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Current Knowledge of Exposure to Tick-borne Pathogens among Rural Population in Cambodia

Introduction: Ticks transmit a greater variety of pathogenic agents than any other blood-feeding arthropods, posing a profound impact on the economy of livestock farming and human health concerns. Cambodia already has an enormously high burden of infectious diseases; however, little is known about potential hotspots of tick-borne pathogens. The diversity and distribution of tick species remain poorly characterized. The medical, veterinary, and socio-economic burdens of tick-borne diseases remain also largely unknown. In the present study, we aim to assess the diversity of tick species and associated pathogens circulating in a rural community of Cambodia and to evaluate the transmission risk of these pathogens in people living in the area where ticks have been collected. Methods: The study was conducted in rural communities of Kampong Thom province located in the central part of Cambodia. Ticks were

collected from animals and the vegetation surrounding human households. All collected ticks were screened for pathogens considered major threats to human health including severe fever with thrombocytopenia syndrome virus (SFTSV), tick-borne encephalitis virus (TBEV), and Crimean-Congo hemorrhagic fever virus (CCHFV), using PCR assays. Human blood samples collected from 200 residents of tick-affected households underwent ELISA assay for detection of IgG antibodies against these pathogens.

Results: From 82 households, 1,433 ticks were collected, primarily from dogs (97.3%). Among them, 91% were adult, dominated by *Rhipicephalus sanguineus* (97.3%) followed by *Rhipicephalus microplus* (2.4%) and *Rhipicephalus haemaphysaloides* (0.3%). None of the targeted viruses were detected. Of the 200 human samples, 56% tested positive for anti-TBEV IgG, 6.7% for anti-SFTSV IgG, 2.5% for anti-CCHFV IgG, 10.5% for anti-scrub typhus IgG, 5% for anti-Borrelia, and 0.6% for anti-Coxiella IgG.

Discussion: Given the absence of highly pathogenic pathogens in our findings, further analysis utilizing metagenomics approaches is necessary to identify and characterize other tick-borne pathogens potentially circulating in Cambodia. The presence of antibodies against tick-borne pathogens in humans, particularly anti-TBEV IgG antibodies, might be overestimated in the present study due to cross-reactions with other flaviviruses. Thus, further confirmatory tests are anticipated for samples positive for anti-SFTSV, TBEV, and CCHFV IgG antibodies using seroneutralization assay.

Conclusion: Our study provided preliminary data on ticks and the potential risks of tick-borne pathogens circulating in the rural community of Cambodia. Large-scale studies implementing one health approach must be considered to better assess the threats of tick-borne diseases at the intersection of animal health, human health, and the environment in Cambodia.

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