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Abstract
The Maruca vitrate multiple nucleopolyhedrovirus (MaviMNPV), isolated from infected larvae of legume pod borer, its genome has been sequenced and identified containing 111,953 bp. The genomic analysis of MaviMNPV revailed that its genome encoded 126 ORFs with G+C content of 38.62%. There are 125 ORFs of MaviMNPV also possessed by RoMNPV, while 124 ORFs possessed by both AcMNPV and BmNPV. One gene is homologues with ORF 34 of ChchNPV. One hundred and twenty-four ORFs among the total 126 ORFs of MaviMNPV showed highly homologues to the respected ORFs encoded by AcMNPV, RoMNPV and BmNPV. The MaviMNPV belong to the small NPV group might contributed to lacking repetitive bro gene. Only four repetitive genes, iap-1 and iap-2, ORF113 and ORF118 are encoded by MaviMNPV. MaviMNPV is shortage of odv-e66 and fgf gene which are encoded by all the baculovirus of Lepidoptera. There are five homologous regions (hrs) distributed in MaviMNPV genome, each of the hr contains the core sequence flanking by 1-GxTTTxC-7 and 22-TxGxAAAxC-30 conserved sequence. The arrangement of the ORFs and hrs in the genome of MaviMNPV adopt the similar profile with AcMNPV, RoMNPV and BmNPV. The phylogenetic analysis based on single gene (polyhedrin gene) or full genome suggested that MaviMNPV is a member of groupI NPVs and most closely to a subgroup containing AcMNPV, RoMNPV, PlxyMNPV and BmNPV. The transient expression assay approved that hr2 of MaviMNPV could enhance promoter activity of both ie-0 and ie-1 gene of MaviMNPV. The effort to estimate the minimal amount of genomic DNA that could be detected by PCR reaction showed that five picogram of genomic DNA from both MaviMNPV and AcMNPV could amplify the 680bp fragment of polyhedrin gene. Then, the RFLP analysis of the PCR product that digested by DraIII and HpaI restriction enzymes could discriminate the MaviMNPV from other NPV.
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