Abstract

Viruses are the major force that shapes the evolution of both pro- and eukaryotic organisms. They have a simple inner organization and contain only a few, usually well-described RNAs. In the case of +(ss)RNA viruses, their genomic RNA serves also as mRNA. This makes them a perfect model system for searching for new mRNA modifications as well as for understanding the role of already known modifications.

In this work, Human Immunodeficiency Virus type 1 (HIV-1) from the *Retroviridae* family was used as a model system. In the following study, four representatives from the *Picornaviridae* family were tested for RNA methylation profile. To get the information, a combination of two techniques was developed, liquid chromatography- mass spectrometry (LC-MS) and sequencing techniques. Results of LC-MS reveal a surprisingly high amount of 1-methyladenosine (m^1A) in RNA isolated from HIV-1. Nevertheless, the m^1A mapping sequencing technique confirm m^1A position only in co-packed tRNA. This led to the recalculation of HIV-1 virion RNA composition.

In the case of *Picornaviridae*, LC-MS revealed m^1A and 5-methylcytidine (m^5C) in two insect viruses (Sacbrood virus, SBV and Deformed wing virus, DWV). RNA seq techniques (m^1A mapping and bisulfite sequencing) confirmed the presence of m^1A and m^5C only in tRNA. Further analysis revealed that tRNAs are present in the form of 3′ and 5′ fragments. This finding shows that also other viruses co-pack tRNAs. Surprisingly, the types of co-packed tRNAs are similar in distinct virus families: HIV-1 and *Picornaviridae*. This finding may indicate that particular co-packed tRNAs play some important general role in viral infection.

Key words: RNA modifications, LC-MS, RNA-seq, 1-methyladenosine, HIV-1, *Picornaviridae*, tRNA, tRNA fragments