Genome of a *Bombyx mori* Nucleopolyhedrovirus Strain Isolated from India

Hai-Wei Fan,* Xue-Chao Zhang,* Yi-Peng Xu,* Xiao-Wen Cheng,* and Chuan-Xi Zhang*  
Agriculture Key Laboratory of Agricultural Entomology, Institute of Insect Science, Zhejiang University, Hangzhou, China,* and Department of Microbiology, Miami University, Oxford, Ohio, USA*  

*Bombyx mori* nucleopolyhedrovirus (BmNPV), a member of the *Baculoviridae*, is a major pathogen of silkworm and has also been recently developed as an expression vector for heterologous gene expression in the silkworm larvae and pupae. To better understand the diversity of this important baculovirus, we sequenced the complete genome of the BmNPV strain isolated from India, where its host is available throughout the year due to its tropical climate. The genome of the Indian strain consists of 127,879 nucleotides, with a G+C content of 40.36%. There are 138 open reading frames (ORFs) encoding the predicted proteins of more than 50 amino acids. Genomic comparison of the Indian strain with 3 other reported BmNPV strains showed that the baculovirus repeat ORFs (bro) and homologous repeat regions (hr’s) are highly variable. These results suggest that the BmNPV strain heterogeneity is mainly caused by single-nucleotide polymorphisms (SNPs) and changes in the hr’s and bro genes.

B. mori nucleopolyhedrovirus (BmNPV) selectively infects the domestic silkworm and causes great losses to sericulture. Currently, BmNPV has been developed as an expression vector for heterologous gene expression in the silkworm larvae and pupae. Sericulture in a temperate area such as China is usually practiced only by two cocoon crops per annum. However, in tropical countries such as India, sericulture can be practiced year-round. Thus, the disease causing BmNPV has hosts for infection and genome replication throughout the year, which may allow faster speciation in the tropics than in temperate regions. To better understand the diversity of this important baculovirus, we sequenced the complete genome of a BmNPV strain isolated from tropical India and compared it with the reported strains.

The virus strain was isolated from a diseased silkworm in Nagpur, India. The virus was plaque purified in BmN cells, propagated by infecting fifth-instar larvae of the silkworm. Genomic DNA was extracted from the purified occlusion bodies. The entire genome was sequenced, assembled, and analyzed as reported previously (1).

The genome of the BmNPV Indian strain consists of 126,879 nucleotides, with a G+C content of 40.34%. The size and G+C content most closely resembled those of the other three reported BmNPV isolates, the T3 strain (128,413 bp; G+C content, 40.4%) (2), the S1 strain (126,770 bp; G+C content, 40.2%) (3), and the Cubic strain (127,465 bp; G+C content, 40.36%) (1). There were 138 open reading frames encoding the predicted proteins of more than 50 amino acids, beginning with the polyhedrin gene. The differences in genome size among the BmNPV strains are mostly due to the divergence in *bro* genes and homologous repeat regions (hr’s). Similar to the S1 strain, the Indian strain has only two subgroups of *bro* genes (*bro-d* of subgroup A and *bro-a* and *bro-c* of subgroup B), lacking *bro* genes of subgroup C, while the T3 strain and the Cubic strain have three subgroups (A, B, and C) of *bro* genes. There are 8 hr’s (*hr2L*, *hr2R*, *hr3*, *hr4a*, *hr4b*, *hr4c*, *hr5*, and *hr1*) present in the genome of the Indian strain, the same as the T3, Cubic, and S1 strains. However, the total numbers and distribution of their inner palindromes are somewhat different. The total numbers of palindromes for the Indian, T3, S1, and Cubic strains are 46, 42, 42, and 41, respectively, with the Indian strain having the most number of palindromes.

Among the four strains, the Indian strain showed the highest infectivity to the second-instar larvae of *B. mori* (Dazao strain). This might be due to its differences in genome compared to the other three strains. More specifically, the Indian strain has shockingly the most mutations in *per os* infectivity factors (PIFs), with 7, 19, 2, 4, and 8 amino acids changes in *P74*, *PIF1*, *PIF2*, *PIF3*, and ODV-E56, respectively, compared with those in the T3 strain. Some of these mutations might be related to its higher infectivity of occlusion body than the other three strains, but this needs to be confirmed in further studies.

**Nucleotide sequence accession number.** The GenBank accession number of the BmNPV Indian strain is JQ991010.

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**REFERENCES**

