**RISK ASSESSMENT FOR THE TRANSMISSION OF EMERGING ZOONOTIC VIRUSES IN MYANMAR**

*Ohnmar Aung, MBBS, MA, Marc T. Valitutto, VMD, Theingi Win Myat, MBBS, MSc, PhD, Moh Moh Htun, MBBS, MMedSc, PhD, Htin Lin, MBBS, MMedSc, Wai Zin Thein, BVSc, Kyaw Yan Naing Tun, BVSc, MSc, PhD , Dawn M. Zimmerman, DVM, MS, Suzan Murray, DVM, DACZM*

**Abstract**

Myanmar is currently one of the last regional countries to have preserved large areas of forest which is home to many wildlife species.  However, internal conflicts and disagreements between the military government and various ethnic armed forces have led to severe mismanagement allowing for unregulated deforestation and animal trade. After nearly five decades of political isolation, with the recently democratized government together with lifted U.S. sanctions, Myanmar has become quite appealing to international developers, animal traders, and tourists.   The influx of industry has had direct effects on the economy, ecosystem, environment, and public health. These changes have obvious in the forests and waterway developments, especially in patterns of displacement of endemic wildlife and increasing reports of human disease of unknown causes.  Traditional practices that require locals to be in close contact with wildlife persist; there have also been an increase in poaching due to access and demand.

As these changes are likely to continue to occur at a rapid pace, it is essential to evaluate the effects of development. USAID’s PREDICT project has been implemented in Myanmar to evaluate the effects of these changes as they pertain to human health, animal health, and environmental health, with a special focus on the emergence of zoonotic diseases.  Traditional practices such as the consumption of wildlife (e.g rats and bats) and guano collection are being examined alongside the burgeoning tourism industry and the application of advanced agricultural practices.  In collaboration with the Ministries of (1) Health & Sports, (2) Livestock, Agriculture & Irrigation, and (3) Natural Resources & Environmental Conservation, as well as WHO and FAO, the PREDICT project has been working to detect zoonotic viruses through concurrent biological sampling of priority wildlife, livestock, and humans which demonstrate an observable interface and risk.  Samples will be evaluated for viral families known to include zoonotic diseases that have had clear pandemic impacts through consensus PCR analysis.  Results will be presented as they correlate to the unique cultural practices and development occurring in Myanmar.

**Background**

In the past decade, the emergence of zoonotic diseases has become an alarming issue around the world, seriously affecting the health of both humans and animals. Over 70% of infectious diseases in humans are of zoonotic origin including transmissions from both wildlife and livestock. Southeast Asia has experienced several infectious diseases that have spilled over from animals including pandemic diseases like avian influenza and severe acute respiratory syndrome (SARS) as well as those of an endemic nature including leptospirosis and rabies.

Myanmar, a developing nation of Southeast Asia, has a high incidence of high-risk zoonotic disease transmission opportunities from animals to humans. Increased trade, mobility of animals and humans, commercialization of farming and animal production, occupancy of forest areas for new development and urbanization, the promotion of ecotourism, and traditional practices, such as the consumption of wildlife (e.g rats and bats) and guano collection are only some of the factors contributing to the changes.

It is essential to evaluate the effects of rapid changes and development immediately. USAID’s PREDICT project has recently been implemented in Myanmar to evaluate the effects of these changes as they pertain to human health, animal health, and environmental health, with an emphasis on the emergence of zoonotic diseases. This evaluation will include various socioeconomic factors related to the rapid development of Myanmar, cultural practices, and livelihood, which may increase the potential risk of disease transmission interface among wildlife, livestock, and humans.

**Goal and Objectives**

**Overall goal:**

* To identify animal reservoirs and amplification hosts for zoonotic viruses, strengthen human and animal disease surveillance system capacities in hotspot regions, and establish collaborative One Health platforms to reduce the risk of disease spillover, amplification, and spread

**Specific objectives:**

* To detect and characterize new and known viruses of epidemic and pandemic potential in high-risk communities
* To identify biological, behavioral, and ecological factors influencing the risk of viral spillover, amplification, and spread
* To determine potential targets for intervention based on high-risk human behaviors and practices that amplify disease transmission in hotspots for viral evolution, spillover, amplification, and spread.

**Methodology**

**Site selection**

A preliminary assessment was conducted to identify the geographical areas and communities with the highest risk of human-wildlife interface. Two sites, that were evaluated to be high-risk, were selected in Hpa-an and Yangon; locals in both sites are heavily dependent on the commercialization of agriculture, involve themselves in religious practices that require them to be in close contact with wildlife, and currently reside in locations where ecotourism is being highly promoted. Livestock and agricultural industries are also very active in the selected areas; as a result, locals are considered to be at risk of human-wildlife-livestock interface.

**Study design and study period**

An analytical study on concurrent human and animal biological surveillance and human behavioral risk characterization in two selected sites in Yangon and Hpaan. The study began in April 2017 and will be continued until September 2019, for a total of 2.5 years.

**Study population**

* People currently residing near bat caves in Hpa An, Kayin State — those who are occupationally exposed to bats through bat guano collection to use in agriculture and who are working within close ranges of the caves for religious purposes.
* People residing in the surroundings of Hlawga National Park, Hmawbi, Yangon region — those who are working and visiting the park frequently, where about 2,000 non-human primates are present. Rodents and bats are also prevalent in this park. Domestic animals in or near the park include cattle, chickens, ducks and dogs.

**Data collection method**

This study is being conducted by the PREDICT Myanmar team, in collaboration with the Department of Medical Research, Myanmar (DMR) and Livestock, Breeding and Veterinary Department (LBVD). Data collection is done in the dry and wet seasons of each year. All field research procedures, including biological sampling and interviews, will be conducted by local individuals trained by the survey team, whose members are already familiar with the PREDICT data collection protocols and training materials. Patients/participants volunteer approximately 1 hour of their time to participate in the study; they mainly provide biological samples and complete questionnaires.Face-to-face interviews are conducted using a structured questionnaire and biological sampling methods, which include the collection of oral swab, nasal swab, blood, serum, urine and feces.

**Data analysis**

Analysis of quantitative data, laboratory test results and viral sequences will be done at the end of 2018 for the whole period of the project. It will involve the calculation of metrics of contact for each risk group in the study, such as the proportion of respondents indicating they have butchered live animals, seen wildlife in their homes, been bitten or scratched by animals, etc. Comparisons of metrics of contact between men and women, children and adults, and different communities will be conducted in order to explore the environmental and social factors (gender, age, occupation/religion, socioeconomic status (SES)) that influence contact with animals and to determine who is at the highest risk, in relation with different types of human-animal contact.

Virus detection in human samples will be performed using a combination of consensus PCR (cPCR) and high throughput sequencing (HTS) to detect and discover known novel viruses from different sample types. Viral families/genera targeted are of potential pandemic or epidemic significance and are previously associated with ILI, SARI, FUO, and hemorrhagic diseases; they may include coronavirus, paramyxovirus, influenza virus and filovirus.

Test results and viral sequences obtained from human and animal (wildlife and livestock) samples will be compared; at the same time, phylogenetic analyses will be performed to document viral sharing between animals and humans. Results will be analyzed according to the context of the questionnaire data to identify high-risk human-animal interactions and behaviors or practices that are associated with viral spillover and/or sharing.

**Current process of data collection**

**Table 1: Number of animal/human samples by taxa (as of December 2017)**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Wildlife |  |  |  | Domestic |  |  | Humans |
| rodents/ shrews | bats | non-human primates | carnivores | poultry/ other fowl | goats/ sheep | swine | humans |
| **439** | **1555** | **326** | **1** | **52** | **57** | **64** | **347** |

**Preliminary findings**

All interviewee data were checked on the day of interview to ensure accuracy and completeness. Data were entered into the EIDITH data system and analyzed for each risk group and disease interface, such as animal production, crop production, zoo & sanctuaries and natural areas. Risk behaviors include coming into different types of contact with animals, such as handling, rearing**,** butchering live animals, seen wildlife in their homes, been bitten or scratched by animals, etc.

A total of 347 people were involved in high risk behavior sampling until December 2017. 50.4% were female, and 49.6% male. The mean age was 40 years old and the majority were between the age range of 31-50 (48%). 69% of respondents have been staying in these areas for more than 10 years. This table below shows that the majority of the respondents in the 4 disease interfaces have high percentages of disease exposure and disease transmission from wildlife and livestock through different kinds of contact.

**Table 2: Disease interface and risk behaviors of sampled human**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Risk behavior directly exposed to animals last year** | **Animal production N=25** | **Animal and crop production N=165** | **Animal, crop production, dwelling and temp settlement N=69** | **Natural area, animal and crop production**  **N=50** | **Zoo and sanctuaries N=38** |
| Handled | 76% | 87% | 100% | 82% | 95% |
| Raised | 72% | 85% | 97% | 52% | 79% |
| Pet in dwelling | 88% | 80% | 87% | 70% | 97% |
| Come in dwelling | 72% | 91% | 100% | 60% | 87% |
| Eaten sick animal | 0% | 50% | 64% | 4% | 68% |
| Eaten dead animal | 20% | 64% | 86% | 12% | 66% |
| Hunted animal | 0% | 6% | 6% | 0% | 3% |
| Sold dead | 0% | 48% | 55% | 2% | 66% |
| Scratched by animal | 24% | 55% | 61% | 12% | 71% |

**Table 3: Exposure of wildlife and livestock of sampled human through animal contacts**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Number of sampled people** | **No exposure** | **Direct exposure** | | |
| **Wildlife (bat, rat, non-human primate)** | **Livestock (fowl, pig, goat)** | **Wildlife and livestock** |
| **N=347** | **37 (11%)** | **160 (46%)** | **299 (86%)** | **149 (43%)** |

**Conclusion**

High levels of risk exposure and reported practices in animal handling and consumption reveal that all the people in this study engage in high-risk behavior due to their livelihood methods, and traditional practices regarding wildlife consumption. These, in turn, are influenced by the socio-cultural and economic changes within the country. Surveillance samples collected concurrently from wildlife, livestock, and humans are being analyzed to evaluate zoonotic disease presence and sharing between species. Pairing our results from our behavioral study with our biological sample results will give us a greater understanding of the high-risk activities demonstrated in Mynamar.

Preliminary findings revealed that although most of the respondents are worried about disease outbreak in their live animals, which is critical for their livelihood, they are not aware of the potential risks of zoonotic diseases transmission associated with their lifestyles, occupation and traditional practices.

**Continued process and recommendations**

Data collection including face to face interviews to high-risk communities and viral surveillance for human and animal is being conducted in both wet and dry season of each year. Viral analysis for 155 samples from 105 animals including 55 bats, and 50 rodents and shrews, are in process. Viral analysis will be conducted for both human and animals in laboratories in DMR and LBVD with trained laboratory team by following PREDICT protocol.

This study intends to identify the risk of viral spillover and determine potential target populations and areas for implementation related to zoonotic disease transmission and the One Health concept. It is also a step towards highly structured research that will elaborate on risk perception and traditional beliefs of high risk communities in more detail. This needs to be addressed in future One Health implementations aiming for prevention and reduction of disease burdens.

**Contact Information**

* Dr. Theingi Win Myat, Deputy Director/ Head, Virology Research Division, Department of Medical Research, Yangon (Ph: 095140652, email: [drtheingiwinmyat@gmail.com](mailto:drtheingiwinmyat@gmail.com) )
* Dr. Ohnmar Aung, Project Coordinator, PREDICT Myanmar, Smithsonian Conservation Biology Institute (Ph: 09254011694, email: [ohnmara@gmail.com](mailto:ohnmara@gmail.com))
* Dr. Marc Valitutto, Myanmar Project Liaison & Wildlife Veterinary Medical Officer, Global Health Program, Smithsonian Conservation Biology Institute (email: [valituttoM@si.edu)](mailto:valituttoM@si.edu))