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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 smallicosahedral 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 pHsp68 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 domain 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 pHsp68 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.

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 GenBank accession number of PiDNV is JX645046.

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