

## Cloning and Genomic Structure Analysis of *Cotesia plutellae* Polydnavirus using Plasmid Capture System

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*Cotesia plutellae* polydnavirus (CpBV) have a segmented genome consisting of multiple circular double stranded DNAs. Recently, we have developed an easy, simple and convenient system based on Tn7 transposition in order to clone genomic segments of CpBV in *Escherichia coli* cell and designated plasmid capture system (PCS). The PCS donor-S transferred a pUC19 origin of replication and an ampicillin resistance marker into CpBV genomic DNA by *in vitro* transposition. Through PCS system, we were able to clone 53 genomic clones ranging from 0.1 to 25.5 kb and further they were classified 29 segments by their sizes and restriction endonuclease patterns. Among them, a complete nucleotide sequence of CpBV-S28 segment was determined and 10 putative genes were predicted from this segment. Interestingly, nine of ten putative ORFs had high level of similarities with catalytic domain of protein tyrosine phosphatase. Also, ORF2810 showed similarity with EP1-like proteins of *C. congregata* polydnavirus.