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miRNA based phylogeny reveals regulatory relationship between *Rehusus lympho Cryptovirus* and *Epstein barr virus*

Ruchi Yadav, Sarita Jha, Manish Kumar and Prachi Srivastava
Amity University, India

RNA interference or RNAi is a naturally occurring endogenous process of reducing the expression of messenger via a short double stranded sequence of ribonucleic acid is called siRNA and miRNA. RNAi mechanism is used by cells to regulate the expression of genes & replication of viruses. The undesirable production of certain proteins (gene expression) is a substantial factor in many human diseases. The abnormality may be due to defective gene, over or under production of a protein by a “normal” gene, or by the expression of genes from viruses or bacteria. This abnormal protein production may have direct effects on cells within the body or may initiate a series of events involving other proteins, thereby producing diseases. In this paper we have done phylogenetic analysis of miRNA among ten different viruses viz (Bandicoot Papillomatosis Carcinomatosis Virus Type 1 and Type2, Bovine Herpes Virus1, Bovine Leukemia Virus, Epstein Barr Virus, Human Herpes Virus6b, HIV, Mouse Cytomegalovirus, Pseudorabies, Rehusus Lymphocryptovirus, Rhesus Monkey Rhadinovirus, Simian Virus 40) study shows that there is functional relationship between Epstein Barr Virus and Rehusus Lymphocryptovirus, sharing 21 clades with a confidence bootstrap value from 80-100%. This shows that RLV infection in rhesus monkeys have a similarity with EBV infection in humans. Present study shows that there is a close relationship in regulatory mechanism of Rehusus lympho cryptovirus and Epstein Barr Virus. Hence Rehusus lympho cryptovirus can be used as a model system to study molecular mechanism of pathogenesis and new drug development process for Epstein Barr Virus.

Biography

Mrs. Ruchi Yadav has done M.Sc. in Bioinformatics and M.Tech in Biotechnology also pursuing Ph.D in Biotechnology specialisation Bioinformatics. She has 7 years of experience in teaching, presently working as Assistant Professor in AMITY Institute of Biotechnology, AMITY University, Uttar Pradesh Lucknow. She has presented more than 15 papers in national and international conferences and interested in application of bioinformatics analysis in life sciences, Genome and proteome analysis, microarray analysis, phylogenetics and miRNA analysis are her major area of research

ryadav@lko.amity.edu
ruchi.amity@gmail.com

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