

Conclusions: The results obtained by sequencing confirmed the presence of *C. parvum* in pre-weaned calves, demonstrating the relationship between the age of infected calves and the species/genotype of *Cryptosporidium*, highlighting the importance of infection in young animals which are usually infected by zoonotic species.

Board 70. The Importance of Enzootic Stability in Explaining the Spatio-temporal Pattern of Hemorrhagic Disease in White-tailed Deer

K. Magori¹, D.E. Stallknecht², B.A. White¹, A.W. Park¹; ¹Odum School of Ecology, University of Georgia, Athens, GA, USA, ²Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA, USA.

Background: Hemorrhagic disease (HD) is the most important infectious disease affecting white-tailed deer (WTD) in North America, causing a range of clinical symptoms from morbidity to outbreaks with massive mortality. HD is caused by several serotypes of related orbiviruses, such as the Epizootic Hemorrhagic Disease Virus (EHDV) and Blue-tongue Virus (BTV), both transmitted by *Culicoides* biting midges. A particular characteristic of HD is enzootic stability, defined as the absence of clinical disease despite high levels of infection in the host population. Enzootic stability in HD occurs in the Southern US (particularly in TX, OK and KS), where HD is not reported despite virus isolation and close to 100% seroprevalence detected for EHDV and BTV in WTD. **Methods:** Capitalizing on a 30-year surveillance dataset by the Southeastern Cooperative Wildlife Disease Study group (SCWDS), we characterize the complex spatio-temporal pattern of HD. We elucidate the mechanisms responsible for enzootic stability for HD in WTD using a conceptual model. We use statistical models to explain the spatio-temporal pattern of HD across the United States. **Results:** Our conceptual model reproduces the pattern of enzootic stability for HD in WTD through the mechanisms of maternal protection of fawns by antibodies secreted in the milk of does, and partial cross-immunity between serotypes of EHDV and BTV. Statistical models incorporating enzootic stability in the Southern US can explain the annual epizootics of HD viruses and their persistence at the continental scale. The statistical framework incorporating enzootic stability provides reliable probability estimates for the presence of infection, morbidity and mortality, and reporting in a particular county for WTD, which correlate with local risk of infection to livestock. **Conclusions:** Enzootic stability for HD, operating through maternal protection and partial cross-immunity, is a critical phenomenon to incorporate in order to understand the spatio-temporal dynamics of HD and to predict the presence of HD in WTD as well as the risk of infection to livestock.

Board 71. Mathematical Modeling of H3N8 Canine Influenza Virus Transmission in Shelter Facilities

T.C. Anderson, P.C. Crawford, E.P. Gibbs, J.J. Pohedra, C.C. Lord; University of Florida, Gainesville, FL, USA.

Background: Canine influenza virus subtype H3N8 (H3N8 CIV) is a highly contagious respiratory infection. Dogs housed in communal settings are at greatest risk of infection. The objective of this study was to develop a mathematical model of H3N8 CIV transmission in shelters in order to assess the importance of multiple factors in the likelihood of an epidemic following virus introduction. **Methods:** A deterministic mathematical model was developed for fixed capacity, high turnover shelters. Model classes included susceptible, latent, infectious clinical, infectious subclinical, and recovered dogs, and fomites. Differential equations, representing the change over time for each class during a simulation, were programmed in MATLAB. Model parameters accounted for virus transmission factors, and immigration and emigration due to typical dog movements. Parameter ranges, most probable values, and distributions were established using published literature, experimental data, and expert opinion. Sensitivity analyses were performed to refine these ranges. Latin hypercube sampling was used to generate 500 parameter sets for simulations. Model outputs included: epidemic occurrence, establishment of endemic infection, epidemic duration, numbers of infected

dogs, and the relative contribution of direct and indirect transmission to epidemic dynamics. Stepwise linear regression was conducted to assess the effect of model parameters on select outputs. **Results:** H3N8 CIV epidemics occurred in 498/500 (99.6%) simulations. Endemic infection was established in 100%. The average epidemic lasted 38 days, and large numbers of dogs were affected. Model parameters associated with indirect virus transmission and shelter size most significantly influenced these outcomes. Of 498 epidemics, 21% were primarily due to direct virus transmission, 63% were primarily due to indirect virus transmission, and 16% were due to both. **Conclusions:** Given the model structure and parameter ranges used, and in the face of no interventions, a canine influenza epidemic almost always occurred when an infected dog was introduced into a shelter. Prevention and control strategies that reduce transmission between dogs and fomites and manage the number of incoming susceptible dogs will likely reduce the impact of H3N8 CIV epidemics in shelters.

Viral Hepatitis

Monday, March 12 | 12:30 PM – 1:30 PM | Grand Hall

Board 72. Underestimated Burden of Hepatitis E: Contribution of Small Clusters Identified in Bangladesh

H.M. Sazzad¹, E.S. Gurley¹, J. Hossain¹, A.B. Labrique², S.K. Saha^{3,4}, S.K. Chowdhury¹, S. Islam¹, Y. Khudyakov⁵, C.-G. Teo⁵, M. Rahman⁶, S.P. Luby^{1,5}; ¹ICDDR,B, Dhaka, Bangladesh, ²Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, ³Popular Diagnostic Centre Ltd., Dhaka, Bangladesh, ⁴Department of Microbiology, Dhaka Shishu Hospital, Dhaka, Bangladesh, ⁵Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, ⁶Institute of Epidemiology Disease Control and Research (IEDCR), Dhaka, Bangladesh.

Background: Hepatitis E is usually reported in the literature as large outbreaks with thousands of cases associated with contaminated drinking water systems. Small clusters of hepatitis E may occur in endemic areas, but may be less frequently reported to public health authorities. The objective of this analysis was to report on the frequency of small clusters of hepatitis E identified through event based outbreak surveillance and a research project in Bangladesh. **Methods:** We defined a small cluster as at least 2 cases who were <100 anti-HEV-IgM positive with clinical jaundice and developed illness within 2 months of each other and were residing in the same home, neighborhoods or workplaces. We identified these clusters through ongoing outbreak surveillance by IEDCR and ICDDR,B and from a research study in an urban private laboratory in Dhaka. We used an ELISA produced by Diagnostic Systems to identify the cases. **Results:** During November 2008 thru July 2011, we identified 30 small clusters of hepatitis E in Bangladesh. The mean number of clusters was 1 (range: 1 - 4) per month. The median number of cases in each cluster was 3 (range: 2 - 74). The only cluster reported through outbreak surveillance consisted of 74 cases and occurred in a rural area. The remaining 29 clusters were identified from the diagnostic laboratory in urban Dhaka. Seventeen (60%) of urban clusters occurred within families or neighborhoods. Two clusters originated in residential hostels for medical professionals, including the rural one. The remaining eleven were associated with the workplace, including 3 physicians from a pediatric hospital and 10 co-workers at a bank. **Conclusion:** The multiple small clusters of hepatitis E in Bangladesh that we identified through limited surveillance and diagnostics reflect the underestimated burden of hepatitis E in Bangladesh. Many similar small clusters almost certainly occur but remain unrecognized. Burden estimates that only consider the large reported outbreaks may underestimate true burden by missing a substantial number of such cases. Subsequent investigations should focus on describing transmission routes associated with small clusters. Improved surveillance for and early intervention with small clusters could prevent future large hepatitis E outbreaks that may start as a small clusters.