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Improving the Algorithm to Predict RNA Structures for Frameshifting in the Expression of Overlapping Viral Genes

ABSTRACT

In many viral genomes made up of ribonucleic acids (RNA), there are overlaps of open reading frames (ORFs) for producing major viral proteins. A frameshifting mechanism in reading nucleotide sequence is observed during the expression of overlapping genes. In many cases, the gene expression uses a mechanism called "-1 ORF frameshifting" in which the reading process shifts backward one nucleotide position. Most known frameshifting mechanisms reported to date are induced by either pseudoknots or stem-loop structures that trigger the frame shift. Another essential requirement for frameshifting is the presence of a heptanucleotide slippery sequence, which is usually a string in the form of XXX YYY N (where X = A,T, or G; Y = A or T; and N = A, T, C), before the pseudoknot or stem-loop structure. While there are well established dynamic programming type algorithms for stem-loop structures, the efficiency of pseudoknot prediction based on minimization of free energy remains to be improved even for short RNA sequences of about 200 bases. We are implementing algorithms on an IBM p690 multiprocessor machine to predict optimal RNA secondary structures for longer segments. This talk presents our pursuit to understand the possible frameshifting mechanism in two overlapping ORFs designated X1 and X2 and located at bases 25268-26089 and 25689-26150 respectively on the SARS coronavirus genome.

All are welcome

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