Insight of Zoonotic Viruses at Human-Animal Interfaces in Cambodia

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improvement of global health needs a collaborative, multisectoral, and transdisciplinary approach, acting at the local, regional and global levels. This concept becomes paramount when taking into account that most diseases affecting humans in the last decades - not only COVID-19 - have been caused by pathogens originated in animals.

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S1: One Health session: Serosurveillance of High Consequence Zoonotic Viruses at the Human-Animal Interface

Date: Friday, Nov 18, 2022 Time: 10:30-12:00

Venue: Banquet Hall Level 3

INSIGHT OF ZOONOTIC VIRUSES AT HUMAN-ANIMAL INTERFACES IN CAMBODIA

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Emerging infectious diseases have been causing outbreaks in humans for centuries and most infectious diseases originate in animals. Re-emerging zoonotic pathogens are rapidly increasing in prevalence or geographic range and causing a significant and growing threat to global health. The present work provides an insight of zoonotic viruses risk at human-bat/rodent interfaces in Cambodia.

We conducted studies to investigate the circulation of zoonotic viruses and the risk of exposure in human living at the interfaces with bats and rodents. Rodent's samples were collected in rural and urban areas of Cambodia. Organs were tested for Hantavirus, Orthohepevirus species C and Arenavirus. Bat's samples were collected in Steung Treng for Sarbecovirus and in Battambang and Kandal for Nipah virus detection. People working/living at the human-animal interfaces were screened for IgG antibodies.

In rodents (750), hantavirus was detected in 3.3% rodents from urban areas only. Seoul orthohantavirus was the most predominant virus followed by Thottapalayam virus. HEV-C was detected only in rodents from urban settings (1.8%). Arenavirus was detected in both rural (6.8%) and urban (2.5%) areas. In humans (788), the seroprevalence of IgG antibodies against hantavirus, HEV-A and Arenavirus was 10.0%, 24% and 23.4% respectively.

NiV was detected in flying fox's urines collected between 2013-2016 in Kandal (0.63%) and in Battambang (1.03%). Blood samples collected in both provinces were negative for NiV antibodies.

SARS-CoV-2 related virus was detected in Rhinolphus shameli in Steung Treng in 2010, 2020 and 2021. Blood samples from people living at the vicinity of positive bats were positive for antibodies against CoV (7.7%), but no specific neutralizing SARS-CoV2 antibodies were detected.

Our studies provided insight of the risk of zoonoses in Cambodia and highlighted the importance of zoonotic surveillance and further One Health effort to prevent, detect, and respond to future cross-species transmission.

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S2: Clinical management of hard to treat infections (case-based discussions) – (in collaboration with MSIDC)

Date: Friday, Nov 18, 2022 Time: 10:30-12:00

Venue: Conference Hall 3, Level 3

MANAGEMENT OF (RECURRENT OR) PERSISTENT MRSA INFECTION

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MRSA infections are often difficult to treat mainly because of difficulty in source control in cases of biofilm infections associated with prostheses or endovascular infections. Drug toxicities and MIC creep can also complicate treatment of MRSA infections although with new agents, this is less of a concern in recent years. Ultimately, the key to successful management of difficult and complex MRSA infections is understanding the pharmacokinetics and pharmacodynamics of the agents used and shared decision making with the patient. This will be illustrated with a series of cases.

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DRUG-RESISTANT ENTERIC PATHOGENS

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In 2010, WHO declared that AMR is one of the top 10 global public health threats facing humanity. Without adequate intervention, global death rates attributable to AMR are projected to surpass that of cancer and reach 10 million deaths per year by 2050. The transmission and spread of multi-drug resistant organisms (MDROs) are facilitated by the increase in travel and trade across the globe over the last few decades. Antimicrobial resistance imposes a drastic burden in terms of healthcare costs, morbidity and mortality. The human gastrointestinal (GI) tract has the potential to transmit MDROs, with the gut microbiome containing an estimated 1014 microorganisms. The gut is a key conduit for the genesis and spread of antimicrobial resistance in enteric bacterial pathogens. Invasive enteropathogens, that exist as bacterial commensals can inflict dysbiosis and disease when exposed