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Fig. 1. Phylogenetic tree constructed using the complete polyprotein amino acid sequences of viruses in the family *Potyviridae*, aligned with MUSCLE. Confidence values were calculated by bootstrapping with 1000 repetitions using the Neighbor-Joining method implemented in MEGA 11. The proposed new species in the genus *Potyvirus* are highlighted in yellow, and those in the proposed new genus *Phragmivirus* are highlighted in blue.