

study, we determined the prevalent strains of *O. tsutsugamushi* circulating in Assam and their origin with respect to 56 kDa TSA gene.

Methods & Materials: 370 clinical serum samples from suspected scrub typhus and other unidentified fever cases were received from tertiary hospitals in Assam. Serological screening was done using Scrub Typhus Detect IgM ELISA (InBios International, Inc., USA). Positive and equivocal samples were subjected to PCR. Nested PCR was performed using primers specific for *O. tsutsugamushi* 56 kDa gene. Phylogenetic analysis was performed using MEGA 6 software.

Results: 19.4% sera (72/370) were found to be IgM positive and 6.4% (24/370) were equivocal. 13 of these samples were PCR positive for 56 kDa gene. Phylogenetic analysis of study strains showed variations in sequence homologies that formed 3 distinct clades that clustered with reference strains from: 1) India 2) Taiwan and 3) Thailand.

Conclusion: In summary, we have identified strains of *O. tsutsugamushi* circulating in Assam and established their evolutionary relationship with reference strains by analyzing a variable portion of 56 kDa gene. Understanding the evolution of the prevalent strains is important to understand the genetic differences which may help in planning control strategies as well as prophylactic measures including development of vaccines.

<http://dx.doi.org/10.1016/j.ijid.2016.02.421>

Type: Poster Presentation

Final Abstract Number: 41.234

Session: Poster Session I

Date: Thursday, March 3, 2016

Time: 12:45-14:15

Room: Hall 3 (Posters & Exhibition)

Uganda National Acute Febrile Illness Agent Detection Serosurvey 2004-2005



G. Kharod^{1,*}, D. haberling², M. Person², A. Folkema³, R. Galloway², M. Elrod², J. Perniciaro², W. Nicholson², N. Patel², J. Bwogi⁴, H. Bukonya⁴, C. Drakeley⁵, S. Mbulaiteye⁶, D. Blaney², S. Shadomy²

¹ CDC, Atlanta, Georgia, USA

² CDC, Atlanta, USA

³ Region of Waterloo Public Health, CDC, Ontario, Canada

⁴ UVRI, Entebbe, Uganda

⁵ The London School of Hygiene and Tropical Medicine, London, United Kingdom

⁶ NIH, Bethesda, USA

Background: Due to their non-specific clinical presentation, acute febrile illnesses (AFI) are often diagnosed clinically as diseases known to be endemic to the region in which they are found. Uganda has been the site of multiple emerging-disease outbreaks, and there are several diseases that present with undifferentiated AFI, requiring further laboratory confirmation; however, limited laboratory capacity can impair timely diagnosis and public health interventions. This results in misdiagnosis and underreporting of emerging diseases of public health importance. The 2004-2005 Uganda National AFI Agent Detection Serosurvey (AFI serosurvey)—a retrospective investigation of seroprevalence of exposure to selected infectious agents—involved testing a subset of banked sera from the 2004-2005 Uganda HIV/AIDS Serobehavioural Survey (UHSBS).

The AFI serosurvey is part of a multi-phase collaboration between Uganda Ministry of Health, Uganda Virus Research Institute (UVRI) and CDC-Atlanta/CDC-Uganda to investigate AFI in Uganda.

Methods & Materials: We selected a random 3097-sample subset from 19,656 UHSBS banked sera for inclusion in the AFI serosurvey; 2705 were ultimately analyzed after applying exclusion criteria. Data from laboratory testing were analyzed and mapped using SAS v9.3 and ArcGIS 10, respectively.

Results: Laboratory diagnostic testing results demonstrated: leptospirosis ELISA and microagglutination test (MAT) (10.4% weighted proportion, SE = 1.2%), brucellosis MAT (0.3% weighted proportion, SE = 0.1%), spotted fever group rickettsiae ELISA (56.7% weighted proportion, SE = 1.4%) and typhus group rickettsiae ELISA (41.6% weighted proportion, SE = 1.4%), malaria MSP119 ELISA (88.4% weighted proportion, SE = 0.7%), orthopoxvirus IgG ELISA (13.5% weighted proportion, SE = 0.8%), chikungunya IgM ELISA (31.1% weighted proportion, SE = 1.0%), dengue IgM ELISA (1.0% weighted proportion, SE = 0.2%) and IgG ELISA (0.7% weighted proportion, SE = 0.2%). A specimen subset (n = 198) was tested for melioidosis using indirect hemagglutination (IHA); 4.6% were seropositive.

Conclusion: Pre-existing national serosurveys can be a source of information on prevalence of AFI etiologic agents. This AFI serosurvey describes the distribution, regional risk, and interregional variability for selected diseases contributing to AFI across Uganda; it will inform prioritization of infectious disease surveillance and laboratory capacity-building activities. Results from this study combined with similarly obtained results from the ongoing testing from the 2011 Uganda AIDS Indicator Survey-based serosurvey will demonstrate changing seroprevalence patterns, allowing for evaluation of potential ecologic drivers for disease distribution variances.

<http://dx.doi.org/10.1016/j.ijid.2016.02.422>

Type: Poster Presentation

Final Abstract Number: 41.235

Session: Poster Session I

Date: Thursday, March 3, 2016

Time: 12:45-14:15

Room: Hall 3 (Posters & Exhibition)

Spotted fever group and typhus fever group rickettsiosis in South Western India



M. Koralar^{1,*}, I. Bairy², M. Varma³, E. Athan⁴, J. Stenos⁵

¹ Kasturba Medical College, Manipal, Karnataka, India

² Melaka Manipal Medical College, Manipal Campus, Manipal, India

³ KMC Manipal, Manipal, India

⁴ Barwon Health, Victoria, Australia

⁵ Australian Rickettsial Reference Laboratory, Vic, Australia

Background: Rickettsial diseases are a group of zoonotic acute febrile illness transmitted to humans by vectors. They are classified into spotted fever group (SFG), typhus fever group (TG) and scrub typhus group (STG). STG remains the major cause of acute febrile illness requiring hospitalization in the tsutsugamushi triangle, however, the true picture of the SFG and TG rickettsiosis is not clear in India. Immunofluorescence assay (IFA) is the serological gold standard test for the diagnosis of rickettsial disease and