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Long-read sequencing uncovers a hidden complexity of the herpesvirus transcriptome

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Herpesviruses are large, enveloped, double-stranded DNA viruses. Although, the members of the three subfamilies (α-, β-, and γ-herpesviruses) differ in tissue tropisms and in many aspects of molecular pathogenesis, the basic mechanisms of their DNA replication and transcription are largely conserved. The herpesvirus transcriptome have already been investigated by various techniques, including Northern-blot and microarray analyses, as well as short-read sequencing supplemented with other techniques such as primer extension, or S1 nuclease analyses. However, these techiques are inefficient for the detection of embedded RNAs, transcript isoforms, polycistronic RNAs, and transcritional overlaps. Long-read sequencing can circumvent these problems. We used two sequencing platforms, the RS II and Sequel methods from Pacific Biosciences and the cDNA and direct RNA sequencig methods from Oxford Nanopore Technology for studying the transcriptome of various herpesviruses including herpes simplex virus type 1, varicella-zoster virus, pseudorabies virus, and human cytomegalovirus. Our investigations revealed a much more complex transcritional landscape than it has been known earlier. We identified novel protein-coding genes, which are embededd into longer host genes. Our analysis detected a number of novel non-coding RNAs, polycistronic transcripts and various transcript isoforms including splice variants as well as transcript start sites and transcript end sites variants. Additionally, our studies uncovered a genome-wide meshwork of transcritional overlaps. This latter phenomenon suggests the existence of a transcriptional interference network controlling the global gene expression through the interactions between the transcritional machineries at the ovelapping regions.

Biography

Zsolt Boldogkoi has completed his PhD from Szent Itvan University and Postdoctoral studies from University of Bonn, School of Medicine. He is the Director of the Department of Medical Biology, University of Szeged. He has published close to 100 papers in reputed journals.

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