

JOINT EVENT

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## Comprehensive analysis of vaccinia virus transcriptome by third-generation sequencing

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The Vaccinia virus (VACV) is a prototype member of the Poxviridae family, it has a relatively large double-stranded DNA genome containing about 220 protein coding genes. The VACV encodes DNA and RNA polymerases, transcription factors, enzymes for capping and polyadenylation, which allows VACV to replicate in the cytoplasm, rather than in the nucleus of the infected cell. The VACV is a historically important virus: it has been successfully applied as a vaccine for immunization against human smallpox, which had been eradicated in 1980 as a result of global vaccination. The most virulent strain of VACV, the Western Reserve (WR) was used in this study. For the thorough analysis of VACV transcriptome, we utilized the currently available third-generation sequencers (TGS) such as the Pacific Biosciences (PacBio) RSII and the Sequel, as well as the Oxford Nanopore Technologies (ONT) MinION, which in contrast to the next-generation sequencing approaches enables to identify full-length RNA isoforms, and distinguish between overlapping RNAs. We have characterized the static VACV transcriptome by using the RSII and MinION, while the Sequel and Minion was applied for the detailed analysis of the transcriptional dynamics of the viral RNAs. Our detailed study redefined the VACV transcriptome. Our data showed that the VACV transcriptome profile is much more complex than it was previously known. We have identified hundreds of novel transcripts and isoforms. We have described hundreds of bi-, polycistronic, and complex transcripts. These forms were not known before our study. These RNA molecules together represent very long transcriptional overlaps.

### Biography

Dora Tombacz has completed her MSc in Biology (2006) and PhD in Medical Sciences (2010) from the University of Szeged, Hungary. She is working in the Department of Medical Biology as an Assistant Professor at the same university in the Genomics & Gene Technology group. She has published more than 30 papers in reputed journals. Her primary field of interest is transcriptomics, the analysis of different organisms at the RNA level. She is currently working with next- and 3rd generation sequencing techniques at the University of Szeged, and as a Visiting Assistant Professor at the Stanford University, USA.

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