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The transcriptome of the adenovirus infected cell

Virology

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A n important aspect of the interaction between adenovirus and its host is the regulation of host cell gene expression. To investigate the deregulation of cellular gene expression at different stages of a human adenovirus type 2 (Ad2) infection, deep sequencing analysis of small noncoding RNA and mRNA were performed. Nineteen new Ad2-encoded small RNAs of 25 to 35 nucleotides long were identified. These small viral RNAs displayed different expression profile during the course of the infection suggesting that they have different functions. Computer prediction showed that the most significant targets for the earliest small RNAs were genes involved in signaling pathway. Furthermore, more than 100 cellular microRNAs were identified as the most significant differentially expressed more than 2-fold in Ad2 infected cells. miRNAs are important gene regulators and often promote destabilization of mRNA targets. The biological significant of differentially expressed miRNAs was studied by computational prediction of their potential targets. Finally, the expression profiles of miRNAs were correlated with the mRNAs abundance at genome-wide level.

Biography

I received her Ph.D from Karolinska Institute, Sweden. During this time, I focused on the molecular mechanism that governs the assembly of enveloped RNA viruses, Semliki Forest virus and influenza A virus (1990 – 1996). I did my postdoc at the Dept of Molecular Biosciences, Faculty of Veterinary Medicine and Animal Science, at the Swedish University of Agricultural Sciences in 1998. Most of my studies emphasized the analysis of cellular processing of bovine prion protein. Since 2000, I began as a research assistant at the Dept. of Immunology, Genetics and Pathology at Uppsala University, Sweden. The main aim of my research is to investigate the overall impact of adenovirus infections on host cell gene expression using high throughput technology.

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