

GLOBAL MEDICAL MICROBIOLOGY SUMMIT & EXPO

November 28-29, 2016 San Francisco, USA

Full-length isoform sequencing reveals a hidden complexity in the transcriptome of a herpesvirus

Zsolt Boldogkoi

University of Szeged, Hungary

A single molecule long-read sequencing platform was used to characterize the polyadenylated fraction of the lytic transcriptome of pseudorabies virus (PRV). Both amplified and non-amplified isoform sequencing protocols were applied to complete the transcriptional annotation of the viral genes. Our analyses revealed previously unrecognized protein-coding and non-coding genes, novel mono and polycistronic transcription units, as well as extensive transcriptional overlaps between neighboring and distal genes. Our investigations identified several non-coding transcripts overlapping all three replication origins of the PRV. This study revealed that the entire PRV genome is utilized for transcription, including both DNA strands in all coding and intergenic regions. The genome-wide presence of transcript overlaps suggests a crosstalk between genes through the interaction of transcription apparatuses with a potential function in the control of gene expression. The Ori-overlapping transcripts are supposed to represent an interaction between the transcription and replication machineries, which might play a role in the control of DNA synthesis. This study also demonstrated the utility of Pacific Biosciences RS II platform for the analysis of quantitative data, since we could evaluate the relative amounts of transcripts produced throughout the viral life cycle.

Biography

Zsolt Boldogkoi has received his PhD in Molecular Biology from Szent Istvan University at Godollo. He has worked at the Wistar Institute, Philadelphia, USA as a PhD student then had Post-doctoral training at University of Bonn. His primary field of interest is the molecular biology of herpesviruses, the regulation of gene expression analysis and utilization of herpesviruses as tools. He has published more than 70 papers in reputed journals. He is currently the Head of Department of Medical Biology at Faculty of Medicine of University of Szeged.

boldogkoi@gmail.com

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