



Manuscript Number: 2279 NAAS Rating: 4.47

Molecular Diversity of *Bombyx mori* Nuclear Polyhedrosis Virus (BmNPV) Isolates using AFLP Markers

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Abstract: Amplified fragment length polymorphism (AFLP) was used to characterize five *silkworm* (Bombyx mori L. Nuclear Polyhedrosis Virus) BmNPV isolates. A total of 235 bands were scored for four AFLP primer combnations, of which 202 (86%) were polymorphic with an average of 50 polymorphic bands per primer combination. Polymorphism information content (PIC) ranged from 0.29 (for E-CAT/M-GTG& E-CAG/M-GTG) to 0.31 (E-CAG/M-GCC). Marker index (MI) ranged from 12.90 (E-CAA/M-GCC) to 17.98 (E-CAT/M-GTG). Primer E-CAG/M-GCC revealed higher values for both PIC (0.31) and MI (14.83). Cluster analysis based on AFLP markers exhibited concordant relationships among the isolates in relation to geographical origin with high bootstrap values. Survey of unique AFLP bands across five BmNPV isolates revealed correlation between number of unique bands noticed for each isolate and their existing genetic relationships. Mandya isolate was most distinct among five isolates and perhaps other four isolates have evolved from this due to higher sequence variation reflected from the number of unique bands.

Key Words: AFLP, Bombyx mori nuclear polyhedrosis virus, Genetic diversity