A lineage of begomoviruses encode Rep and AC4 proteins of enigmatic ancestry: hints on the evolution of geminiviruses in the New World.

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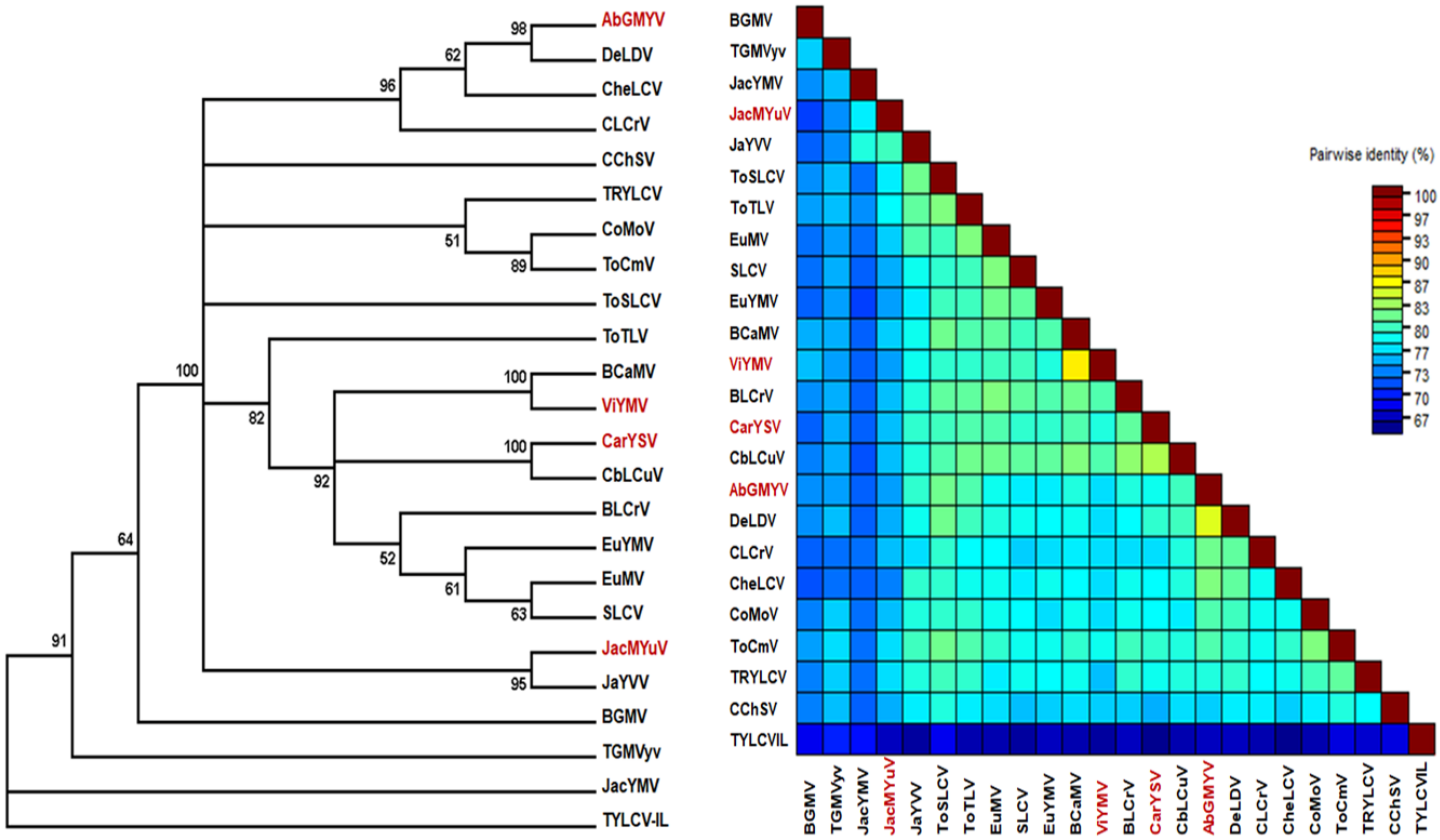
Supplementary Figure S2

Phylogenetic tree and matrix of pairwise sequence identity based on DNA-A sequences of the isolated begomoviruses and their relatives.



Supplementary Figure 2. Maximum likelihood phylogenetic tree and matrix of pairwise sequence identity based on full length sequences of genome components A. ML phylogenies were constructed by multiple alignments of complete DNA-A sequences. ML tree in MEGA 7 was based on the Tamura-Nei model and the tree support was tested by bootstrapping with 1000 replicates. SDTv software was used for the matrix of pairwise sequence identity.