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Recombination in natural populations of Dengue virus serotype 2 from Mexico

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Dengue (DEN) is a major cause of mortality and morbidity in the world including Mexico, where the infection is endemic. Some of the states with higher rate of dengue cases are Oaxaca and Veracruz. The cause of DEN is a positive-sense RNA virus named dengue virus (DENV) that evolves rapidly increasing its variability which results in enhancement of viral adaptation, including the escape from host immune responses. Furthermore, recombination may play a role in driving the evolution of DENV, which may affect virulence and host tropism changes. We have studied recombination in Mexican strains and the relevance in virus evolution in the endemic states, Oaxaca and Veracruz, where the four serotypes of DENV are circulating. We obtain the sequence of 6 different isolates of DENV-2 Asian/American genotype from the outbreak 2005-6, one clone of the C-prM-E-NS1 structural genes, and 10 clones of the E gene from the isolate MEX_OAX_1656_05 to determined whether there are isolates from Oaxaca having recombination. Strains from Veracruz are currently in study. Evidence of recombination was found using two softwares: RDP3 and GARD. The Oaxaca MEX_OAX_1656_05 and MEX_OAX_1038_05 isolates sequenced in this study were recombinant viruses, incorporating the genome sequence from the Cosmopolitan genotype. Furthermore the clone of the E gene namely MEX_OAX_165607_05 from this study was also recombinant, incorporating genome sequence from the American genotype. Our results represent the first report of recombination in DENV-2 in México. In conclusion, recombination could play a significant role in the DENV evolution and must be considered as a potentially important mechanism generating genetic variation in this virus with serious implications in vaccine and drug treatment. We acknowledge the support by the "Instituto de Ciencia y Tecnología del D.F."

Biography

Dr. Maria de Lourdes Munoz made her PhD. at the Department of Genetics and Molecular Biology (Centro de Investigación y de Estudios Avanzados del IPN). She held a position as visiting fellow for Advanced Research Experience at the National Institute of Health, Bethesda, Maryland, USA and has been working at the Department of Genetics and Molecular Biology (CINVESTAV-IPN) since 1985 in the following research areas: Identification of Dengue virus receptors in the midgut of mosquito epithelial cells; and Populations genetics of dengue virus and the mosquito vector *Aedes aegypti*.