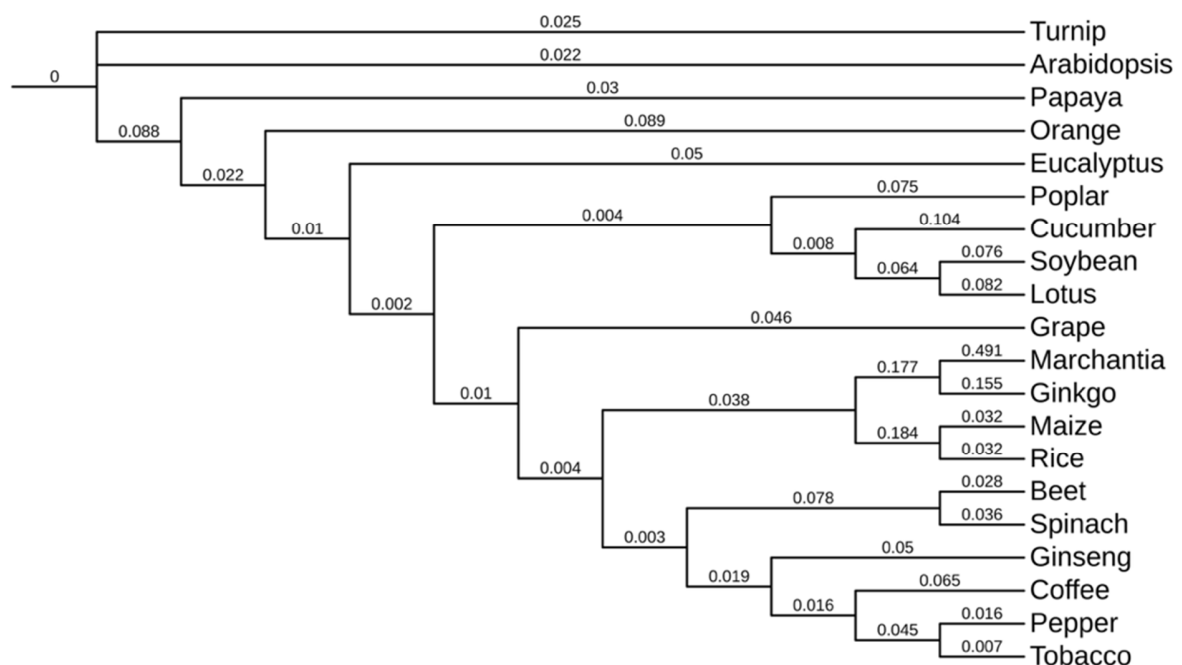


Supplementary Note

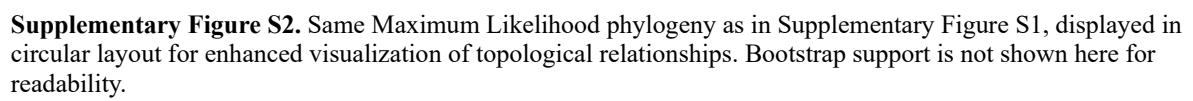
The phylogenetic trees shown in Supplementary Figures S1 and S2 were generated using IQ-TREE v3.0.1 with automatic model selection (-m TEST) and ultrafast bootstrap approximation (-bb 1000) applied to the trimmed supermatrix of 16 chloroplast barcoding genes. The rectangular (S1) and circular (S2) layouts complement the gene-specific Neighbor-Joining trees (Figure 2 in main text) by offering a robust maximum likelihood topology with quantified node support.

These figures reinforce the major clades observed in individual gene trees, including strong separation of bryophytes (*Marchantia polymorpha*), gymnosperms (*Ginkgo biloba*), monocots (*Oryza sativa*, *Zea mays*), and various eudicots. The high bootstrap values at major nodes (>95%) further support the reliability of the inferred evolutionary relationships based on plastid barcoding loci.

Supplementary Figures



Supplementary Figure S1. Maximum Likelihood phylogenetic tree of 20 plant species constructed from a concatenated alignment of 16 chloroplast barcoding genes. Branch lengths reflect sequence divergence, and numerical values at nodes represent ultrafast bootstrap support (1,000 replicates). The tree was midpoint rooted and rendered in rectangular layout for clarity.



Supplementary Figure S2. Same Maximum Likelihood phylogeny as in Supplementary Figure S1, displayed in circular layout for enhanced visualization of topological relationships. Bootstrap support is not shown here for readability.