A putative DNA helicase and novel oligoribonuclease in the Diachasmimorpha longicaudata entomopoxvirus (DlEPV).

Abstract:

Diachasmimorpha longicaudata entomopoxvirus (DlEPV) is a symbiotic entomopoxvirus (EPV) of the parasitic wasp Diachasmimorpha longicaudata. It has a double-stranded DNA genome of 250-300 kb and is >60% A-T rich. We describe ten ORFs (RI-35-1 to -10) contained within a 5.64 kb clone, RI-35, from a DlEPV EcoRI genomic library. Our goal was to identify unique motifs and compare them with others in the database, particularly those of poxviruses. Two ORFs (RI-35-1 and RI-35-7, respectively) encode putative proteins (113 aa and 219 aa) that are probably involved in regulating gene expression based on their predicted nuclear localization and the presence of SPxx motifs, leucine-zipper like sequences (113 aa), and a basic domain (219 aa). The largest gene (RI-35-3) is under the control of an intermediate/late promoter and is presumed to encode a cytoplasmic 480 aa DNA-dependent DNA helicase with conserved motifs that are characteristic of DExH helicases. Amino acid analysis of the DNA helicase sequence showed that DlEPV is close to but distinct from the Genus B EPVs. The DlEPV helicase is also distinct from that of the Diadromus pulchellus ascovirus 1a from the D. pulchellus parasitic wasp, with less than 10% amino acid identity. DlEPV encodes a 207 aa oligoribonuclease (RI-35-8) of the DEDDh family of exoribonucleases. The second largest ORF (RI-35-9) is under the control of a poxvirus early promoter and encodes a protein of 329 aa that is likely DlEPV-specific. Three ORFs (RI-35-4, -5, and -6) overlap (in the anti-sense strand) with ORFs encoding putatively important virus replication proteins (which were also under the control of intermediate promoters) and are presumably not expressed in DlEPV. These results support earlier reports that DlEPV is a member of the sub-family Entomopoxvirinae, most likely in Group C, and is the first symbiotic EPV described to date from a parasitic wasp.