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ANNUAL MEETING

Sheraton New Orleans and New Orleans Marriott | New Orleans, LA USA

October 28 – November 1, 2018

ABSTRACT BOOK

"There will be epidemics..."

EBOLA: WORLD GOES ON RED ALERT -2014

Six Dead, 17 Sick From Drug-Resistant TB -2017

Panic as 1,500 Die of Malaria -1998

Spread of Spanish Flu Menaces War Production -1918

Cholera Epidemic in Yemen Now Affects One Million People -2017

Charity to Help Fight Malaria in Africa -2010

Ebola Out of Control -2014

Death Toll Growing as Influenza Claims Many Score Victims -1918

Success in Tests of Yellow Fever Serum Reported -1932

Brace for Dengue -2017

Dengue Dengue EVERYWHERE -2017

Officials: Texas Sees Growing Number of Typhus Cases -2017

FDA Busts Fake Malaria Medicines -2013

New Hope for AIDS Drug -1996

African Countries to Plot New Malaria Vaccine -2017

ZIKA THREAT ON OUR DOORSTEP -2016

DIPHTHERIA: Why Is It Back? -2017

Zika Spreads Worldwide -2016

Island Declares State of Emergency Over Zika Virus, Dengue Fever Outbreak -2016

ASTMH Annual Meeting Canceled Due to Spanish Flu Outbreak -1918

QUARANTINE WANTED as Yellow Fever Spreads -1878

An American Plague: Yellow Fever Epidemic of 1793 -2003

Been to an Ebola-affected country? Stay away from ASTMH meeting, Louisiana says -2014

Malaria Cases on the Rise in Last 3 Years -2016

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Supplement to
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%), *Bartonella spp* (0.8%), and *Babesia spp* (0.4 %). The high analytical sensitivity suggests potential for the duo 4-plex qPCR for detection of common TBZ.

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APPLICATION OF WHOLE GENOME SEQUENCING TO STUDY THE GENETIC DIVERSITY OF FIELD COLLECTED *ORNITHODORUS* TICKS AND THE PATHOGENS THEY CARRY FROM NIGERIA

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Ornithodorus ticks are established vectors of relapsing fever in humans caused by *Borrelia* species and have also been reported to be potential vector for the recently emerging Alkhurma haemorrhagic fever virus. They have been reported from various parts of the world. However, there are not much genomic data utilizing sensitive techniques from Africa. Whole Genome Sequencing (WGS) using MinION (Oxford Nanopore), is a new and rapid third generation sequencing technology that has been successfully utilized to determine species of mosquito vectors and detect a variety of vector borne viruses. Using qPCR and WGS, we attempt to determine the species of *Ornithodorus* ticks and the pathogen they carry from a semi-arid Northeastern Nigeria. The sequence data generated was used to infer phylogenetic relationships among ticks as well as the pathogens detected. Genomic DNA was extracted from field collected ticks pooled by life stages. PCR analysis to identify tick species using primers against tick 16S gene and Sanger sequencing of resulting amplicons was initially carried out. The preliminary results by qPCR revealed the species of ticks to be *Ornithodoros savignyi.* Samples were further screened for the presence of *Borrelia* by sequencing of 16S, flagellin and IGS regions which revealed the presence of *Candidatus* Borrelia kalaharica. A recently proposed species that caused relapsing fever in a returning traveller from Southern Africa to Germany. The complete results from more extensive field sampling and analyses from sequence generated from the MinION will be presented at the meeting. This is the first report of relapsing fever *Borrelia* of public health importance from Nigeria. Furthermore, genomic data generated could help in better understanding of the diversity of tick species and for improved vector-borne disease diagnostics.

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SYNANTHROPIC RODENTS AS CARRIERS OF IMPORTANT ZOONOTIC PATHOGENS - FIRST REPORT FROM BHUTAN

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The number of acute undifferentiated febrile illness cases (AUFI) has been on the rise recently in Bhutan leading to misdiagnosis and inadequate treatment. Bhutan is a small country known for its rich biodiversity and strong conservation policies. It has approximately 80 rodent species. Rodents are well known reservoirs and vectors of many emerging and re-emerging infectious diseases, but little is known about their potential role in zoonotic disease transmission in Bhutan. A cross-sectional study of zoonotic disease pathogens in rodents was performed in Chukha district, Bhutan where many AUFI cases have been detected in people. Field collections were performed in 2016 and 2017. Rodents in and around houses and agricultural fields were trapped using live wire mesh traps. Following euthanasia, liver and kidney tissues were removed and tested by Polymerase Chain Reaction (PCR) for *O. tsutsugamushi* and other bacterial and rickettsial pathogens causing Bartonellosis, Borreliosis, human monocytic ehrlichiosis (HME), human granulocytic anaplasmosis (HGA), leptospirosis, and rickettsiosis. A phylogenetic analysis was performed on all rodent species captured and pathogens detected. Four out of the twelve rodents (33%) sampled in 2016 tested positive by PCR for a zoonotic pathogen. *Anaplasma phagocytophilum*, *Bartonella grahamii*, and *B. queenslandensis* were identified for the first time in Bhutan. *Leptospira interrogans* was also detected for the first time from rodents in Bhutan. Twenty-four additional rodents were collected in 2017, the results from these samples are still being analyzed and the final results will be presented during the meeting. Our study shows that sampling even a few rodents in Bhutan can provide important information about potential risks of rodent-borne zoonotic diseases. This is first of this kind of study conducted in Bhutan and more studies are warranted with a larger sample size and that cover more localities and diverse landscapes. We expect interesting findings from rodents sampled in 2017 and ongoing studies. This data will be used to better quantify the risk of rodent-borne zoonotic diseases in Bhutan.

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INCIDENCE OF HUMAN MONOCYTIC EHRLICHIOSIS IN SITES WHERE LONE STAR TICK INFESTATIONS HAVE RECENTLY EMERGED

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The Lone Star tick (*Amblyomma americanum*), has greatly expanded its distribution in the northeastern United States within the last decade. Once largely restricted to western Long Island and New Jersey south to Florida and westward to Texas, sporadic specimens have now been recorded from all northeastern states, and focal perpetuating infestations have been identified in Massachusetts. This aggressively human biting tick is a known vector for STARI/Masters Disease, human monocytic ehrlichiosis (HME), *Ehrlichia ewingii* ehrlichiosis, Rocky Mountain spotted fever, and tularemia; a common symbiont of Lone Star ticks, *Rickettsia amblyommatis*, is suspected of causing febrile illness in people. The public health burden of new Lone Star tick infestations has not been determined. We analyzed 37,133 blood samples submitted by clinical practices in CT, MA, RI, ME, NH, and VT during 2016-2017 for evidence of *Ehrlichia chaffeensis* (the agent of HME) DNA by polymerase chain reaction. By comparison, 21,082 blood samples were similarly analyzed from NJ, NY, PA, and MD, where Lone Star ticks have been endemic for at least two decades. Only two samples (0.005%) were positive from the New England sites whereas 0.63% of those from sites farther south were positive. We conclude that risk of acquiring HME and likely that of the other less common zoonotic infections transmitted by Lone Star ticks is very small in sites where they have recently invaded.

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RISK OF TICK-BORNE ENCEPHALITIS VIRUS INFECTION IN NORTHERN KAZAKHSTAN

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Tick-borne encephalitis (TBE) is becoming a growing public health problem in Kazakhstan. Recognized areas of spread of this infection are the eastern and south-eastern regions. At the same time, in recent years, there have been registered cases of TBE infection in the northern region of the republic, in particular in the Akmola region (24 cases in the period