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Microbial comparative genome for *in-silico* DNA marker extraction

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Next-Generation Sequencing (NGS) technologies have developed progressively in microbial genomic research and clinical applications. Also, genetic fingerprinting has been used in molecular epidemiologic studies. Therefore, it is essential that a connection or a link is established between them for discovering DNA marker in whole genome for using in molecular epidemiology and bacterial diagnosis. Bioinformatics and comparative genome analysis tools lead to further and deeper understanding of genomic variation in the bacterial species. Bacterial comparative genome analyses can be used for evolutionary processes, structure and function annotations, and importantly in unique DNA marker extraction. These unique probes are suitable for high-throughput diagnostic methods such as micro-array. Finally, setting up a procedure for comparative analysis will be useful for a wide range of microbial researches and clinical applications.

Predicting a novel hypothetical miRNA encoded by Hepatitis C virus

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HCV infection is a prevalent disease with approximately 170 million individuals (3%) chronically infected worldwide. MicroRNAs (miRNAs) are small (17-23 nucleotides) non-coding RNAs that serve as post-transcriptional regulators of gene expression. Viruses can also encode viral miRNAs to alter host physiology or to influence its replication. The purpose of this study was to predict a novel miRNA encoded by 5'-UTR hepatitis C virus (HCV) genome. RNA secondary structure prediction tool, Blastn, and multiple sequence alignment tools were used for identify new member of miRNA and its target. In this study, a novel small RNA encoded by 5'-UTR hepatitis C virus (HCV) genome has been predicted that regulated fork-head box K2 (FOXK2) gene. Predictionally, the small RNA could down regulate a human transcription factor known as Interleukin enhancer binding factor (FOXK2) via RNAi pathway in human cells. FOXK2 activates interleukin-2 gene and then induces the human immune responses. Possibly, HCV interferes with the human immune system by generating viral encoded small RNA to knock down its target the FOXK2 mRNA.