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The Transcription Strategy of *Bombyx mori* Bidensovirus and a Characterization of the Viral Structural Proteins

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Bombyx mori bidensiovirus (BmBDV) is a species of Bidensovirus that has been was placed into a new genus within the new family Bidnaviridae by the International Committee on Taxonomy of Viruses. BmBDV causes fatal flacherie disease in silkworms, which causes large losses to the sericulture industry. BmBDV contains two sets of complementary linear single-stranded DNAs of approximately 6.5 kb (viral DNA 1, VD1) and 6.0 kb (viral DNA 2, VD2). VD1 and VD2 are encapsidated in separate icosahedral non-enveloped capsids, which are similar in size and shape. However, the complete mRNA procession profile remains unclear. In this work, we investigated the expression strategies of BmBDV non-structural proteins and structural proteins. Total RNA was obtained from the midgut of infected silk worm at 5th instar. RACE methods were used to identify the 5' and 3' transcription ends. Meanwhile, a total of six structural proteins were separated by two-dimensional electrophoresis and shown to be encoded by the BmBDV VP gene via mass spectrometry. The transmission electron microscopy results showed that co-expression of the BmBDV VP and SP structural proteins in Spodoptera frugiperda sf9 cells resulted in the formation of 22–24 nm virus-like particles. Furthermore, a mutation of the major structural protein-encoding VP gene, in which the second in-frame ATG codon was mutated to GCG, abrogated the production of several structural proteins, indicating that this strategy of expressing BmBDV VP is dependent on a leaky scanning translation mechanism.