological data for greater area prediction models that will bridge the uncertainty in RVF spatial and temporal patterns in East, South, and West Africa (22, 72, 75, 76).

While this review focuses on reports of major epidemics and illustrates the geographical pattern of the disease with pockets in East, West, and Southern Africa, RVF endemic status may be underreported due to lack of surveillance and diagnostic capacity in other countries as shown in Fig. 2. The unexpected RVF epidemiological shift to Egypt, Sudan in 1988–89 (80), Arabian Peninsula in 2000, and isolated landmasses like Madagascar, Mayotte, and Comoros may be driven by climatic and ecological factors conducive for robust vector emergence that coincides with the presence of circulating virus dispersed by livestock trade and human migration. Due to unreliable national livestock disease surveillance systems, there is a dearth of livestock mortality figures; thus, our attempt to aggregate the sparse human studies to provide mortality and outbreak maps may be severely underestimated (Figs. 2 and 3).

We have highlighted epidemiological and ecological studies focusing on humans and animals as well as risk factors, molecular and genetic diversity, spatiotemporal and predictive risk mapping for RVF. However, there is a need to contextualize socioeconomic impacts and to quantify long-term disease burden of RVF as evidenced in Table 1 (81–83). Clearly, there is an urgent need for global collaboration and prioritized research funding to tackle RVF and other emerging zoonotic diseases (84).

Disclaimer

The findings and conclusions in this paper are by the authors and views expressed in this publication do not necessarily represent the decisions, policy, or views of their institutions.

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Predicting the global spread of H5N1 avian influenza

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The spread of highly pathogenic H5N1 avian influenza into Asia, Europe, and Africa has resulted in enormous impacts on the poultry industry and presents an important threat to human health. The pathways by which the virus has and will spread between countries have been debated extensively, but have yet to be analyzed comprehensively and quantitatively. We integrated data on phylogenetic relationships of virus isolates, migratory bird movements, and trade in poultry and wild birds to determine the pathway for 52 individual introduction events into countries and predict future spread. We show that 9 of 21 of H5N1 introductions to countries in Asia were most likely through poultry, and 3 of 21 were most likely through migrating birds. In contrast, spread to most (20/23) countries in Europe was most likely through migratory birds. Spread in Africa was likely partly by poultry (2/8 introductions) and partly by migrating birds (3/8). Our analyses predict that H5N1 is more likely to be introduced into the Western Hemisphere through infected poultry and into the mainland United States by subsequent movement of migrating birds from neighboring countries, rather than from eastern Siberia. These results highlight the potential synergism between trade and wild animal movement in the emergence and pandemic spread of pathogens and demonstrate the value of predictive models for disease control.

emerging | introduced species | model | trade | zoonotic disease

Highly pathogenic H5N1 avian influenza emerged in Hong Kong in 1996–1997 (1) and by early October 2006 had subsequently caused outbreaks in poultry or wild birds in 53 countries and 256 human cases, including 151 deaths (www.who.int/csr/disease/avian_influenza/en/). Hundreds of millions of chickens, ducks, turkeys, and geese have died or have been culled to prevent the spread of the virus. Coupled with export bans on affected countries the disease has had an economic impact of >$10 billion (2). Despite efforts to eradicate H5N1 in southeast Asia it has spread to central Asia, Europe, and Africa. Migratory birds, the transport of poultry and poultry products, and the trade in wild birds all have been hypothesized as pathways of introduction. However, their role in individual H5N1 introduction events and in future spread is not well understood and has been debated extensively (3–9).

Determining the pathways by which H5N1 is spread has critical implications for predicting and preventing the future spread of this virus (10). If the risk of H5N1 spread to a country is highest through the movement of migratory birds, then surveillance at migratory stopovers such as Alaska will likely yield the first evidence of introduction, a strategy that matches current U.S. Department of Interior and Agriculture policy (11). In this scenario, the timing of the highest risk of introduction would coincide with periods of peak bird movement and pathways of migration (12). Prevention of future outbreaks would be facilitated by eliminating contact between farmed poultry and migrating birds, as was attempted by several European countries in 2005–2006. Alternatively, if the risk of H5N1 introduction is higher via the trade in poultry and poultry products, then monitoring poultry imports and eliminating imports from high-risk countries should be a higher priority for reducing the probability of H5N1 introduction. Finally, H5N1 has been found in wild birds imported into Europe and other countries as part of commercial trade in wild birds (4), making this another potentially important pathway unless all imported birds are quarantined, tested for avian influenza, and culled where necessary.

We determined the most likely pathways for the introduction of H5N1 into each of 52 countries by using global data on country-to-country imports and exports of live poultry, trade in wild birds, and the migratory and cold weather movements of wild ducks, geese, and swans, which are considered to be the main reservoirs for highly pathogenic H5 and H7 subtypes of avian influenza, including H5N1 (6, 13, 14). For each of these three pathways we estimated risk as the number of H5N1-infectious bird days for an introduction by multiplying the number of birds entering or passing through a country by an estimate of the prevalence of H5N1 and by an estimate of the number of days that each bird would shed virus. We then used data on the trade in poultry and wild birds and the migration patterns of wild birds to predict the future risk of spread of H5N1 to new countries. Because of the variability in trade restrictions and the delays of several days to over a month between the start of an H5N1 outbreak and the implementation of trade bans, we predicted future spread under two scenarios. First, we estimated the number of infectious bird days caused by the poultry trade assuming no restrictions on the poultry trade were imposed on H5N1-infected countries. Second, we predicted the risk of introduction assuming that no country would import poultry from another country that had reported H5N1 in poultry (unless that country was considered H5N1-free), but that countries reporting H5N1 in wild birds could export poultry freely, and that these exports might contain infected birds.

Results and Discussion

Past Spread of H5N1. We found that estimated numbers of H5N1-infectious bird days associated with poultry trade was >100-fold higher than for the two other pathways (wild bird trade and migratory birds) for introductions of H5N1 into Indonesia, Vietnam, Cambodia, Laos, Malaysia, Kazakhstan, Azerbaijan, Iraq, and Cote D'Ivoire and 57-fold higher for Sudan [Fig. 1*a* and supporting information (SI) Data Set]. In contrast, the number of infectious bird days was >58-fold higher for migrating birds passing first through regions with H5N1 and then to Thailand, Croatia, Ukraine, Niger, Bosnia and Herzegovina, Slovakia, Switzerland, Serbia, Burkina Faso, Poland, Denmark, Israel, the United Kingdom, and Djibouti at the time of H5N1 outbreaks than for imports of poultry and captive wild birds (Fig. 1*a* and SI Data Set). In addition, the number of infectious bird days associated with movements of wild birds after a cold weather event in Eastern Europe in January 2006

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The authors declare no conflict of interest.

Abbreviation: IBA, important bird area.

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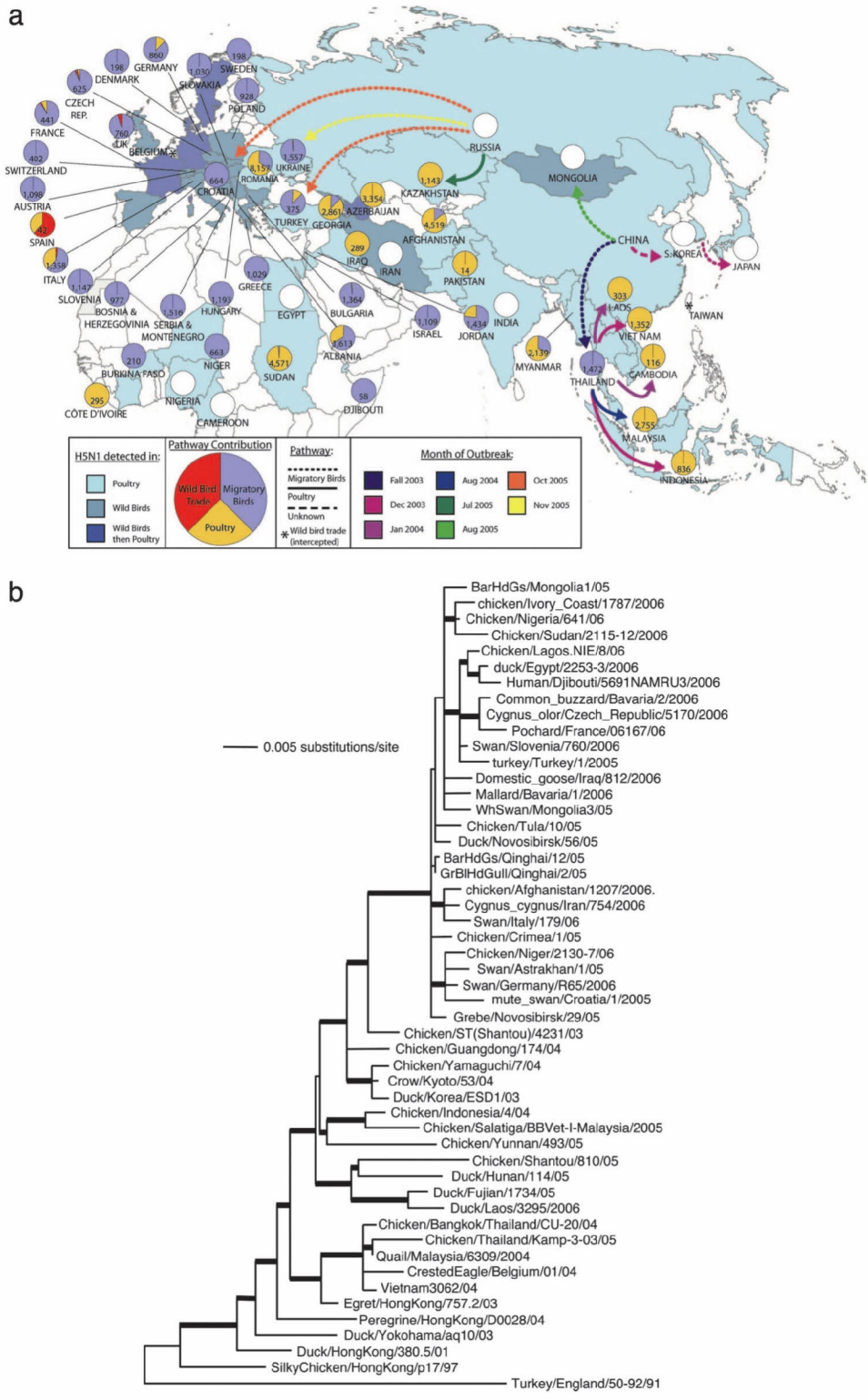

Fig. 1. Spread of H5N1 avian influenza and phylogenetic relationship of viral isolates. (*a*) Spread of H5N1 in Asia, Europe, and Africa. Pie charts show the total number of infectious bird days (number of infected birds × days shedding virus) and fraction from each pathway for birds moving between previous H5N1 outbreak countries and the focal country. Arrows give the month of the outbreak and hypothesized direction of spread for 2003–2005 introductions. The introductions of H5N1 into some countries (white pie charts) were inconsistent with reported wild bird and poultry trade (no imports from an H5N1-infected country were reported) and the direction of migratory birds in the months of the outbreaks (outbreaks occurred outside periods of bird movement; see *Methods*). Introductions into Belgium and Taiwan through the trade in wild birds were intercepted and did not lead to outbreaks in poultry or wild birds. (*b*) Maximum-likelihood phylogram showing the genetic relationship between samples of strains of H5N1 avian influenza isolated between 1997 and 2006 (with England 1991 as an outgroup) for the hemagglutinin gene. Nodes with thick, gray lines have bootstrap support >70%, based on 100 replicates.

were >100-fold greater than the trade in poultry or wild birds for H5N1 introductions into other European countries (Greece, Bulgaria, Hungary, Slovenia, Sweden, Austria, Bosnia and Herzegovina, Slovakia, Switzerland, and Serbia and Montenegro) (Fig. 1*a* and SI Data Set). The fact that poultry were not subsequently found infected in most of the countries in these latter two groups (all but Denmark and Sweden) after H5N1 was detected in migratory birds also argues against the involvement of the trade in live poultry, in which the virus usually causes substantial mortality. Migratory birds, the trade in wild birds, and the trade in poultry were all possible pathways for H5N1 introductions to Turkey, Romania (which imports poultry from Turkey), Albania, Italy, France, Germany, Georgia, Afghanistan, Myanmar, Jordan, and Spain (Fig. 1*a* and SI Data Set). However, genetic analyses (see below) and the details of the outbreaks for Italy, France, and Germany suggest that introduction by cold weather-induced movement of wild birds was more likely (www.oie.int/downld/AVIAN%20INFLUENZA/A_AI-Asia.htm). In summary, the synergistic spread of H5N1 first by poultry in Southeast Asia and then by migratory birds to Europe facilitated rapid dissemination and introductions into many countries that would likely have remained free of the virus without this synergism.

H5N1 outbreaks in South Korea, Japan, Russia, Mongolia, Nigeria, India, Pakistan, and Cameroon were inconsistent with both reported poultry trade (no poultry imports were reported from H5N1-infected countries) and the timing and direction of migratory bird travel in the month of the outbreaks. This finding suggests that unreported or illegal trade of poultry or poultry products [e.g., chicken feces for fertilizer and aquaculture (7)], the trade in wild birds, movement of free-grazing domestic ducks (15), or irregular movements of wild birds led to these introductions and may have contributed to others. Alternatively, H5N1 may have been introduced earlier by migratory birds, but not detected until later (e.g., when it spread to poultry). This sequence of events is highly likely for introductions into Russia, Mongolia, Nigeria (9), and Spain, which occurred 1–2 months after periods of peak migration and involved isolates that were genetically closest relatives to isolates along migratory bird routes (see below).

The phylogenetic relationships of the H5N1 isolates currently available strongly support the spreading pattern outlined in Fig. 1*a* and provide additional insight into the introduction of H5N1 into Japan, Russia, Mongolia, Turkey, Italy, and France, and thus clarify three introductions that could not be resolved based on trade data. The recent isolates from South Korea and Japan (eastern clade) and Qinghai (China), Russia, Mongolia, Europe, and Africa (western clade) formed well supported clades, suggesting a common ancestor for each of these groups of isolates (Fig. 1*b*). Thus, the introduction into Japan was most likely from migratory birds passing through South Korea (16) and not from China (neither of which reported poultry exports to Japan in 2003), whereas the introductions into Russia and Mongolia likely originated from China. The France, Italy, and Turkey isolates formed a well supported clade with Russian (Novosibirsk, Tula) and Ukraine (Crimea) isolates (the source for migrating birds) that was distinct from south Asian isolates where poultry imports into France and Italy (India) and Turkey (Thailand) originate.

Birds imported into the United Kingdom, Belgium, and Taiwan from Southeast Asia (Fig. 1*a*) as part of the wild bird trade also tested positive for H5N1, although none of these introductions resulted in outbreaks in poultry or wild birds (4). The trade in wild birds may also have played a part in the introductions into Japan, Indonesia, and Malaysia, where imports number in the thousands per year.

These results represent an important advance over earlier general assertions that the spread of H5N1 involves both poultry and wild birds in Asia and Europe, respectively (5, 6, 12, 17, 18). Most importantly, they identify the most likely individual pathway for 36 of 52 H5N1 introduction events, which is not possible based solely on phylogenetic relationships of viral isolates (17). Our results demonstrate that the spread of H5N1 through Asia and Africa involved both migratory birds and poultry, whereas wild bird movements were the most important pathway for the spread into and throughout Europe.

Predicting Future Spread. In the absence of trade bans, H5N1 may be introduced through poultry to the remaining countries in Europe, throughout much of Africa, and to the Americas in the near future (Fig. 2*a*). However, even if countries with current outbreaks of H5N1 in poultry cease exports, the risk of H5N1 spread continuing through Europe, Africa, and into the Americas is possible through poultry exports (Fig. 2*b*) from countries with H5N1 in wild birds (which has repeatedly spilled over into poultry; Fig. 1*a*). In addition, because few birds regularly migrate between the Americas and areas of the Old World where H5N1 has been reported (Fig. 2*d*; H5N1 has not been reported in eastern Siberia or Ireland) both poultry and the trade in wild birds currently represent a larger risk than migratory birds for the spread of H5N1 to the Americas (Fig. 2 *b* and *c*) unless all birds are quarantined and tested for influenza on import (as they are in the United States). However, if H5N1 spreads into northeastern Siberia (including Wrangel Island), then the risk of introduction into the mainland United States by migratory birds will increase substantially, because several species of ducks, geese, and swans regularly cross the Bering Sea between their breeding and wintering grounds (3, 19) (Fig. 2*d*).

Our analyses demonstrate an important consequence of the synergistic spread of H5N1 by both poultry trade and wild birds (Fig. 1*a*): Although the risk of H5N1 introduction into the mainland United States by any single pathway is relatively low (Fig. 2), the risk of introduction by poultry to other countries in the Americas, including Canada, Mexico, and Brazil, is substantial unless all imported poultry is tested for H5N1 or trade restrictions on imports from the old world are imposed (Fig. 2 *a* and *b*). Subsequent spread by >4 million migratory ducks, geese, and swans (representing ≈2,600 H5N1 infectious bird days) from the south would then make introduction into the United States likely (Fig. 2*d*). Thus, current American surveillance plans (11) that focus primarily on the Alaskan migratory bird pathway may fail to detect the introduction of H5N1 into the United States in time to prevent its spread into domestic poultry.

Examination of previous outbreaks and surveillance efforts also provides insight into the most effective means of surveillance. Of the 23 H5N1 primary outbreaks detected first in wild birds (Fig. 1*a*), 17 were in dead or sick swans (*Cygnus* spp.) and the other 6 were in dead or sick geese or ducks (other species, including a gull and several birds of prey were also occasionally found infected with H5N1) (www.oie.int/downld/AVIAN%20INFLUENZA/A_AI-Asia.htm). Surveillance of live birds, even in areas where H5N1 is known to be circulating, has shown that the prevalence of H5N1 is quite low (0.0013 ± 0.00052) (17). These findings suggest that surveillance measures should focus on sick or dead birds such as swans and other waterfowl (family Anatidae) for the early detection of H5N1.

In this analysis, we used data on the numbers of migratory birds and the magnitude of the trade in poultry and wild birds to understand previous spreading events and predict the risk of introduction of H5N1 to currently uninfected countries. Although we were not able to account for illegal and unreported poultry trade, it is unlikely that doing so would alter the following four conclusions: (*i*) the spread of H5N1 in Asia and Africa included introductions both by poultry and wild birds, whereas the spread to European countries was more consistent with the movements of wild birds (Fig. 1); (*ii*) currently, the highest risk of H5N1 introduction to the Americas is through the trade in poultry, not from migratory birds (Fig. 2*b*); (*iii*) because of

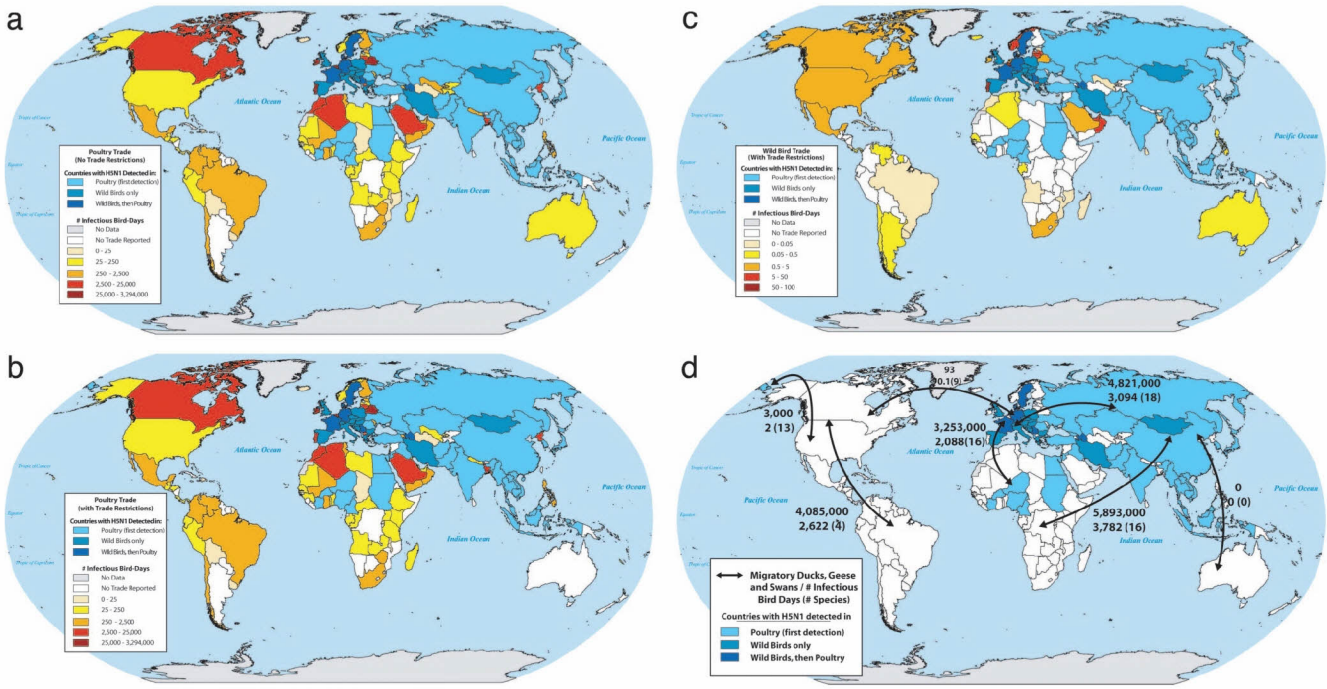

Fig. 2. Predicted risk of H5N1 avian influenza introduction from countries that have had H5N1 outbreaks (in blue). (*a–c*) Risk was estimated as the number of infectious bird days (number of infected birds × days shedding virus) caused by trade (presented as yearly totals/12 months) in: live poultry with no trade restrictions (*a*), live poultry with no exports from countries reporting H5N1 in poultry (France, Denmark, Sweden, and Germany are considered H5N1-free) (*b*), and captive wild birds with no exports from countries reporting H5N1 in poultry (*c*) as in *b*. (*d*) Estimated number of ducks, geese, and swans migrating between mainland continents, number of infectious bird days, and number of species (in parentheses). Numbers given between Asia and North America include only those that breed on mainland Asia and winter in North America south of Alaska; an additional 200,000–400,000 ducks breed in Siberia and molt or winter in or off the coast of Alaska. In addition, ≈20,000 geese migrate between Ireland and North America.

synergy between poultry and migratory bird pathways, countries adjacent to poultry importers, including the United States, are at higher risk for H5N1 introduction (Fig. 2*c*); and (*iv*) surveillance for H5N1 introduction in wild birds should focus on searching for and testing sick and dead (rather than live) birds arriving from the south and the north. We conclude that the most effective strategy to prevent H5N1 from being introduced into the western hemisphere would be strict controls or a ban on the importation of poultry and wild birds into the Americas and stronger enforcement to curb illegal trade. More broadly, our results highlight an important consequence of trade and globalization and show how predictive modeling can be used as a valuable tool for controlling the spread of pathogens.

Methods

To examine the past and future spread of H5N1 avian influenza, we determined the number of infectious bird days for each pathway as the simple product of three quantities: (*i*) the number of birds entering a country, (*ii*) the prevalence of infection, and (*iii*) the number of days that infected birds would be likely to shed virus. We obtained data on the country-to-country trade in poultry and wild birds from the Food and Agricultural Organization of the United Nations (http://unstats.un.org/unsd/comtrade/) and the U.S. Census Bureau, Foreign Trade Division. For poultry we used commodity code H1-0105 (live poultry, domestic fowls, ducks, geese, etc.). For wild bird trade we summed the totals from three commodity codes: H2-010632 [live birds (order Psittaciformes), including parrots, parakeets, macaws, and cockatoos], H2-010631 (live birds of prey), and H2–010639 [live birds (excluding H2-010631 and H2-010632)]. These numbers include all reported trade in wild birds, but do not include illegal or unreported trade.

Trade data were reported in dollar values and either kilograms or numbers of birds. We converted all of the data to numbers of live birds by using the median number of birds per kilogram (obtained from trade data where both were reported), 10.61 for poultry (most traded poultry are domestic fowl <185 g) and 1.92 for wild birds. To minimize errors in trade data caused by underreporting we used the maximum of the two quantities: (*i*) imports reported by country A from country B; and (*ii*) exports reported by country B to country A. To provide an additional check on the Food and Agriculture Organization of the United Nations (FAO) wild bird trade data, we also compared the 2003 FAO data to the 2003 Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) bird trade data (http://sea.unep-wcmc.org/citestrade/trade.cfm) (the most recent complete data). We found that, on average, wild bird trade reported to FAO was 41.7 times higher than CITES trade (which only includes species of conservation concern), with only two countries reporting trade >100 birds per year having CITES numbers >15% higher than those reported to FAO (Bahrain and Portugal, with 1,000 per year and 7,520 per year, respectively).

We quantified migratory birds as a possible mechanism for H5N1 outbreaks reported in the months of peak migration [spring: March-May in Europe and Asia and February-April in Africa; fall: September-November (20)]. To obtain the most robust estimate, we used up to three different methods to calculate the number of ducks, geese, and swans (Anseriformes: Anatidae) migrating between H5N1-affected countries (SI Data Set). We included both diving ducks and dabbling ducks in the analysis, but dabblers were >75% of the total number of individuals for all countries considered. We multiplied estimates of the population size for each subpopulation (using midpoints if a range was given) (21) of waterfowl by the approximate

fraction of each subpopulation whose migration pathway from their breeding grounds to their wintering grounds would result in them passing both over an area with a reported H5N1 outbreak and then over the outbreak area (within a ≈50-mile radius) in the focal country. For many species where migration pathways are unknown we estimated this fraction by drawing parallel lines along the migration pathways connecting the breeding and wintering areas. We used the same method to determine the number of waterfowl migrating between continents. Given the uncertainty in the population estimates (21) and migration routes for each species our estimates for the total number of migrating waterfowl along each pathway have an estimated coefficient of variation of 50% (i.e., estimates are accurate within a 3- to 5-fold range).

We used two additional methods to estimate the number of migratory birds that may have introduced H5N1 into European countries in 2005. First, we summed the average of the minimum and maximum numbers of duck, goose, and swan species recorded as nonbreeding (excluding summer nonbreeders) or passage birds in important bird areas (IBAs) (22) within 50 miles of an outbreak in a focal country for species whose migratory pathway (19, 23) is likely to have passed through an H5N1 outbreak area. Approximately one-quarter of the IBAs near the H5N1 outbreak in Turkey had no data, so we divided the IBA estimate for this country by 0.75. Second, we obtained estimates of the mean wintering populations in H5N1 outbreak countries for the same species considered in the first two methods (24).

The first of our three methods estimated the fraction of each species that passed through an infected area and then into or through the focal country based on the size of breeding and wintering areas and approximate migratory routes. The second technique was based on actual counts at sites near focal country outbreaks and is likely to be the most accurate for species that congregate in large numbers on IBAs and are easily counted (geese and swans). Although some of these counts may be overestimates caused by double-counting of the same individuals at different sites, for most species they are likely to underestimate the number of individuals of species that migrate through, rather than winter in, IBAs, because single or repeated counts cannot account for turnover of individuals. In addition, several species migrate through the affected areas in small groups and are not concentrated into IBAs, and thus are unlikely to be accurately counted (e.g., Garganey, *Anas querquedula*). The third technique estimates the total population for each species in the entire country, rather than just within 50 miles of the outbreak area. It is likely to be more accurate for species that winter in substantial numbers near the H5N1 outbreak, but outside of IBAs, but may overestimate the number of individuals of a species that may have introduced H5N1 to a country if that species winters in areas far from the outbreak area (e.g., eastern Turkey). Our qualitative conclusions for determining the most likely pathway for European H5N1 introductions were identical with all three methods. For the 2003–2005 H5N1 introductions in Fig. 1*a* we used the mean of the estimates from the first and second methods for the number of migratory birds that may have introduced H5N1 into a country.

In January 2006, a period of cold weather in eastern Europe resulted in the movement of large numbers of waterfowl to the north and west and these birds may have introduced H5N1 in their movements. We estimated the number of birds that may have been responsible for these introductions by calculating the numbers of ducks, geese, and swans that overwinter in countries that were previously affected by H5N1 in the late fall of 2005 (Turkey, Romania, Croatia, and Ukraine). We assumed that 5–25% of the birds wintering in these countries would have flown west to other European countries, with the fraction decreasing with the distance between these countries (e.g., 5% of the waterfowl wintering in Turkey was estimated to reach France). Although these estimates involve substantial uncertainty, our qualitative conclusions were unaffected by a 5-fold increase or decrease in these fractions.

We did not include migratory shorebirds (Charadriidae) in our calculations because, although they can become infected with H5N1 (12), they appear to shed low quantities of virus (25) and as a group are generally thought to carry different types of influenza (14). Including shorebirds in our calculations would have increased the predicted future risk of H5N1 introduction (Fig. 2*d*) to two areas, Australia and Southern Africa. Neither of these regions are wintering grounds for migratory ducks, geese, or swans summering in Europe or Asia, but both are used by large numbers (>1 million) of shorebirds that breed in Asia and Europe (21).

To analyze the previous spread of H5N1 we compared migratory bird numbers to trade data from 2003 if H5N1 was first detected in 2003 or January 2004, and 2004 trade data if the first detection of H5N1 occurred between February 2004 and December 2004, and 2005 trade data for introductions that occurred in 2005 through July 2006. However, several countries had not yet reported trade data for 2005, and Vietnam did not report in 2004 or 2005. We used 2003 data for Vietnam and an average of 2003–2004 data for the others. To examine past spread, we assumed that a country's poultry exports were infected only if it reported H5N1 in poultry. In addition, we assumed that poultry exports from France, Germany, Denmark, and Sweden were not infected, because these countries had at most two infected farms with no subsequent outbreaks.

To compare the risk for H5N1 introduction of poultry and wild bird trade to migratory birds we divided the yearly import/export numbers by 12 months, and the migratory bird numbers by 2 because the peak period of migration for individual migratory species is ≈2 months (20). To compare the number of migratory birds and poultry that might be shedding H5N1 we multiplied the numbers generated above by estimates of periods of viral shedding, 2 ± SD = 1.0 d for poultry (26) and 6.0 ± 0.95 d for migratory ducks (17), and 3 ± 3 d for the trade in wild birds (this was unknown so a wide range was assumed); and prevalence, 6/4,674 (0.0012 ± SE 0.00052) for highly pathogenic H5N1 in asymptomatic migrating ducks, 6/13,115 (0.00046 ± 0.00020) for highly pathogenic H5N1 in all wild birds tested (which may underestimate prevalence in traded wild birds because of crowded shipping conditions), and 512/51,121 (0.010 ± 0.00044) for H5N1 in apparently healthy poultry, based on large-scale surveillance efforts in China (17). Another smaller-scale study in Russia found 22 of 466 wild birds were positive for H5 by PCR, including 4 that were positive for H5N1 (pathogenicity was not reported) in the Republic of Kalmikya, a region that had not yet reported H5N1 in poultry (27). These data confirm the presence of H5N1 in wild birds away from outbreak areas. We estimated confidence bounds on the contribution of each pathway to each introduction (Fig. 1*a*) and categorized introductions as being more likely the result of one of the pathways if the lower limit of the 95% confidence interval for the pathway with the greatest number of infectious bird days was at least 5-fold higher than the mean value for the next most important pathway (SI Data Set).

DNA sequences for the hemagglutinin gene (and a subset of neuraminidase sequences including isolates from India) of H5N1 influenza A viruses were downloaded from GenBank. Initially, all sequences that could be easily aligned were examined (>475 sequences) and used in a simple analysis of phylogenetic relationships (these trees are available from R.C.F.). We then pared down the data set to 50 sequences that represented the variation within particular clades or geographic regions of interest, with a goal of at least two isolates per country. We used the sequence from a 1991 isolate from a turkey in the United Kingdom as an outgroup. Maximum-parsimony (MP), maximum-likelihood (ML), and neighbor-joining (NJ) analyses were used to recon-

struct relationships among the sequences (28). For ML and NJ analyses, we used a Kimura two-parameter model of sequence evolution. All analyses resulted in very similar trees, with strong support by bootstrap for a number of the possible clades. Bootstraps of 1,000 replicates were conducted for the MP and NJ analyses and of 100 replicates for the ML tree.

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RESEARCH ADVANCE

Updates to the zoonotic niche map of Ebola virus disease in Africa

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Abstract As the outbreak of Ebola virus disease (EVD) in West Africa is now contained, attention is turning from control to future outbreak prediction and prevention. Building on a previously published zoonotic niche map (***Pigott et al., 2014***), this study incorporates new human and animal occurrence data and expands upon the way in which potential bat EVD reservoir species are incorporated. This update demonstrates the potential for incorporating and updating data used to generate the predicted suitability map. A new data portal for sharing such maps is discussed. This output represents the most up-to-date estimate of the extent of EVD zoonotic risk in Africa. These maps can assist in strengthening surveillance and response capacity to contain viral haemorrhagic fevers.

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Introduction

Since the index case in 2013, the West African Ebola epidemic has killed more than 11,000 people (***World Heath Organization, 2016***) and exposed national and international inadequacies in pandemic preparedness and response (***Moon et al., 2015***). In 2014 a zoonotic niche map for Ebola virus disease (EVD) was produced (***Pigott et al., 2014***) in part to assess the expected geographical extent of spillover risk. This research was then expanded to explore how changes in demography and international connectivity may have facilitated the establishment and rapid subsequent spread of the epidemic (***Bogoch et al., 2015***). The West African outbreak of EVD has again highlighted key information gaps that exist with respect to the broader epidemiology of Ebola virus, particularly concerning viral persistence in reservoirs (***Funk and Piot, 2014***; ***Mari Saez et al., 2015***; ***Leendertz, 2016***), and prompted a variety of questions concerning the role bats play in transmission (***Leendertz et al., 2016***). Identifying reservoirs of zoonotic disease is a complex process (***Viana et al., 2014***; ***Haydon et al., 2002***) and whilst considerable sampling effort has been undertaken over the years (***Kuhn, 2008***; ***Leirs et al., 1999***), isolation of Ebolavirus from living animals has been rare (***Leroy et al., 2005***). The original eLife study only incorporated the three bat species found to be RNA-positive (***Leroy et al., 2005***). Whilst this remains currently the best evidence for an animal reservoir species, it is important to consider that other sampling efforts may by chance represent false negatives, particularly if infection is rare.

Consequently, to contribute to these broader discussions, the original paper (**Pigott et al., 2014**) was updated with new occurrence data and expanded to consider a wider range of potential bat reservoir species. Bats remained the priority mammalian order given the previous viral isolation and the repeated anecdotal implications in previous outbreaks (**Leroy et al., 2009**; **Mari Saez et al., 2015**). Since there are a large number of bat species found in Africa, we defined three groupings, based upon the strength of evidence supporting their potential Ebola reservoir status. As a result, not only were the original three RNA-positive bats included (**Leroy et al., 2005**), but also those species with serological evidence of EVD infection (**Olival and Hayman, 2014**) and those identified through trait-based machine learning approaches as being similar to species already reporting filoviral infection (**Han et al., 2016**).

Results

Six additional records of EVD were incorporated into the disease occurrence database: one human outbreak in the Democratic Republic of Congo (**Maganga et al., 2014**); two reports of infections in animals in Zambia (**Ogawa et al., 2015**); and three animal infections in Central African Republic (**Morvan et al., 1999**) (**Figure 1**). Of these new occurrences, two in southern Central African Republic are found in areas predicted to be at-risk by the previous model (**Pigott et al., 2014**), with the index case from the Democratic Republic of Congo located in close proximity (<10 km) to at-risk areas. The occurrences in Zambia and northern Central African Republic lie, respectively, to the south and north of previously predicted at-risk regions.

Figure 2 depicts the three new consolidated bat distributions. The revised distribution of the Group 1 bats (*i.e.* those found to have been Ebolavirus RNA positive) is broadly consistent with that published in the original paper except that the peripheries of Central Africa are now predicted to be environmentally suitable for these bats, as well as some parts of East Africa, particularly Tanzania, Mozambique and Madagascar. The Group 2 and Group 3 bat species are predicted to be distributed across much of Africa stretching from West to East Sub-Saharan Africa, as well as much of the coastline of the continent.

The revised niche map, incorporating the updated bat covariates and disease occurrence database, is presented in **Figure 3**. The map shows the predicted areas of environmental suitability for zoonotic Ebola virus transmission to be consistent with previous attempts, but the relative environmental suitability within this distribution differs from the previous estimates. **Figure 3—figure supplement 1** demonstrates that Cameroon, Gabon, Republic of Congo and mainland Equatorial Guinea are now predicted to be more environmentally suitable than in the previous analysis. The regions of Central Africa (particularly Gabon and the Republic of Congo) identified as being most environmentally suitable for zoonotic EVD transmission in the previous analysis remain so in this analysis. The revised number of predicted at-risk countries, determined by thresholding the map by a probability that captures 95% of the occurrence dataset, is 23 (**Table 1**).

The similar AUC values (0.85 0.04 compared to 0.8236 0.080) between the previous and current iterations suggest that the updated model fits the new occurrence dataset as well as the previous model fitted the older dataset. Mean enhanced vegetation index (EVI) remains the highest relative predictor covariate for zoonotic EVD transmission while the relative importance of Group 1 bat distributions moved from being the fifth most important to the second. Mean night-time land surface temperature (LST), elevation and mean daytime LST complete the top five predictors (**Table 2**).

When separate bat layers were used in the model, as opposed to the consolidated covariates, the predictions were geographically similar (**Figure 3—figure supplement 2**) however, four bat species were identified as explaining more of the variation than the rest; *Hypsignathus monstrosus, Epomops franqueti* (from both of which Ebolavirus RNA has been isolated), *Otomops martiensseni* and *Epomophorus labiatus* (both from Group 3). The explanatory power of this model (evaluated using AUC) was comparable to the model results described above (AUC = 0.819 0.080).

Discussion

This research advance integrates new data as well as a more thorough consideration of the bat species that act as a reservoir for the virus in order to update our modelled estimate of the zoonotic

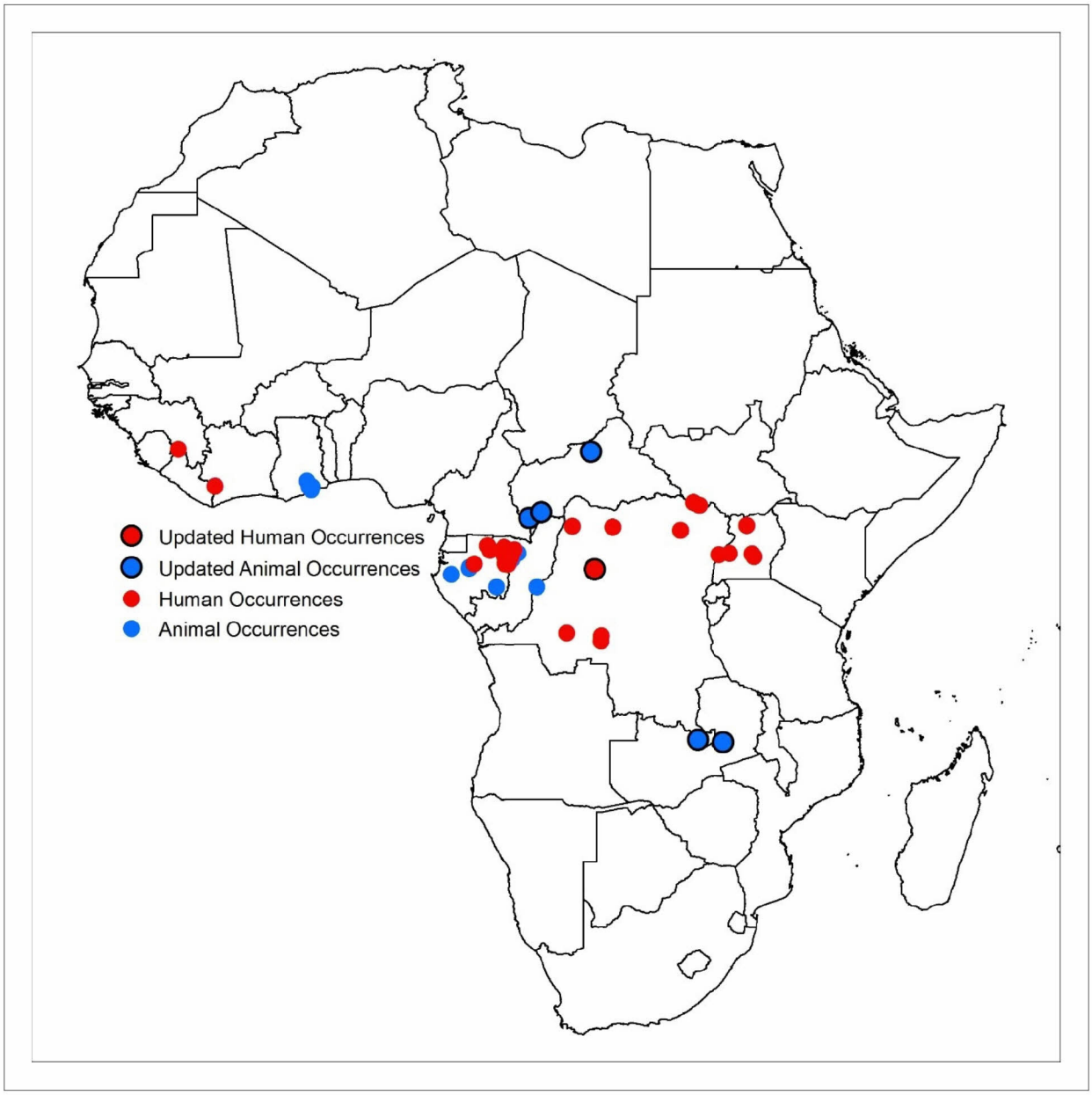

Figure 1. Updated Ebola virus disease occurrence database. Human index cases are represented by red circles, animal occurrences in blue. New occurrence information is indicated by the black circle. The coordinates of polygon centroids are displayed for occurrences defined by an area greater than 5 km x 5 km.

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niche of EVD. The area estimated to be at potential risk of zoonotic EVD transmission has now expanded to include Kenya and the influence of additional bat species demonstrates that continued focus should be placed on rigorously identifying reservoir species and the role they play in sustaining viral transmission (***Leendertz, 2016***). The fact that *O. martiensseni* and *E. labiatus* contribute explanatory power to the model, in comparison with their distributions on the eastern and southern periphery of reported cases of EVD (***Figure 2—figure supplement 3***) suggests that different regions of the continent may support transmission cycles with differing reservoir species. This, coupled with the potential for each of the pathogenic species of *Ebolavirus* potentially having differing distributions (***Peterson et al., 2004***), cannot currently be explored more rigorously due to insufficient data.

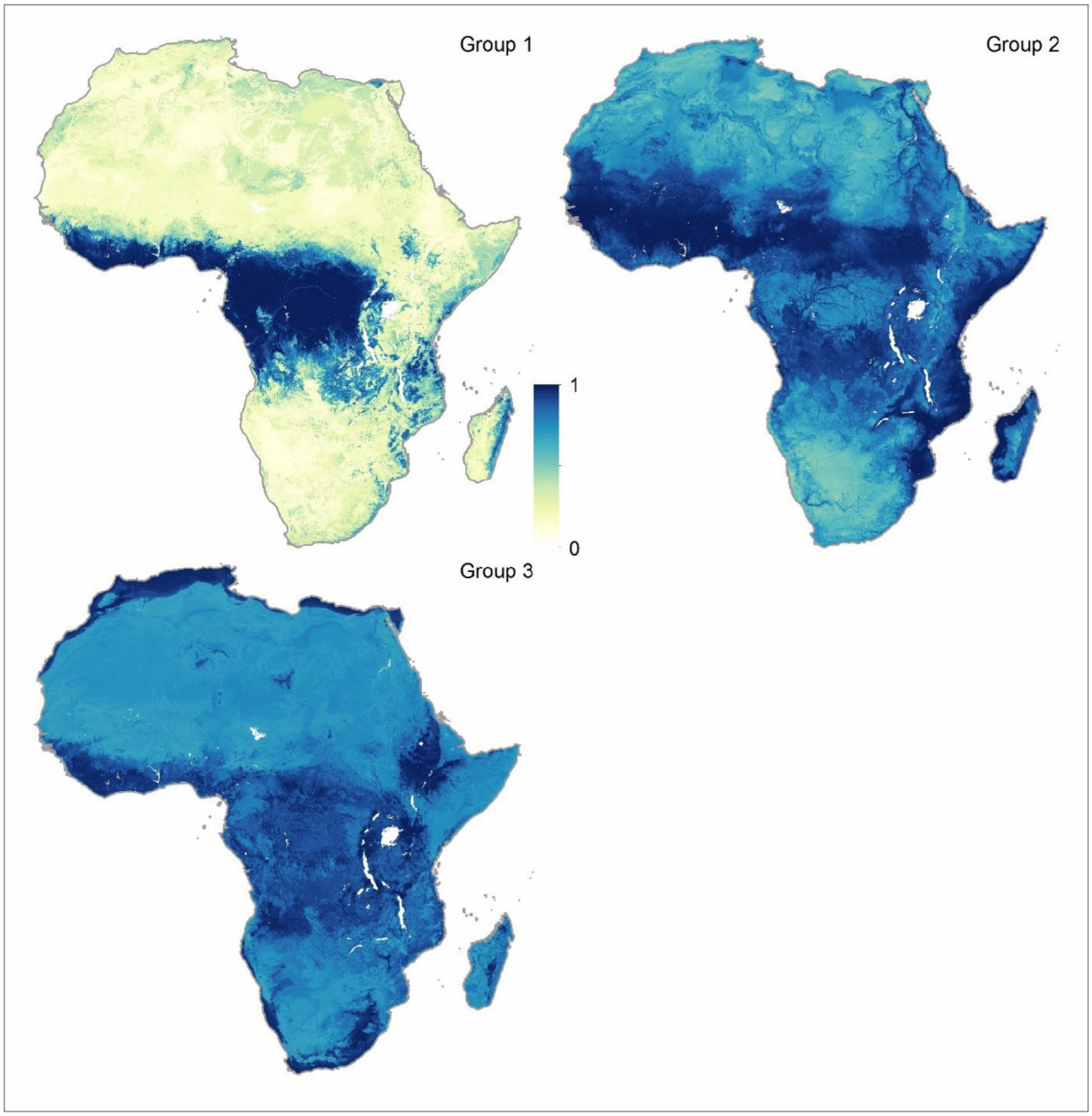

Figure 2. Combined suitability surfaces for each of the potential reservoir bat groupings. For each layer the species specific suitability maps were combined to produce a surface approximating the probability that any bat species in that group may be present. Regions in blue (1) are most environmentally similar to locations reporting bat records. Areas in yellow (0) are the least environmentally similar. The top left panel depicts Group 1, top right Group 2 and bottom left Group 3 bats.

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The following figure supplements are available for figure 2:

Figure supplement 1. Group 1 bat distributions.

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Figure supplement 2. Group 2 bat distributions.

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Figure supplement 3. Group 3 bat distributions.

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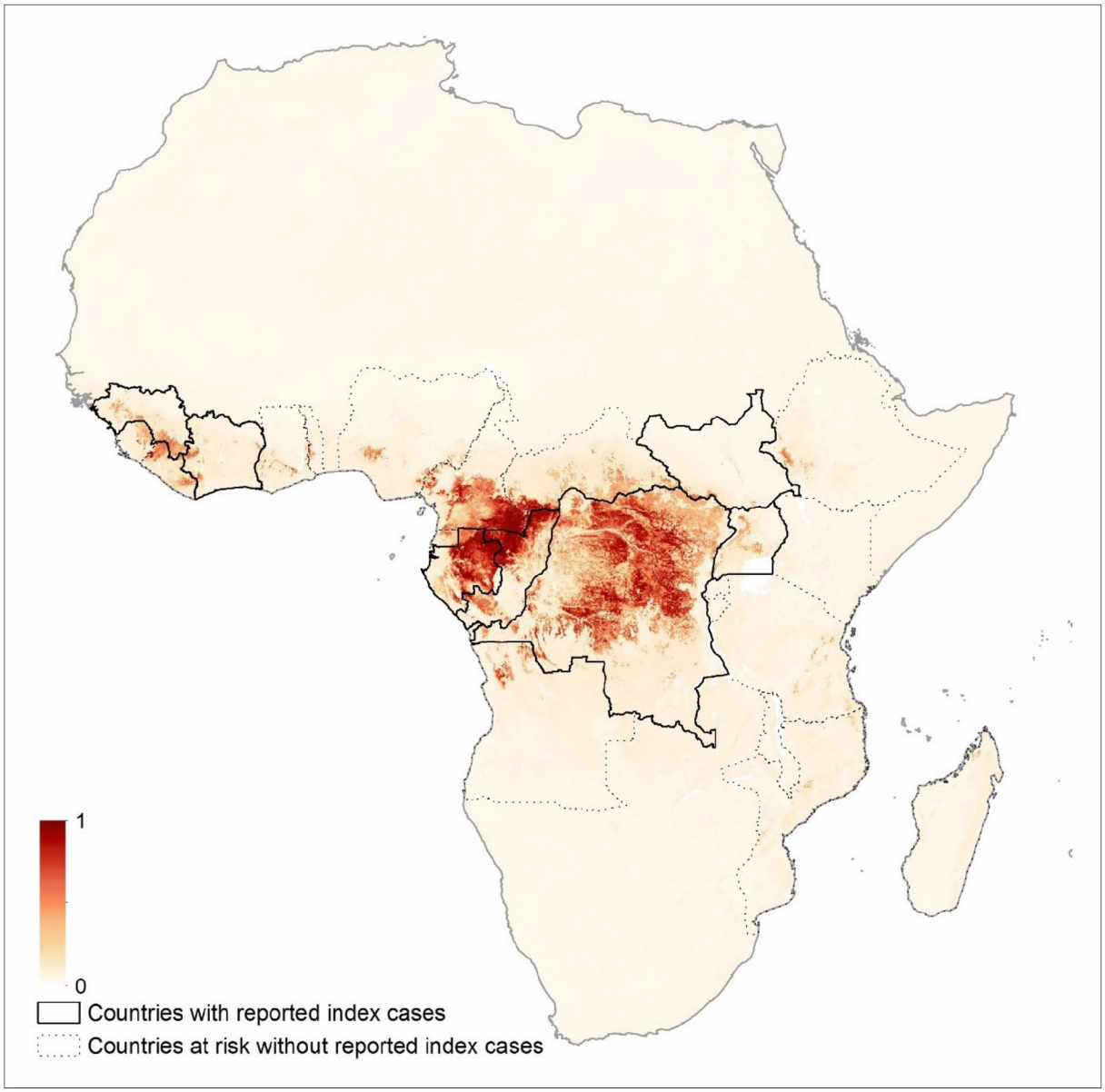

Figure 3. Updated map showing areas most environmentally suitable for the zoonotic transmission of Ebola virus. Areas closer to dark red (1) are most environmentally similar to locations reporting Ebola virus occurrences; areas in light yellow (0) are least similar. Countries with borders outlined are those which are predicted to contain at-risk areas for zoonotic transmission based on a thresholding approach. Output displayed generated from model using the three consolidated bat covariates.

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The following figure supplements are available for figure 3:

Figure supplement 1. Absolute differences between previous and revised maps.

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Figure supplement 2. Zoonotic niche map based upon inclusion of individual bat covariate layers.

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As with the original publication, it must be reiterated that environmental suitability does not inevitably lead to spillover events. Currently absolute human population residing in at-risk pixels is used as a proxy for spillover likelihood, however, a variety of factors will influence the outbreak risk within each location (***Plowright et al., 2015***) and only by including covariates that consider human behaviour (***Woldehanna and Zimicki, 2015***), patterns of susceptibility in other animals (***Walsh et al.,***

Table 1. National populations at risk.

	Country	Population-at-risk (in 100,000s)
Countries previously reporting index cases	Democratic Republic of the Congo	170.18
	Uganda	21.58
	Guinea	17.61
	Côte d'Ivoire	4.08
	Gabon	3.65
	South Sudan	1.80
	Republic of Congo	1.07
Countries with no reported index cases	Nigeria	29.13
	Cameroon	22.90
	Central African Republic	7.62
	Liberia	5.88
	Ghana	4.04
	Sierra Leone	3.94
	Angola	3.25
	Togo	1.78
	Ethiopia	1.75
	Equatorial Guinea	1.22
	Tanzania	1.18
	Burundi	1.07
	Mozambique	0.55
	Madagascar	<0.1
	Kenya	<0.1
	Malawi	<0.1

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2007; ***2009***), impacts of land use change (***Rosales-Chilama et al., 2015***) and within-host viral dynamics (***Amman et al., 2012***; ***Hayman, 2015***) can an approximation of spillover risk be defined.

These updates demonstrate the ease and speed with which new data and covariate considerations can be incorporated within existing empirical models (***Kraemer et al., 2016***). As the wider discussion on EVD turns to focus on strategies to prevent or contain future spillover events as well as developing long-term in-country containment capacities (***Currie et al., 2016***), it is hoped that maps

Table 2. Comparison of previous and revised niche models.

	Revised niche map (with summary bat layers)	Revised niche map (with individual bat layers)	Previous eLife niche map (*Pigott et al., 2014*)
AUC	0.8236 0.08	0.8195 0.08	0.85 0.04
Occurrences	n = 57 (animals), n = 31 (humans)	n = 57 (animals), n = 31 (humans)	n = 51 (animals), n = 30 (humans)
Ranked relative contributions	EVI mean (0.55)	EVI mean (0.46)	EVI mean (0.65)
	Group 1 bat distribution (0.18)	*Hypsignathus monstrosus* (0.15)	Elevation (0.12)
	LST mean (night) (0.08)	*Epomops franqueti* (0.08)	LST mean (night) (0.08)
	Elevation (0.06)	*Otomops martiensseni* (0.06)	PET mean (0.06)
	LST mean (day) (0.04)	*Epomophorus labiatus* (0.04)	Bat distribution (0.04)

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such as these convey the heterogeneities in spillover risk that exist within Africa. To better enable researchers and policymakers to consider EVD preparedness and necessary contingencies, a new online tool has been developed which allows users to interrogate the revised maps in more detail, in areas of specific interest (http://vizhub.healthdata.org/ebola). As part of this tool, the zoonotic niche output and Group 1 bat layers are now available, along with filters for identifying at-risk countries and locations of previous index cases from outbreaks.

Geographic datasets such as these provide context to broader discussions as our aspirations transition from controlling outbreaks to mitigating the risk of future spillover events prioritised by their potential for more widespread epidemics. Such data are particularly important for determining where best to investigate the frequency of potentially transmissible contacts between reservoir and susceptible species and humans. Previous niche maps served as an important impetus in the search for potential reservoirs (**Peterson et al., 2004**) and these iterations can continue to inform such work. As researchers and policy makers seek to resolve outstanding questions about EVD epidemiology, it is hoped that the continued updating and dissemination of this information can contribute to this discussion.

Materials and methods

Updating the occurrence database

Since the previous publication, an outbreak of EVD occurred in humans in the Democratic Republic of the Congo (**Maganga et al., 2014**). The outbreak is thought to have originated in Inkanamongo, a village near Boende, Équateur province and resulted in 66 probable and confirmed cases and 49 probable and confirmed deaths (**Rosello et al., 2015**). A polygon of radius 10 km centered on the town of Boende was included to capture the location of the index case, increasing the database of assumed independent animal-to-human spillover events to 31 as part of 24 distinct reported outbreaks (**Mylne et al., 2014**).

In addition, a re-analysis of the literature available on infections in animal species was completed on 7th October 2015. Due to the poor differential capacity of immunological tests to discriminate Ebola virus from other viruses we retained the following inclusion criteria for the database; for susceptible species mortality events linked to Ebolavirus by any diagnostic methodology *or* PCR-positive diagnosis of Ebolavirus were included. Inclusion criteria for potential bat reservoir species were either PCR-positivity or serological evidence suggesting Ebolavirus infection. Serological studies were included without fatal outcomes (unlike with susceptible species) due to the hypothesised asymptomatic nature of infection in the reservoir hosts. As a result of these inclusion criteria, studies with serological detection of Ebolavirus in healthy non-Chiropteran species were excluded, such as surveys in dogs (**Allela et al., 2005**).

In total six new records of EVD occurrence in animals were identified and included within the database to increase the total to 57. These records were obtained from two research articles. The first of these assessed Ebolavirus load in a variety of mammal species and identified PCR-positivity in a number of small mammals across three sites in Central African Republic (**Morvan et al., 1999**). In total, four separate occurrences, consisting of three different species, were identified as being PCR positive: a member of the *Praomys* complex, Peter's mouse (*Mus setulosus*) and the greater forest shrew (*Sylvisorex ollula*). The second study investigated serological responses in straw-coloured fruit bats (*Eidolon helvum*) caught in two districts in Zambia (**Ogawa et al., 2015**). Specific latitudes and longitudes of the study sites were supplied for the Central African Republic study and were used to generate point occurrences. For the Zambian study it was necessary to use administrative data representing the two districts where the bats were caught (Serenje and Ndola districts).

Expanding potential bat reservoir species

Potential bat reservoir species were stratified into three groupings based upon the strength of evidence suggesting their reservoir status (**Table 3**). Group 1 contained the three species of bat from which Ebolavirus RNA has been detected and therefore have the strongest evidence to support potential reservoir status (**Leroy et al., 2005**). Group 2 species are those that, using a variety of serological tests, have been reported to be Ebolavirus seropositive, suggesting potential reservoir status. A previous review (**Olival and Hayman, 2014**), identified nine species as seropositive for

Table 3. Final bats included in analysis classified by evidence grouping.

Grouping	Bat	Occurrences
Group 1	Franquet's epauletted fruit bat (*Epomops franqueti*)	442
	Hammerheaded fruit bat (*Hypsignathus monstrosus*)	254
	Little collared fruit bat (*Myonycteris torquata*)	107
Group 2	Angolan free-tailed bat (*Tadarida condylura*, formerly *Mops condylurus*)	179
	Egyptian fruit bat (*Rousettus aegyptiacus*)	177
	Gambian epauletted fruit bat (*Epomophorus gambianus*)	166
	Peter's dwarf epauletted fruit bat (*Micropteropus pusillus*)	208
	Straw-coloured fruit bat (*Eidolon helvum*)	282
Group 3	Buettikofer's epauletted fruit bat (*Epomops buettikoferi*)	50
	Common bent-wing bat (*Miniopterus schreibersii*)	31
	Eloquent horseshoe bat (*Rhinolophus eloquens*)	61
	Ethiopian epauletted fruit bat (*Epomophorus labiatus*)	187
	Giant leaf-nosed bat (*Hipposideros gigas*)	21
	Greater long-fingered bat (*Miniopterus inflatus*)	56
	Large-eared free-tailed bat (*Otomops martiensseni*)	33

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Ebolavirus. This was reduced to five species after the removal of the three species already categorised in Group 1 and Leschenault's Rousette, *Rousettus leschenaultii*, which is not found in Africa.

Finally, Group 3 species were identified *via* generalized boosted regression analysis, which discriminates the bats reported to be filovirus-positive by learning trait patterns that distinguish them from all other bat species (***Han et al., 2016***). Generalized boosted regression (***Elith et al., 2008***) was applied to traits describing all bat species, including life history, physiological, ecological, morphological and demographic variables collected from numerous published sources. In addition to traits, the filovirus status of each bat species was assigned as a binary score (0 – not currently known to be positive for any filoviruses; 1 – published evidence). This analysis produces a rank list of all bat species according to their probability of being a filovirus carrier on the basis of their trait similarities with known filovirus-positive bat species. Bats found in the 90th percentile of likely filovirus carriers were initially considered, and then filtered to include only those which have home ranges in Africa (***Schipper et al., 2008***). As per the original publication, occurrence records were extracted from the Global Biodiversity Information Facility (GBIF). Species for which there were fewer than 20 unique GBIF records in Africa were dropped from the analysis due to data paucity. ***Table 3*** reports the bat species and corresponding numbers of occurrences included in the analysis.

For Group 1 species, occurrence records were supplemented by searching PubMed and Web of Knowledge for additional reports. A literature review was completed on the 8th September 2015 using the following sets of keywords:

- '*Hypsignathus monstrosus*' or 'hammer-headed bat' or 'hammer headed bat' or 'hammer-headed bat' or 'big-lipped bat' or 'big lipped bat' or '*Hypsignathus labrosus*' or '*Hypsignathus macrocephalus*'
- '*Myonycteris torquata*' or 'little collared fruit bat' or '*Myonycteris collaris*' or '*Myonycteris leptodon*' or '*Myonycteris wroughtoni*'
- 'Epomops franqueti' or "Franquet's epauletted fruit bat" or 'Epomops comptus' or 'Epomops strepitans'

A total of 34 articles were identified for inclusion, from which 564 additional occurrences were sourced.

All bat species were modelled separately using boosted regression trees (***Elith et al., 2008***) utilising the same modelling procedure as outlined in the original article except that 100, rather than 50, bootstrap models were fitted. This resulted in 15 individual environmental suitability maps for bat species (see ***Figure 2—figure supplements 1***, ***2*** and ***3***), as well as three consolidated bat layers combining the environmental suitability maps for the bats within each of the three groupings (***Figure 2***).

Revising the predicted zoonotic niche map

A species distribution model, specifically a boosted regression trees approach (***Elith et al., 2008***), was implemented. The model generates regression trees based upon binary splits of linked covariates, which are iteratively improved upon by boosting. The regression trees are capable of characterising complex environmental interactions and correlations since each tree is built from a hierarchy of multiple nodes, each based upon different successive binary splits of the covariates. The model extracts environmental information for each reported occurrence of Ebolavirus to define an optimal relationship between presence of the disease and environmental factors. Predictive performance is improved by including a comparison background dataset that acts as a hypothesised environmental negative control (***Phillips et al., 2009***). As per the previous analysis, this dataset was generated by randomly sampling across Africa biased towards areas of high population density. By including human population density in this way, some potential sampling biases present in human index case reporting can be mitigated as cases are more likely to be reported in more populous areas. The boosted regression trees were re-run using the same parameters and covariates (elevation, mean evapotranspiration rate, and mean and range measures of enhanced vegetation index, daytime land surface temperature (LST), and night-time LST) as the previous publication except for the inclusion of the new occurrence data outlined above and the new bat layers. Two model iterations were run: one with the three consolidated bat layers (i.e. Groups 1, 2 and 3) and the other with all the bat species layers considered separately.

Estimating populations at risk

The continuous suitability surface was converted into a binary at-risk versus not-at-risk surface by determining a threshold value that included 95% of the estimated suitability values of pixels with reported human index cases (***Pigott et al., 2015***). For sites represented by a specific latitude and longitude the suitability score was taken from the corresponding pixel; for polygon estimates covering a number of cells, the mean suitability was taken across all pixels covered by the polygon.

Whilst not included directly as a covariate in the modelling process, human population layers were assessed in at-risk locations as a potential proxy for spillover frequency. The populations living within the gridded cells thought to be at-risk of potential Ebolavirus transmission from zoonotic sources were calculated using an updated contemporary gridded estimate of population (***WorldPop Project, 2015***).

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SIH: Reviewing editor, *eLife*. The other authors declare that no competing interests exist.

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Additional files

Major datasets

The following dataset was generated:

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Sympatric Occurrence of 3 Arenaviruses, Tanzania

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To determine the specificity of Morogoro virus for its reservoir host, we studied its host range and genetic diversity in Tanzania. We found that 2 rodent species other than *Mastomys natalensis* mice carry arenaviruses. Analysis of 340 nt of the viral RNA polymerase gene showed sympatric occurrence of 3 distinct arenaviruses.

Arenaviruses are RNA viruses, primarily rodent borne, that include the etiologic agents of lymphocytic choriomeningitis and hemorrhagic fevers in humans. On the basis of their antigenic properties, arenaviruses have been divided in 2 groups: New World and Old World (*1*). In Africa, 2 arenaviruses are known to be highly pathogenic to humans: Lassa virus in West Africa and the recently described Lujo virus from southern Africa (*2*). Rodents from the subfamily Murinae are the principal hosts of the Old World arenaviruses. The multimammate mouse, *Mastomys natalensis*, is the reservoir host of Lassa virus in western Africa (*3*) and Mopeia virus, for which human pathogenicity has not been reported, in eastern Africa (*4*,*5*).

Previously, a serosurvey of small mammals from Tanzania identified a hot spot of arenavirus circulation in Morogoro (*6*). Molecular screening detected a new arenavirus in *M. natalensis* mice: Morogoro virus, closely related to Mopeia virus (*6*). This virus seems a promising model for studying virus–host dynamics and testing rodent control measures for arenaviruses for which *M. natalensis* mice are host. However, before being used as a model, the degree of specificity of Morogoro virus for its reservoir host must be assessed because secondary reservoir species may play a role in the transmission and maintenance of the virus in natural habitats. Our objective, therefore, was to determine the limit of specificity of the Morogoro virus.

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The Study

From October 13 through December 3, 2008, a total of 555 small mammals were trapped in Morogoro, Tanzania (6.84°S, 37.65°E). This period corresponds to the end of the dry season, when the density *of M. natalensis* mice is usually high (*7*). Sherman traps were set in habitats where these mice were expected to occur in high density (*7*). Dried blood samples were preserved on calibrated, prepunched filter papers. Blood samples (1 punch ≈15μL/rodent) were eluted in 300 μL of phosphate-buffered saline and tested for antibodies to arenaviruses by indirect immunofluorescence antibody (IFA) testing using Morogoro virus as antigen. In addition, total RNA was extracted from another punch of blood by using 300 μL of AVL buffer (QIAGEN, Venlo, the Netherlands). The lysate, plus 300 μL of ethanol, was centrifuged in a silica column (Zymo Research, Orange, CA, USA). The column was washed with 400 μL of AW1 and AW2 buffers (QIAGEN). RNA was eluted with 15 μL of water. A 1-step reverse transcription–PCR (RT-PCR) selective for the Morogoro virus RNA polymerase (large [L]) gene was performed as described (*6*); it was based on a pan–Old World arenavirus RT-PCR approach (*8*), but primers were adjusted to detect the Morogoro virus (*6*). Products were shown by agarose gel electrophoresis. A subset of the amplicons was purified and unidirectionally sequenced by using MoroL3359-fwd primer (*6*). Amplicons derived from *Lemniscomys rosalia* and *Mus minutoides* mouse blood samples were bidirectionally sequenced. Nucleotide and amino acid sequences were aligned by using BioEdit software (*9*). Old World arenaviruses and 2 representatives of New World arenaviruses were used to estimate nucleotide and amino acid pairwise divergence (p-distance) with MEGA 4 (*10*). A phylogram was reconstructed by using the neighbor-joining algorithm in MEGA 4.

We trapped 511 *M. natalensis* mice and 44 individuals from 7 other small mammal species (Table 1). IFA results were positive for 58 blood samples from *M. natalensis*, 1 from *L. rosalia*, and 1 from *M. minutoides* mice (Table 1). *M. rosalia* mice were trapped in woodlands, whereas *M. minutoides* mice were trapped in vegetable gardens and fallow fields. These results are consistent with recently reported results from a study in the same locality 20 years ago, in which mice from the genera *Lemniscomys* and *Mus* were seropositive for arenaviruses according to IFA with Lassa virus as antigen (*6*). In our 2008 study, the antibody prevalence for *M. natalensis* mice was 12.1%, which is low compared with 50% antibody prevalence reported for 2004 and 2007 (*6*), suggesting high fluctuation of interannual or seasonal prevalence of Morogoro virus in its host.

Table 1. Arenavirus antibodies and arenaviruses in blood samples of small mammals around Morogoro, Tanzania, October 13–December 3, 2008

Species	No. trapped	Antibodies*		Arenaviruses†		Total positive, no. (%)
		No. examined	No. (%) positive	No. examined	No. (%) positive	
Acomys spinosissimus	1	1	0	1	0	0
Crocidura sp.	20	11	0	12	0	0
Dasymys incomtus	1	1	0	1	0	0
Lemniscomys rosalia‡	3	3	1 (33.3)	3	1 (33.3)	2 (66)
Mastomys natalensis	511	480	58 (12.1)	489	41 (8.4)	93 (19)
Mus minutoides‡	7	5	1 (20)	5	1 (20)	2 (40)
Rattus rattus	1	1	0	1	0	0
Gerbilliscus robustus	11	11	0	11	0	0
Total	555	513	60 (11.7)	523	43 (8.2)	97 (18.5)

*Detected by indirect immunofluorescent antibody testing.
†Large segment. Detected by reverse transcription–PCR.
‡Species identification was confirmed by sequencing mitochondrial cytochrome b gene.

Using RT-PCR selective for the arenavirus L gene, we obtained positive results for 43 mice: 41 *M. natalensis*, 1 *L. rosalia*, and 1 *M. minutoides*. In total, 6 samples were positive according to IFA and RT-PCR. We sequenced 33 RT-PCR amplicons. The sequences derived from *M. natalensis* mice (286 bp used for the analysis) showed 97.1%–100% amino acid homology with the Morogoro prototype L sequence (GenBank accession no. EU914104). In contrast, the 2 sequences derived from the blood samples of *L. rosalia* and *M. minutoides* mice showed only 69.3% and 65.2% aa homology with the Morogoro prototype L sequence. These sequences (320 bp) were compared with sequences of the Old World arenaviruses (Table 2). The virus amino acid sequence from *M. minutoides* mice clustered at 93.7% homology with that of the Kodoko virus, in the lymphocytic choriomeningitis clade (Figure; Table 2): thus, the arenavirus of *M. minutoides* mice seems to be a strain of the Kodoko virus originally isolated from 2 *M. minutoides* mice in Guinea (*11*). Our finding supports *M. minutoides* mice as the true reservoir of Kodoko virus in Africa.

The amino acid sequence of the virus isolated from *L. rosalia* mice clusters with the Ippy virus sequence (Figure). Ippy virus was isolated in the Central African Republic from *Arvicanthis niloticus* rodents (*12*). For the portion of L gene sequenced (320 bp), the level of amino acid divergence between the 2 is 17.3%, higher than the level of divergence between other Old World arenavirus species (e.g., 14.5% aa divergence between Mobala and Lassa viruses; Table 2). Thus, the arenavirus found in *L. rosalia* mice appears to be a new species of Old World arenavirus. The genus *Lemniscomys* is more closely related to the genus *Arvicanthis* than to the genera *Mus* and *Mastomys*.

Table 2. Nucleotide and amino acid p-distances of 2 arenaviruses in blood of *Mus minutoides* and *Lemniscomys rosalia* mice in Morogoro, Tanzania, October 13–December 3, 2008, compared with Old World and 2 New World arenaviruses*

Virus sequence†	Old World arenaviruses											New World arenaviruses	
	Dandedong	Ippy	Kodoko	Mobala	Mopeia	Morogoro	Lassa	LCMV	Lujo	Lemn	Minu	Pirital	Pichinde
Dandedong		0.282	0.073	0.218	0.255	0.282	0.209	0.027	0.355	**0.245**	**0.091**	0.418	0.409
Ippy	0.345		0.264	0.227	0.209	0.209	0.191	0.300	0.345	**0.173**	**0.273**	0.491	0.482
Kodoko	0.244	0.354		0.200	0.227	0.255	0.227	0.091	0.336	**0.236**	**0.073**	0.409	0.409
Mobala	0.318	0.315	0.315		0.136	0.127	0.145	0.227	0.327	**0.209**	**0.236**	0.482	0.464
Mopeia	0.310	0.295	0.351	0.256		0.055	0.145	0.273	0.345	**0.182**	**0.255**	0.482	0.464
Morogoro	0.327	0.324	0.360	0.262	0.241		0.136	0.282	0.364	**0.209**	**0.282**	0.491	0.473
Lassa	0.286	0.283	0.366	0.286	0.271	0.262		0.209	0.364	**0.200**	**0.236**	0.473	0.436
LCMV	0.182	0.354	0.223	0.339	0.324	0.345	0.330		0.373	**0.264**	**0.109**	0.436	0.409
Lujo	0.351	0.393	0.360	0.372	0.387	0.405	0.399	0.357		**0.373**	**0.336**	0.500	0.500
Lemn	**0.333**	**0.315**	**0.336**	**0.292**	**0.313**	**0.307**	**0.301**	**0.327**	**0.351**		**0.227**	0.482	0.464
Minu	**0.211**	**0.360**	**0.241**	**0.301**	**0.348**	**0.348**	**0.339**	**0.244**	**0.354**	**0.324**		0.436	0.409
Pirital	0.440	0.467	0.429	0.420	0.452	0.443	0.455	0.432	0.476	0.473	0.417		0.173
Pichinde	0.426	0.446	0.432	0.458	0.476	0.467	0.473	0.452	0.446	0.443	0.435	0.268	

*Nucleotides below diagonal; amino acids above diagonal. LCMV, lymphocytic choriomeningitis virus; Lemn, virus sequenced from *Lemniscomys rosalia* mice (indicated by **boldface**); Minu, virus sequenced from *Mus minutoides* mice (indicated by **boldface**).
†Strains and GenBank accession numbers of the sequences used: Dandenong (0710-2678, EU136039), Ippy (Dak An B 188 d, DQ328878), Kodoko (KD42, EF179865), Mobala (Acar 3080, DQ328876), Mopeia (Mozambique, DQ328875), Morogoro (3017/2004, EU914104), Lassa (Josiah, AY628202), LCMV (Armstrong,,AY847351), Lujo (NC_012777), Pirital (VAV 488, AY216505), Pichinde (AN3739, NC_006439). Sequences of arenaviruses in *L. rosalia* and *M. minutoides* mice have been deposited in GenBank under accession nos. GU182412 and GU182413, respectively.

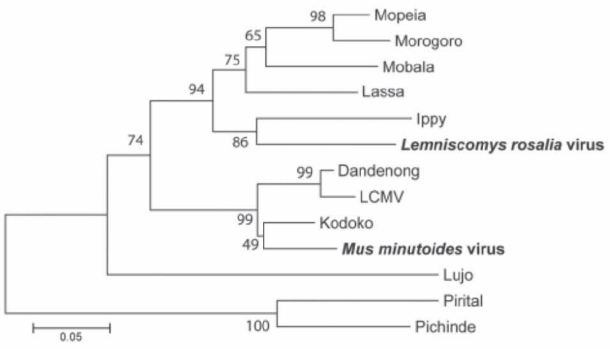

Figure. Neighbor-joining tree of Old World arenaviruses, showing position of 2 arenaviruses found in blood samples of *Lemniscomys rosalia* and *Mus minutoides* mice (**boldface**), based on the analysis of partial sequences of the RNA polymerase gene. Phylogeny was estimated by neighbor-joining of amino acid pairwise distance in MEGA 4 (*10*). Numbers represent percentage bootstrap support (1,000 replicates). Two New World arenaviruses, Pirital and Pichinde, were used as outgroups. See Table 2 for virus strains and GenBank accession numbers. Scale bar indicates amino acid substitutions per site. LCMV, lymphocytic choriomeningitis virus.

Conclusions

In high-density habitats of *M. natalensis* mice, where Morogoro arenavirus transmission occurs, sympatric murine species do not seem to be secondary reservoirs for the virus. In contrast, 2 mouse species, *L. rosalia* and *M. minutoides*, seem to be reservoirs of 2 other Old World arenaviruses, 1 of which may be a new species. Our study emphasizes the complementary nature of serologic and genetic-based approaches for arenavirus detection. Because of the cross-reactivity of Morogoro antigens with immune serum from individuals infected with other arenaviruses, a serology-only approach might have led to the conclusion that an extended set of hosts exists for the Morogoro virus. Because of its high cost, a genetics-only approach might never have indicated the hot spot of arenavirus around Morogoro that was shown by IFA (*6*). However, critically, genetics then enable cross-reactivity to be decomposed.

Our study demonstrates the presence of 3 Old World arenaviruses in a single location. To date, only 5 Old World arenavirus species and 17 New World arenaviruses have been recognized by the International Committee for Taxonomy of Viruses (*13*). Although the likely presence of additional arenaviruses in Africa has long been suggested (*14*,*15*), the discovery of new Old World arenaviruses is rare. Our study illustrates that arenaviruses in Africa may be highly diverse and demonstrates the efficiency of the recently developed pan–Old World arenavirus RT-PCR for identifying new Old World arenaviruses (*8*). To isolate and describe the new arenavirus of *L. rosalia* mice and the strain of Kodoko virus, additional sampling and genotyping are being conducted. In particular, determining the sequence of the S segment will further clarify evolutionary relationships within the Old World group.

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Isolation of Genetically Diverse Marburg Viruses from Egyptian Fruit Bats

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Abstract

In July and September 2007, miners working in Kitaka Cave, Uganda, were diagnosed with Marburg hemorrhagic fever. The likely source of infection in the cave was Egyptian fruit bats (*Rousettus aegyptiacus*) based on detection of Marburg virus RNA in 31/611 (5.1%) bats, virus-specific antibody in bat sera, and isolation of genetically diverse virus from bat tissues. The virus isolates were collected nine months apart, demonstrating long-term virus circulation. The bat colony was estimated to be over 100,000 animals using mark and re-capture methods, predicting the presence of over 5,000 virus-infected bats. The genetically diverse virus genome sequences from bats and miners closely matched. These data indicate common Egyptian fruit bats can represent a major natural reservoir and source of Marburg virus with potential for spillover into humans.

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Introduction

Viruses of the *Marburgvirus* and *Ebolavirus* genera (family *Filoviridae*) cause outbreaks of hemorrhagic fever in Africa characterized by person-to-person spread and high case fatality. Humans have on occasion acquired infection from contact with tissues of diseased nonhuman primates and perhaps herbivores, but the susceptibility of these animals to fatal infection renders it unlikely that they could serve as filoviruses reservoir hosts.

Although the source of filoviruses in nature has not been definitively identified, the cumulative evidence suggests that bats are involved. The infected monkeys consigned from Uganda to Europe in 1967, which resulted in the first recognized outbreaks of Marburg hemorrhagic fever (MHF), were caught on the shores of Lake Victoria and on islands where fruit bats are prevalent [1]. In 1975, the second recorded outbreak of MHF involved tourists who slept at two locations in Zimbabwe in rooms containing insectivorous bats followed by a purported visit to Chinhoyi caves (formerly Sinoia caves) where bats may also have been present [2]. In the first recognized outbreak of Ebola hemorrhagic fever (EHF) in 1976, the first six patients worked in a room where bats roosted in a cotton factory in Sudan [3]. In 1980 and 1987, two patients who developed MHF in Kenya both visited a cave inhabited by bats shortly before becoming ill [4,5]. In 1994, chimpanzees which developed EHF in Cote d'Ivoire had been observed feeding in a wild fig tree together with fruit bats for two weeks before developing the disease [6]. The Reston ebolavirus, which is apparently nonpathogenic for humans, was introduced into the USA and Europe on several occasions via imported infected monkeys from the Philippines, and each time the animals originated from a single export facility located on the grounds of a former fruit orchard where they were potentially exposed to the excreta of fruit bats [7]. In1996, it was shown that experimentally infected fruit bats were capable of supporting replication of ebolavirus without developing overt disease [8]. In 1998–2000, a protracted outbreak of MHF in Durba village in northeastern Democratic Republic of the Congo (DRC) consisted of repeated occurrences of short transmission chains arising in workers in Goroumbwa Mine where large numbers of bats roosted. The impression that there were recurrent introductions of infection into

Author Summary

Marburg virus, similar to its close cousin Ebola virus, can cause large outbreaks of hemorrhagic fever (HF) in rural Africa with case fatalities approaching 90%. For decades, a long-standing enigma has been the identity of the natural reservoir of this deadly virus. In this report, we identify the cave-dwelling Egyptian fruit bat (*Rousettus aegyptiacus*) as a natural host of Marburg virus based on multiple lines of evidence which include, for the first time ever, the isolation of virus directly from wild-caught and apparently healthy bats. The species *R. aegyptiacus* is common throughout Africa with distribution into the eastern Mediterranean and Middle East. Our finding of active virus infection in approximately 5% of *R. aegyptiacus* bats and their population exceeding 100,000 in Kitaka cave in Uganda suggests there are likely over 5,000 Marburg virus–infected bats in this cave, which is only one of many such cave populations throughout Africa. Clearly, these bats could serve as a major source of virus with potential to initiate human epidemics, and the implications for public health are striking. Additionally, we found highly divergent (21%) genome sequences among viruses circulating in these bat populations, a level of diversity that would result from a long-term association with a suitable reservoir host of large population size.

humans from a natural source was supported by finding that multiple genetic lineages of virus circulated during the outbreak [9]. Significantly, diverse genetic lineages of Marburg virus were detected in Egyptian fruit bats, *Rousettus aegyptiacus*, and two species of insectivorous bat in the mine, and the outbreak ceased when the mine flooded, but no live virus was isolated from bats [10]. In 2002, ebolavirus RNA was detected in three forest-dwelling species of fruit bat in Gabon during an investigation which followed outbreaks of EHF [11] and in 2005 nucleic acid of Marburg virus was detected in *R. aegyptiacus* bats in the same country in the absence of a corresponding outbreak of disease [12]. On both occasions it again proved impossible to isolate live virus.

In July 2007, a small outbreak of MHF occurred in workers mining lead and gold in Kitaka Cave near Ibanda village in western Uganda. Large numbers of *R. aegyptiacus* and insectivorous *Hipposideros species* bats were present in this mine. Ecological investigations were conducted in August 2007 and May 2008, and the findings are presented here.

Results/Discussion

Identification of MHF in Kitaka miners

Kitaka Cave was first mined in the 1930s and eventually became a large producer of lead ore in Uganda, but was closed in 1979. It was reopened in January 2007, and in July a miner working in the cave fell ill and died with disease confirmed at Centers for Disease Control and Prevention, USA (CDC) to be MHF (patient A, Table 1). The Ugandan Ministry of Health closed the mine shortly thereafter. Following the month-long ecological investigation in August 2007, a second miner (patient B, Table 1) was confirmed to have MHF. The timing of his onset of symptoms in September, plus a lack of epidemiologic linkage to the first case, suggested that he re-entered the mine surreptitiously shortly after the departure of the investigating team. Thus, it appears that the ecological study was conducted at a time when Marburg virus activity was continuing. Marburg virus was isolated from each of the two miners, and full-length genome sequences were determined (01Uga2007 and 02Uga2007 respectively). Retrospective analysis of Patient A's contacts found two additional Kitaka miners positive for Marburg virus-specific IgG (data not shown). Both of these miners reported symptoms consistent with MHF in the month prior to Patient A falling ill.

Detection of Marburg virus by Q-RT-PCR, virus isolation, IgG ELISA, and immunohistochemistry in bats found in Kitaka Cave

Marburg virus nucleic acid was detected by Q-RT-PCR in a total of 32 bats, and for the first time, live virus was isolated from five of the bats (Tables 2 and 3). There was a direct correlation between RNA levels (viral load) determined by Q-RT-PCR and the ability to isolate virus; 4/5 bats which yielded isolates had the highest RNA levels (lowest Ct values) (Table 3). Although rigorous quantitative analysis was not performed, the highest viral load measured (a Ct value of 24 recorded in bat 371), if compared to a liquid sample, corresponded to an approximate infectious titer of 1×10^5 pfu/ml. This suggests that some infected individuals contain high levels of virus and may be shedding, perhaps infecting other animals, including humans. The fact that four isolates were obtained from *R. aegyptiacus* bats caught in 2007 and the fifth isolate came from a bat of the same species caught nine months later in 2008 implies that *R. aegyptiacus* colonies can harbor Marburg virus for extended periods of time. Previous studies [10,11,12] indicated that a modest prevalence of low-titered virus could be expected in liver and spleen samples. Possible reasons for the success in isolating live virus in the present study include the fact that an effort was made to sample relatively large numbers of bats and to flash freeze and preserve samples in liquid nitrogen directly after dissection. Moreover, the limited size of the outbreak in humans allowed the investigators to concentrate on implementing the initial ecological study shortly after the outbreak started, while virus activity in the bat colony was probably still high.

By equating RNA-positivity with virus infection, it is possible to derive preliminary conclusions on the dynamics of Marburg virus activity in bat populations. Although there was a similar frequency of RNA-positivity in bats collected in August 2007 and May 2008, the fact that a total of 31/611 (5.1%) *R. aegyptiacus* bats in both collections tested positive in comparison to only 1/609 (0.2%)

Table 1. Summary of Marburg virus diagnostic test results for samples sent to CDC from patients A and B.

Patient	Sample ID No.	Days post onset	Ag	IgG	Q-RT-PCR (Ct)	NP PCR	VP35 PCR	L PCR	Isolation
A	200702854	NA	Pos	Neg	Pos (22)	Pos	Pos	Pos	Pos
B	200703648	7	Neg	Neg	Pos (32)	Pos	Pos	Neg	Pos
B	200703658	10	Neg	Neg	Pos (34)	NA	NA	NA	NA
B	200706136	20	Neg	Pos	Neg	NA	NA	NA	NA

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Table 2. Summary of species, gender and age of all bats captured and tested from the August 2007 and April–May 2008 collections.

Collection	Species	Total	No. PCR positive	% of total
August '07	*R. aegyptiacus*	411	22	5.6
	Male	184	8	5.7
	Female	226	14	5.5
	Female (pregnant)	182	4	2.1
	Adult	333	14	4.2
	Juvenile	78	8	10.3
	Hipposideros spp.	407	1	0.2
	Male	198	0	ND
	Female	209	1	ND
April–May '08	*R. aegyptiacus*	200	9	4.5
	Male	84	6	7.1
	Female	116	3	2.5
	Adult	140	8	5.7
	Juvenile	60	1	1.6
	Hipposideros spp.	202	0	ND
	Male	87	0	ND
	Female	115	0	ND

Listed by species is the total number of bats for each gender or age classification, with the percentage of Marburg virus positive bats (by Q-RT-PCR) within each classification listed in the column to the right.
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Hipposideros spp. bat (Table 2), suggests that infection in the latter species represented spillover from circulation of virus in *R. aegyptiacus* bats. In contrast, approximately equal proportions (3.0–3.6%) of *R. aegyptiacus* and two species of insectivorous bats were found positive for Marburg virus RNA in Goroumbwa Mine, DRC, in 1999 [10,11,12], but meaningful comparisons are precluded by differences in sample size and the inadequacy of population estimates.

Serologic testing found 13/546 (2.4%) *R. aegyptiacus* bats (data not shown), all adults, clearly positive for Marburg virus-specific IgG antibody (titer≥400, sum OD>0.95), two of which (#s 273 and 278) were also weakly positive by Q-RT-PCR. The testing found 455/546 (83.3%) bats to be clearly negative, while another 78 *R. aegyptiacus* bats had indeterminate antibody levels (titer = 100, sum OD≥0.33≤0.95). None of the *Hipposideros spp.* bats had detectable IgG to Marburg virus. It is unclear why only a low percentage of the *R. aegyptiacus* bat population is found positive for Marburg virus reactive IgG antibody. Perhaps a greater proportion of the population was previously infected, but antibody levels are below the conservative IgG assay cut-off used here. This would be consistent with low Marburg virus reactive antibody levels reported in previous bat studies [10,12]. The finding that only 2/13 IgG positive bats had detectable virus nucleic acid would suggest the majority of virus is being cleared prior to Marburg virus reactive antibody becoming detectable.

All bats caught in 2007 and 2008 appeared healthy enough to leave their roosts to forage for food, the ratio of male to female *R. aegyptiacus* was similar in the two collections, and there appeared to be no gender bias in the evidence for Marburg virus infection (Table 2). However, the proportions of *R. aegyptiacus* juveniles and pregnant females present in the 2007 and 2008 collections differed markedly, and this appears to be consistent with the fact that the species is known to give birth in March and September in Uganda [13,14]. After a gestation period of 105–7 days, females usually give birth to a single pup which is carried attached to a nipple on the female for 6 weeks, then left at the roosting site and fed with regurgitated food for 9–10 weeks, before flying and fending for itself [15]. Thus, in August 2007, 182/226 (80.5%) *R. aegyptiacus* females were found to be pregnant ahead of giving birth in September, and juveniles, mostly weaned, represented 78/411 (19%) of the collection. The prevalence of Marburg virus RNA detected in the juveniles, 8/78 (10.3%), was significantly higher than in adult *R. aegyptiacus* bats, 14/333 (4.2%) ($p<.05$, Fisher's exact test; Table 2). Only 4/182 (2.1%) of the pregnant females were RNA-positive, and their placentas all tested negative. Additionally, a single RNA-positive mother nursing an RNA-negative newborn pup was identified. In May 2008, no *R. aegyptiacus* females were found to be pregnant, although microscopic examination of uterine tissues were not performed, and juveniles, presumably born mostly in March, represented 60/200 (30%) of the collection, but only 1/60 (1.6%) of the juveniles were RNA-positive (Table 2).

It can be concluded that there was no evidence of vertical transmission of infection in *R. aegyptiacus*, but that juveniles are exposed to virus at a stage of their development possibly determined by factors such as waning maternal immunity or seasonal occurrence of infection in external hosts such as arthropods. Limited tests on arthropod parasites of bats in the present study were negative for evidence of Marburg virus infection (data not shown), and the same was true for larger numbers of parasitic and cave-associated arthropods tested in the investigations in the DRC in 1999 [10]. It seems more likely that there is horizontal transmission of infection among susceptible bats, as was proposed for Hendra virus [16] and Nipah virus [17]. However, no Marburg virus RNA was detected in oral swabs taken from bats, including those with virus RNA-positive liver and spleen samples (data not shown), suggesting that transmission via masticated fruit spats as suggested for Nipah virus, is an unlikely route for Marburg virus. Transmission via bat urine or feces would be another possible mechanism. It is notable that ebolavirus was found to be shed in the feces of experimentally infected fruit bats for up to 3 weeks [8], but limited immunohistochemical analyses of formalin-fixed kidneys of our RT-PCR positive bats have thus far been negative, tentatively suggesting that transmission via urine may be less likely than through feces. However, it would be premature to rule out transmission though urine, feces or saliva given the limited number of bats tested to date, and the lesser sensitivity of immunohistochemical methods relative to RT-PCR. The determination of virus transmission mechanisms will be best addressed in the future through experimental infection of *R. aegyptiacus* bats.

For ebolavirus, it has been suggested that outbreaks in nonhuman primates follow seasonal patterns which may reflect changes in diet or reproductive status of reservoir hosts, and that infection of the primates could be initiated through consumption of fruit contaminated with blood and placentas during parturition of infected bats [18,19]. Our data indicating the lack of evidence for vertical transmission of Marburg virus would suggest blood and placentas generated during parturition are unlikely to be source of virus infecting primates, at least for Marburg virus.

Histopathological examination of liver and spleen samples of 30 *R. aegyptiacus* bats and one *Hipposideros spp.* bat which produced positive PCR results, and 49 bats which were uniformly negative in Q-RT-PCR plus NP and VP35 RT-PCR assays, revealed no lesions which could specifically or consistently be ascribed to Marburg virus infection. Viral antigens were detected by IHC in

Table 3. Summary of all Marburg virus positive bats in each collection period.

Collection	Bat No.	Species	Sex	Status	Ct	RT-PCR NP-VP35	Virus isolation	Sample ID/ Virus isolate No.
August '07	**44**	*R. aegyptiacus*	F	Adult	35.0	**Yes**	**Yes**	**200704525/811274**
	77	*R. aegyptiacus*	F	Adult	38.2			
	97	*R. aegyptiacus*	M	Adult	38.7			
	188	*R. aegyptiacus*	F	Adult	28.6	**Yes**	**Yes**	**200704669/811275**
	208	*R. aegyptiacus*	F	Adult (Preg)	39.4			
	209	*R. aegyptiacus*	F	Adult	38.8			
	238	*R. aegyptiacus*	M	Adult	39.4			
	273	*R. aegyptiacus*	M	Adult	35.0			
	276	*R. aegyptiacus*	M	Adult	39.6	**Yes**		
	278	*R. aegyptiacus*	F	Adult (Preg)	39.3			
	288	*R. aegyptiacus*	F	Juvenile	35.0	**Yes**		
	291	*R. aegyptiacus*	F	Juvenile	35.9	**Yes**		
	311	*R. aegyptiacus*	F	Adult w/pup (neg)	38.7			
	323	*R. aegyptiacus*	F	Adult (Preg)	36.8			
	328	*R. aegyptiacus*	M	Juvenile	30.7	**Yes**		
	331	*R. aegyptiacus*	M	Juvenile	29.1	**Yes**	**Yes**	**200703992/811276**
	371	*R. aegyptiacus*	F	Juvenile	24.0	**Yes**	**Yes**	**200704852/811277**
	374	*R. aegyptiacus*	F	Juvenile	34.4			
	427	*Hipposideros spp*	F	Adult	32.0	**Yes**		
	721	*R. aegyptiacus*	M	Adult	37.1			
	756	*R. aegyptiacus*	F	Adult (Preg)	38.6			
	772	*R. aegyptiacus*	F	Juvenile	37.1	**Yes**		
	782	*R. aegyptiacus*	M	Juvenile	36.9	**Yes**		
April '08	**839**	*R. aegyptiacus*	F	Adult	39.2			
	883	*R. aegyptiacus*	M	Juvenile	34.8	**Yes**		
	901	*R. aegyptiacus*	F	Adult	38.8			
	924	*R. aegyptiacus*	M	Adult	39.4			
	931	*R. aegyptiacus*	F	Adult	39.5			
	946	*R. aegyptiacus*	M	Adult	36.9			
	982	*R. aegyptiacus*	M	Adult	31.8	**Yes**	**Yes**	**200805444/811391**
	989	*R. aegyptiacus*	M	Adult	38.5			
	1013	*R. aegyptiacus*	M	Adult	35.0	**Yes**		

Listed for each bat is the species, sex, status and specific Q-RT-PCR, conventional RT-PCR (NP and VP35), and virus isolation test result. Shown in the far right column are the unique identification numbers for the tissues from which virus was isolated. Note that Marburg virus was isolated from liver/spleen tissues that tended to have the highest viral loads (lower Ct values) as measured by Q-RT-PCR.

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the livers of two bats which yielded Marburg virus isolates in culture (bats 331 and 371, Table 3) and were distributed predominantly in a perimembranous pattern around small, relatively isolated foci of hepatocytes. These foci were often associated with small accumulations of mononuclear inflammatory cells and highly localized hepatocyte necrosis (Figures 1A–E). Rare Marburg virus antigens were observed in the spleen of only one bat, number 371, and were localized to the cytoplasm of isolated mononuclear cells (Figure 1F). This represents the first time that filovirus antigens have been visualized in tissues of naturally infected bats. From the sparse and highly focal nature of the infected sites, it can be surmised that the methods used to sample and test bats, including the Q-RT-PCR, are likely to produce underestimates of the prevalence of active infection. The paucity of hepatic lesions and viral antigens detected by IHC in wild-caught *R. aegyptiacus* contrasts markedly with the abundant and extensively distributed Marburg virus antigens observed in the livers of infected humans and non-human primates [20,21]. The histopathologic and immunohistochemical findings of Marburg virus infection in these naturally infected *R. aegyptiacus* are consistent with observations made for hemorrhagic fever viruses of the families *Arenaviridae*, *Bunyaviridae*, and *Paramyxoviridae* in their small-mammal reservoir hosts [22,23,24], and lend additional support to the contention that *R. aegyptiacus* is a reservoir for Marburg virus.

Estimation of *R. aegyptiacus* colony size

During the 2008 field trip a total of seven of 1,329 marked bats at the Kitaka mine were recaptured at a rate of about 1% of total nightly catches (data not shown), and from these data it was calculated that approximately 112,000 *R. aegyptiacus* bats roosted in Kitaka mine. By extrapolation from the approximately 5% viral

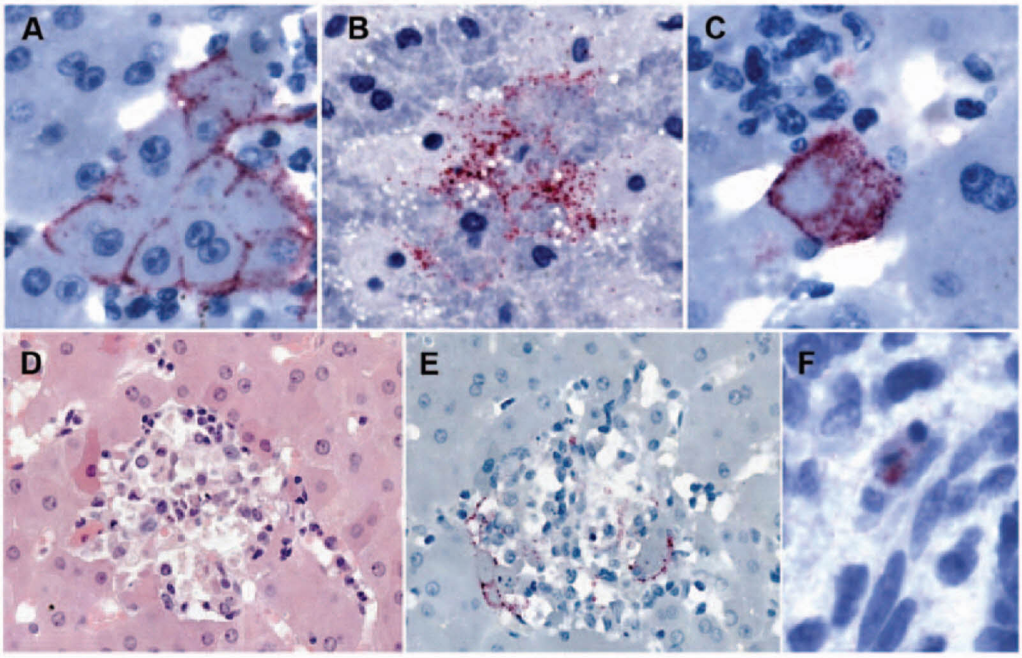

Figure 1. Immunohistochemical localization of Marburg virus antigens in *Roussetus aegypticus* tissues. In the liver, viral antigens were distributed in and around hepatocytes in a dense (A) or loose (B) perimembranous pattern. Rarely, entire hepatocytes were involved (C). These infected foci were characteristically sparse and were often associated with small collections of mononuclear inflammatory cells and hepatocyte necrosis (D and E), although infected cells could also be identified without conspicuous inflammatory infiltrates. Only rare viral antigens were seen in a few mononuclear cells of the spleen of 1 bat (F). Immunoalkaline phosphatase with napthol fast-red and hematoxylin counterstain (A–C, E, F), and hematoxylin and eosin (D); original magnifications ×100 (A, B, D, E) and ×258 (C, F).
doi:10.1371/journal.ppat.1000536.g001

RNA-positive levels detected by Q-RT-PCR in the bats tested in 2007 and 2008, it follows that there could be >5,000 infected bats within the colony at any one time, suggesting that there is a high risk of infection for humans who spend extended periods in close proximity to the bats. In fact, in December 2007 and again in July 2008, an American and Dutch tourist acquired non-fatal and fatal Marburg virus infections respectively after encountering *R. aegyptiacus* bats in Python Cave in the Queen Elizabeth National Park, <30 miles from Kitaka mine [25,26].

Phylogenetic analysis of Marburg virus sequences from bats and miners

The results of Bayesian analysis of the nucleotide differences among full-length virus genome sequences of the isolates from the two miners (01Uga2007 and 02Uga2007), plus the five isolates from bats (44, 188, 331, 371 and 982, Table 3), and 18 representative historical Marburg virus isolates, is shown in Figure 2A. Isolate 01Uga2007 falls into the prototypic clade containing the majority of known Marburg virus sequences. The second human isolate, 02Uga2007, which differs by 21% (nucleotide level) from 01Uga2007, is closely related to members of the highly distinct Ravn lineage, first isolated in 1987 from a patient (RavKen1987) who ostensibly acquired infection in Kitum Cave, Kenya [5]. Thus, it is clear that the Kitaka mine outbreak represented two independent introductions of infection from the natural reservoir hosts into the human population. Two of the bat isolates group with the majority of historical Marburg virus sequences and are most closely related (99.3% identical) to the sequence from miner A (01Uga2007), while the other 3 bat isolates reside within the Ravn lineage (RavKen1987) and are closely related (99.2–99.9% identical) to the sequence from miner B (02Uga2007).

In order to extend the phylogenetic analysis to virus RNA-positive bats from which no isolates were obtained, concatenated partial NP and VP35 gene sequences determined for 14 bats during the present study, plus 2 equivalent sequences derived from the human isolates, and 48 sequences derived from data for historical Marburg virus isolates (Genbank accession numbers in Table S1), were subjected to Bayesian analysis (Figure 2B). No sequences could be determined for a further 17 bats which were positive for viral RNA by Q-RT-PCR, possibly because the viral loads were too low for conventional NP and VP35 RT-PCR to detect. Nevertheless, it was clear that diverse Marburg virus lineages were circulating in the Kitaka mine bats, and that some were identical or near-identical to the human isolates across the genome fragments examined. Sequences from bats 291 and 772 were either identical or within one nucleotide, respectively, of isolate 01Uga2007 (miner A), while sequences from bats 44, 188, 276, 288 and 328 closely matched 02Uga2007 (miner B). The identification of virus lineages circulating in bats within Kitaka mine was probably incomplete, but even these limited genetic data suggest recent common ancestry for closely matching genomes found in bats and humans and strongly implicate *R. aegyptiacus* as the primary source of human infection. The structure of the outbreak was strikingly similar to that seen in 1999 in Durba, DRC, as that outbreak also involved multiple introductions of virus from the natural reservoir, putatively bats, into the human population, plus the co-circulation of highly divergent Marburg viruses in a single geographic location [9,10].

Concluding remarks

The generation and perpetuation of such diverse genetic lineages of virus, with ≥21% nucleotide differences, imply the need for a long association of the virus with its reservoir host, plus

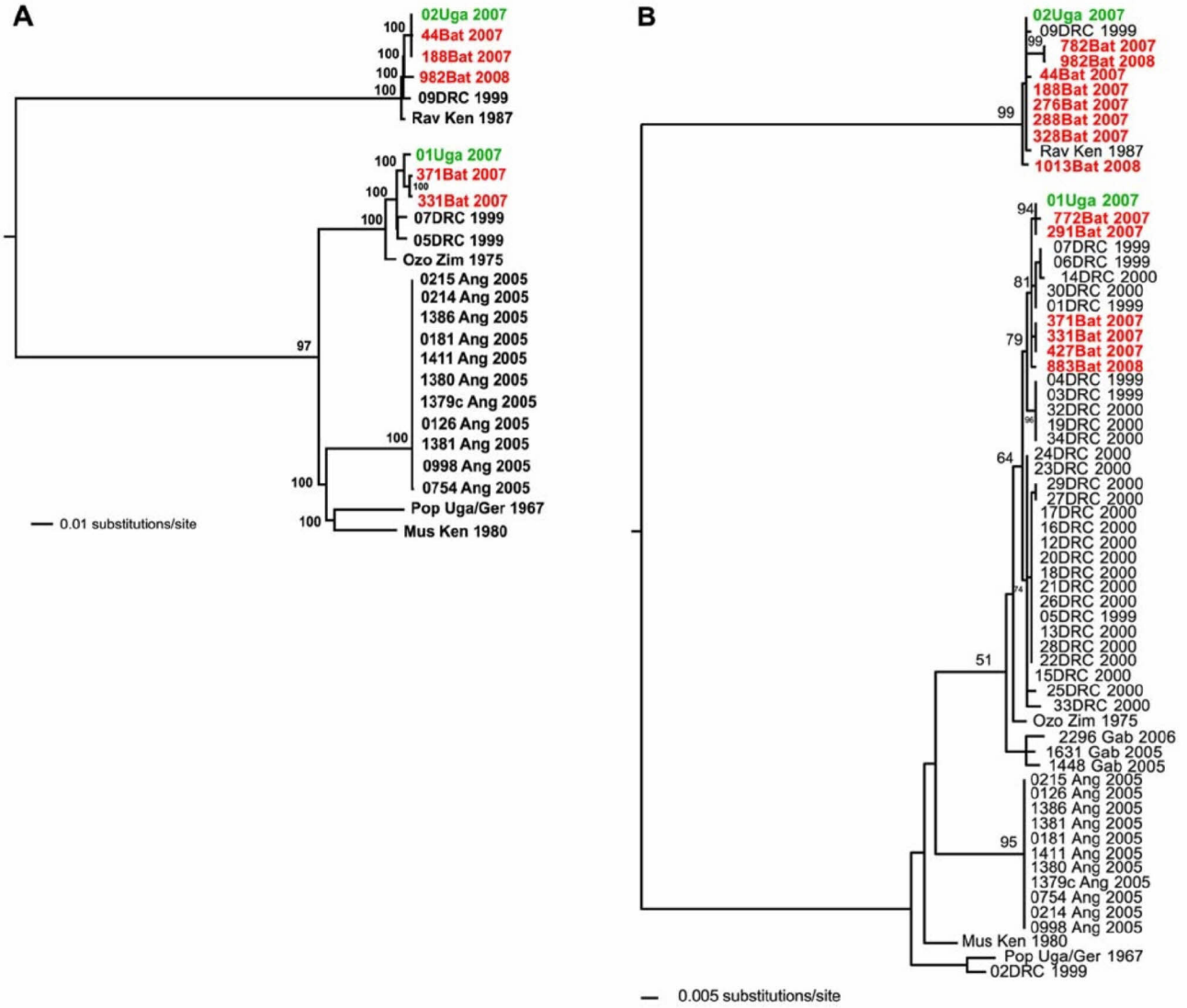

Figure 2. Phylogenetic analysis of full-length or partial genomes of Marburg viruses isolated from humans or bats (see Table S1 for Genbank accession numbers). Trees shown are maximum-likelihood analyses with Bayesian posterior probabilities >50 listed at the appropriate nodes. The ebolavirus outgroup used during the Bayesian phylogenetic analyses are denoted by the small twig at the root of the tree. Marburg virus sequences from 2007 human cases in Uganda are in green, while those from bats are listed in red. (A) Analysis of full-length genomes of five Marburg virus bat isolates, 18 historical isolates, and the isolates from patients A and B (01Uga07 and 02Uga07 respectively). (B) Phylogenetic analysis of concatenated NP and VP35 sequence fragments obtained from each bat specimen compared to corresponding regions from 48 historical isolates and those from 01Uga07 and 02Uga07.
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the need for a large host population with constant recruitment of naïve individuals. The estimated population of 112,000 *R. aegyptiacus* bats in Kitaka mine could probably produce up to 100,000 offspring with two breeding seasons a year. Moreover the species is widely distributed in Africa, with many large colonies in proximity in East Africa alone, including the Kitum Cave complex on Mount Elgon, and numerous caves in western Uganda. It has been observed in South Africa that large proportions of the bats within *R. aegyptiacus* colonies migrate ≥300 miles to other colonies on a seasonal basis [27]. Hence the potential pool of vertebrate hosts for Marburg virus may extend to tens of millions of bats across a large geographic range.

Although diverse Marburg virus lineages were found to co-circulate at single geographic locations in Kitaka mine in Uganda and Goroumbwa Mine in the DRC, it is noteworthy that very closely related lineages have also been found at widely separated geographic locations, in some instances over 2000 km apart. For example, Marburg virus sequences found in bats in Gabon are closely related to isolates from Zimbabwe, Uganda and DRC. Isolates of the Ravn lineage have been found in Kenya, DRC and Uganda. In fact, an isolation-by-distance analysis of the data presented here (Mantel test) found no correlation between genetic and geographic distances ($p>0.3$). The geospatial separation of the closely related Marburg virus lineages is most consistent with mobility of their natural host, a dynamic easily accomplished by the enormous meta-population of *R. aegyptiacus* present in Africa.

Longitudinal studies of naturally infected *R. aegyptiacus* colonies would provide valuable insights into the dynamics of immune status, as well as the shedding, transmission and persistence of Marburg virus in bat populations, and help to determine if the

proportions of infected individuals relative to age are periodic or stochastic. The studies should be supplemented by experimental infections to observe the dynamics of infection within individual bats. Given the detection of infectious ebolavirus in privileged sites, such as testes, up to three months after onset of symptoms in human infections [28], careful examination of multiple tissues from infected bats is also warranted.

Materials and Methods

Human samples

Blood samples collected during acute illness and submitted as diagnostic samples to the Centers for Disease Control and Prevention (CDC), Atlanta, USA, were tested for Marburg virus antigen and IgG antibody by enzyme-linked immunoassay as described previously [29,30]. The samples were also tested for presence of Marburg virus nucleic acid by reverse transcriptase-polymerase chain reaction (RT-PCR), and cultured for isolation of virus as described below.

Bat samples

According to an institutionally reviewed IACUC protocol, bats were captured with mist nets or harp traps at the opening of the mine, euthanized with Isoflurane, and samples of liver, spleen and placenta (where applicable) collected by dissection, using safety precautions described previously [31]. Liver and spleen were selected for sampling based upon previous studies [10,11,12] and because these organs are affected in filovirus infections of primates. Aliquots of tissue were preserved in chaotrope (Cellular Lysis Buffer, Applied Biosystems) for analysis by RT-PCR, while replicate samples were frozen in liquid nitrogen for culture of virus, and fixed in formalin for histopathological examination. Blood was also taken from each bat for RT-PCR and antibody analyses as described below. Bats were identified morphometrically [32], their measurements and breeding status recorded, and the carcasses preserved in 10% formalin for at least 1 week and later changed to 70% ethanol for long-term storage. To minimize the potential for cross-contamination between bat samples, all dissection instruments were used only once during each nightly necropsy session, and in between sessions, all instruments were soaked in 3% Lysol for $\geq$15 minutes followed by disinfection in 10% bleach for $\geq$15 minutes.

To maximize the chances of isolating virus, large numbers of each of the two species of bat found in the mine, the fruit bat *R. aegyptiacus* and the insectivorous *Hipposideros* spp. bats, were sampled during the first field trip in August 2007. Smaller numbers were sampled during the second field trip which was undertaken in May 2008, during the putative breeding season of *R. aegyptiacus* bats in Uganda, mainly to seek evidence of continued circulation of virus and possible vertical transmission of infection. Opportunity was taken to collect oral swabs from the bats sampled in May to determine the likelihood of virus transmission through saliva or respiratory aerosols. A mark and recapture study was also conducted in May to estimate the size of the *R. aegyptiacus* population, and to possibly allow for later determination of foraging and migration distances of the bats. A total of 1,329 *R. aegyptiacus* bats were tagged with coded aluminum necklaces or leg bands over a period of two weeks, and recaptures which were recorded once the number of marked bats reached 1,000, were used in the Jolly-Seber model for estimating the abundance of an open population [33,34].

Collection of additional fauna within the mine

Limited numbers of arthropod parasites of bats were collected and frozen, including 25 wingless flies (Family *Nycteribiidae*) found in the pelage of bats during dissection, and 100 adult and nymphal argasid ticks (*Carios faini*) taken from crevices in the rocks near bat roosting sites. Apart from dermestid beetles, spiders, crickets, moth flies and cockroaches, the only other fauna seen in the cave consisted of a target rat (*Stochomys longicaudatus*) and forest cobras (*Naja melanoleuca*).

RT-PCR analysis

Total RNA was extracted in one of two ways. 50 µ liquid samples (blood and eluates of oral swabs) were extracted using non-cellular lysis buffer (Applied Biosystems) [35] while RNA from tissue (100 mg) were extracted with cellular lysis buffer (Applied Biosystems) [12]. RT-PCR based assays for the NP, VP35 and VP40 genes, were performed as described previously [9,12,36], except that the VP40 quantitative RT-PCR assay (Q-RT-PCR) assay was modified to include two reporter-labeled probes 5′Fam-ATCCTAAACAGGC"T"TGTCTTCTCTGGGACTT-3′ and 5′Fam-ATCCTGAATAAGC"T"CGTCTTCTCTGGGACTT-3′ in addition to the forward primer 5′-GGACCACTGCTGGC-CATATC-3′and reverse primer 5′-GAGAACATITCGGCAG-GAAG-3′. The quencher BHQ1 was placed internally in the probes at the "T" sites.

All human and bat samples were screened by Q-RT-PCR, designed to detect RNA of all known lineages of Marburg virus, and bat samples found positive (Ct<40) were re-analyzed by extracting RNA from frozen tissue using RNAeasy mini-kits (Qiagen) after overnight incubation at 4°C in lysis buffer. The extracts were subjected to the Q-RT-PCR and conventional RT-PCR based on the NP and VP35 genes. Tissues from 39 bats found negative in the initial Q-RT-PCR were also re-extracted and subjected to Q-RT-PCR and NP and VP35 gene RT-PCR. Nycteribid flies and argasid ticks were individually ground in cellular lysis buffer and extracted RNA tested by Q-RT-PCR.

Virus isolation

For human samples, 100 µl of blood was inoculated onto Vero E6 monolayers in 25 cm^2 flasks and incubated for 14 days at 37°C/5% CO_2 in MEM/2% fetal calf serum with a media change after day 7. Cultures were monitored daily for CPE with cell scrapes at days 7 and 14 tested by IFA. For bat samples, 10% suspensions of freshly thawed ~250 mg frozen tissue sections were homogenized on ice in viral transport medium (HBSS/5% fetal calf serum) with a plastic pestle and ~250 mg sterile alundum (Fisher cat# A634-3) in 15 ml conical tubes. The homogenate was clarified by low speed centrifugation and 100 µl of supernatant fluid was inoculated onto Vero E6 cell cultures in 25 cm^2 flasks at 37°C/5% CO_2 for 1 hr with gentle rocking followed by media replacement with MEM/2% fetal calf serum. Inoculated flasks were monitored daily for 14 days (with media change after day 7) for the appearance of CPE and by IFA of cell scrapes on days 7 and 14. Cultures positive by IFA for Marburg virus were additionally analyzed by RT-PCR (see below).

Nucleotide sequencing of PCR products and virus isolates

Sequencing of Marburg virus whole genomes and partial gene sequences (NP and VP35) were performed as previously described [12,36].

IgG detection in bats

Blood samples from bats were tested by enzyme-linked immunoassay for the presence of IgG antibody reactive with Marburg virus as described previously [29,30] but with the

following modifications: 1) 96-well plates were coated with Marburg virus infected cell lysate (diluted 1:1000 final concentration) generated from Marburg virus isolates # 188 (Ravn lineage) and #371 (main lineage), 2) sera were initially diluted 1:100 in 5% nonfat milk rehydrated in PBS-T containing normal Vero E6 cell slurry diluted 1:25 and then further diluted 4-fold through 1:6400 in PBS-T/5% nonfat milk, and 3) bound bat-specific IgG was detected using HRP-conjugated goat anti-bat IgG (Bethyl-L cat# A140-118P) diluted 1:2000. The mean and SD of the adjusted sum ODs from the entire collection (both species) were used to plot a frequency distribution and calculate a value greater than the mean+3 SD. Sera with repeatable adjusted sum ODs greater than this cutoff value (0.95) and whose titers were ≥1:400 were considered positive.

Phylogenetic analyses

Genbank accession numbers are described in Table S1. Phylogenetic analyses were performed separately on two sets of data: one comprising 25 whole genome sequences including those of 18 representative historical Marburg isolates, plus the 2 isolates obtained from miners and 5 isolates obtained from bats during the present investigations, and the second data set was comprised of 64 concatenated partial NP and VP35 gene sequences including 48 derived from historical Marburg isolates plus 2 derived from the isolates obtained from miners and 14 determined for PCR products obtained from bats during the present study. A representative sample of Ebola Zaire (Genbank accession NC 002549) was used as an outgroup.

Modeltest 3.730 [37] was used to examine 56 models of nucleotide substitution to determine the model most appropriate for the data. For whole genome analysis, the General Time Reversible model incorporating invariant sites and a gamma distribution (GTR+I+G) was selected using the Akaike Information Criterion (AIC). Nucleotide frequencies were A = 0.326, C = 0.195, G = 0.185, T = 0.294, the proportion of invariant sites = 0.451, and the gamma shape parameter = 7.244. The Kimura 3-parameter model with unequal base frequencies and a proportion of invariant sites (K81uf+I) was selected for the concatenated NP-VP35 dataset. Nucleotide frequencies were A = 0.310, C = 0.233, G = 0.202, T = 0.255, and the proportion of invariant sites = 0.659. Maximum likelihood analyses were subsequently performed in PAUP*4.0b10 [38] using the GTR+I+G or K81uf+I model parameters.

In addition, Bayesian phylogenetic analyses were conducted for each of the datasets in MrBayes 3.2 [39] using the GTR+I+G model of nucleotide substitution. For each dataset, two simultaneous analyses, each with four Markov chains, were run for 10,000,000–40,000,000 generations, sampling every 100 generations. Prior to termination of the run, the AWTY program was used to assess convergence to ensure that the length of the analysis was sufficient [40]. Trees generated before the stabilization of the likelihood scores were discarded as burn-in, and the remaining trees were used to construct a consensus tree. Nodal support was assessed by posterior probability values (≥95 = statistical support).

Histopathological examination of bat tissues

To determine if marburg virus infection caused lesions in infected bats, sections were cut from paraffin-embedded blocks prepared from formalin-fixed liver and spleen samples from 32 bats found positive by Q-RT-PCR, and examined in parallel with the tissues of 39 bats found negative in both the Q-RT-PCR and conventional RT-PCR. Hematoxylin and eosin (H&E) stained sections of the tissues were examined for lesions, and sections stained by an immunoalkaline phosphatase technique [41] with a polyclonal rabbit anti-Marburg virus antiserum diluted to 1/1000. Samples were evaluated without prior knowledge of the PCR and virus culture results.

Supporting Information

Table S1 Genbank Accession numbers used for phylogenetic analysis

Found at: doi:10.1371/journal.ppat.1000536.s001 (0.08 MB DOC)

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Author Contributions

Conceived and designed the experiments: JST BRA STN PER. Performed the experiments: JST BRA TKS SARC JAC AK RS CDP SB MLK PBHF CGA DMM ZDR JTK JNM DLC PWG ECF JWT PER. Analyzed the data: JST BRA TKS SARC JAC AK RS CDP MLK DMM ZDR JNM DLC SRZ TGK STN PER. Contributed reagents/materials/analysis tools: JST BRA PBHF EB PA SO EKM RD JWT SRZ TGK STN PER. Wrote the paper: JST BRA SARC RS CDP STN PER.

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MARBURG-VIRUS DISEASE IN KENYA

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Summary The third known outbreak of Marburg-virus disease occurred in Kenya in 1980. The index patient acquired infection in western Kenya, and a doctor in close contact with the patient terminally during a massive haematemesis developed infection in Nairobi. There was no further evidence of nosocomial transmission. Surveillance in western Kenya provided no evidence of Marburg-virus disease but suggested the presence of Ebola haemorrhagic fever.

Introduction

IN January, 1980, a doctor became ill with a febrile disease subsequently shown to be Marburg-virus disease (MVD). 9 days previously he had attempted to resuscitate a man admitted to the Nairobi Hospital with liver failure and a haemorrhagic diathesis. The patient died 6 h after admission. Necropsy showed extensive hepatic necrosis, and virus particles were subsequently identified in formalin-fixed renal tissue.

Only two previous outbreaks of MVD have been recognised. The first was in Europe, where 31 cases with 7 deaths occurred in 1967 in Germany[1] and Yugoslavia.[2] Infection was acquired from vervet monkeys (*Cercopithecus aethiops*) imported from Uganda.[3] In the second outbreak, in South Africa in 1974,[4] there were 3 cases and 1 death, and the primary case was believed to have become infected in Zimbabwe.[5] We now report a third outbreak of MVD in 2 Kenyan residents, the first almost certainly acquiring the infection in a defined area of western Kenya.

Case-reports

Case 1

A 56-year-old Frenchman working as an electrical engineer in a sugar factory in Nzoia, near Bungoma in Western Province, fell ill on Jan. 8, 1980, with a sudden febrile illness. Early features included headache, myalgia, and malaise. Diarrhoea and vomiting began on the 3rd day. He was admitted to a private hospital in Kisumu where, despite rehydration and antibiotics, his condition worsened. He was transferred by air to Nairobi on Jan. 15. During the journey he had a substantial haematemesis. On arrival in Nairobi he was deeply jaundiced and collapsed from massive gastrointestinal haemorrhage. He was also bleeding from the nose and mouth. Resuscitation attempts failed, and he died 6 h after admission.

Haemoglobin was 12·3 g/dl; white-cell count $8·6 \times 10^9$/l; urea 15 mmol/l; bilirubin 204 μmol/l; serum-aspartate-aminotransferase 6000 units; serum-alanine-aminotransferase 3000 units/ml; alkaline phosphatase 120 units/ml. Necropsy showed extensive hepatic necrosis and confirmed the haemorrhagic diathesis. The cause of death was reported as fulminating hepatitis with haemorrhagic complications.

Case 2

The doctor who attended the first patient fell sick on Jan. 24, 1980, 9 days after attempting resuscitation of the first patient. Early symptoms included fever, headache, severe backache, and sore throat. He took chloroquine and later chloramphenicol and continued working until the 4th day of illness, when severe diarrhoea and vomiting developed.

He was admitted to a single room on the medical ward of the Nairobi Hospital.

The diarrhoea continued, and on several occasions blood was observed in the stool. Investigation failed to identify the aetiology of the disease. On Feb. 4 ultrasound examination suggested a possible liver abscess. Laparotomy was carried out next day, but no cause for his illness was found. A liver biopsy was done, and he was transferred to the intensive-care unit.

Renal function deteriorated, and the prospect of renal dialysis led to an intensified search for the cause of his illness. Paired sera from Jan. 30 (7th day of illness) and Feb. 6 (14th day of illness) were inoculated into cultures of Vero LLC-MK-2,V_3A (vervet monkey kidney), L132, and primary baboon kidney cells for virus isolation. Serum samples were sent to the Centers for Disease Control (C.D.C.), Atlanta, to be tested for antibodies against Marburg, Ebola, Crimean-Congo, and Rift Valley fever viruses. The paired sera showed a rise in titre from 1:4 to 1:256 against Marburg virus. The cell cultures were harvested approximately 48 h after inoculation, and samples were sent to C.D.C. on dry-ice. Passage in Vero cells resulted in isolation of Marburg virus from Vero cells and M_2K fluids which had been inoculated with the serum sample of Jan. 30 (fig. 1). Further virus isolation attempts from serum, urine, and conjunctival swabs proved negative, but virus was recovered from seminal fluid collected 2 months after clinical recovery.

Other Possible Cases

The nurse who assisted the doctor (case 2) in the resuscitation of the first patient fell ill 11 days later on Jan. 26 with fever, malaise, headache, and backache. On the 5th day of illness she noticed a faint macular rash on the upper arms which desquamated 2 weeks later. She remained unwell for 3 weeks. The white-cell count fell from $5·7 \times 10^9$ to $4·6 \times 10^9$/dl. The blood film showed atypical mononuclear cells, and the Paul Bunnell and monospot tests remained negative. Serum-aspartate-aminotransferase was 65

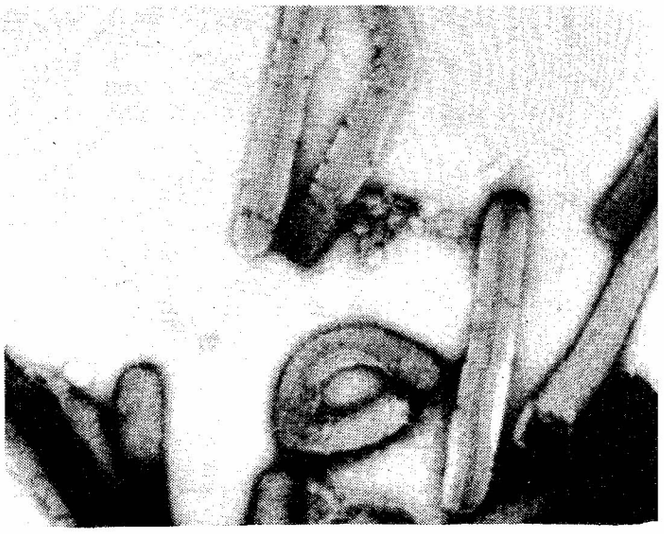

Fig. 1—Case 2: electron micrograph of Marburg-virus particles.
Reduced by half from ×143 640.

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units/ml and serum-alanine-aminotransferase 82 units/ml. There were no haemorrhagic features apart from an unusually heavy and prolonged menstrual period. Virus-isolation attempts on serum samples as early as day 4 proved negative, and she did not develop antibodies against Marburg virus.

Another nurse, who nursed the second patient, developed a febrile illness at the same time, but she was subsequently found to have hepatitis A.

Outbreak Containment

The diagnosis of MVD was made in case 2 on the 17th day of illness, and a containment programme was then instituted. This consisted of isolation of the patient, provision of laboratory support, quarantine of close contacts, and surveillance of all other contacts.

Isolation of Patients

At confirmation of the diagnosis case 2 was being nursed in a single room in the intensive-care unit. The rest of the unit was closed, and strict barrier nursing by a limited number of volunteer staff from those already exposed was introduced. Initial barrier nursing was carried out with disposable gowns, masks, and gloves, but within 48 h Vickers positive-pressure respirators were made available.

At diagnosis the patient was being intensively investigated. Management depended on continuing laboratory investigation. A small laboratory was set up in the intensive-care unit, with a class-I safety cabinet and a technician wearing full protective clothing. When investigation beyond the capacity of this laboratory was required, samples were processed in the main hospital laboratory after normal working hours: the staff were fully protected and equipment was decontaminated after use.

Contact Containment

A list of all contacts of case 2 was prepared, giving both the time and type of contact. Contacts were classed as either close contacts (those who had direct contact with the patient or direct contact with his excretions or laboratory samples) or remote contacts (mostly visitors and friends). The close contacts were grouped into cohorts according to the date of their most recent contact exposure, and contact groups were placed in quarantine for 14 days from their last exposure. Further contact with adequate protection did not extend this period.

The interval between the death of the first patient and identification of the outbreak was well beyond the accepted incubation period, and in the absence of further cases, action was limited to the follow-up of all contacts for history of illness and serum collection.

Close contacts.—In all, 67 individuals were considered as close contacts, the majority of whom worked and lived at the hospital. This group included nurses, doctors, attendants, and laboratory staff as well as the surgical team. They were quarantined in the hospital and nurses' home in groups according to their last date of exposure. Groups were kept separate. Surveillance was maintained by twice-daily temperature recording and reporting of sickness. Blood samples were collected to provide a baseline white-cell count and a serum sample. Most of the laboratory staff had been exposed. In order to allow the laboratory to remain functional staff continued to work during the quarantine period. The only modification to normal procedure was that samples were brought to the laboratory instead of being collected by laboratory staff from the wards. Two individuals became ill during quarantine. A theatre-sister developed a fever and respiratory symptoms, and a physician had a 4-day illness with malaise and low-grade fever. In neither case was MVD considered likely, but both were isolated until virus-isolation attempts proved negative. Neither developed antibodies against Marburg virus.

Remote contacts.—76 individuals had remote contact with the second patient. Most were staff and friends who had visited him during his illness but had not taken part in direct patient care. All remote contacts were asked to take their temperatures daily and to report any illness. They were told to restrict their contacts for a period of 14 days. They were visited regularly during the period, and blood samples were collected from 56.

Source of Infection

The diagnosis of MVD in the primary case was made retrospectively on fixed tissue obtained at necropsy. Characteristic virus particles were seen on electron microscopy of formalin-fixed renal tissue (fig. 2) but not in liver tissue. Fluorescence microscopy of renal tissue with the trypsin treatment described by Swoveland and Johnson[6] confirmed that the particles were Marburg virus.

The first patient had been working as an electrical engineer in the Nzoia sugar factory (fig. 3). He had been resident in Kenya for 6 months before falling ill on Jan. 8, 1980. He was admitted to the Agha Khan Hospital in Kisumu on Jan. 12 and transferred to Nairobi on Jan. 15. Contacts during his illness included friends and colleagues at his place of work, hospital staff in Kisumu and Nairobi, and those who took part in his transportation between Nzoia, Kisumu, and Nairobi. All contacts were interviewed for recent illness, and blood samples were collected.

During the 2 weeks before the onset of his illness he had worked in the sugar factory. His job was to maintain the electrical equipment, and he had little contact with raw sugar-cane or its processing. The factory was new, well maintained, and with no evidence of infestation with rodents, bats, or other animals apart from spiders. He lived on the sugar estate some 2 miles from the factory. He usually walked to work across the cane fields. In the week preceding his illness there had been several cane fires which could have caused animals or birds to move from their usual habitats in the cane fields. He lived alone apart from a house-servant. There was no

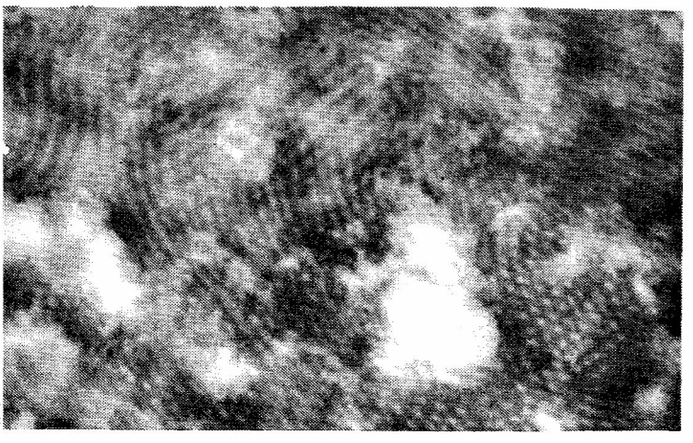

Fig. 2—Case 1: electron micrograph of Marburg-virus-like inclusions in renal tissue.

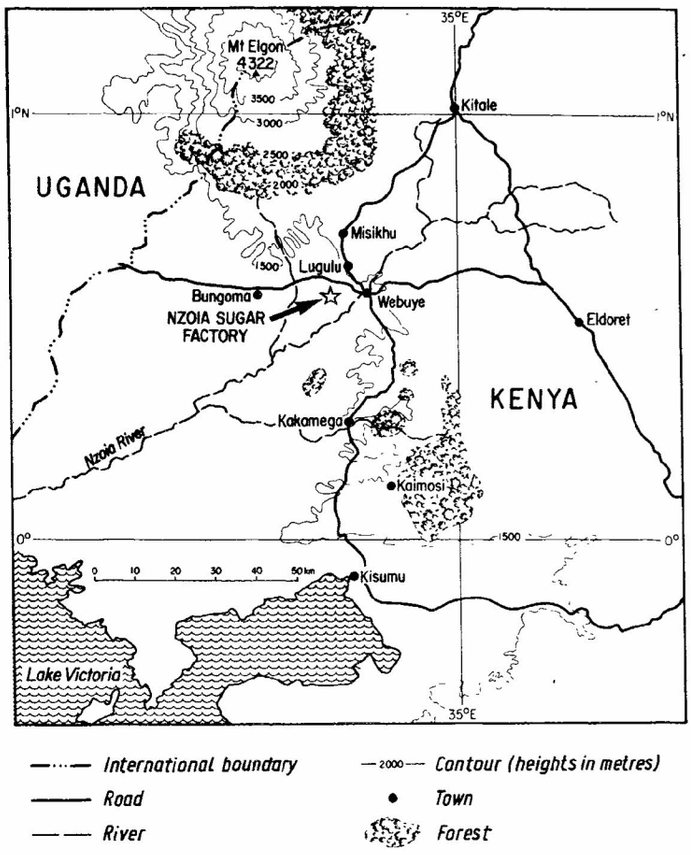

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Fig. 3—Map of Western Kenya showing origin of primary case.

evidence of rodent or bat infestation in his home. Within his compound a pair of pied crows (*Corvus albus*) nested, and one of the birds had become partially tame and would enter the house for food. There was also a colony of black-headed weaver birds (*Ploceus cucullatus*) in a tree near to his house. His neighbour recalled that in the month before he became sick he had brought a small sick bird into the house and it had died.

He had made few visits outside the area in the 2 weeks before falling ill. On Christmas Day, 15 days before he became sick, he visited the Mount Elgon National Park with two friends. He entered the Elgon caves, which harbour large bat populations. He also visited neighbouring towns for shopping. He frequently visited small forested areas in the vicinity, taking food for animals and birds. It could not be established with certainty that he had visited any of these areas in the 2 weeks before becoming ill.

He had little contact with other senior staff at the factory. His social life appeared to centre around Eldoret, where he had become friendly with a group of young women, at least three of whom had visited him shortly before his illness. His usual house-servant went on holiday in mid-December: a replacement maid (maid A) helped for 2 weeks (Dec. 22–Jan. 4) and was then replaced by maid B, who looked after him during the first 5 days of his illness.

Serological Investigation

Sera collected during the investigation were stored at −80°C in Nairobi and transported to the National Institute for Virology (N.I.V.), Johannesburg, and C.D.C., Atlanta, where they were examined by indirect fluorescent-antibody test by means of slide antigens prepared at C.D.C. with monospecific, triple (Ebola/Lassa/Marburg), and five-antigen (Crimea Congo/Rift Valley/Ebola/Lassa/Marburg) slides.

Interpretation of results was complicated by the variability in reporting of results between the two laboratories. With regard to Marburg-virus antibodies, results reported by N.I.V. were consistently of a lower order of sensitivity, with fewer positive results and lower titres in those positive. In an attempt to overcome this difficulty sera reported here as positive were confirmed in both laboratories at a titre of 1:16 or more.

Contact Serology

Sera were collected from 186 contacts of the 2 patients with MVD. 68 were contacts of patient 1, 65 were close contacts of patient 2, and 53 were remote contacts of patient 2. By the above criteria only 2 contacts were considered positive. The first, maid A, had contact with the first patient until 4 days before he became ill. Her serum remained positive at the same titre for 6 months. She denied recent illness. She was born in western Kenya and had lived there throughout her life. The second was a laboratory nurse who had handled samples from patient 2. She was born in western Kenya and had been nursing in Nairobi for 4 years. She also denied recent illness.

Population Serology

224 sera from populations in the area of residence of the first patient were examined. A random sample of 63 employees of the Nzoia sugar factory and 79 cane cutters and growers were also examined. Subsequently blood samples were taken from 44 workers from a nearby road-construction camp and 100 medical staff from three hospitals in the area. Three staff members of the Friends Hospital at Kaimosi were found to have antibody titres of 1:16 or greater against Marburg virus.

Prospective Surveillance

At the time of the initial investigation all hospitals and health facilities in the area were visited. Staff were interviewed and, where available, hospital records were examined. There were no evidence of previous cases or outbreaks of viral haemorrhagic fever. During these visits staff were briefed on the diagnosis and management of suspect cases and requested to notify suspicious febrile illness, especially with subsequent diarrhoea, jaundice, or haemorrhagic manifestations. Protective clothing was issued after notification of a suspect case. A public-health officer was assigned to surveillance in the area for the identification of suspects, documentation, sample collection, and investigation of families and close contacts.

In the 6 months following confirmation of MVD, 17 suspect cases were notified and investigated. In 6 individuals MVD was considered possible on clinical grounds. In no instance was virus isolated from either blood or liver tissue (obtained post mortem). Serological investigation was negative in all 6 cases investigated for Marburg-virus disease.

In 2 episodes evidence for infection with Ebola virus was obtained from serological investigation of either the patient or family contacts. In the first instance, a young girl died in Lugulu Hospital with a febrile illness in June, 1980. She had become jaundiced and developed haemorrhagic manifestations. A friend who had nursed the girl who died had also fallen sick with fever. She was found to have a titre to Ebol

virus of 1:128. A serological survey of the family and close neighbours showed that 4 of 84 had titres of 1:16 or more to Ebola virus. The second instance occurred in October, 1980, in the nearby Misikhu Mission Hospital, where a young girl from a local school was admitted with fever with subsequent haemorrhagic features. She was found to have antibodies against Ebola rising from 1:32 to 1:256 a week later. In neither instance was there evidence of nosocomial spread of infection, although no initial precautions were taken to protect hospital staff.

Discussion

Identification of the first outbreak of MVD in Kenya resulted from the investigation of an unexplained febrile illness in a doctor working in a Nairobi hospital. Whereas the early features of his disease suggested a viral haemorrhagic fever the course of the illness was less typical. Haemorrhage was limited to intermittent intestinal bleeding. Intensive investigation in the hospital did not at first indicate a diagnosis, which was suspected more on epidemiological grounds: the sick doctor was working in the intensive-care unit of a busy hospital admitting patients from throughout Kenya and neighbouring countries, in particular the Southern Sudan, where recent outbreaks of Ebola-virus fever had occurred. Further investigation leading to diagnosis was precipitated by the possibility of renal dialysis, and in most circumstances pertaining in Africa this limited outbreak would have passed unnoticed.

Identification of the primary case and subsequent confirmation were made possible by the excellent record-keeping system in the hospital and because necropsy was routinely carried out on patients whose deaths were unexplained.

The differential diagnosis of viral haemorrhagic fevers may present problems.[4,8,9] In the first patient a diagnosis of fulminating hepatitis was made and apparently confirmed post mortem, although the absence of an inflammatory response accompanying the massive hepatic necrosis was unlike viral hepatitis. Overt jaundice has seldom been described in either Marburg[1,4] or Ebola[8,9] virus disease and appears to be a terminal event. In patient 2 the differential diagnosis had originally included malaria and typhoid and later septicaemia, infectious mononucleosis, trypanosomiasis, and liver abscess. The incubation period was clearly established as 9 days. The liver biopsy was not typical of MVD and it is possible that the illness was complicated by a second infection, possibly a septicaemia.

The diagnosis still presents many difficulties. Few laboratories are equipped to conduct the necessary investigations in safety. The presence of specific antibodies is of value only later in the disease, especially when titres rise. It is of no value in the early stages of the disease and the investigation of sporadic cases. Diagnosis therefore rests on virus isolation early in the course of the illness. Electron microscopy of blood, urine, or necropsy specimens may demonstrate virus particles. Virus was identified in case 1 only in renal tissue. Liver tissue is usually recommended for post-mortem diagnosis of both MVD and Ebola fever, but in this case liver tissue was negative. Trypsin digestion of formalin-fixed tissue before fluorescence microscopy allowed a specific diagnosis of MVD to be made in the first patient, differentiating it in particular from Ebola fever. This technique appears especially suitable for retrospective investigation of stored tissues.

The diagnosis once established had important implications to the entire hospital. The patient, a doctor working in the same hospital, had been intensively nursed for 2 weeks. The entire staff of the intensive-care unit had been exposed, and the majority of doctors in the hospital had taken part in his clinical care, including 2 of the busiest surgeons. The laboratory staff had collected and examined many samples. Attempts were made during the necessary containment programme to allow hospital function to continue. To this end the patient and a small laboratory were housed in a contained unit and staffed by a minimum compatible with good patient-care. Grouping contacts into time cohorts reduced the quarantine period for many and allowed them to resume work at the earliest opportunity. The hospital was virtually returned to normal function after 10 days.

Little apprehension was apparent in those kept in quarantine or under surveillance. Their main concern was for their sick colleague. Daily meetings between clinical staff, nursing staff, and epidemiologists did much to reduce problems. Those in quarantine were allowed access to the grounds for exercise and recreation within their own group. Once the patient started to get better morale among his contacts strikingly improved.

In this outbreak 207 individuals had contact with persons infected with Marburg virus. Of the 64 contacts of case 1, there was 1 confirmed case (case 2) and 1 clinically suspect case who did not subsequently develop antibodies. Of the 143 contacts of case 2, 67 were considered to have had close tissue contact with the patient or with laboratory samples. He had been nursed in a single room with no precautions. Containment was begun on day 14, at which time he was probably aviraemic, although virus persisted for 2 months in seminal fluid. The absence of further transmission seems to indicate relatively low transmissibility of MVD. Case 2 had very close contact with case 1. He had attempted to do a tracheal intubation during massive haematemesis and recalled that his arms were heavily contaminated with the patient's blood. The nurse who assisted him became equally contaminated. She had an illness suggestive of MVD but diagnosis could not be confirmed by virus isolation or antibody development.

The three reported outbreaks of MVD seem similar and contrast with outbreaks of Ebola haemorrhagic fever. Of the 36 known cases of MVD 27 were primary cases and 9 secondary. Transmission has not gone beyond a second generation. The mortality is 25% and appears less in secondary cases. In contrast, during the outbreaks of Ebola fever in southern Sudan and Zaire, 602 cases were identified and in all but 40 direct man-to-man transmission could be traced.[7,10] The majority were therefore secondary cases, and in Sudan transmission could be demonstrated through at least 12 generations.[7] One obvious difference between outbreaks of MVD and Ebola fever was the standard of medical care. Syringe passage was clearly demonstrated in Zaire;[10] and, in general, hospitals involved in outbreaks of Ebola fever were clearly less sophisticated than those involved in the outbreaks of MVD in Europe, Johannesburg, and Nairobi. Nevertheless, in outbreaks of MVD strict barrier nursing has not been implemented until late. In Nzara in southern Sudan most of the outbreak occurred outside the hospital, where there was no medical care, and in this situation Ebola-fever transmission was observed through 8 generations. It is possible that the transmissibility of these two viruses is different.

If serological positivity is limited to subjects found positive both at C.D.C. and at N.I.V. then only 2 contacts were considered positive from the 186 samples examined. Both

had spent most of their lives in western Kenya (Bungoma and Kitale), neither had an illness suggestive of MVD, and neither showed a rise in titre. The nurse's contact with laboratory samples was brief and distant. Maid A had her last contact with the first patient 4 days before the onset of his illness. It seems unlikely that either was a secondary case.

Virus persisted in the seminal fluid of patient 2 for 2 months after clinical recovery, and sexual transmission of MVD is known to occur.[1] The potential for sexual transmission should be further investigated, since it could provide a means of virus spread.

Preliminary serological and ecological investigations in the area of the sugar factory 10 km south-east of Bungoma township failed to indicate the source or route of infection of the primary case. The area (fig. 3), at an altitude of 1450 m, is among the most densely populated in Kenya. The land, some 40% of which is under cultivation with maize and sugar-cane, is open savannah and forms the base of Mount Elgon, which rises to 4321 m to the north-east astride the Uganda border. Remnant patches of forest with affinities to the West African Congo forest type are found in the area, the flora and fauna of which are unique in Kenya, many species being found elsewhere only in West and Central Africa. The area is close to the Lake Kyoga area of Uganda, where monkeys incriminated in the original European outbreaks were collected.

Attempts to develop a surveillance system for viral haemorrhagic fevers have emphasised the difficulties inherent in such programmes. Patients present late in their illness, when they are unlikely to be viraemic. Necropsy is rarely carried out, and indeed in the primary case in this outbreak virus particles were not found in liver tissue. Active surveillance in the area since the outbreak has failed to provide definite evidence of MVD in the area of residence of the primary case, apart from seropositivity in 4 residents. Present evidence, however, suggests the presence of Ebola virus. 1 surviving patient showed a significant rise in antibody titre against Ebola virus, and a close friend of an Ebola suspect who died was sick and had a significant antibody titre. In addition 4 of 84 individuals in the immediate area had significant antibody titres against Ebola virus. Radioimmunoassay may prove a more specific indicator of infection and was strongly positive in 1 of our suspected cases of Ebola fever (K. M. Johnson, unpublished).

Once suspected, isolation of individuals is mandatory until the diagnostic results are known. The technical, financial, and logistic implications of surveillance and clinical investigation require close examination to ensure that health resources are used to maximum advantage, especially in countries with limited health resources. Nosocomial transmission can probably be prevented with simple procedures, and close tissue contact seems necessary to effect transmission. Simple barrier-nursing techniques and limitation of laboratory investigation except with adequate containment should be established in areas of virus activity. The indirect fluorescent-antibody test appears to be unsatisfactory especially for epidemiological investigations, and efforts should be increased to develop tests with greater specificity.

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OUTBREAK OF COXSACKIE A1 GASTROENTERITIS: A COMPLICATION OF BONE-MARROW TRANSPLANTATION

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Summary In a three-week period 7 of 14 transplan recipients were infected with coxsackie A virus. Diarrhoea and mortality were significantly associate with infection (7 of 7 infected compared with 0 of 7 nor infected, and 6 of 7 infected compared with 1 of 7 nor infected, respectively). Early in the outbreak, the diarrhoe was presumed to be due to acute graft-versus-host diseas (AGVHD). However, the distribution of AGVHD amon infected and non-infected patients was nearly equal, and a necropsy 3 of 6 infected patients who had had diarrhoe showed no evidence of gastrointestinal involvement wit AGVHD. Infection with viral enteric pathogens may be a important factor in the clinical course of transplai recipients.

Introduction

BONE-MARROW transplantation (BMT) is effective therap for aplastic anaemia and lymphoreticular malignancies.[1]