

Type: Poster Presentation

Final Abstract Number: 51.015
 Session: Emerging Infectious Diseases
Date: Friday, April 4, 2014
 Time: 12:45–14:15
 Room: Ballroom

Rickettsia felis and related bacteria: An epidemiological enigma


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Background: Recent works identified a novel healthcare problem in Africa: acute *Rickettsia felis*-induced fever that mimics malaria. The epidemiology of these diseases remains to be characterized. Indeed, the natural reservoirs of *R. felis* are not known. Since the first clinical descriptions of *R. felis*-associated fever, the cat and dog fleas *Ctenocephalides felis* and *C. canis* were implicated as the most probable vectors in many countries, but not in Senegal.

Methods & Materials: Arthropods (ticks, mites, fleas, tsetse flies, biting midges, mosquitoes, bed bugs) and environmental samples (dust and water samples) were collected in the villages of Dielmo and Ndiop where *R. felis*-associated acute fevers contribute up to 8% of all acute fevers with the incidence of 6.7 per 100 person-years. DNA extracted from all samples was tested by *Rickettsia* genus-specific qPCR and by two different *R. felis*-specific qPCR. Positive environmental samples were subjected to PCR with the universal eukaryotic cytochrome oxidase I-based primers followed by cloning of the amplicons with pGem vectors. Isolation was performed in XTC cell line using the shell-vial technique. Characterization of the isolated strains was done by sequencing of *gltA* and 16S rRNA genes.

Results: Arthropods (ticks, mites, fleas, tsetse flies, biting midges, mosquitoes, bed bugs) and environmental samples (dust and water samples) were collected in the villages of Dielmo and Ndiop where *R. felis*-associated acute fevers contribute up to 8% of all acute fevers with the incidence of 6.7 per 100 person-years. DNA extracted from all samples was tested by *Rickettsia* genus-specific qPCR and by two different *R. felis*-specific qPCR. Positive environmental samples were subjected to PCR with the universal eukaryotic cytochrome oxidase I (COI)-based primers followed by cloning of the amplicons with pGem vectors. Isolation was performed in XTC cell line using the shell-vial technique. Characterization of the isolated strains was done by sequencing of *gltA* and 16S rRNA genes.

Conclusion: This is the first evidence of the presence of *R. felis* in arthropods in the endemic focus or *R. felis* infection in Senegal. The roles of *Siteroptidae* mites in the hosting and transmission of the *R. felis* is to be further investigated

<http://dx.doi.org/10.1016/j.ijid.2014.03.883>

Type: Poster Presentation

Final Abstract Number: 51.016
 Session: Emerging Infectious Diseases
Date: Friday, April 4, 2014
 Time: 12:45–14:15
 Room: Ballroom

Burden of human rhinovirus infections in influenza like illnesses in Kenya


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Background: There have been several recent reports of respiratory outbreaks with associated mortality due to human rhinovirus (HRV) infection. Studies on viral etiologies of Influenza-like illness have shown that many patients are infected with more than one viral agent with frequencies of co-infection being as high as 20%. From these studies, human rhinovirus has been shown as one of the most prominent respiratory viruses that co-infect patients with influenza. In Kenya, the ongoing Influenza surveillance has provided data that now allows for exploration of other respiratory viruses that cause influenza-like illnesses. Currently, there is scanty information on the patterns of HRV circulation throughout the country.

Methods & Materials: This study utilized a retrospective cross-sectional descriptive design. It involved the use of 517 archived samples from the ongoing country-wide influenza Surveillance protocol. The archived nasopharyngeal specimens were collected from a study population comprising persons from two months of age onwards who attended outpatient clinics in the year 2008, in hospitals located in 8 different regions in Kenya presenting with influenza like illnesses. Viral RNA was extracted from the samples followed by real-time RT-PCR assays with HRV-specific primers for screening for HRV.

Results: A total of 131 (25%) of the samples were positive for HRV. The highest prevalence (33%) was recorded from samples obtained from the Coast region of the country, followed by Western region (32.7%) while Eastern region had the lowest prevalence (11%). Children aged between 2 months–7 years were mostly infected while the age group ≥ 60 years was least affected. There was no significant difference in HRV infection in relation to gender.

Conclusion: The study notes that HRV infection is a significant viral etiology of morbidity throughout the country. However, disparities were observed between different regions. The more humid regions in the country (Western and Coast) had the highest HRV prevalence. At the same time, children below 7 years were at a greater risk of HRV infection. Determination of the molecular characteristics of the rhinovirus strains to enable specific identification of the species and the evolutionary relationships is ongoing.

<http://dx.doi.org/10.1016/j.ijid.2014.03.884>