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Pseudoplusia includens Densovirus Genome Organization and Expression Strategy

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The genome of a densovirus of a major phytophagous pest, Pseudoplusia includens, was analyzed. It contained 5,990 nucleotides (nt) and included inverted terminal repeats of 540 nt with terminal Y-shaped hairpins of 120 nt. Its DNA sequence and ambisense organization with 4 typical open reading frames demonstrated that it belonged to the genus Densovirus in the subfamily Densovirinae of the family Parvoviridae.

The distribution of the polyphagous soybean looper pest, Pseudoplusia includens (syn., Chrysodeixis includens [Hübner] [Noctuidae, Plusiinae, Lepidoptera]), is restricted to the Western Hemisphere, occurring from southern Canada to southern South America (1). In addition to the soybean, it may feed on a large number of crops of economic importance (8, 9). Previously, two small isosahedral viruses have been isolated from the soybean looper, a picornavirus and a smaller virus with biophysical properties that seem to match those of the densoviruses (2).

Densoviruses are notoriously unstable upon cloning (7, 10–13), and densovirus entries in GenBank, such as those from Junonia coenia (JcDNV) (3) and Diatraea saccharalis (DsDNV) (NC_001899), often lack significant parts of their inverted terminal repeats (ITRs). DNA purified from Pseudoplusia includens DNV (PiDNV) in phosphate-buffered saline (PBS) had a size of around 6 kb. This DNA was blunt ended by a mixture of Klenow fragment and T4 DNA polymerase and cloned into a linear pljazz vector (from Lucigen Corp.), which lacks transcription into the insert and torsional stress (5) to prevent recombination and deletion of insert fragments. Six clones, or about 0.3%, had full-length inserts and could be stably subcloned into circular vectors.

Four complete clones were sequenced in both directions, using Sanger’s method and the primer-walking method as described before (11), and the contigs were assembled by the CAP3 program (http://pbil.univ-lyon1.fr/cap3.php) (6). The difficulties encountered with sequencing of the terminal hairpins were solved by sequencing after (i) digestion near the middle of the hairpin with BstUI restriction enzyme or (ii) amplifying the hairpin with primers that include 5′ nucleotides at their 3′ end and 3′ nucleotides at their 5′ end by using Sanger’s method and the primer-walking method as described before (11). The large ORF1 (nt 1355 to 3019) on the plus strand had a coding capacity for NS1 of 554 amino acids (aa), ORF2 corresponded to NS2 (nt 1362 to 3019) with 275 aa, and ORF3 (nt 647 to 1348) corresponded to NS3 with 233 aa. On the complementary minus strand, a large ORF (also on the 5′ half at nt 3060 to 5423) with a potential coding region of 805 aa corresponded well to those of the VP structural proteins of related densoviruses. The distribution of the putative coding sequences implied an ambisense organization and expression, and PiDNV contained the typical NS-1 helicase superfamily III and VP phospholipase A2 (14) motifs observed in other parvoviruses.

Nucleotide sequence accession number. The GenBank accession number of PiDNV is JX645046.

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REFERENCES


