**Conclusion:** SSU based PCR-RFLP tool discriminated Cryptosporidium into two species and *C. hominis* was more prevalent in this area. GFP60 sequence based subtyping has revealed the coexistence of *C. hominis* with *C. meleagridis/C. parvum* and also *C. hominis* subtypes. These species were missed by SSU rRNA based RFLP analysis which detected only *C. hominis* in concurrent infections. The existence of many *C. hominis* and *C. parvum* subgenotype families and subtypes within the subgenotype families reveals the complexity of Cryptosporidium transmission and this heterogeneity indicates stable cryptosporidiosis transmission in North India.

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**A survey of preparedness and risk communication in US and Thai zoos: using highly pathogenic Avian influenza as a model**

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**Background:** The ecology of zoonotic infections are particularly complex in zoological garden settings. It involves endangered and non-endangered resident zoo animals, free living wildlife, millions of human visitors, zookeepers that can come into very intimate contact with animals. Thus, Zoos are potentially one critical point for wildlife zoonosis to emerge. The best known recent examples of this phenomenon are the episodes of Highly Pathogenic Avian Influenza H5N1 (HPAI) and West Nile virus. Meanwhile, zoos are also the place where the public seeks information during zoonotic disease outbreaks that involve any kind of wildlife and a major setting for conservation education.

**Methods:** This study aimed to assess the existing stance of zoos in Thailand and United States concerning the communication of potential risks using HPAI as a model. We used a convenience sampling strategy for collection of data targeting personnel from 8 zoos in Thailand and in the United States. The survey was a self-administered, web based instrument which included 22 questions focusing on respondent demographics, mental models for HPAI, adherence to risk communication principles as expounded by Peter Sandman and assessment of zoo preparedness.

**Results:** Based on 38 responses, 95% agreed that the outbreak of HPAI can cause negative emotion or outrage. When we probed the underlying mental model for the negative emotions or outrage, the top three categories included the catastrophic nature of HPAI, trust accrued by communicating authority or agency and the inherent dread of a high mortality, high impact disease. Timing of zoo response, as the outbreak continued, was characterized by 37% indicating they would be likely to communicate with the public immediately, 5% would wait until a greater number of cases was available and 37% would wait for official declaration of the outbreak. If HPAI were to occur in a zoo, the respondents felt that wild bird “stop over” was the most likely cause. Zoos indicate that preparedness status was much more than enough (3%), more than enough (16%), enough (35%), not enough (32%), nearly nothing (14%).

**Conclusion:** The effect of location, country, and respondent strata was analyzed.

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**Emergence of dengue virus genotype 3 subgenotype III in Malaysia**


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**Background:** Malaysia is hyperendemic country for dengue, where all four dengue viruses (DENV) are co-circulating within the community. The presence of DENV genotype 3 (DENV-3) was first described by Lim *et al* as the main causative agent responsible for the 1973 dengue epidemics in Malaysia. From then on, DENV-3 became ubiquitous in Malaysia that exhibited a cyclical outbreak pattern at interval of seven to eight years. Several studies have demonstrated the presence of DENV-3 subgenotypes I and II in Malaysia. Here, we present evidence at emergence of subgenotype III in Malaysia.

**Methods:** A random subset of DENV-3 virus samples, isolated in year 2010, was obtained from Diagnostic Virology Repository at University Malaya Medical Center. The virus was propagated through one round passage in cell culture. Viral RNA was extracted from cell culture supernatant and the virus envelope (E) gene was amplified and sequenced. Complete E gene sequences of DENV-3 were examined in the study, together with sequences retrieved from the GenBank. Phylogenetic relationship of these viruses is presented.

**Results:** The phylogenetic analysis based on the complete E gene of DENV-3 isolated from Malaysia along with representative strains obtained from the GenBank demonstrates the presence of 5 distinct DENV-3 subgenotypes. All the Malaysia isolates in this study clustered under the subgenotype III group, which forms a distinct Malaysia lineage. This Malaysia lineage grouped closely with DENV-3 strain isolated from Singapore during the 2005 outbreaks. These viruses formed a geographically distinctive clade within the subgenotype III group.

**Conclusion:** In summary, our study demonstrates the emergence of DENV-3 subgenotype III in Malaysia in 2010. Further study is underway to monitor and evaluate the possibility of this new subgenotype to emerge as the dominant circulating DENV-3 in Malaysia.

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