



V 6 Analysis of complete genomes of the Far-Eastern subtype of tick-borne encephalitis virus with different pathogenicity for man

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We compared the genomes of 2 groups of strains of tick-borne encephalitis virus that caused a diametrically opposite severity of disease. Nine strains pathogenic to humans were isolated from people who died of encephalitis. Twenty strains causing subclinical forms of the disease were isolated from the blood of patients after a tick bite. Two groups of strains had 16 specific amino acid substitutions in the protein-coding part of the genome. Most of these changes did not significantly change the properties of amino acids, and only 4 substitutions led to a significant change in hydrophobicity of amino acids. One change was the deletion of an amino acid: 111 at the C end of the capsid protein, the second mutation of 917 Ser → Gly in protein NS1, the third mutation 1534 Ser → Phe, localized near the catalytic center of virus protease, and the fourth mutation 3235 Ala → Ser in protein NS5. These 4 substitutions were key causing a change in pathogenicity of strains of the Far-Eastern subtype of tick-borne encephalitis virus. The cumulative effect of several minor mutations that differ in 2 groups of strains may have some effect on the pathogenicity of strains. But apparently, most of these mutations did not affect the pathogenicity and were the result of natural accumulation of mutations in the evolution of the virus.