The role of post-transcriptional editing of herpes simplex virus 1 miR-H2 during latency

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Herpes simplex virus 1 (HSV-1), an important human pathogen, has been shown to encode 29 microRNAs (miRNAs), the function of which is yet to be revealed. The functions of miRNAs are defined by their sequences, as only one nucleotide difference can dramatically change the specificity of miRNA for its target. Using advanced bioinformatics tools, we recently found that miR-H2, an HSV-1 miRNA targeting important virus gene ICP0, is extensively edited by the function of the adenosine deaminase acting on RNA (ADAR) in latently infected human ganglia. The ADAR proteins deaminate adenosines to inosine (recognized as guanosine), they have a critical role in homeostasis, and it is possible that expression of ADAR proteins in neuronal tissue specifically regulates the establishment and maintenance of latency. This editing function could indicate that the virus is using cellular processes to broaden the scope of possible miRNA targets, including viral and host targets, or to affect their stability. Furthermore, to comprehensively investigate this phenomenon and biological relevance, we used biological approaches to test the relevance of a few most important bioinformatically predicted targets of edited HSV-1 miR-H2. In addition, to extensively analyze this phenomenon during infection with other viruses, we analyzed many publicly available small-RNA deep-sequencing data sets including samples infected with Epstein–Barr virus, Kaposi's Sarcoma-associated herpesvirus, cytomegalovirus, human herpesvirus 6 and human papillomavirus and our preliminary results show that many viruses employ this phenomenon to specifically change the crucial part of the miRNA sequence important for binding to its target or have effect on host miRNAome during the course of the infection. Understanding this novel aspect of non-coding RNA biology will not only shed light on an incredibly complex life cycle of HSV-1 but also might reveal important cellular pathways.