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Interaction between the transcriptional machineries in pseudorabies virus

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Earlier we proposed that the transcriptional interactions form a network play important roles in the regulation of global gene expression in all taxa of living beings. We used a herpesvirus model for the investigation of this issue. The genome of pseudorabies virus (PRV) is very compact. We have shown that most of the PRV transcripts overlap with each other in various manners including convergent, divergent and parallel orientations. We have shown that this interactions result in a inverse pattern of gene expressions. We used the following techniques for these investigations: Real-time RT-PCR, Illumina HiScanSQ and PacBio RS II platforms.

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