Table

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**Figure S1** Multiple sequence alignment of the cysteine-rich zinc finger-like motif identified in the hypothetical proteins encoded by dsRNA2 of TaPmV-1and other polymycoviruses.

Text

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**Figure S2** Multiple sequence alignment of the catalytic MTR motif identified in the proteins encoded by dsRNA3 of TaPmV-1 and other polymycoviruses.

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**Figure S3** Multiple sequence alignment of the regions of proteins putatively encoded by TaPmV-1, AaPmV1, AfuTmV-1, AfuPmV-1 and AspTmV-1 that mediate the in 5’- capping of RNA.

Logo

Description automatically generated with medium confidence

**Figure S4** Predicted secondary structures of 5’-UTRs and 3’-UTRs of dsRNAs 1-6 of TaPmV-1. (A) Secondary structures of the 5’-UTRs of dsRNA1-dsRNA6. (B) Secondary structures of the 3’-UTRs of dsRNA1- dsRNA6.

A picture containing box and whisker chart

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**Figure S5** Phylogenetic analyses of TaPmV-1 and selected polymycoviruses. Phylogenetic analyses of TaPmV-l based on the sequences of MTP.

Diagram

Description automatically generated

**Figure S6** Phylogenetic analyses of TaPmV-1 and selected polymycoviruses. Phylogenetic analyses of TaPmV-l based on the sequences of PASrp.

A picture containing diagram

Description automatically generated

**Figure S7** Detection of TaPmV-1 in *T. amestolkiae*. (A) Detection of TaPmV-1 in *T. amestolkiae* following treatment with the protoplast preparation and regeneration approach, using CF11 cellulose columns for extraction followed by gel electrophoresis. (B) The presence of the TaPmV-1 genome in the strain LSH3 and the absence of the TaPmV-1 genome in the strain LSH3VF were confirmed by RT-PCR.