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Editorial Open access

Isolation of the Tick-Borne Encephalitis Virus from Mosquito in Khabarovsk Region of the Far East of Russia

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Editorial

Background: Flaviviruses are subdivided into three groups—mosquito-borne, tick-borne and no-known vector viruses. Tick-borne encephalitis virus (TBEV) is the most widely spread flavivirus in Eurasia which is transmitted to man by tick bytes and causes severe neuroinfection with lethal outcomes. Ticks are main carriers and reservoir hosts of the TBEV in nature. Their ability to feed on a variety of vertebrate animals, intracellular digestion of blood, their long life cycle up to 3-6 years at each stage of development and transovarial transmission of the TBEV make them ideal vectors. Natural TBEV infection had been revealed for 16 species of ixodid ticks.

Methods: TBEV strains were isolated from a pool of mosquito Aedes vexans and ticks Ixodes persulcatus Schulze in new-born mice and porcine embryo kidney cells. Nucleotide sequences of reverse transcription-PCR products were determined using DNA analyzer ABI 3500 (Applied Biosystems, USA). Assembling of the nucleotide sequences into complete genomes of the TBEV strains, their alignment and phylogenetic analysis were performed using MEGA 6.06.

Results: TBEV strain Lazo MP36 (GenBank accesson number KT001073) had been isolated from a pool of mosquito Aedes vexans in Lazo region of Khabarovsk territory of the Far East of Russia in September 2014 by intracerebral infection of new-born mice. Phylogenetic analyses showed its close relationship with the TBEV strains of Far Eastern subtype isolated in the same Khabarovsk region of Russia both from ticks (strain 1230 (KF880805) and Khekhtzir 9-13, 10-13, 17-13 (KT001070- KT001072) and mosquito (Malishevo (KJ744034) isolated from Aedes vexans nipponii in 1978). The fusion peptide of the strain Lazo MP36 responsible for the flavivirus entry remains a canonical structure 98 DRGWGNHCGLFGKGSI 113 (protein E numbering) of all tick-borne flaviviruses except Powassan and deer tick virus. The principle change H104G typical for the mosquito-borne flaviviruses was not found. Secondary structures of 5’- and 3’ untranslated regions as well as cyclisation sequences were typical for the TBEV (92-97% homology within the Far Eastern subtype of the TBEV).

Conclusions: The TBEV with fusion peptide and untranslated regulatory regions specific for the Far Eastern subtype can be isolated from mosquito Aedes vexans. Two TBEV strains isolated from mosquito in 1978 (Malishevo) and 2014 (Lazo MP36) have 94% homology of their complete genomes similar to homology between Far Eastern strains isolated from ticks.

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