Cloning and Sequence Analysis of *Cotesia plutellae* Polydnavirus Genomic Segments

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Cotesia plutellae polydnavirus (CpBV) is obligate mutualistic insect virus found in parasitic wasp, *Cotesia plutellae*, which has been recommended as useful component to apply integrated pest management of the diamondback moth, *Plutella xylostella*, in southeastern Asia. The CpBV causes several obvious physiological changes such as immune suppression and developmental disturbance in parasitized hosts, *P. xylostella* larvae. Genomes of CpBV consist of several double-stranded, circular DNA molecules with variable size. In this study, we cloned CpBV genomic segments using plasmid capture system (PCS), pPCS-S into *Escherichia coli* cell. The pPCS-S may transfer a pUC19 origin of replication and an ampicillin resistance marker inserted between Tn7 left (L) and right (R) end, and this pPCS-S donor was applied to clone segments of CpBV genome by *in vitro* transposition using TnsABC* transposase. In result, 53 genomic clones ranging from 0.3 to 26 kb were cloned and they were classified 29 different segments by their size and restriction endonuclease pattern. Among these clones, the complete nucleotide sequence of CpBV-S30 clone was determined and 9 putative ORFs were predicted with FGENESV0. Comparison of the nucleotide sequences with EMBL databases or of the hypothetical proteins with SWISS-PROT databases using BLAST revealed that each ORF showed homology with EP1 of *C. congregata* polydnavirus, CkV2.0 of *C. kariyai* polydnavirus, 94k of baculoviruses, catalytic domain of protein tyrosine phosphatase or histone H4 proteins, respectively.