

Detection of the Insect-Specific Flavivirus Chaoyang in Mosquitoes in the Jewish Autonomous Region of the Far East of Russia

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Background

Metagenomics research revealed enormous diversity of viruses up to 1000 and their possible role as global drivers of evolution. Using molecular genetic methods, numerous unknown viruses were detected during the entomological surveillance [1]. Among them insect-specific flaviviruses (ISFVs) with significant divergence from all known flaviviruses could represent an ancient primordial form of flaviviruses