Vector-based metagenomics for animal virus surveillance

T.F.F. Ng1,*, D. Wilner2, C. Nilsson3, Y.W. Lim1, R. Schmieder2, B. Chau2, Y. Ruan3, F. Rohwer2, M. Breitbart1

1 University of South Florida, Saint Petersburg, FL, USA
2 San Diego State University, San Diego, CA, USA
3 Genome Institute of Singapore, Singapore, Singapore

Background: Recent epidemics have underscored the importance of non-human viral reservoirs and the devastating impact of emerging viruses on human health. Broad understanding of the animal viruses circulating in a given region is crucial for monitoring emerging diseases, but is hindered by the inability to sample enough individuals and the difficulty of characterizing previously undescribed viruses. As mosquitoes draw blood from animals and humans and are known to carry a number of viruses, metagenomic sequencing of viral particles purified from mosquitoes enables surveillance of the animal viruses circulating in a given region.

Methods: To characterize actively circulating viruses and provide a baseline for detection of emerging viruses, viral metagenomics was performed on mosquitoes captured from San Diego, California. Virus particles were purified from mosquitoes through filtration, chloroform, and nuclease treatment. Nucleic acids were then extracted from the purified viral particles, and subjected to metagenomic sequencing followed by bioinformatic analysis.

Results: This study identified a number of previously unknown DNA and RNA viruses from the mosquito virome. Highly diverse novel single-stranded DNA viruses were discovered, with limited amino acid identity (40-63%) to known human anellovirus and animal circovirus genomes in GenBank. One of the circoviruses showed a unique genomic organization with characteristics of several ssDNA viral types. Several closely related virus genomes were recovered from individual samples; however, viruses from different samples varied widely, indicating distinct virus profiles. A number of partial sequences from novel RNA animal viruses were also identified. New RNA viruses characterized from the mosquitoes had only extremely limited amino acid identity to members of the Bunyaviridae and Rhabdoviridae families.

Conclusion: In summary, this study has identified a diversity of novel DNA and RNA viruses, successfully demonstrating that numerous unknown viral species are circulating in mosquitoes. Through the use of vector-based viral metagenomics, the animal viruses present in a given region can be characterized and used as a baseline to monitor emerging viruses of relevance to human and animal health.

doi:10.1016/j.ijid.2010.02.460

76.017

Epidemiological, clinical and zoonotic evidences for the existence of Lyme disease in Central of Mexico

G. Gordillo1,*, F. Solorzano Santos2, J. Torres3, E. Velazquez2, G. Ramon2, R. Garcia2, M. Vargas4

1 Instituto Mexicano Del Seguro Social, Mexico City, Mexico
2 Hospital de pediatria, Centro Medico Nacional SXXI, IMSS, Mexico, DISTRITO FEDERAL, Mexico
3 Hospital De Pediatría Centro Medico Nacional Sxii, Imss, Mexico, Distrito Federal, Mexico
4 Facultad de Medicina Veterinaria y Zootecnia, Mexico, Michoacan, Mexico

Background: Lyme borreliosis, caused by Borrelia burgdorferi, is the most commonly reported vector-borne disease in the United States. Infection is transmitted to humans by Ixodes tick-bite, and causes a disease affecting skin, nervous system, heart, and joints. Recent studies in Mexico documented cutaneous clinical cases infected with B. burgdorferi and ticks from the Northeast of the country infected with B. burgdorferi sensu stricto.

Aim: To document Borrelia infection in patients with suggestive Lyme disease in Central of Mexico, and to search for the presence of B. burgdorferi-infected competent vectors and reservoirs.

Methods: We studied 800 patients suggestive of Lyme disease in one Pediatric and one General hospital. Sera, biopsies, and cerebrospinal fluids were tested for infection using immunological, microbiological, and molecular test. Ticks and mice were collected in forest areas, which patients visited, and infection studied by culture and molecular tests.

MEXICAN PATIENT WITH EM.