

Sequence analysis of a putative DNA helicase and four peptides encoded by ORFs of the *Diachasmimorpha longicaudata* entomopoxvirus (DIEPV)

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Abstract

DIEPV is a symbiotic entomopoxvirus (EPV) of the parasitic wasp *Diachasmimorpha longicaudata*(Dl). It has a double stranded DNA genome of 250-300 kb and is >60% A-T rich. We describe five DIEPV open reading frames (ORFs) within the first 2.87 kb of the 5' region of clone #35 (RI-35) from a DIEPV EcoRI genomic library. Our goal was to identify unique motifs and compare them with others in the database, particularly those of poxviruses, using Sequencher, PROSITE, and SwissPROT. RI-35-I encodes a putative nuclear peptide of 113 aa, contains a late promoter (TAAATG) and an early transcription stop sequence (TTTTTCT) three nucleotides downstream of the stop codon, and is likely an early/late gene. RI-35-2 is a late gene that presumably encodes a 117 aa cytoplasmic peptide and contains a leucine zipper-like sequence that is predicted to bind DNA, and is probably a transcription factor that regulates viral gene expression. RI-35-3 is a presumed DNA helicase gene whose protein of 480 aa is highly homologous to those of *Melanoplus sanguinipes*EPV (72%), *Amsacta moorei*EPV (72%) and vaccinia virus (69%). DNA helicases unwind the DNA helix during replication and transcription. The DIEPV-encoded enzyme contains six conserved motifs that characterize helicases and is likely a member of the DEXH DNA and RNA helicases. Like its homologs, the RI-35-3 protein has a predicted cytoplasmic location and is probably an intermediate/late gene. RI-35-4 and -5 encode 81 and 106 aa respectively, and are predicted to be cytoplasmic proteins expressed during the intermediate phase of viral morphogenesis. Our results provide additional evidence that DIEPV is a member of the Entomopoxvirinae and is the first symbiotic EPV described to date. Support from the National Science Foundation grants, IBN 9514583 and 9986076 to POL is gratefully acknowledged.