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## Long read sequencing of herpesvirus transcriptomes revealed widespread transcriptional interactions

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High-throughput sequencing methods have revolutionized genomics, including RNA-sequencing; however the widespread short read-sequencing techniques cannot distinguish between the different transcript isoforms and overlaps. The third-generation, long-read sequencers (TGS) are enabled to identify full-length isoforms. For the deep analysis herpesvirus transcriptomes, we utilized the Pacific Biosciences (PacBio) RSII and the Sequel TGS machines, as well as the Oxford Nanopore Technologies (ONT) MinION device. In this project, we characterized the RNA profiles of the following viruses: human herpesvirus-1 (HSV-1), pseudorabies (PRV), varicella zoster virus (VZV), human cytomegalovirus (HCMV), Epstein-Barr virus (EBV). For the analysis of the static transcriptome of HSV, PRV and HCMV the PacBio IsoSeq protocol was used. For the analysis of the dynamic properties of PRV transcript isoforms we applied the PacBio non-amplified method. To obtain a more comprehensive picture about the RNA variants, the ONT cDNA and direct RNA sequencing protocols, as well as a CAP-selection method combined with ONT cDNA sequencing were also utilized. These ONT approaches were applied for the analysis of EBV and VZV transcriptomes. Our surveys redefined the herpesvirus transcriptomes profiles. We discovered that the herpesvirus genomes are much more complex and the transcriptional-read-throughs between the genes are more common than it was known. Our data revealed that these read-throughs can generate very long RNAs including some containing oppositely oriented ORFs, which have been classified as complex transcripts. The applied TGS techniques have been shown that the extensive RNA variations are common among herpesviruses.

### 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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