

عنوان مقاله:

Analysis of synonymous codon usage bias and nucleotide and amino acid composition in 13 species of Flaviviridae

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خلاصه مقاله:

The family, Flaviviridae includes viruses which cause several diseases including Dengue fever, Japanese encephalitis, Murray Valley encephalitis, Tick-borne encephalitis, West Nile encephalitis, Yellow fever and Hepatitis C virus infection. Members of this family have monopartite, linear, single-stranded RNA genomes of positive polarity with 9.6-12.3 kb in length. Here, we analyzed the codon usage of 13 species of this family by using gene infinity package. Base analysis was performed by CAIcal server and amino acid composition was calculated by PseAAC web-server. The results showed that the highest number of A, G and C bases were seen in the RNA genome of Dengue virus 2, Tick borne encephalitis virus and Hepatitis C virus, respectively. Although the number of U bases used in RNA genomes was very close, the highest U nucleotide amount was 23.77% in Wesselsbron virus. The lowest number of C, G, U and A bases was seen in Bovine viral diarrhea virus, Dengue virus 2, Tick borne encephalitis virus and Hepatitis C virus, respectively. In this study, it was found that the complete genome of classical swine fever virus has a lower GC content and genome of Tickborne encephalitis virus, Hepatitis C virus and Powassan virus have the highest GC content among other examined species. We also classified the amino acids as rare (Phenylalanine, Cysteine, Histidine, Methionine, Asparagine, Glutamine, Tryptophan and Tyrosine), frequent (Alanine, Glutamic acid, Glycine, Leucine, Valine and Threonine), and intermediate (all others). The highest numbers of preferred codons exist in Wesselsbron virus and the lowest in West Nile virus

کلمات کلیدی:

Flaviviridae, codon usage bias, amino acid composition, nucleotide composition

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