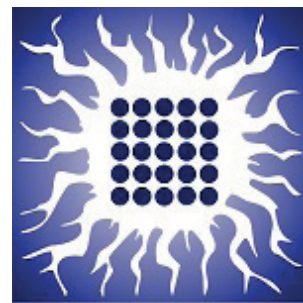


# Biologia Serbica

Department of Biology and Ecology,  
Faculty of Sciences, University of Novi Sad, Serbia



Book of Abstracts  
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## Bioinformatics analysis of eukaryotic positively oriented single stranded RNA viruses

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### Abstract

Positively oriented single stranded RNA viruses [ssRNA(+)] persistently affect health and well-being of all eukaryotes, including plants, animals and humans (i.e. SARS-CoV-2, yellow fever, hepatitis C, zika, West Nile, pepper mild mottle virus, etc.). How come these viruses are so wide spread and hard to eradicate? Besides their high changeability, another major reason is their ability to mimic host processes upon entering the host. Only recently it was revealed that ssRNA(+) viruses undergo methylation inside the host in the process that is similar to the methylation of the hosts' own mRNAs. Such process may enable or disable virus to avoid some of the host's defense mechanisms, but it inevitably impacts viral stability and fitness.

Studies on this topic have only started, opening even more questions, with major ones being: how ssRNA(+) methylation, that occurs in the host, impacts viral pathogenicity and are these methylation patterns different in different hosts and for different ssRNA(+) viruses or do these viral methylomes share more universal pattern in concordance with their similar genome organization? Among numerous different methylation patterns of RNA, this research focused on N6-methyladenosine (m6A), as the most common and abundant methylation in eukaryotes, which was confirmed to be present in ssRNA(+) viruses as well.

This study searched for patterns in the primary sequences and secondary structures of ssRNA(+) that are associated to m6A methylation sites relying on the experimentally obtained m6A datasets for eukaryotes and eukaryotic ssRNA(+) viruses. The results are discussed in view of datasets characteristics and study approach.

### Keywords:

bioinformatics, m6A, methylome pattern, single stranded RNA viruses, ssRNA(+)

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