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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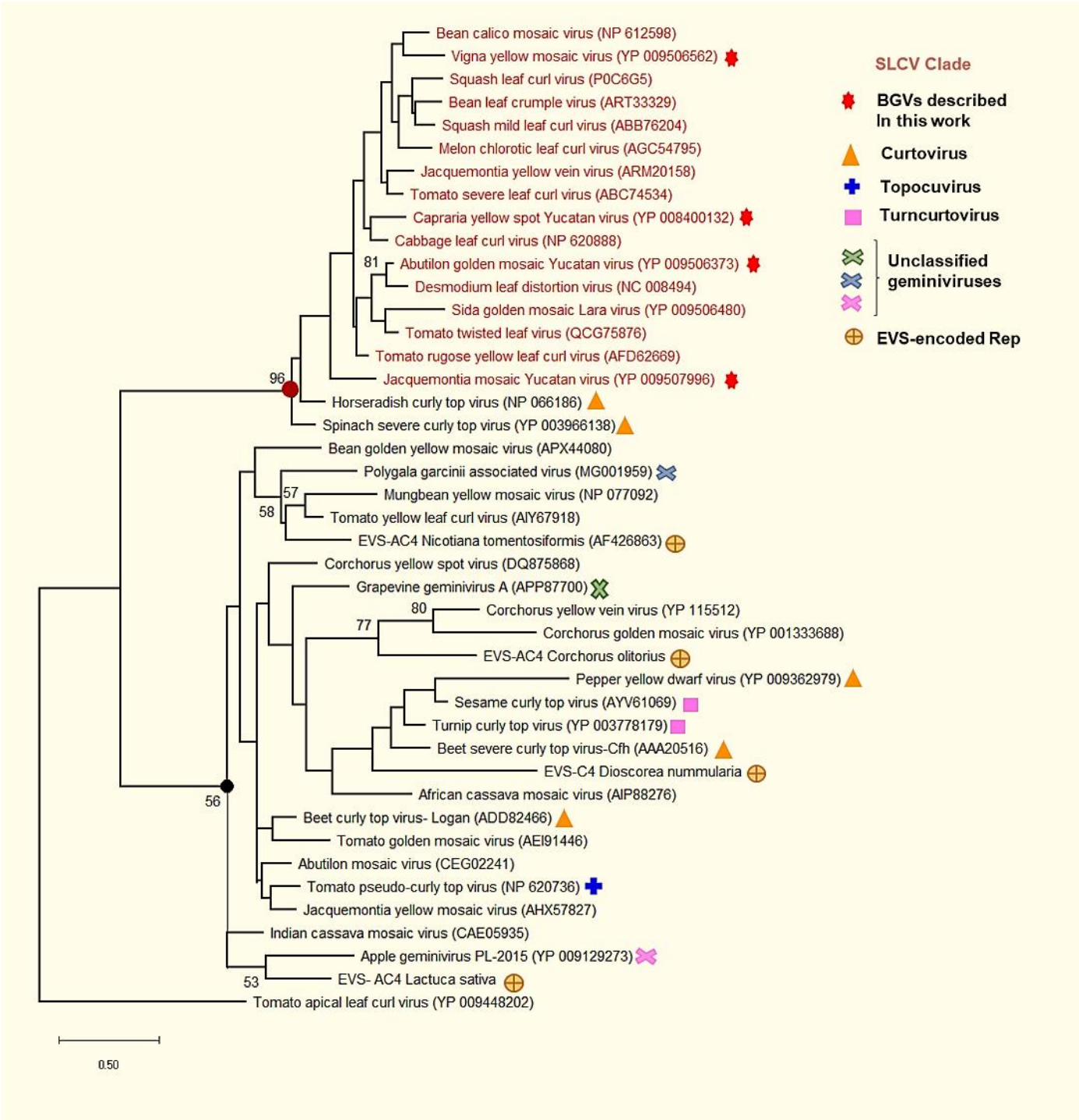
Supplementary Figure 6



Supplementary Figure 6. Phylogenetic relationships between AC4 proteins encoded by SLCV-Lin members (highlighted in red) and those of other geminivirus subgroups. The phylogenetic tree was inferred by using the Maximum Likelihood method based on the JTT matrix-based model. The percentage of trees in which the associated taxa clustered together is shown next to the branches (1000 iterations). Red filled circle indicates the node of the S-Lin BGVs, and the black filled circle indicates the main branch of other geminiviruses.