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Bioinformatic analysis of zika virus miRNAs interacting with host genes

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MicroRNA (miRNA) is a non-coding RNA molecule consisting of about 2-24 nucleotides that control gene expression and are present in various organisms. It mainly forms base pairs with mRNAs with complementary sequences, leading to the decomposition of mRNAs, and disrupts gene expression by blocking the process of mRNA translation. It is highly conserved in plants and animals, it is considered an essential, evolutionarily ancient genetic regulatory element. When the gene for a miRNA is expressed, a primary miRNA with a hairpin structure is formed, and through a processing process including two cleavage processes, a complete form of miRNA is created. In the case of viruses, it is not yet fully known whether they can produce their own miRNAs, but in some viruses, it is known that miRNAs that have regulatory functions and have the same sequence as RNA viruses exist. In the case of flaviviruses, there are miRNA mechanisms that play roles, such as interfering with replication, translation, and host-host control. In this study, we performed machine learning-based miRNA prediction analysis on the genome of ZIKV, a flavivirus, to identify similar hairpin structures of miRNAs and, based on this, to identify potential miRNA-based interactions between human miRNAs and viral genes. As a result, 343 hairpin structure sequences were extracted from the ZIKV genome, and according to the prediction results, nine were inferred to be precursor miRNAs. The targeting analysis showed that ten viral mature miRNA-like sequences could target 412 different human genes. Through this, several genes involved in the transcription process of human genes were identified as primary potential viral miRNAs predicted. It can support the fact that you can be a target. In addition, human miRNAs are involved in suppressing the viral transcription process by targeting ORF genes that regulate the lifespan of the virus. Based on these research results, it is expected to be applied to developing new treatments using ZIKV, Flavivirus, and human miRNA mechanisms and further utilized in vaccine development technology.