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In-Silico prediction of miRNAs in Viral Genomes and Interaction studies with different Proteins and Drugs

Abstract

The miRNA are the latest thing happening in the world of RNA, genetics and science. These wonderful tiny little things can possess the potential to provide a new way to treat the dreaded diseases prevalent in the past. Chemotherapy brought a surge in the medical field when it had the magical healing ability and cured most of the diseases but now that trend is ending due to development of the resistance by the causative agents towards the classical method of treatment. These miRNA are going to take the role and change the future of medicine.

In genetics, microRNAs (miRNA) are about 21-23 nucleotides in length single-stranded RNA molecules thought to regulate the expression of other genes. RNA genes that are transcribed from DNA encode the miRNAs but these are not translated into protein; instead they are processed from primary transcripts known as pri-miRNA to short stem-loop structures called pre-miRNA and finally to functional miRNA. miRNA molecules on maturity are complementary to regions in one or more messenger RNA (mRNA) molecules, which they target for degradation. Hence these are conserved, endogenous non coding RNA molecules that regulate protein coding gene expression in the plants and animals via the RNA silencing machinery.

In here we have predicted miRNAs in the viral genomes of Japanese encephalitis virus, Usutu virus, and West nile virus. All causing deadly diseases. The approach was simple and logistic as we worked over the exact mechanism of the miRNA biogenesis and its processing. Then implementing the same in-silico we predicted the stem loop structures first in the complete genome of the viruses by following a set of rules being obeyed by the stem loop precursors. Then we filtered out these precursors on the basis of some elucidated parameters which included energy parameters and that would satisfy the miRNA criteria. The selected precursors were then submitted to the MEME online server for motif elicitation. This would rank them on the basis of some inbuilt score and give a conserved motif in a cluster of precursor sequences. A cut off value was set that would

filter out the motif with higher values. These motifs were then traced back in the hairpin loop as they would satisfy all the conditions and hence we can conclude about it as the predicted miRNA in the viral genome.

Hence we have taken up this project with the soul purpose of making advancement in the medical therapy of the dreaded diseases, basically supporting the existing methods of chemotherapy and the restoration of the resistant drugs by the novel approach of RNA interference.