

SUPPORTING INFORMATION

Climate-influenced boreotropical survival and rampant introgressions explain the thriving of New World grapes in the north temperate region

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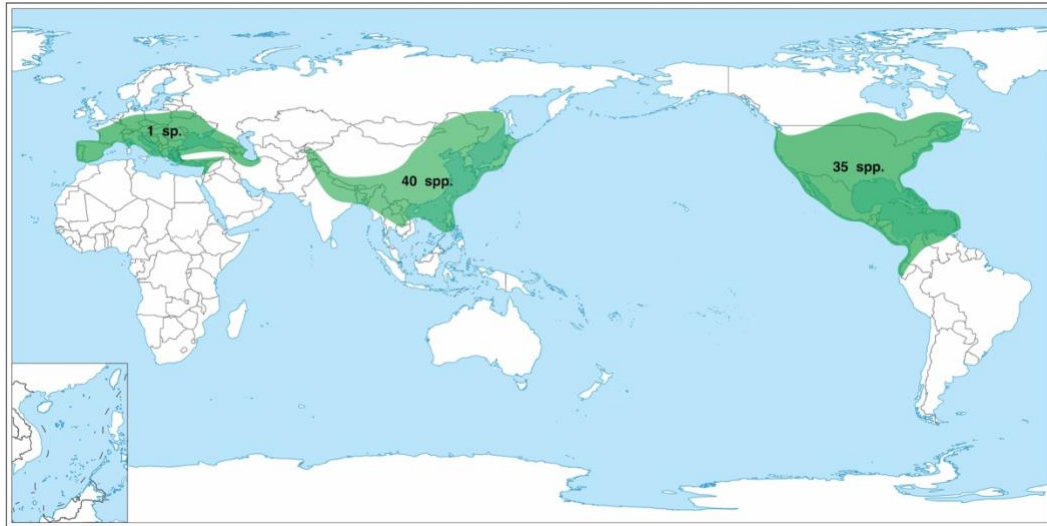


Figure S1. Distribution map with species numbers of the genus *Vitis* in the world.

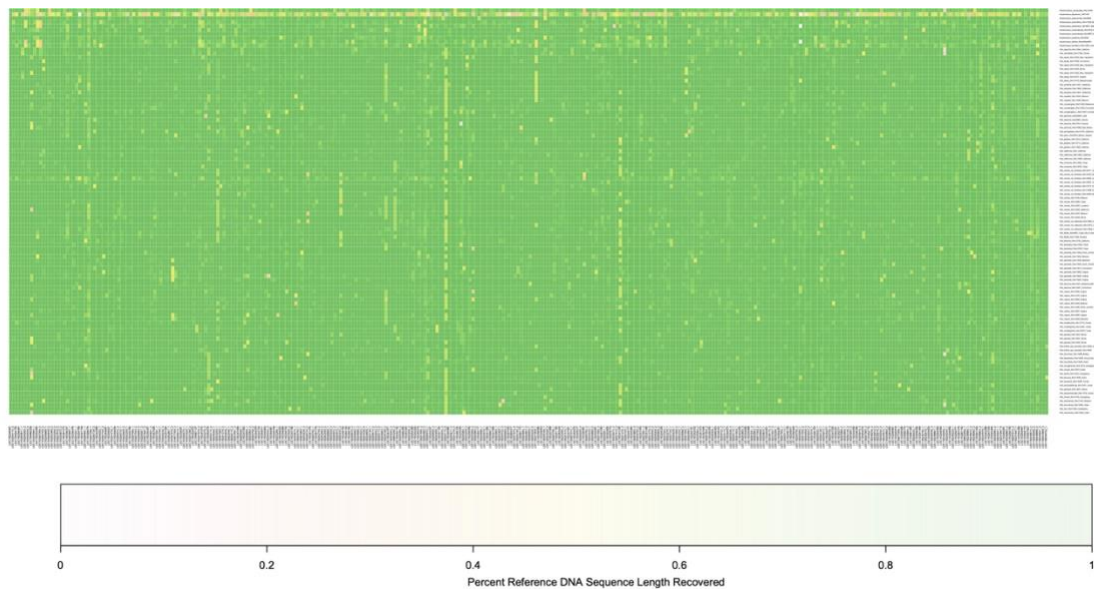
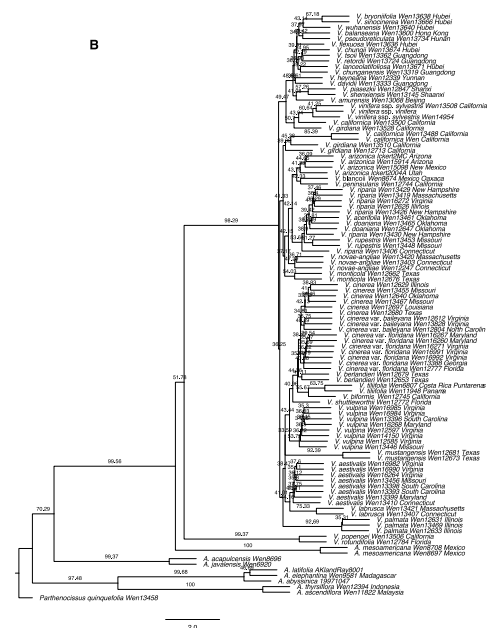
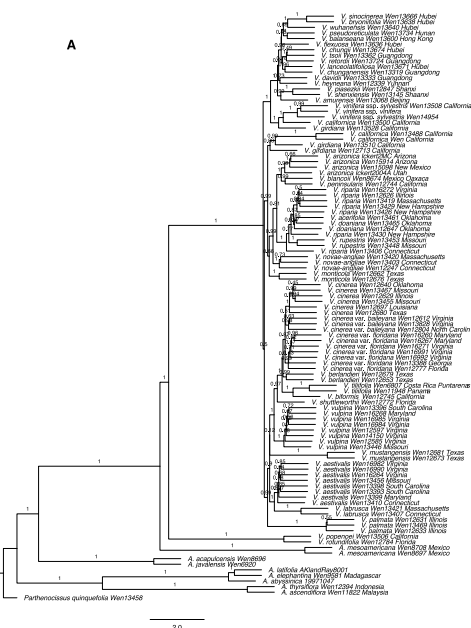


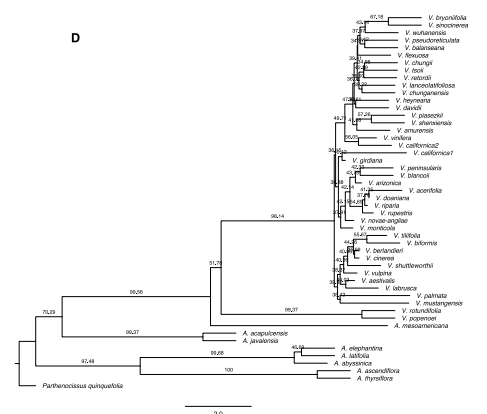
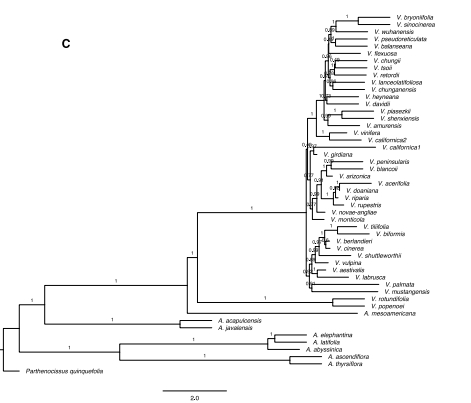
Figure S2. Recovery efficiency of a set of 346 target loci recovered by HybPiper.
Each row shows a sample, and each column is a gene. The amount of color in each box corresponds to the length of the gene recovered for that sample, relative to the length of the reference gene (maximum of 1.0).

B



C

D



E

F

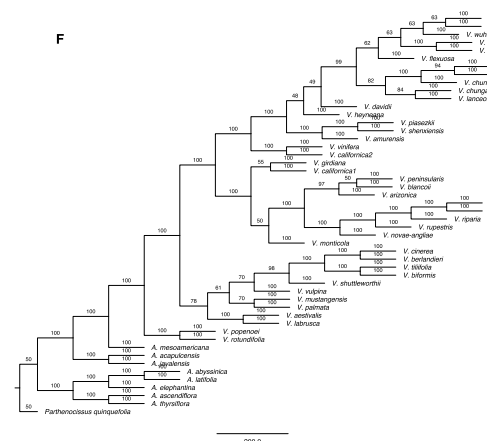
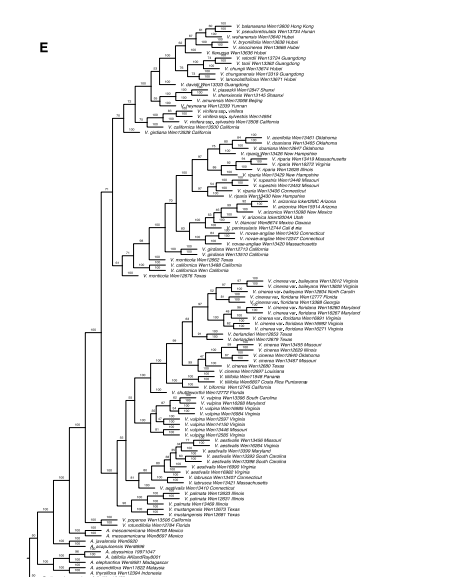


Figure S3. Coalescent analyses of *Vitis* and related taxa. Species trees inferred from Astral-III with numbers above the branches indicating the branch support values measuring the support for a local posterior possibility (A) and quartet scores (B). Species trees inferred from Astral-III on the species level with all individuals assigned to each species identity, with numbers above the branches indicating the branch support values measuring the support for a local posterior possibility (C) and quartet scores (D). Species trees estimated from SVDquartets including all individuals (E) or assigned to species identity (F) with numbers above branches indicating bootstrap supports.



Figure S4. Maximum likelihood phylogeny of *Vitis* and related taxa inferred from RAxML analyses of three plastid dataset.

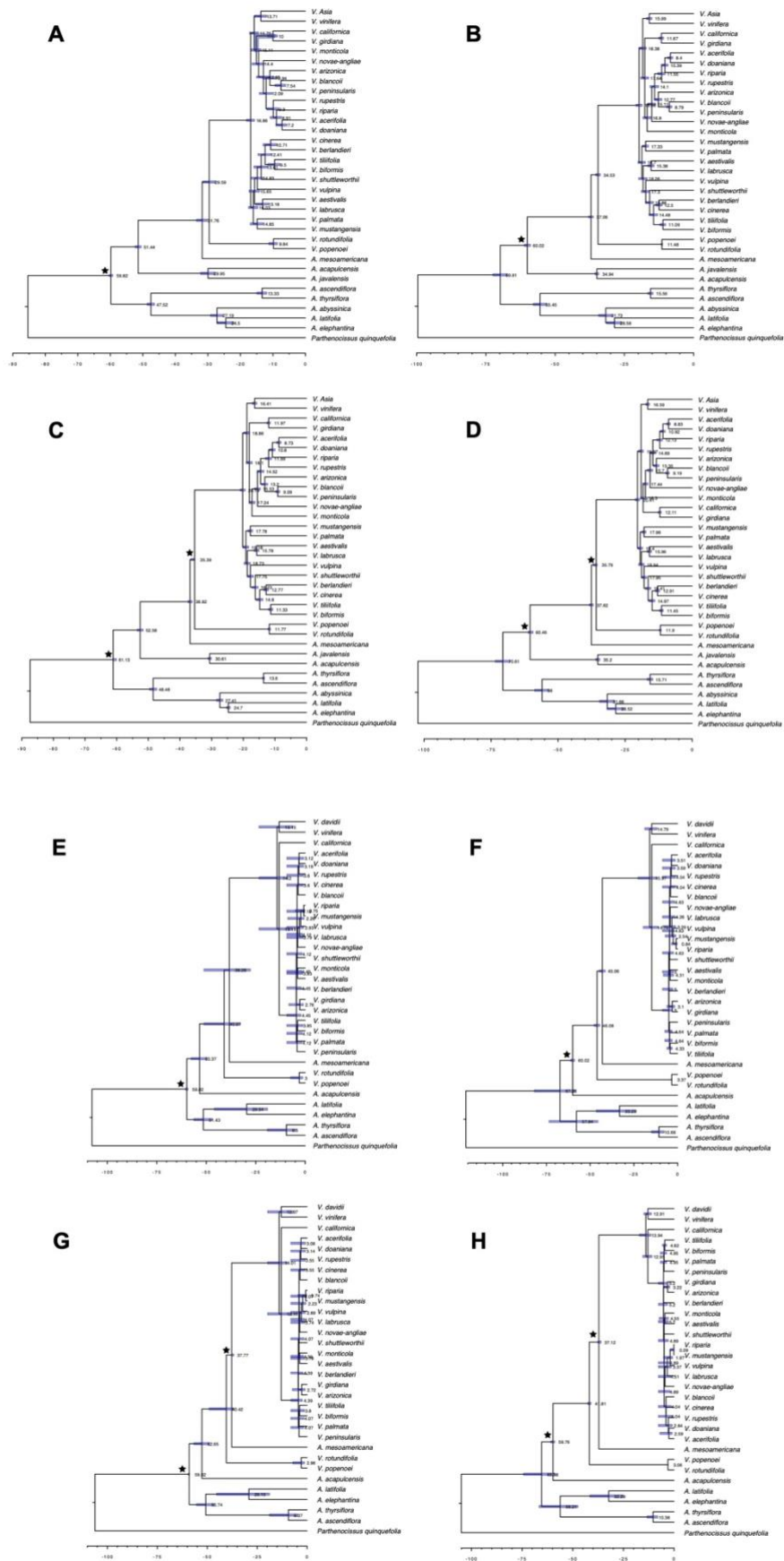


Figure S5. Time estimations of *Vitis* with four calibrated schemes based on nuclear species tree (A-D) and plastid dataset (E-H). Stars indicate calibration points according to fossil evidence.

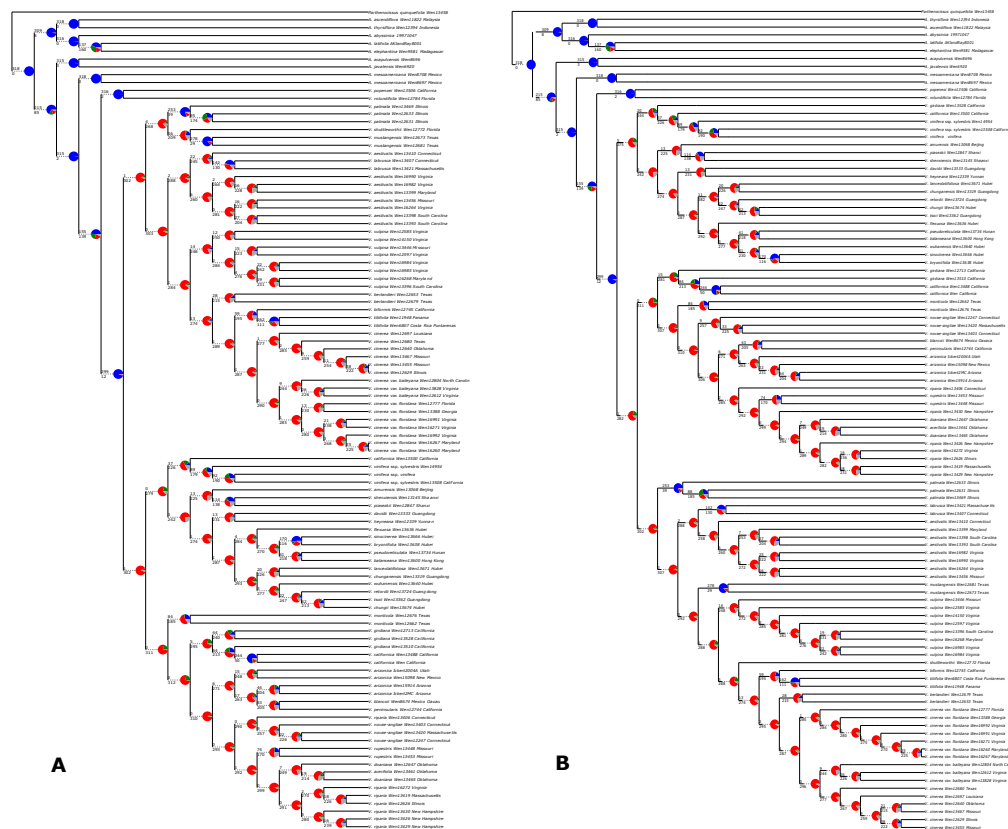


Figure S6. PhyPart analyses of *Vitis* and related taxa based on concatenated gene tree (A) and coalescent species tree (B). Numbers above branches indicate the number of gene trees concordant/conflicting with that node in the species tree. Numbers below the branches are the Internode Certainty All (ICA) score. Pie charts on nodes present the proportion of gene trees that support that clade (blue), the proportion that support the main alternative bifurcation (green), the proportion that support the remaining alternatives (red), and the proportion (conflict or support) that have < 50% bootstrap support (gray).

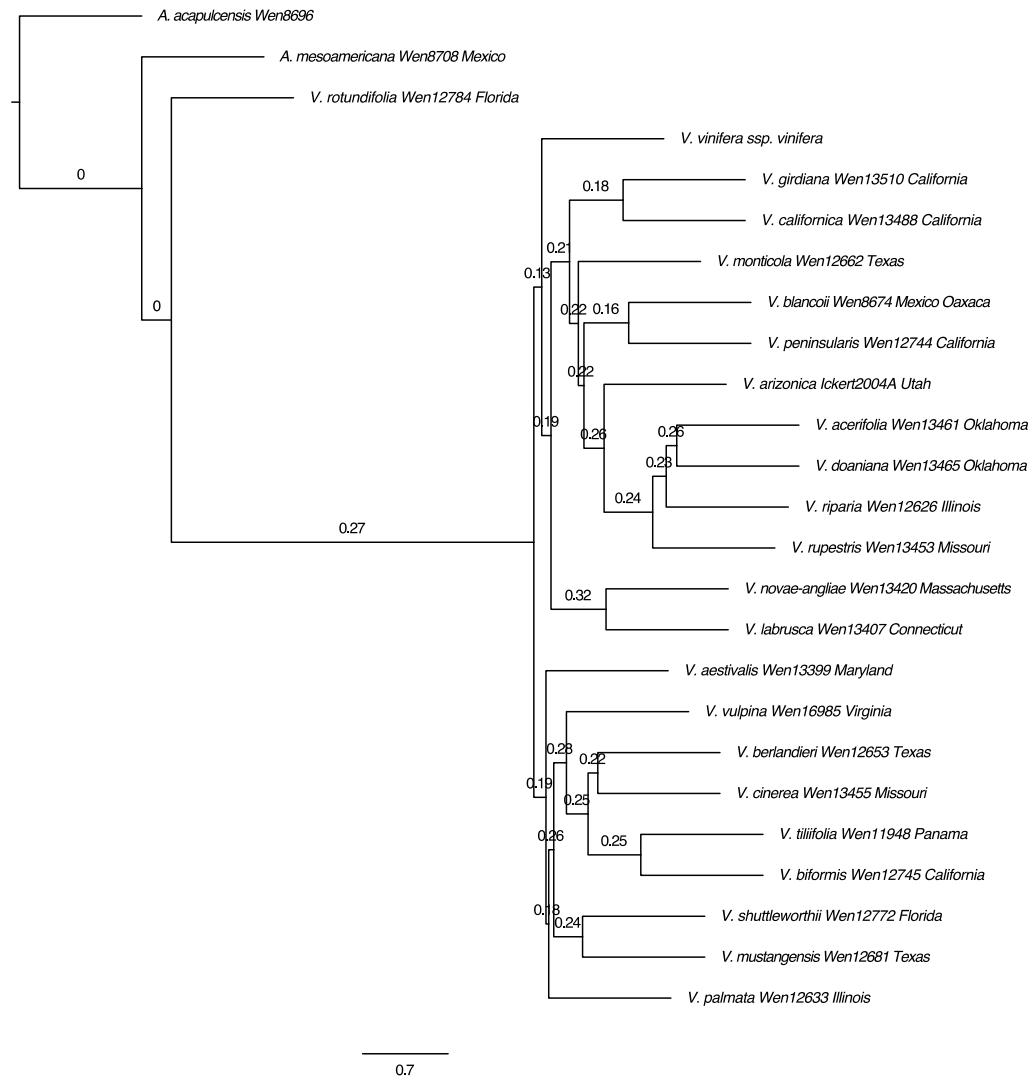


Figure S8. Reticulate Index analysis of *Vitis* and related taxa based on 25 exemplars from Figure 2. Numbers above branches show Reticulate Index.

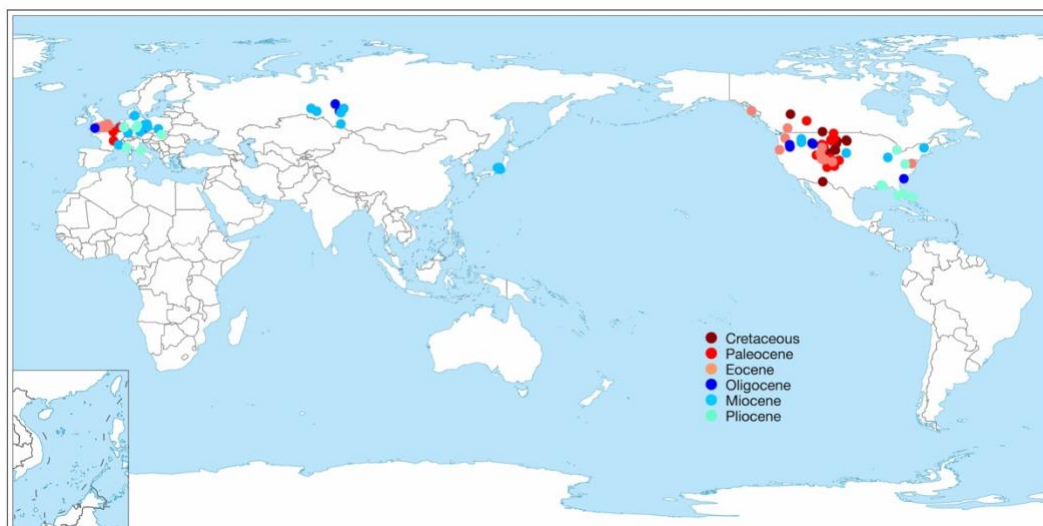


Figure S9. Global distribution of fossil data from *Vitis* based on records from Table S3.