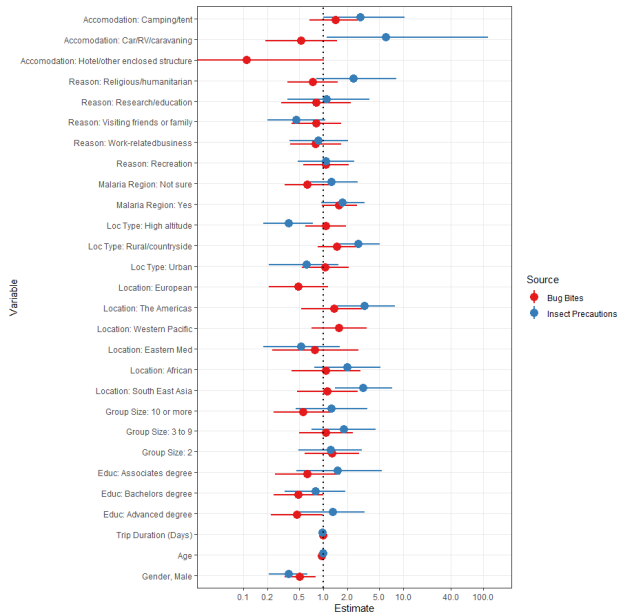


Results. A total of 463 individuals completed the survey and were included in our analytic sample. The majority of respondents (80%) reported using insect repellent, and close to half (45%) reported bug bites. Insect repellent use was positively associated with visiting rural/countryside (OR 2.78, 95% CI 1.50 – 5.15), and traveling to South East Asia (OR 3.16, 95% CI 1.40 – 7.26), or Americas regions (OR 3.34, 95% CI 1.45 – 7.92). Being of male gender (OR 0.37, 95% CI 0.21 – 0.64) or traveling to high altitude locations (OR 0.37, 95% CI 0.18 – 0.74) was negatively associated with using insect repellent. Longer trip duration (OR 1.01, 95% CI 1.00 – 1.02) was positively associated with reporting insect bites, while male gender (OR 0.51, 95% CI 0.33 – 0.80), older age (OR 0.96, 95% CI 0.95 – 0.98), and having an advanced degree (OR 0.47, 95% CI 0.22 – 0.99) were negatively associated.

Estimated Risk Factors of Insect Bites and Insect Repellent Use



Characteristics of international travelers were self-reported in a cross-sectional study. Use of insect repellent and reporting bug bites despite repellent use was examined through multivariate logistic regression and used to calculate odds ratios and 95% confidence intervals. Due to multicollinearity and data skewness, the following variables were omitted from the insect repellent model: Accommodation: Hotel/other enclosed structure, Location: European, Location: and Western Pacific. Reference categories are Gender: Female, Education: High school diploma/GED or less, Group size: 1 (Traveled alone), Location type: Urban, and Malaria region: No. All other categories are not mutually exclusive and evaluated as separate binary variables.

Conclusion. We show that gender, age, trip duration, and education level were associated with self-reported bug bites during travel abroad. Given the number of vector-borne diseases affecting health of travelers, our findings will contribute towards strategies to advise travelers for disease prevention.

Disclosures. All Authors: No reported disclosures

740. Elucidation of the Mode of *Clostridioides difficile* Transmission Based on One Health Approach

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Session: P-35. Global Health

Background. Community-onset *Clostridioides difficile* (*C. difficile*) infection (CACDI) has been increasing in recent years. To explore the transmission route of CACDI, we performed the whole-genome sequencing of *C. difficile* isolated from CACDI patients and compared it to the isolates from livestock, companion animals, and soil.

Methods. From October 2020 until April 2021, fecal specimens of cattle, poultry, swine, felines, canines, CACDI patients, their families, and soil from the CACDI patients' living environment were applied for isolation of *C. difficile*. Whole-genome sequencing of *C. difficile* was performed on the MiSeq system (Illumina). Using the draft genome obtained from these analyses, the house-keeping gene (*tpi*), MLST, toxin genes (*tcdA*, *tcdB*, *cdtA*, *cdtB*), and resistance genes (*gyrA*, *gyrB*, *rpoA*, *rpoB*, *rpoC*) were comprehensively analyzed.

Results. As of March 31, 2021, 275 specimens were collected. Forty-five fecal specimens of companion animal origin (23 feline and 22 canines) were collected and the positive rate of *C. difficile* was 28.9% (2 felines, 11 canines). In MLST analysis, ST 15 (4 strains), ST 26 (2 strains), ST 42, ST 3, ST 28, ST 100, and ST 185 were detected in canines, and ST 203 and ST 297 strains were detected in felines. Samples of livestock origin were collected from 135 cattle, 41 poultries, and 20 swine. The detection rate in cattle was 11%, toxin-gene positivity was 60%. MLST analysis of 9 strains revealed ST 11 (5 strains), ST 2, ST 15, ST 58, and ST 101. No isolates were found from poultry

or swine. Patient-derived strains of CACDI were collected from 14 patients at 2 sites. MLST analysis revealed ST42, ST37, ST100, and ST203 (two isolates, respectively), ST 224, ST 81, ST 28, and ST 47. 2 isolates were unclassifiable. One case was a healthy 1-year-old girl, whose family revealed no isolation of *C. difficile*. Impressively, the soil in the parks (A and B) related to the child detected *C. difficile* from 4/4 samples (toxin-gene positivity; 75% in Park A and 1/4 samples (toxin-gene positive) in Park B. MLST analysis demonstrated ST 42, the same as that in the affected child and core-genome single-nucleotide polymorphisms (SNPs) analysis suggested closely related strain.

Conclusion. Our results suggest one health approach is fundamental to prevent the transmission of *C. difficile*.

Disclosures. All Authors: No reported disclosures

741. Ehrlichia chaffeensis Induced Hemophagocytic lymphohistiocytosis: A Descriptive Case Series

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Session: P-35. Global Health

Background. Hemophagocytic lymphohistiocytosis (HLH) secondary to tick borne illnesses is rarely reported. Clinical signs and symptoms of tick borne illnesses and HLH might overlap with fever, cytopenias and increased liver enzymes being common. We describe findings from case series of ehrlichiosis induced HLH.

Fever	16/16 (100%)
Splenomegaly (%)	5/16 (31%)
Cytopenias of 2 or more lineages	13/14 (92.8%)
Hypertriglyceridemia > 265mg/dL	13/16 (80%)
Fibrinogen (<1.5 g/dL)	4/13 (31%)
Soluble CD25 >2400 U/mL	7/7 (100%)
NK activity (low or absent)	N/A
Hemophagocytosis on Bone marrow	10/14 (71%)

Methods. We reviewed patients with ICD-10 codes corresponding to a diagnosis of HLH or macrophage activation syndrome (MAS) at University of Kentucky Medical Center between January 2008 and April 2020. Inpatients who were >18 years of age without known immune compromise were included. 4 cases with confirmed underlying ehrlichiosis were identified at our institution. We searched PubMed for English-language articles containing the terms "Hemophagocytic lymphohistiocytosis" and "infection" or "tick borne" or "Ehrlichia". Data on patient demographics, clinical signs and symptoms, laboratory data such as ferritin, platelet count, IL-2, NK cell activity, and outcomes were collected.

Results. We identified 16 cases of ehrlichiosis (1 had a coinfection with Rocky Mountain Spotted fever). Eleven out of 16 (68%) were male, median age was 58. All patients were febrile and thrombocytopenic on presentation and 8/14 (57%) were neutropenic. All had elevated ferritin (mean 36187 ng/mL, range 860 – more than 100000). CNS involvement was reported in 4 patients with a positive CSF Ehrlichia chaffeensis PCR. All patients met at least 5 2004-HLH defining criteria and 10/14 (71%) patients had evidence of hemophagocytosis on bone marrow biopsy (table 1). Fourteen out of 15 (93%) patients received doxycycline and 9/15 (60%) received steroids +/- etoposide. Mortality for Ehrlichia induced HLH was 12.5%, significantly lower than that reported for all secondary HLH mortality (45%).

Conclusion. This review highlights the importance of considering Ehrlichiosis as a cause of HLH in endemic areas particularly as clinical signs and symptoms of the 2 entities overlap. While overall mortality rate due to HLH is elevated, Ehrlichia induced HLH seems to have a much favorable prognosis with prompt institution antimicrobial treatment. Additional prognostic factors that correlate with a more severe course dictate need for immunosuppressive treatment need to be further elucidated.

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