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Protein domains of ns5 antigen of Zika virus

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Introduction. *Zika virus* (ZIKV) is an arthropod-borne virus in the genus *Flavivirus* from the family *Flaviviridae*. ZIKV was first isolated from insects (mosquitoes) and nonhuman primates. Usually ZIKV is transmitted by the bite of infected insects. It was shown that Ns5 antigen of ZIKV determines pathogenic properties. Ns5 antigen has also important virulence properties. Some methods of ZIKV identification are based on Ns5 antigen determination, especially by serological methods. Properties and structure of Ns5 antigen have not yet been completely detected.

The aim of this study was to build the model of Ns5 antigen and detect its biochemical properties using bioinformatics methods.

Material and methods. Protein domains of Ns5 antigen amino acid sequence were detected by DELTA-BLAST program. Ns5 antigen structure was calculated by SWISS-MODEL online program.

Results and discussion. In result of researching there were 4 domains of Ns5 antigen detected:

1) S-adenosylmethionine-dependent methyltransferases (SAM or AdoMet-MTase) domain. AdoMet-MTases are domains that use S-adenosyl-L-methionine (SAM or AdoMet) as a substrate for methyltransfer, creating the product S-adenosyl-L-homocysteine (AdoHcy). There are at least five structurally distinct families of AdoMet-MTases, class I being the largest and most diverse. Within this class enzymes can be classified by different substrate specificities (small molecules, lipids, nucleic acids, etc.) and different target atoms for methylation (nitrogen, oxygen, carbon, sulfur, etc.).

2) RNA_dep_RNAP domain: RNA-dependent RNA polymerase (RdRp) is an essential protein encoded in the genomes of all RNA containing viruses with no DNA stage. RdRp catalyzes synthesis of the RNA strand complementary to a given RNA template. RdRps of many viruses are products of processing of polyproteins. Some RdRps consist of one polypeptide chain, and others are complexes of several subunits. The domain organization and the 3D structure of the catalytic center of a wide range of RdRps, including those with a low overall sequence homology, are conserved. The catalytic center is formed by several motifs containing a number of conserved amino acid residues. This subfamily represents the RNA-dependent RNA polymerases from all positive-strand RNA eukaryotic viruses with no DNA stage.

3) RT_like domain: Reverse transcriptase (RT, RNA-dependent DNA polymerase)_like family. An RT gene is usually indicative of a mobile element such as a retrotransposon or retrovirus. RTs occur in a variety of mobile elements, including retrotransposons, retroviruses, group II introns, bacterial msDNAs, hepadnaviruses, and caulimoviruses. These elements can be divided into two major groups. One group contains retroviruses and DNA viruses whose propagation involves an RNA intermediate. They are grouped together with transposable elements containing long terminal repeats (LTRs). The other group, also called poly(A)-type retrotransposons, contain fungal mitochondrial introns and transposable elements that lack LTRs.

4) FtsJ domain. FtsJ's substrate is the 23S rRNA. The 1.5 Å crystal structure of FtsJ in complex with its cofactor Sadenosylmethionine revealed that FtsJ

has a methyltransferase fold. FtsJ domain also includes the N terminus of flaviviral NS5 protein. It has been hypothesized that the N-terminal domain of NS5 is a methyltransferase involved in viral RNA capping.

Ns5 antigen structure was building by SWISS-MODEL program (Fig. 1).



Fig. 1. Ns5 antigen structure built by SWISS-MODEL

Conclusions. Ns5 antigen is widespread among the primates. Finally there were detected 4 domains (FtsJ, SAM, RdRp, RT) in Ns5 antigen.

