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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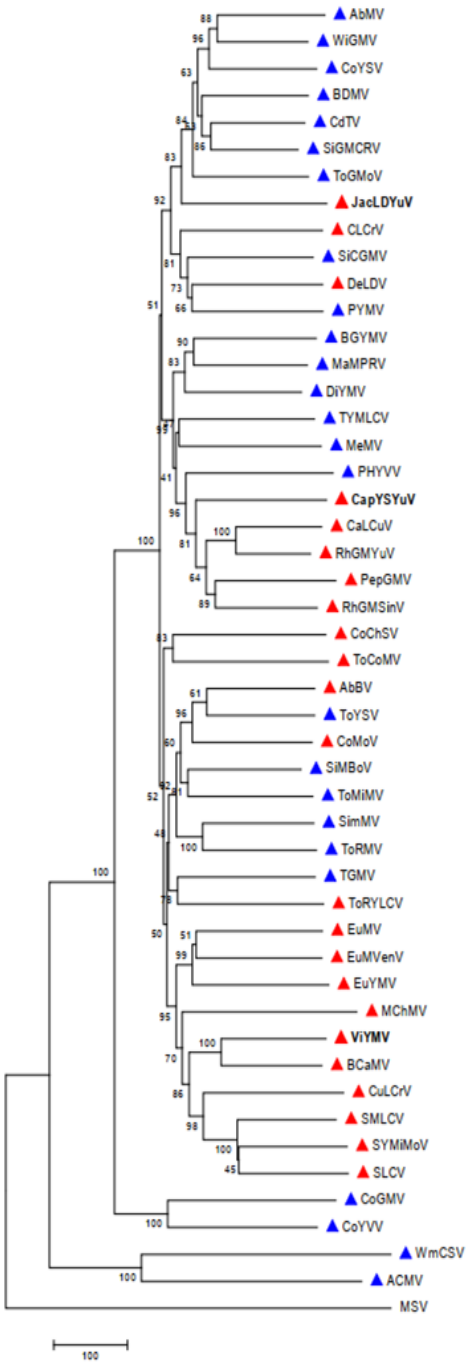
Supplementary Figure S5

DNA-B inferred evolutionary relationships of viruses isolated in this work compared with selected begomoviruses



Supplementary Figure 5. DNA-B inferred evolutionary relationships of viruses isolated in this work compared with selected begomoviruses. Phylogenetic tree indicating the relationship between the DNA-B genomic component of viruses isolated in this work (AbGMYuV, CarYSYuV, JacMYuV and, ViYMV) and selected begomoviruses is shown. The SLCV clade members are denoted with a red triangle depicted before the name. *Maize streak virus* (MSV, a mastrevirus) was used as outgroup. Genome B phylogeny was inferred with a total of 1470 positions in the final dataset using the Neighbor-Joining method. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the number of differences method and are in the units of the number of base differences per sequence. The analysis involved 46 nucleotide sequences. All positions containing gaps and missing data were eliminated. Tree support was tested by bootstrapping with 1000 replicates.