



GENETIC CHARACTERIZATION OF AN ALPHABACULOVIRUS CAUSING TIGER BAND DISEASE IN THE OAK TASAR SILKWORM, *ANTHRAEA PROYLEI* J (LEPIDOPTERA: SATURNIIDAE)

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ABSTRACT

In the recent decade, a dreadful viral disease commonly known as tiger band disease affecting the oak tasar silkworm, *Antheraea proylei* has caused severe loss in the production of silk. The virus was isolated and the complete viral genome was determined, unveiling that a group I alphabaculovirus i.e., *Antheraea proylei* nucleopolyhedrovirus (AnprNPV) is the causal agent of this disease. The genome is 126,930 bp in length with 53.46 % G+C content. It encodes 147 open reading frames (ORFs), consisting of 37 core genes, 25 lepidopteran baculovirus conserved genes, 11 lepidopteran NPVs genes, 41 genes found in all Group I NPVs, 27 genes found in some Group I NPVs, 5 genes found specifically in NPVs of saturniid silkworms and also with 1 additional unique gene, *he65-like* (Anpr35). There are 109 intergenic regions distributed ranging from 1 to 454 bp, contributing to 7.33 % of the whole genome. Within intergenic regions, 239 microsatellites (SSRs) motifs having mono to hexa-nucleotide repeats were distributed where trinucleotides had maximum abundance (47.89 %). Six homologous regions (Hr1 to Hr6) present in the genome have perfect / imperfect palindromes of 30 bp sequence, CGBTTTTTCNAGNHTGDYYRTNCTYGAAAANC associating with a direct repeat, TCRGCGCTGA. Phylogenetic analysis showed the clustering of AnprNPV in the same clade as the alphabaculovirus group I of the saturniid silkworms *A. pernyi* and *Philosamia cynthia ricini* indicating a close relationship with those viruses. Furthermore, AnprNPV and *A. pernyi* nucleopolyhedrovirus (AnpeNPV) isolates had a nucleotide sequence identity above 95 %, which strongly suggest that AnprNPV is a regional variant of AnpeNPV.

Key words: *Antheraea proylei*, nucleopolyhedrovirus, saturniid silkworm, viral genome.