

Genomic sequencing and analyses of *Lymantria xyлина* multiple nucleopolyhedrovirus.

ABSTRACT

BACKGROUND: Outbreaks of the casuarina moth, *Lymantria xyлина* Swinehoe (Lepidoptera: Lymantriidae), which is a very important forest pest in Taiwan, have occurred every five to 10 years. This moth has expanded its range of host plants to include more than 65 species of broadleaf trees. LyxyMNPV (*L. xyлина* multiple nucleopolyhedrovirus) is highly virulent to the casuarina moth and has been investigated as a possible biopesticide for controlling this moth. LdMNPV-like virus has also been isolated from *Lymantria xyлина* larvae but LyxyMNPV was more virulent than LdMNPV-like virus both in NTU-LY and IPLB-LD-652Y cell lines. To better understand LyxyMNPV, the nucleotide sequence of the LyxyMNPV DNA genome was determined and analysed. **RESULTS:** The genome of LyxyMNPV consists of 156,344 bases, has a G+C content of 53.4% and contains 157 putative open reading frames (ORFs). The gene content and gene order of LyxyMNPV were similar to those of LdMNPV, with 151 ORFs identified as homologous to those reported in the LdMNPV genome. Two genes (Lyxy49 and Lyxy123) were homologous to other baculoviruses, and four unique LyxyMNPV ORFs (Lyxy11, Lyxy19, Lyxy130 and Lyxy131) were identified in the LyxyMNPV genome, including a gag-like gene that was not reported in baculoviruses. LdMNPV contains 23 ORFs that are absent in LyxyMNPV. Readily identifiable homologues of the gene host range factor-1 (hrf-1), which appears to be involved in the susceptibility of *L. dispar* to NPV infection, were not present in LyxyMNPV. Additionally, two putative odv-e27 homologues were identified in LyxyMNPV. The LyxyMNPV genome encoded 14 bro genes compared with 16 in LdMNPV, which occupied more than 8% of the LyxyMNPV genome. Thirteen homologous regions (hrs) were identified containing 48 repeated sequences composed of 30-bp imperfect palindromes. However, they differed in the relative positions, number of repeats and orientation in the genome compared to LdMNPV. **CONCLUSION:** The gene parity plot analysis, percent identity of the gene homologues and a phylogenetic analysis suggested that LyxyMNPV is a Group II NPV that is most closely related to LdMNPV but with a highly distinct genomic organisation.

Keyword: Genome; *Lymantria xyлина*; Multiple nucleopolyhedrovirus.