

JOINT EVENT

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## Characterization of the ACMNPV transcriptome using long-read real-time sequencing

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The *Autographa californica* multiple nucleopolyhedrovirus (AcMNPV) is an insect virus belonging to the Baculoviridae family. The 134 kbp long double-stranded circular DNA of the virus encompasses 150 tightly packed open reading frames. Genes of the AcMNPV are expressed in three phases: early, late and very late. Promoters of early genes are recognized by the host RNA polymerase, and usually consist of a canonical TATA motif located upstream of the transcriptional start site. At the same time some early transcripts start from the arthropod initiator element (CAGT). Late and very late genes are transcribed by the viral RNA polymerase, which recognizes a late initiator sequence (TAAG). A short-read sequencing technique was used previously to elucidate the structure of the AcMNPV transcripts; however short-read sequencing cannot tackle the highly complex, overlapping nature of the viral transcriptome. In this study we found and annotated four novel putative protein coding, four non-coding transcripts and forty-seven novel length isoforms of previously annotated transcripts using the Oxford Nanopore Technologies' MinION and the Pacific Biosciences Sequel platforms. We demonstrated that the canonical promoters and initiators of a transcript are in concordance with the motifs found upstream of its isoforms. We also discovered the extensive overlapping nature of the viral transcriptome. Additionally we determined the expression characteristics of novel transcript isoforms and revised it for the already annotated transcripts using long-read real-time sequencing of the AcMNPV transcriptome.

### Biography

Norbert Moldovan graduated in Biology from Babes-Bolyai University and now is a PhD student at the University of Szeged, Faculty of General Medicine. His area of research is in molecular genetics of human and non-human pathogenic viruses. His main focus is in structural and expressional characterization of viral mRNAs using third-generation sequencing. He has published seven papers on these subjects in reputed journals during his two years of doctoral studies.

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